

**NOMINATION OF DR. ERIC S. LANDER,
NOMINEE TO BE DIRECTOR, OFFICE OF SCIENCE
AND TECHNOLOGY POLICY (OSTP)**

HEARING

BEFORE THE

**COMMITTEE ON COMMERCE,
SCIENCE, AND TRANSPORTATION
UNITED STATES SENATE**

ONE HUNDRED SEVENTEENTH CONGRESS

FIRST SESSION

APRIL 29, 2021

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SENATE COMMITTEE ON COMMERCE, SCIENCE, AND TRANSPORTATION

ONE HUNDRED SEVENTEENTH CONGRESS

FIRST SESSION

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**NOMINATION OF DR. ERIC S. LANDER,
NOMINEE TO BE DIRECTOR, OFFICE OF
SCIENCE AND TECHNOLOGY POLICY (OSTP)**

THURSDAY, APRIL 29, 2021

U.S. SENATE,
COMMITTEE ON COMMERCE, SCIENCE, AND TRANSPORTATION,
Washington, DC.

The Committee met, pursuant to notice, at 10 a.m., in room SR-253, Russell Senate Office Building, Hon. Tammy Duckworth, presiding.

Present: Senators Duckworth [presiding], Klobuchar, Blumenthal, Markey, Peters, Tester, Sinema, Rosen, Luján, Hickenlooper, Warnock, Wicker, Thune, Blunt, Fischer, Moran, Blackburn, Young, Lee, Johnson, Scott, and Lummis.

**OPENING STATEMENT OF HON. TAMMY DUCKWORTH,
U.S. SENATOR FROM ILLINOIS**

Senator DUCKWORTH. Good morning and welcome. Today, the Senate Committee on Commerce, Science, and Transportation will consider the nomination of Dr. Eric Lander, to be the Director of the Office of Science and Technology Policy. Dr. Lander, I welcome you and your family, and it is good to see you again.

The position that you have been nominated for, is charged with advising the President on a broad range of scientific and technological policies to address national problems. For the first time in our country's history, President Biden has elevated this position to a Cabinet-level post, underscoring its significance and the Administration's commitment to follow the science.

You are an accomplished geneticist, molecular biologist, and mathematician—all subjects I got a C- in—

[Laughter.]

Senator DUCKWORTH. Who has spear-headed scientific efforts to increase our understanding of the human genome. You have answered the call to public service, previously serving as the Co-Chair of President Obama's Counsel of Advisors on Science and Technology.

Our Nation is facing a critical moment, one with incredible challenges, but also with infinite possibilities. We are simultaneously facing a global pandemic and experiencing the daily effects of a changing climate. And yet, we are on the cusp of discoveries that could help us meet these challenges and so many others facing our Nation today. And science has never been more important.

Although science is often considered the Great Equalizer, the truth is that gender and minority representation in science, technology, engineering, and math, or the STEM fields, are anything but equal. While the United States is a leader in scientific and technological innovation, we have fallen short of consistently recruiting, retaining, and promoting women and diverse individuals in the STEM fields.

My home state of Illinois is proud to host two thriving national labs, Fermilab and Argonne National Laboratory. These crown jewels of scientific innovation would not be possible without the contributions of women and diverse scientist and engineers. To continue serving as a leader in scientific research, the United States must tap as wide a talent pool as possible. After all, more women in science, greater diversity in science, ultimately, leads to better science and greater breakthrough that benefit us all. One may need look no further than the recipients of the Nobel Prize in Chemistry last year, for their ground-breaking work on CRISPR, Dr. Jennifer Doudna and Dr. Emmanuelle Charpentier, to see why female representation is so important in the STEM fields.

Addressing gender, racial, and ethnic disparities in STEM is a national priority. As a Nation, and as leaders in our government, we need to do more to ensure that gender equality exists, and that diverse candidates have meaningful representation across scientific and engineering fields. Increasing the number of women and diverse individuals in science, requires intentional recruitment and promotion.

However, that alone will not be enough. We also need inspiration. That means recognizing the accomplishments and successes of women and minorities in science, technology, engineering, and math. We need to inspire the next generation of great minds to encourage scientific study in all children, and to provide all children with the opportunity to succeed.

On this note, Dr. Lander, I must admit that I am troubled by issues that have been raised surrounding your nomination. You have been criticized for downplaying the contributions of the female Nobel laureates I just mentioned, for toasting a well-known racist, misogynistic, anti-Semite, and for attending lunch meetings with the late, disgraced Jeffery Epstein. You have provided responses to this committee, to these allegations, and I plan to ask you about them today.

The bottom line is that, if confirmed, you will have the authority to promote the representation of women and minorities in STEM fields. So, I strongly encourage you to use this hearing as an opportunity to explain how you have learned from your past mistakes. Nobody enjoys reflecting on previous errors that may be embarrassing, shameful, or worst of all, may have harmed individuals, or a profession that you love. But ultimately, our most productive growth as a leader, occasionally stems from honest reflection and following through on difficult lessons learned.

I hope to learn today how your successes, and failures have made you a better leader, a better scientist, and prepared you to direct our Nation's scientific policy in an inclusive manner, that empowers women and minorities. I know recognize my good friend from Mississippi, Ranking Member Wicker, to give his opening remarks.

**STATEMENT OF HON. ROGER WICKER,
U.S. SENATOR FROM MISSISSIPPI**

Senator WICKER. Thank you very much, Senator Duckworth. This is an important hearing on the nomination of Dr. Eric Lander to be Director of the Office of Science and Technology Policy. I commend Senator Cantwell for allowing the Committee the necessary time to prepare and give a full and thorough review of Dr. Lander's record and qualifications. There is no doubt he has led a long and notable career as a bright and dedicated research scientist. However, as Senator Duckworth has said, our extensive evaluation of Dr. Lander's record has brought to light a number of concerns that deserve further examination by this committee. As Senator Duckworth further said, I hope his testimony today will provide clarity on these topics.

The Director of OSTP has been a critically important position since it was first created. The person occupying this role directly advises the President on the scientific, engineering, and technological aspects of a wide range of Federal Government activity. In addition, it falls to the director of the OSTP to coordinate science and technology policy across all Federal agencies.

Notably, under the Industries of the Future Act, which I had the opportunity to author and see enacted last Congress, the Director of the OSTP is required to submit a report on the Federal Government research and development investments, infrastructure, and workforce development. The report must include a plan to advance U.S. leadership in industries of the future, such as, artificial intelligence and quantum science, as well as a blueprint for boosting annual spending in this area to \$10 billion by 2025. Implementing this new law is one of the many responsibilities of the Director of OSTP.

This position has been made all the more significant by the President's decision to elevate it to the Cabinet-level, hence the need for a comprehensive review by this committee.

I want to thank Dr. Lander to his commitment to public service, and for appearing before us today. I want to welcome our two colleagues, from the Commonwealth of Massachusetts, and I expect this hearing will be informative and useful to the Committee.

Thank you, Madam Chair.

Senator DUCKWORTH. Thank you. I recognize Senator Warren.

**STATEMENT OF HON. ELIZABETH WARREN,
U.S. SENATOR FROM MASSACHUSETTS**

Senator WARREN. Thank you, Chair Duckworth and Ranking Member Wicker. I have the privilege of introducing Dr. Eric Lander, who has been nominated to serve as the Director of the President's Office of Science and Technology.

Now, Eric has an impressive record as a scientist and leader. He received a degree in mathematics from Princeton and a PhD from Oxford, where he was a Rhodes Scholar. He received a MacArthur Genius award in 1987 and was soon tapped to lead the Human Genome project. In 2001, he and his team published the first draft of the Human Genome. In 2003, Eric co-founded the Broad Institute, where he has served as the President and Founding Director. In addition, he is a professor at MIT and, as you noted, Chair

Duckworth, for 8 years during the Obama Administration, Eric also served as the external Co-Chair of the President’s Council of Advisors on Science and Technology.

Now, I have known Eric for a decade. We have had many conversations about a range of topics from hearing aids to cancer vaccines. One recurring topic is women in science. Eric recognizes that the scientific community is strongest when it is diverse and inclusive. Eric does not just mouth the words. Under Eric’s leadership, the Broad has prioritized efforts to support and advance the careers of women scientists and scientists of color.

Let me give you a specific example on this. Eric is a scientist to his bones, and he believes in data. So, to assess and improve diversity and inclusion at the Broad, Eric set in motion a study, to collect data about the Institute. The results showed that, in a field where women are underrepresented, the Broad is modeling a better path. Currently, women make up the majority of the Institutes’ overall employees, the majority of the scientific teams, and the majority of the Senior Leadership team. In order to recognize his support for women in science, in 2020, Eric’s former mentees and trainees raised an endowment to create an award to honor his mentorship of early career women scientists.

Eric’s support for women’s careers has been recognized in the world outside the Broad, as well. This September, for the fourth year in a row, “Working Mother” magazine named the Broad as one of the 100 Best Companies in America for progressive programs related to advancing women, mentoring flexibility, childcare, and parental leave.

Eric’s commitment was on full display during this past year. The pandemic’s impact on working mothers has been devastating, cutting into the career advancement of many women, and forcing many more to leave the workforce all together. Eric was not a passive observer. Instead, Eric led the Broad in setting up its own childcare center and, to ensure the safety of the children and reassure the parents, the Broad conducted onsite COVID-19 testing every few days. Thanks to Eric’s work, women scientists at the Broad did not have to take a step back during the pandemic.

Under Eric’s leadership, the Broad has also operated a flagship diversity and inclusion program for college students. Nearly all of the program’s graduates have enrolled in graduate or medical programs. Some have even won prestigious awards, including three Rhodes Scholars. The Broad has also launched or collaborated on major research projects on racial health disparities, including serving as the largest genome sequencing laboratory for the NIH’s All of U.S. research program.

And one final note. The Broad is internationally famous for its cutting-edge work on genomics. During the coronavirus pandemic, Eric led the Broad to take on a very different role. The Broad ramped up and ran COVID tests night and day, building from scratch a COVID testing lab, that grew into the largest non-commercial lab in America. Described as, “The centerpiece of New England’s testing infrastructure”, a vision of just how much better our national pandemic response might have been. As the need grew, the Broad took on more and more work running, literally, millions

of tests for cities and towns, K-12 schools, and over 100 colleges and universities in seven states.

Now, there is much more that I could say about Eric. I know I am out of time here. But I want to end with one last bit of information, for those of you who do not already know him. Eric is fun. He is a passionate scientist whose enthusiasm for learning is infectious. He listens. He put people and ideas tighter. And best of all, he makes things happen.

I know that, under Eric's leadership, the Office of Science and Technology will push forward cutting-edge policies that benefit everyone and reinvigorate our country's role as a scientific leader. So, welcome, Eric, and congratulations on your nomination.

Senator DUCKWORTH. Thank you. Senator Markey.

**STATEMENT OF HON. EDWARD MARKEY,
U.S. SENATOR FROM MASSACHUSETTS**

Senator MARKEY. Thank you, Senator Duckworth, Senator Wicker. Thank you for hosting us today. And I am pleased, along with Senator Warren, to be here to introduce Dr. Eric Lander as the nominee to be the Director of the White House Office of Science and Technology Policy. And I want to extend a warm welcome to Eric's family, to Lori—his wife, Lori who is here today, and his children, Jessica and Daniel and David. And I can tell you, they are a team. It is a very special family that the Lander have created, and I am so proud of all of you and glad to be with you here today.

Senator Warren is right. Dr. Lander is a visionary scientist and thinker. And he is going to serve with distinction, as Director of the Office of Science and Technology Policy. I often say that Massachusetts is not only the Bay State, it is the Brain State, and Dr. Lander represents the kind of new American pioneer. One committed to exploring horizons defined, not by the boundaries of land and shore, but of genes and genius. A pioneer who does not see limits in biology, but the expanse of possibility. He exemplifies what it means to represent a place where scientific progress is a part of our DNA.

Dr. Lander started his career as a mathematician. He has taught economics and he has been one of the world's foremost biomedical scientists for years. When I was a young boy who refused to do his homework, my mother would threaten that she would donate my brain to Harvard as a completely unused human organ. Somehow—somehow, my mother anticipated Dr. Lander and his work on the Human Genome project.

Senator WICKER. That explains so much about you, Senator.

[Laughter.]

Senator MARKEY. I—mothers know you best. And thank God, there is a Dr. Lander that can help mothers. And so, I am so—I am so proud that my mother can see me here today, introducing Dr. Lander, because I know that she would think that somehow or other, I had defied all expectations that she had for me as a child.

And Dr. Lander's work on the Human Genome project and founding of the Broad Institute at MIT and Harvard, which reflects his deep understanding of how science and policy can inform one another. At the Broad Institute, he pursued collaborative science,

bringing together biologists, clinicians, chemists, engineers, and computational scientists. The transformative model for scientific research that the Broad Institute represents, is a new way to take on the challenges that we face today, bringing scientific discoveries and advances forward more quickly than ever before.

His contribution to science has also demonstrated how impactful research can be. The Human Genome project was a 13-year long project that involved hundreds of scientists across the entire world. This project is an incredible example of a publicly funded project that keeps knowledge in the public domain, and a feat that provided a model for the kind of large-scale cooperative effort that the world's biggest problems require.

The Human Genome project has also had an enormous economic impact with one analysis, from 10 years ago, estimating that the \$3 billion project has produced more than 330,000 jobs and nearly \$800 billion in economic benefit. And that was 10 years ago. Sequencing nearly the entire human genome has already led to countless advances, a trend that is certain to continue into the future. The project discovered genes that are fundamental to thousands of diseases, including heart disease and Alzheimer's and cancer, and paved the way for novel treatments.

Last night, we heard President Biden commit to curing Alzheimer's disease, a disease that my mother died from. I know we will reach that goal and I know Dr. Lander will have played a part in that discovery.

In addition to his groundbreaking research, he has taught MIT's Introductory Biology course for more than 25 years and is one of MIT's most beloved teachers. He has inspired students to grapple with complex issues, helping them become informed and active members of their communities. He has an ability to explain the science of why much better than senators can explain the political science of why not. And that ability to teach and translate is more important than ever before.

I know Dr. Lander has the skill to rebuild the celebration of science that is a hallmark of American excellence. When his country needed him, during the coronavirus pandemic, he moved to build, from scratch to operation, the largest non-commercial COVID testing laboratory in the country. Senator Warren already spoke to that incredible success.

He has been a strong supporter of people of color in science and improving racial equity in science outcomes. He has used science as a tool for justice, playing a key role in the origins of the Innocence Project, as his commitment to justice and forensic science has spanned more than three decades.

The crises we face today, of man and mind and the intersection of those two forces, are daunting. We are confronted by a surging China and its race to dominate the scientific and technological landscape. But Eric's breadth of knowledge, unparalleled experience, and pioneering spirit make him uniquely suitable to lead.

With Dr. Lander at the helm of the Office of Science and Technology Policy, all Americans will be his students, sharing his passion for science, discovery, and achievement. We thank you, Dr. Lander, for trading your microscope for a microphone and we appreciate your service for our country.

Thank you.

Senator DUCKWORTH. Thank you, Senator Markey. Dr. Lander.

**STATEMENT OF DR. ERIC S. LANDER,
NOMINEE TO BE DIRECTOR, OFFICE OF SCIENCE
AND TECHNOLOGY POLICY (OSTP)**

Dr. LANDER. Thank you, Chair Duckworth and Ranking Member Wicker. And thank you to Senators Warren and Markey for your very, very kind introductions.

It is a tremendous honor to come before this committee as President Biden's nominee for Director of the Office of Science and Technology Policy. America has led the world in science and technology for 75 years. That leadership has had profound benefits for our health, economy, our national security, driving medical breakthroughs from cancer to COVID, new industries with millions of jobs, from computers to biotechnology. But today, America's future depends on science and technology like never before. We have amazing opportunities ahead, but also unprecedented challenges and the choices we make now will determine our path for generations to come.

In a recent letter, President Biden recognized we need to rethink our strategy for the next 75 years. He asked OSTP to take the lead, because OSTP is the place where all of science and technology comes together across government, industry, academia, medicine, and society. President Biden posed big questions. What lessons can we learn, in the broadest way, from this pandemic? How do we ensure America is the world leader in the technologies of the future, especially in our competition with China? How can science drive market-driven solutions for climate change? And very importantly, how do we ensure the fruits of science and technology are shared across all America and all Americans?

If confirmed, I would throw my full energies into this and let me explain why. I grew up as a kid in Brooklyn, New York. I was raised by my mom, because my dad suffered from a long illness and died when I was 11 and in my neighborhood, there were no scientists. If New York City had not had a few public STEM high schools, there is no way I would have ever have become a scientist. I knew I was very lucky to have that chance, and I have never forgotten it. Most people never get a chance. And the opportunity is so unevenly distributed across gender and race and geography.

Science has been unwelcoming to women and people of color. It has been concentrated in a few regions of the country. And most Americans lack access to great STEM schools and many even to broadband. And lack of inclusion is not just deeply unfair, it is a risk to America's success. To lead the world, we are going to need everybody. If confirmed to OSTP, I will, as I have done in my career at the Broad, make full inclusion and equitable outcomes a high priority. Including ensuring that OSTP's staff will look like America including by identifying extraordinary women and people of color as candidates in every search. That PCAST, the advisory group, will be the most diverse in history. That OSTP's work will be rooted in equity. And I would work to put in place a plan to increase the numbers of women and underrepresented people in STEM careers by 50 percent. We can do that.

I am also excited to bring other experiences and values. I have seen how science can be a force for justice. As a young scientist in 1989, I testified in one of the first criminal cases using DNA fingerprinting. For such consequential evidence, the quality was shoddy, and I said so. That position was not popular with everyone. But the case forced higher standards for DNA fingerprinting, and it led directly to the founding of the Innocence Project, which has used DNA to reveal that hundreds of innocent people were behind bars, with Black Americans making up a disproportionate share and having served much longer sentences.

A year later, I got to be part of an amazing collaboration, the Human Genome Project. When we set out in 1990, mapping a person's complete genetic code seemed absurd. It would have taken 200 years. But scientists rallied together and drove innovation. We got it done in just 13 years. Today, it takes just hours. And it has unlocked secrets from cancer to Alzheimer's, driving unimaginable progress. And we are going to need this kind of collaboration to tackle much of what is ahead.

After the genome project, I worked with colleagues to find a new kind of research community, the Broad Institute. It is deeply collaborative. It lets scientists, particularly young scientists, dream big and take on challenges at whatever scale is needed, blending the best of individual creativity and large-scale platforms. I am particularly proud it is one of the few such institutions in which women comprise the majority of the overall staff, scientific staff, and senior leadership team. There is a lot more to be done, but we can reimagine how we do science.

Finally, I have learned that good science requires a healthy dose of humility. Scientists' favorite ideas are often wrong, mine included. We constantly need to be open to different perspectives from scientists, non-scientists, and policymakers. I know that this committee has led on so many critical issues in science and technology. Your work has been so collaborative and so bipartisan. If confirmed, I promise to work closely and open-mindedly with each of you.

Thank you for the invitation to come before you and I look forward to your questions.

[The prepared statement and biographical information of Dr. Lander follow:]

PREPARED STATEMENT OF DR. ERIC S. LANDER, NOMINEE TO BE DIRECTOR, OFFICE OF SCIENCE AND TECHNOLOGY POLICY

Thank you, Chair Cantwell and Ranking Member Wicker. And, thank you to Senators Warren and Markey for your kind introductions.

It's a great honor to come before this committee as President Biden's nominee for Director of the Office of Science and Technology Policy.

America has led the world in science and technology for 75 years. That leadership has had profound benefits for our health, economy, and national security—driving medical breakthroughs from cancer to covid; new industries with millions of jobs, from computers to biotechnology.

But, today, America's future depends on science and technology like never before. We see amazing opportunities ahead, but also unprecedented challenges. The choices we make now will determine our path for the generations to come.

In a recent letter, President Biden recognized we need to rethink our strategy for the next 75 years.

He asked OSTP to take the lead, because OSTP is the one place where all of science and technology comes together—across government, industry, academia, medicine, and society.

President Biden posed big questions:

- What lessons can we learn from the pandemic?
- How do we ensure America is the world leader in the technologies of the future, especially in competition with China?
- How can science create market-driven solutions for climate change?
- And, very importantly: How do we ensure the fruits of science and technology are shared across all America and all Americans?

If confirmed, I'd throw my full energies into this work. Let me explain why.

I grew up as a kid in Brooklyn, New York. I was raised by my mom, because my dad suffered from a long illness and died when I was 11.

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Science has been unwelcoming to women and people of color. It's concentrated in a few regions of the country. Most Americans lack access to great STEM schools or many even to broadband.

Lack of inclusion is not only deeply unfair, it's a greatest risk to America's success. To lead the world, we're going to need everyone.

If confirmed to OSTP, I will—as I've done in my career at the Broad Institute—make full inclusion and equitable outcomes a high priority, including that:

- OSTP's staff will look like America, including identifying extraordinary women and people of color as candidates in every search;
- PCAST will be the most diverse in history;
- OSTP's work will be rooted in equity—tackling issues from STEM inclusion to algorithmic bias.
- And, I'd work to put in place a plan to increase the numbers of women and underrepresented people in the science and technology professions by 50 percent. We can do that.

I'm also excited to bring other experiences and values:

I've seen how science can be a force for justice.

As a young scientist in 1989, I testified in one of the first criminal cases using DNA fingerprinting. For such consequential evidence, the quality was shoddy. I said so. That position wasn't popular with everyone.

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Scientists' favorite ideas are often wrong, mine included. We constantly need to be open to different perspectives—from scientists, non-scientists, policymakers.

This committee has led on so many critical issues in science and technology. Your work has been so collaborative and so bipartisan.

If confirmed, I promise to work closely and open-mindedly with each of you.

Thank you. I look forward to your questions.

A. BIOGRAPHICAL INFORMATION

1. Name (Include any former names or nicknames used): Eric Steven Lander.
2. Position to which nominated: Director, Office of Science and Technology Policy.
3. Date of Nomination: Jan 20, 2021.
4. Address (List current place of residence and office addresses):
 Residence: Information not released to the public.
 Office (until January 25, 2021): Broad Institute, 415 Main Street, Cambridge, MA 02142.
5. Date and Place of Birth: February 3, 1957; Brooklyn, New York.
6. Provide the name, position, and place of employment for your spouse (if married) and the names and ages of your children (including stepchildren and children by a previous marriage).
 Lori Weiner Lander—Self-employed artist
 Jessica Ann Lander—33
 Daniel Aaron Lander—29
 David Abraham Lander—26
7. List all college and graduate degrees. Provide year and school attended.
Princeton University, Princeton, New Jersey, 1974–1978
 AB with highest honors in Mathematics, June 1978
Oxford University, Oxford, England, 1978–1981
 D. Phil. in Mathematics, January 1981
8. List all post-undergraduate employment, and highlight all management-level jobs held and any non-managerial jobs that relate to the position for which you are nominated.
Broad Institute of MIT and Harvard
 President and Founding Director, 2003–2021
 Core Faculty Member 2003 to present (on leave)
Massachusetts Institute of Technology, Department of Biology
 Professor, 1993 to present (on leave)
 Associate Professor, 1989–1993
 Visiting Scientist, 1984–1989
Harvard Medical School, Department of Systems Biology
 Professor, 2004 to present (on leave)
Whitehead Institute for Biomedical Research
 Director, Whitehead/MIT Center for Genome Research, 1990–2003
 Member, 1989–2008
 Whitehead Fellow, 1986–1989
Harvard University, Graduate School of Business
 Associate Professor, 1987–1990
 Assistant Professor, 1981–1986
Cold Spring Harbor Laboratory
 Summer Course Lecturer, Summer 1987, 1989, 1990
The Jackson Laboratory
 Summer Course Lecturer, Summer 1987, 1989, 1990
Hampshire College Summer Studies in Mathematics
 Summer Course Faculty, Summer 1975, 1976, 1979
9. Attach a copy of your résumé.
 My CV is attached as Appendix A9 “Résumé”.
10. List any advisory, consultative, honorary, or other part-time service or positions with Federal, State, or local governments, other than those listed above, within the last ten years.
Massachusetts’ COVID–19 Medical Advisory Board: Member, 2020–2021
Defense Innovation Board, Office of the Secretary of Defense: Member, 2016–2020
President’s Council on Jobs and Competitiveness (President’s Jobs Council), Executive Office of the President: Member, 2011–2012

President's Council of Advisors on Science and Technology (PCAST), Executive Office of the President: Co-Chair, 2009–2017

11. List all positions held as an officer, director, trustee, partner, proprietor, agent, representative, or consultant of any corporation, company, firm, partnership, or other business, enterprise, educational, or other institution within the last ten years.

For Profit Companies:

Codiak BioSciences, Board of Directors
 Foundation Medicine, Founding Advisor
 FPrime (formerly Fidelity Biosciences), Scientific Advisory Board
 Infinity Pharmaceuticals, Board of Directors
 Neon Therapeutics, Board of Directors
 Third Rock Ventures, Scientific Advisory Board
 Verastem, Founding Advisor

Non-Profit Organizations or Committees:

Ariadne Labs, Advisory Board Member
 Biden Cancer Initiative, Secretary and Member, Board of Directors
 Boston University, Member, Board of Trustees
 Count Me In, Member, Board of Directors
 Global Alliance for Genomics & Health (GA4GH), Member, Strategic Advisory Board
 Harvard Kennedy School, Belfer Center for Science and International Affairs, Member, Board of Directors
 Innocence Project, Member, Board of Directors
 Institute for Molecular Medicine Finland, Member, Scientific Advisory Board
 Life Science Cares, Member, Board of Advisors
 Massachusetts General Hospital, Member, Research Advisory Council
 Ontario Institute for Cancer Research: Co-Chair Scientific Advisory Board
 Parker Institute for Cancer Immunotherapy (PICI), Member, Board of Trustees
 Parker Institute for Cancer Immunotherapy, Member, Scientific Advisory Board
 Ragon Institute, Member, Scientific Advisory Board
 Salk Institute, Helmsley Center for Genomic Medicine, Advisory Board Member
 Salk Institute for Biological Studies, Non-Resident Fellow
 Society for Science & The Public, Member, Honorary Board

12. Please list each membership you have had during the past ten years or currently hold with any civic, social, charitable, educational, political, professional, fraternal, benevolent or religiously affiliated organization, private club, or other membership organization. (For this question, you do not have to list your religious affiliation or membership in a religious house of worship or institution.). Include dates of membership and any positions you have held with any organization. Please note whether any such club or organization restricts membership on the basis of sex, race, color, religion, national origin, age, or disability.

I am a member of various scientific societies:

American Association for Cancer Research
 New York Academy of Medicine (honorary fellow)
 American Society of Human Genetics
 American Society for Microbiology
 American Academy of Microbiology
 American Association for the Advancement of Science
 New York Academy of Sciences
 Genetics Society of America
 International Society for Computational Biology

I am also a member of

Council on Foreign Relations
 Examiner's Club (which organizes informal talks in Boston)

None of these organizations restricts membership on the basis of sex, race, color, religion, national origin, age, or disability.

13. Have you ever been a candidate for and/or held a public office (elected, non-elected, or appointed)? If so, indicate whether any campaign has any outstanding debt, the amount, and whether you are personally liable for that debt. No.

14. List all memberships and offices held with and services rendered to, whether compensated or not, any political party or election committee within the past ten years. If you have held a paid position or served in a formal or official advisory position (whether compensated or not) in a political campaign within the past ten years, identify the particulars of the campaign, including the candidate, year of the campaign, and your title and responsibilities.

Hillary for America, Science Policy Working Group, Senior Partner (2015–2016) [uncompensated]

15. Itemize all political contributions to any individual, campaign organization, political party, political action committee, or similar entity of \$500 or more for the past ten years.

9/29/11	Barack Obama	\$2,500
9/30/11	Robert Massie	\$500
3/31/12	Barack Obama	\$2,500
3/31/12	Elizabeth Warren	\$2,500
3/31/12	Eiizabeth Warren	\$2,500
10/22/12	DNC	\$5,000
11/2/12	DNC	\$15,000
6/6/13	Democratic State Committee of Massachusetts	\$2,400
6/25/13	Ed Markey	\$2,600
6/24/14	Katherine Clark	\$1,000
7/29/14	Maura Healey	\$500
9/15/15	Hillary Clinton	\$2,700
9/22/16	Democratic Senatorial Campaign Committee	\$2,500
9/27/16	Maggie Hassan	\$1,000
5/31/17	Elizabeth Warren	\$2,700
5/24/19	Ed Markey	\$2,800
6/30/19	Elizabeth Warren	\$250
8/27/19	Elizabeth Warren	\$2,550
10/25/19	Katherine Clark	\$1,000
11/10/19	Jake Auchincloss	\$500
12/31/19	Joe Biden	\$2,800
12/31/19	Elizabeth Warren	\$2,800
12/31/19	Elizabeth Warren	\$250
5/8/20	Ed Markey	\$2,800
8/11/20	Joe Biden	\$2,800

16. List all scholarships, fellowships, honorary degrees, honorary society memberships, military medals, and any other special recognition for outstanding service or achievements.

Honorary Degrees:

Charles University, Czech Republic, Honorary Doctorate, 2020

Ben-Gurion University of the Negev, Israel, Honorary Doctorate, 2017

Université catholique de Louvain, Belgium, Honorary Doctorate, 2017

Brandeis University, Honorary Doctorate, 2014

Worcester Polytechnic Institute, Honorary Doctorate and Commencement Speaker, 2013

Columbia University, Honorary Doctorate, 2008

Lund University, Sweden, Honorary Doctorate, 2007

Northeastern University, Honorary Doctorate and Commencement Speaker, 2005

University of Massachusetts at Lowell, Honorary Doctorate, 2005

Williams College, Honorary Doctorate and Commencement Speaker, 2003

Mount Sinai School of Medicine, Honorary Doctorate, 2001

Medical College of Wisconsin, Honorary Doctorate, 2001

Tel Aviv University, Honorary Doctorate, 2000

Elected or Appointed Academies:

Pontifical Academy of Sciences, 2020
 Royal Swedish Academy of Sciences, Class of Biosciences, 2013
 European Molecular Biology Organization, 2012
 Academy of Athens, 2009
 U.S. Institute of Medicine (now U.S. National Academy of Medicine), 1999
 American Academy of Arts and Sciences, 1999
 American Academy of Achievement, 1999
 U.S. National Academy of Sciences, 1997

Award, Prizes and Other Recognition:

Association for Molecular Pathology (AMP) Award for Excellence in Molecular Diagnostics, 2016
 Friends of Cancer Research Leadership Award, 2016
“for pioneering research unlocking the molecular origins of cancer, leadership guiding our Nation’s scientific priorities, and dedication to empowering a new generation of researchers to accelerate biomedical advancements”
 James R. Killian, Jr. Faculty Achievement Award, MIT, 2016
“for extraordinary professional achievements by an MIT faculty member”
 Fellow, American Association for Cancer Research Academy, 2016 AAAS Philip Hauge Abelson Prize, 2015
“for signal contributions to the advancement of science in the United States”
 Han-Mo Koo Memorial Award, Van Andel Institute, 2015
 Time Magazine’s 10 years of Influence, 2013
 Block Memorial Award for Distinguished Achievement in Cancer Research, Ohio State University, 2013
 Breakthrough Prize in Life Sciences, 2013
“For the discovery of general principles for identifying human disease genes, and enabling their application to medicine through the creation and analysis of genetic, physical and sequence maps of the human genome.”
 Harvey Prize for Human Health, Technion University, Israel, 2012
“In recognition of his significant contributions to the field of genomics, as the driving force behind most of the major advances in this field.”
 Dan David Prize, Genome Research, Tel Aviv University, Israel, 2012
“For the Future Dimension—Genome Research”
 Dart/NYU Biotechnology Achievement Award, 2012
 Albany Prize in Medicine and Biomedical Research, Albany Medical College, 2010
 New York Academy of Medicine Medal for Distinguished Contribution in Biomedical Sciences, 2009
 A. Clifford Barger Excellence in Mentoring Award, Harvard Medical School, 2008–2009
 US News & World Report “America’s Best Leaders,” 2006
 Reenpaa Medal, Finnish Cultural Foundation, 2006
 AAAS Award for Public Understanding of Science and Technology, 2004
“for his excellence in communicating complex scientific ideas, and their implications for society, to the general public and policy-makers, while actively engaged in a demanding and aggressive research program.”
 Research!America Award for Sustained Leadership at the National Level, 2004
 Lila Gruber Cancer Award, American Academy of Dermatology, 2004
 Time Magazine, List of “100 Most Influential People in the World Today,” 2004
 Josiah Willard Gibbs Prize Lecturer, American Mathematical Society, 2004
 American Scientist of the Year Award, R&D Magazine, 2003
 Scientist of the Year Award, National Disease Research Interchange, 2003
 Alfred Benzon Foundation Prize, Denmark, 2002
 Gairdner Foundation International Award, Canada, 2002
“for his major seminal contribution to the sequencing of the human and other genomes”
 John von Neumann Award, Society for Industrial and Applied Mathematics, Philadelphia, 2002

- Special Achievement Award, Miami Nature Biotechnology Winter Symposium, 2002
- City of Medicine Award, 2001, with John Sulston and Robert Waterston Max Delbruck Medal, Berlin, 2001
- J. Allyn Taylor Prize, Canada, 2001
- Novartis Drew Award in Biomedical Research, 2001
- Distinguished Service Award, American College of Neuropsychopharmacology, 2001
- Allen Award, American Society of Human Genetics, 2000
"to the community of scientists that carried out the Human Genome Project",
 accepted on behalf of community, together with Francis Collins and Craig Venter
- Beckman Prize, American Association for Lab Automation, 2000
- Millennium Lecturer, The White House, October 1999
- Pasarow Prize in Cancer, Robert J. and Claire Pasarow Foundation, 1998
- Chiron Prize for Biotechnology, American Society for Microbiology, 1998
- Phi Beta Kappa Associates Award, 1998
"for outstanding work as a scientist"
- Woodrow Wilson Award for Public Service, Princeton University, 1998
"the university's highest award to an alumnus of the undergraduate college"
- American Academy of Microbiology, elected 1997
- Dickson Prize in Medicine, University of Pittsburgh, 1997
- Class of 1960 Fellows Award, Massachusetts Institute of Technology, 1996
"for outstanding teaching"
- Kroc Distinguished Lecturer, University of Washington, Seattle, 1996
- Rhoads Memorial Award, American Association for Cancer Research, 1995
"for excellence in cancer research"
- Herman Beerman Lecturer, Society for Investigative Dermatology, 1995
- Herbert Boyer Lecturer in Genetics, University of California at San Francisco, 1995
- Gladstone Distinguished Lecturer, Gladstone Institute, 1994
- Ralph R. Braund Distinguished Visiting Professor, University of Tennessee, 1994
- Herbert W. Dickerman Award, New York Department of Health, 1993
- Christian A. Herter Distinguished Lecturer, New York University, 1993
- Baker Memorial Prize for Excellence in Undergraduate Teaching, MIT, 1992
- Fellow, American Association for the Advancement of Science, 1990
"for research on the application of mathematical and statistical approaches to molecular genetics"
- MacArthur Prize Fellow, *for research in human genetics and mathematics*, 1987–1992
- Rhodes Scholar, 1978–1981
- Johnson Memorial Bequest, Oxford University, June 1981
for best thesis in mathematics,
- Senior Prize, Oxford University, June 1981
- Valedictorian, Princeton University, June 1978
- Pyne Prize, Princeton University, February 1978
"the highest award the university confers upon an undergraduate"
- Phi Beta Kappa Award, Princeton University, June 1978
"for highest academic achievement"
- Class of 1863 Prize and Andrew Brown Prize in Mathematics, Princeton University, 1976, 1977
- U.S. Mathematical Olympiad Team, Silver Medal, 16th International Mathematical Olympiad, Erfurt, East Germany, 1974
- First Place, Westinghouse Science Talent Search, 1974
17. Please list each book, article, column, Internet blog posting, or other publication you have authored, individually or with others. Include a link to each publication when possible. Also list any speeches that you have given on topics relevant

to the position for which you have been nominated. Do not attach copies of these publications unless otherwise instructed.

BOOK

1. Lander, E.S. (1983). *Symmetric designs: an algebraic approach* (Vol. 74). New York, NY: Cambridge University Press.

EDITED BOOK

2. Lander, E.S., & Waterman, M.S. (Eds.). (1995). *Calculating the secrets of life: Contributions of the mathematical sciences to molecular biology*. Washington, DC: National Academy Press.

ARTICLES

Mathematics

3. Lander, E.S. (1981). *Symmetric designs and self-dual codes*. *Journal of the London Mathematical Society*, 2(2), 193–204.

4. Lander, E.S. (1981). *Characterization of biplanes by their automorphism groups*. In M. Aigner & D. Jungnickel. (Eds.), *Geometries and groups* (pp. 204–218). Berlin Heidelberg, Germany: Springer-Verlag.

5. Lander, E.S. (1988). *Characterizing symmetric designs by their symmetries*. *Journal of Algebra*, 113(1), 1–18.

6. Lander, E.S. (1988). *Restrictions upon multipliers of an abelian difference set*. *Archiv der Mathematik*, 50(3), 241–242.

7. Arratia, R., & Lander, E.S. (1990). *The distribution of clusters in random graphs*. *Advances in Applied Mathematics*, 11(1), 36–48.

8. Chernoff, H., & Lander, E.S. (1995). *Asymptotic distribution of the likelihood ratio test that a mixture of two binomials is a single binomial*. *Journal of Statistical Planning and Inference*, 43(1), 19–40.

Economics

9. Farrell, J., & Lander, E.S. (1989). *Competition between and within teams: The lifeboat principle*. *Economics Letters*, 29(3), 205–208.

Biology

10. Lander, E.S., & Botstein, D. (1986). *Consanguinity and heterogeneity: Cystic fibrosis need not be homogeneous in Italy*. *American Journal of Human Genetics*, 39(2), 282–283. PMID: 3752091; PMCID: PMC1683934.

11. Lander, E.S., & Botstein, D. (1986). *Strategies for studying heterogeneous genetic traits in humans by using a linkage map of restriction fragment length polymorphisms*. *Proceedings of the National Academy of Sciences*, 83(19), 7353–7357. PMID: 2876423; PMCID: PMC386715.

12. Lander, E.S., & Botstein, D. (1986). *Mapping complex genetic traits in humans: new methods using a complete RFLP linkage map*. *Cold Spring Harbor Symposia on Quantitative Biology*, 51(Pt 1), 49–62. PMID: 2884068.

13. Lander, E.S., & Green, P. (1987). *Construction of multilocus genetic linkage maps in humans*. *Proceedings of the National Academy of Sciences USA*, 84(8), 2363–2367. PMID: 3470801; PMCID: PMC304651.

14. Lander, E.S., & Botstein, D. (1987). *Homozygosity mapping: a way to map human recessive traits with the DNA of inbred children*. *Science*, 236(4808), 1567–1570. PMID: 2884728.

15. Green, P., Barker, D., Knowlton, R., Schumm, J., Lander, E.S., Oliphant, A., Willard, H., Akots, G., Brown, V., Gravius, T., Helms, C., Nelson, C., Parker, C., Rediker, K., Watt, D., Weiffenbach, B., & Donis-Keller, H. (1987). *A genetic linkage map of chromosome 7 including the cystic fibrosis region*. In: G. Mastella & P.M. Quinton (Eds.), *Cellular and Molecular Basis of Cystic Fibrosis*. San Francisco, CA: San Francisco Press.

16. Barker, D., Green, P., Knowlton, R., Schumm, J., Lander, E.S., Oliphant, A., Willard, H., Akots, G., Brown, V., Gravius, T., Helms, C., Nelson, C., Parker, C., Rediker, K., Rising, M., Watt, D., Weiffenbach, B., & Donis-Keller, H. (1987). *Genetic linkage map of human chromosome 7 with 63 DNA markers*. *Proceedings of the National Academy of Sciences USA*, 84(22), 8006–8010. PMID: 2891136; PMCID: PMC299465.

17. Lander, E.S., Green, P., Abrahamson, J., Barlow, A., Daly, M.J., Lincoln, S.E., & Newburg, L. (1987). *MAPMAKER: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations*. *Genomics*, 1(2), 174–181. PMID: 3692487.

18. Donis-Keller, H., Green, P., Helms, C., Cartinhour, S., Weiffenbach, B., Stephens, K., Keith, T.P., Bowden, D.W., Smith, D.R., Lander, E.S., Botstein, D., Akots, G., Rediker, K.S., Gravius, T., Brown, V.A., Rising, M.B., Parker, C., Powers, J.A.,

- Watt, D.E., Kauffman, E.R., Bricker, A., Phipps, P., Muller-Kahle, H., Fulton, T.R., Ng, S., Schumm, J.W., Braman, J.C., Knowlton, R.G., Barker, D.F., Crooks, S.M., Lincoln, S., Daly, M.J., & Abrahamson, J. (1987). A genetic linkage map of the human genome. *Cell*, 51(2), 319–337. PMID: 3664638.
19. Lincoln, S.E., & Lander, E.S. (1987). *Constructing genetic linkage maps with MAPMAKER: A tutorial and reference manual*. Whitehead Institute Technical Report, 107.
20. Lander, E.S. (1987). *The new human genetics: Mapping inherited diseases*. *Princeton Alumni Weekly*, (March 25), 10–16.
21. Lander, E.S., & Waterman, M.S. (1988). Genomic mapping by fingerprinting random clones: a mathematical analysis. *Genomics*, 2(3), 231–239. PMID: 3294162.
22. Chang, C., Bowman, J.L., DeJohn, A.W., Lander, E.S., & Meyerowitz, E.M. (1988). Restriction fragment length polymorphism linkage map for *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences USA*, 85(18), 6856–6860. PMID: 2901107; PMCID: PMC282077.
23. Dracopoli, N.C., Stanger, B.Z., Ito, C.Y., Call, K.M., Lincoln, S.E., Lander, E.S., Housman, D.E. (1988). A genetic linkage map of 27 loci from PND to FY on the short arm of human chromosome 1. *American Journal of Human Genetics*, 43(4), 462–470. PMID: 2902785; PMCID: PMC1715484.
24. Lander, E.S., & Lincoln, S.E. (1988). The appropriate threshold for declaring linkage when allowing sex-specific recombination rates. *American Journal of Human Genetics*, 43(4), 396–400. PMID: 3177382; PMCID: PMC1715500.
25. Paterson, A.H., Lander, E.S., Hewitt, J.D., Peterson, S., Lincoln, S.E., & Tanksley, S.D. (1988). Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. *Nature*, 335(6192), 721–726. PMID: 2902517.
26. Lander, E.S. (1988). Splitting schizophrenia. *Nature*, 336(6195), 105–106. PMID: 2903447.
27. Lander, E.S. (1988). Mapping complex genetic traits in humans. In: K. Davies (Ed.), *Genome analysis: A practical approach* (pp. 171–188). Oxford: IRL Press.
28. Lander, E.S. (1988). Restriction fragments: Their properties and uses. In: M. Waterman (Ed.), *Mathematical methods for DNA sequences* (pp. 35–52). Boca Raton, FL: CRC Press.
29. Hulbert, S.H., Ilott, T.W., Legg, E.J., Lincoln, S.E., Lander, E.S., & Michelmore, R.W. (1988). Genetic analysis of the fungus, *Bremia lactucae*, using restriction fragment length polymorphisms. *Genetics*, 120(4), 947–958. PMID: 2906309; PMCID: PMC1203586.
30. Lander, E.S., Mesirov, J.P., & Taylor, W.J. (1988). Protein sequence comparison on a data parallel computer. *Proceedings of the 1988 International Conference on Parallel Processing, August 15–19, 1988/sponsored by Department of Electrical Engineering, Penn State University*
31. Lander, E.S., & Botstein, D. (1989). Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics*, 121(1), 185–199. PMID: 2563713; PMCID: PMC1203601.
32. Pato, C.N., Lander, E.S., & Schulz, S.C. (1989). Prospects for the genetic analysis of schizophrenia. *Schizophrenia Bulletin*, 15(3), 365–372. PMID: 2683037.
33. Lander, E.S. (1989). DNA fingerprinting on trial. *Nature*, 339(6225), 501–505. PMID: 2567496.
34. Lander, E.S. (1989). Population genetic considerations in the forensic use of DNA typing. *Banbury Report*, 32, 143–156.
35. Lander, E.S., & Daly, M.J. (1989). Genetic mapping of the cystic fibrosis region: Multipoint linkage analysis in two-generation pedigrees. In: R.C. Elston, M.A. Spence, S.E. Hodge, & J.W. MacCluer (Eds.), *Genetic Analysis Workshop 6: Multipoint Mapping and Linkage Based upon Affected Pedigree Members*. New York: Alan R. Liss.
36. Lander, E.S., Mesirov, J.P., & Taylor, W.J. (1989). Study of protein sequence comparison metrics on the Connection Machine CM-2. *The Journal of Supercomputing*, 3(4), 255–269.
37. Lander, E.S. (1989). Genetic mapping of polygenic factors causing diabetes in inbred rodent strains. In: *Nordisk Insulin Symposium No. 3: Genes and Gene Products in the Development of Diabetes Mellitus—Basic and Clinical Aspects*, Oslo, Norway. Amsterdam: Elsevier Publishers.
38. Accili, D., Frapier, C., Mosthaf, L., McKeon, C., Elbein, S.C., Permutt, M.A., Ramon, E., Lander, E.S., Ullrich, A., & Taylor, S.I. (1989). A mutation in the insulin receptor gene that impairs transport of the receptor to the plasma membrane and causes insulin-resistant diabetes. *The EMBO Journal*, 8(9), 2509–2517. PMID: 2573522; PMCID: PMC401244.

39. Lander E.S., & Botstein, D. (1989). *Accurate and efficient mapping of quantitative trait loci*. In: T. Helentjaris & B. Burr (Eds.), *Development and Application of Molecular Markers in Problems in Plant Genetics; Current Communications in Molecular Biology* (pp. 89–96). Cold Spring Harbor, NY: Cold Spring Harbor Press.
40. Jones, R., Taylor, W.J., Zhang, X., Mesirov, J.P., & Lander, E.S. (1990). *Protein sequence comparison on the Connection Machine CM-2*. In *Computers and DNA: Proceedings of the Interface Between Computation Science and Nucleic Acid Sequencing Workshop, Dec 12–16, 1988*. Redwood City, Calif.: Addison-Wesley Pub. Co.
41. Lander, E.S., & Lodish, H. (1990). *Mitochondrial diseases: gene mapping and gene therapy*. *Cell*, 61(6), 925–926. PMID: 2190693.
42. Chakravarti, A., & Lander, E.S. (1990). *Genetic approaches to the dissection of complex diseases*. *Banbury Report*, 33, 307–315.
43. Immerman, N., & Lander, E.S. (1990). *Describing graphs: A first-order approach to graph canonization*. In A.L. Selman (Ed.), *Complexity Theory Retrospective* (pp. 59–81). New York, NY: Springer-Verlag.
44. Paterson A.H., Lander, E.S., & Tanksley, S.D. (1990). *Mapping QTLs affecting agriculturally important traits: Some examples from the tomato*. In: J.E. Womack (Ed.), *Mapping the Genomes of Agriculturally Important Animals*. Cold Spring Harbor, NY: Cold Spring Harbor Press.
45. MacMurray, A.J., Weaver, A., Shin, H.S., & Lander, E.S. (1991). *An automated method for DNA preparation from thousands of YAC clones*. *Nucleic Acids Research*, 19(2), 385–390. PMID: 2014175; PMCID: PMC333606.
46. Paterson, A.H., Damon, S., Hewitt, J.D., Zamir, D., Rabinowitch, H.D., Lincoln, S.E., Lander, E.S., & Tanksley, S.D. (1991). *Mendelian factors underlying quantitative traits in tomato: comparison across species, generations, and environments*. *Genetics*, 127(1), 181–197. PMID: 1673106; PMCID: PMC1204303.
47. Lander, E.S., & Green, P. (1991). *Counting algorithms for linkage: correction to Morton and Collins*. *Annals of Human Genetics*, 55(Pt. 1), 33–38. PMID: 2042933.
48. Lander, E.S. (1991). *Molecular Biology: The new frontier for computational science*. *Very Large Scale Computation in the 21st Century*, 25, 138.
49. Green, P., & Lander, E.S. (1991). *Forensic DNA tests and Hardy-Weinberg equilibrium*. *Science*, 253(5023), 1038–1039. PMID: 17775346.
50. Lander, E.S. (1991). *Research on DNA typing catching up with courtroom application*. *American Journal of Human Genetics*, 48(5), 819–823. PMID: 1760000; PMCID: PMC1683053.
51. Lander, E.S. (1991). *Research on DNA typing validated in the literature [Reply]*. *American Journal of Human Genetics* 49, 899–903.
52. Jacob, H.J., Lindpaintner, K., Lincoln, S.E., Kusumi, K., Bunker, R.K., Mao, Y.P., Ganten, D., Dzau, V.J., & Lander, E.S. (1991). *Genetic mapping of a gene causing hypertension in the stroke-prone spontaneously hypertensive rat*. *Cell*, 67(1), 213–224. PMID: 1655275.
53. Arratia, R., Lander, E.S., Tavaré, S., & Waterman, M.S. (1991). *Genomic mapping by anchoring random clones: A mathematical analysis*. *Genomics*, 11(4), 806–827. PMID: 1783390.
54. Lander, E.S., Langridge, R., & Saccocio, D.M. (1991). *Computing in molecular biology: mapping and interpreting biological information*. *Computer*, 24(11), 6–13.
55. Dietrich, W., Katz, H., Lincoln, S.E., Shin, H.S., Friedman, J., Dracopoli, N.C., & Lander, E.S. (1992). *A genetic map of the mouse suitable for typing intraspecific crosses*. *Genetics*, 131(2), 423–447. PMID: 1353738; PMCID: PMC1205016.
56. Stuber, C.W., Lincoln, S.E., Wolff, D.W., Helentjaris, T., & Lander, E.S. (1992). *Identification of genetic factors contributing to heterosis in a hybrid from two elite maize inbred lines using molecular markers*. *Genetics*, 132(3), 823–839. PMID: 1468633; PMCID: PMC1205218.
57. Jacob, H.J., Pettersson, A., Wilson, D., Mao, Y., Lernmark, A., & Lander, E.S. (1992). *Genetic dissection of autoimmune type I diabetes in the BB rat*. *Nature Genetics*, 2(1), 56–60. PMID: 1303251.
58. Lander, E.S. (1992). *DNA fingerprinting: Science, law, and the ultimate identifier*. In: D.J. Kevles & L. Hood (Eds.), *The Code of Codes: Scientific and Social Issues in the Human Genome Project* (pp. 191–210). Cambridge, MA: Harvard University Press.
59. Waterman, M.S., Eggert, M., & Lander, E.S. (1992). *Parametric sequence comparisons*. *Proceedings of the National Academy of Sciences USA*, 89(13), 6090–6093. PMID: 1631095; PMCID: PMC49443.
60. Groot, P.C., Moen, C.J., Dietrich, W., Stoye, J.P., Lander, E.S., & Demant, P. (1992). *The recombinant congenic strains for analysis of multigenic traits: genetic composition*. *The FASEB Journal*, 6(10), 2826–2835. PMID: 1634045.
61. Lincoln, S.E., & Lander, E.S. (1992). *Systematic detection of errors in genetic linkage data*. *Genomics*, 14(3), 604–610. PMID: 1427888.

62. Hästbacka, J., de la Chapelle, A., Kaitila, I., Sistonen, P., Weaver, A., & Lander, E.S. (1992). *Linkage disequilibrium mapping in isolated founder populations: distastrophic dysplasia in Finland. Nature Genetics*, 2(3), 204–211. PMID: 1345170.
63. Goff, D.J., Galvin, K., Katz, H., Westerfield, M., Lander, E.S., & Tabin, C.J. (1992). *Identification of polymorphic simple sequence repeats in the genome of the zebrafish. Genomics*, 14(1), 200–202. PMID: 1427829.
64. Luongo, C., Gould, K.A., Su, L.K., Kinzler, K.W., Vogelstein, B., Dietrich, W., Lander E.S., & Moser, A.R. (1993). *Mapping of multiple intestinal neoplasia (Min) to proximal chromosome 18 of the mouse. Genomics*, 15(1), 3–8. PMID: 8094372.
65. Dietrich, W., Miller, J., Katz, H., Joyce, D., Steen, R., Lincoln, S., Daly, M., Reeve, M.P., Weaver, A., Goodman, N., Dracopoli, N., and Lander, E.S. (1993). *SSLP genetic map of the mouse (Mus musculus) 2N= 40. Genetic Maps*, 4–110.
66. Yi, T.M., & Lander, E.S. (1993). *Protein secondary structure prediction using nearest-neighbor methods. Journal of Molecular Biology*, 232(4), 1117–1129. PMID: 8371270.
67. Kusumi, K., Smith, J.S., Segre, J.A., Koos, D.S., & Lander, E.S. (1993). *Construction of a large-insert yeast artificial chromosome library of the mouse genome. Mammalian Genome*, 4(7), 391–392. PMID: 8358173.
68. Lander, E.S. (1993). *DNA fingerprinting: the NRC report. Science*, 260(5112), 1221. PMID: 8493559.
69. Lander, E.S. (1993). *Finding similarities and differences among genomes. Nature Genetics*, 4(1), 5–6. PMID: 8513322.
70. Lehesjoki, A.E., Koskineniemi, M., Norio, R., Tirrito, S., Sistonen, P., Lander, E.S., & de la Chapelle, A. (1993). *Localization of the EPM1 gene for progressive myoclonus epilepsy on chromosome 21: linkage disequilibrium allows high resolution mapping. Human Molecular Genetics*, 2(8), 1229–1234. PMID: 8104628.
71. Yi, T.M., & Lander, E.S. (1993). *Protein secondary structure prediction using nearest-neighbor methods. Journal of Molecular Biology*, 232(4), 1117–1129. PMID: 8371270.
72. Copeland, N.G., Jenkins, N.A., Gilbert, D.J., Eppig, J.T., Maltais, L.J., Miller, J.C., Dietrich, W.F., Weaver, A., Lincoln, S.E., Steen, R.G., Stein, L.D., Nadeau, J., & Lander, E.S. (1993). *A genetic linkage map of the mouse: current applications and future prospects. Science*, 262(5130), 57–66. PMID: 8211130.
73. Copeland, G., Gilbert, D.J., Jenkins, N.A., Nadeau, J.H., Eppig, J.T., Maltais, L., Miller, J.C., Dietrich, W.F., Steen, R.G., Lincoln, S.E., Weaver, A., Joyce, D.C., Merchant, M., Wessel, M., Katz, H., Stein, L.D., Reeve, M.P., Daly, M.C., Dredge, R.D., Marquis, A., Goodman, N., & Lander, E.S. (1993). *Genome map IV: The mouse. Science*, 262, 67–82.
74. Dietrich, W.F., Lander, E.S., Smith, J.S., Moser, A.R., Gould, K.A., Luongo, C., Borenstein, N., & Dove, W. (1993). *Genetic identification of Mom-1, a major modifier locus affecting Min-induced intestinal neoplasia in the mouse. Cell*, 75(4), 631–639. PMID: 8242739.
75. Lisitsyn, N.A., Segre, J.A., Kusumi, K., Lisitsyn, N.M., Nadeau, J.H., Frankel, W.N., Wigler, M., & Lander, E.S. (1994). *Direct isolation of polymorphic markers linked to a trait by genetically directed representational difference analysis. Nature Genetics*, 6(1), 57–63. PMID: 8136836.
76. Wiseman, R.W., Cochran, C., Dietrich, W., Lander, E.S., & Söderkvist, P. (1994). *Allelotyping of butadiene-induced lung and mammary adenocarcinomas of B6C3F1 mice: frequent losses of heterozygosity in regions homologous to human tumor-suppressor genes. Proceedings of the National Academy of Sciences USA*, 91(9), 3759–3763. PMID: 8170984; PMCID: PMC43661.
77. Dietrich, W.F., Miller, J.C., Steen, R.G., Merchant, M., Damron, D., Nahf, R., Gross A., Joyce, D.C., Wessel, M., Dredge, R.D., & Marquis, A. (1994). *A genetic map of the mouse with 4,006 simple sequence length polymorphisms. Nature Genetics*, 7(2 Spec No), 220–245. PMID: 7920646.
78. Hsu, L.C., Kennan, W.S., Shepel, L.A., Jacob, H.J., Szpirer, C., Szpirer, J., Lander, E.S., & Gould, M.N. (1994). *Genetic identification of Mcs-1, a rat mammary carcinoma suppressor gene. Cancer Research*, 54(10), 2765–2770. PMID: 8168109.
79. Yi, T.M., & Lander, E.S. (1994). *Recognition of related proteins by iterative template refinement (ITR). Protein Science*, 3(8), 1315–1328. PMID: 7987226; PMCID: PMC2142931.
80. Lander, E.S., & Schork, N.J. (1994). *Genetic dissection of complex traits. Science*, 265(5181), 2037–2048. PMID: 8091226.
81. Dietrich, W.F., Radany, E.H., Smith, J.S., Bishop, J.M., Hanahan, D., & Lander, E.S. (1994). *Genome-wide search for loss of heterozygosity in transgenic mouse tumors reveals candidate tumor suppressor genes on chromosomes 9 and 16. Proceedings of the National Academy of Sciences USA*, 91(20), 9451–9455. PMID: 7937788; PMCID: PMC44830.

82. Hästbacka, J., de la Chapelle, A., Mahtani, M.M., Clines, G., Reeve-Daly, M.P., Daly, M.J., Hamilton, B.A., Kusumi, K., Trivedi, B., Weaver, A., Coloma, A., Lovett, M., Buckler, A., Ilkka, K., & Lander, E.S. (1994). *The diastrophic dysplasia gene encodes a novel sulfate transporter: positional cloning by fine-structure linkage disequilibrium mapping*. *Cell*, 78(6), 1073-1087. PMID: 7923357.
83. Cox, D.R., Green, E.D., Lander, E.S., Cohen, D., & Myers, R.M. (1994). *Assessing mapping progress in the Human Genome Project*. *Science*, 265(5181), 2031-2032. PMID: 8091223.
84. Lander, E.S., & Budowle, B. (1994). *DNA fingerprinting dispute laid to rest*. *Nature*, 371(6500), 735-738. PMID: 7818670.
85. Hegi, M.E., Devereux, T.R., Dietrich, W.F., Cochran, C.J., Lander, E.S., Foley, J.F., Maronpot R.R., Anderson M.W., & Wiseman, R.W. (1994). *Allelotype analysis of mouse lung carcinomas reveals frequent allelic losses on chromosome 4 and an association between allelic imbalances on chromosome 6 and K-ras activation*. *Cancer Research*, 54(23), 6257-6264. PMID: 7954475.
86. Haldi, M., Perrot, V., Saumier, M., Desai, T., Cohen, D., Cherif, D., Ward, D., & Lander, E.S. (1994). *Large human YACs constructed in a rad52 strain show a reduced rate of chimerism*. *Genomics*, 24(3), 478-484. PMID: 7713499.
87. Truett, G.E., Jacob, H.J., Miller, J., Drouin, G., Bahary, N., Smoller, J.W., Lander, E.S., & Leibel, R.L. (1995). *Genetic map of rat chromosome 5 including the fatty (fa) locus*. *Mammalian Genome*, 6(1), 25-30. PMID: 7719022.
88. Lander, E.S., & Kruglyak, L. (1995). *Genetic dissection of complex traits*. *Nature Genetics*, 11(3), 241-247. PMID: 7581446.
89. Chernoff, H., & Lander, E.S. (1995). *Asymptotic distribution of the likelihood ratio test that a mixture of two binomials is a single binomial*. *Journal of Statistical Planning and Inference*, 43(1), 19-40.
90. Lander, E.S. (1995). *Mapping heredity: Using probabilistic models and algorithms to map genes and genomes*. In: E.S. Lander & M.S. Waterman (Eds.), *Calculating the Secrets of Life: Contributions of the Mathematical Sciences to Molecular Biology* (pp. 25-55). Washington, DC: National Academy Press.
91. Lander, E.S., & Waterman, M.S. (1995). *The Secrets of Life: A Mathematician's Introduction to Molecular Biology*. In: E.S. Lander & M.S. Waterman (Eds.), *Calculating the Secrets of Life: Contributions of the Mathematical Sciences to Molecular Biology* (pp. 25-55). Washington, DC: National Academy Press.
92. Kruglyak, L., Daly, M.J., & Lander, E.S. (1995). *Rapid multipoint linkage analysis of recessive traits in nuclear families, including homozygosity mapping*. *American Journal of Human Genetics*, 56(2), 519-527. PMID: 7847388; PMCID: PMC1801139.
93. Jacob, H.J., Brown, D.M., Bunker, R.K., Daly, M.J., Dzau, V.J., Goodman, A., Kren, V., Kurtz, T., Lernmark, A., Levan, G., Mao, Y.P., Pettersson, A., Pravenec, M., Simon, J.S., Szpirer, C., Szpirer, J., Trolliet, M.R., Winer, E.S., & Lander, E.S. (1995). *A genetic linkage map of the laboratory rat, Rattus norvegicus*. *Nature Genetics*, 9(1), 63-69. PMID: 7704027.
94. Kruglyak, L., & Lander, E.S. (1995). *A nonparametric approach for mapping quantitative trait loci*. *Genetics*, 139(3), 1421-1428. PMID: 7768449; PMCID: PMC1206467.
95. Lander, E.S. (1995). *Mapping heredity: Using probabilistic models and algorithms to map genes and genomes (Part I)*. *Notices of the AMS*, 42, 747-753.
96. Lander, E.S. (1995). *Mapping Heredity: Using probabilistic models and algorithms to map genes and genomes (Part II)*. *Notices of the AMS*, 42(8), 854-858.
97. Bell, C.J., Budarf, M.L., Nieuwenhuijsen, B.W., Barnoski, B.L., Buetow, K.H., Campbell, K., Colbert A., Collins J., Desjardins, P.R., DeZwaan, T., Eckman, B., Fischbeck, K.H., Foote, S., Hart, K., Hiester, K., Van Het Hoog, M.J., Hopper, E., McDermid, H.E., Overton, C., Reeve-Daly, M.P., Searls, D.B., Watson, E., Winston, R., Valmiki, V.H., Nussbaum, R.L., Lander, E.S., Emanuel, B.S., & Hudson, T.J. (1995). *Integration of physical, breakpoint and genetic maps of chromosome 22. Localization of 587 yeast artificial chromosomes with 238 mapped markers*. *Human Molecular Genetics*, 4(1), 59-69. PMID: 7711735.
98. Dietrich, W.F., Damron, D.M., Isberg, R.R., Lander, E.S., & Swanson, M.S. (1995). *Lgn1, a gene that determines susceptibility to Legionella pneumophila, maps to mouse chromosome 13*. *Genomics*, 26(3), 443-450. PMID: 7607666.
99. Kruglyak, L., & Lander, E.S. (1995). *High-resolution genetic mapping of complex traits*. *American Journal of Human Genetics*, 56(5), 1212-1223. PMID: 7726179; PMCID: PMC1801437.
100. Kruglyak, L., & Lander, E.S. (1995). *Complete multipoint sib-pair analysis of qualitative and quantitative traits*. *American Journal of Human Genetics*, 57(2), 439-454. PMID: 7668271; PMCID: PMC1801561.

101. Segre, J.A., Nemhauser, J.L., Taylor, B.A., Nadeau, J.H., & Lander, E.S. (1995). *Positional cloning of the nude locus: genetic, physical, and transcription maps of the region and mutations in the mouse and rat. Genomics*, 28(3), 549–559. PMID: 7490093.
102. Pettersson, A., Wilson, D., Daniels, T., Tobin, S., Jacob, H.J., Lander, E.S., & Lernmark, A. (1995). *Thyroiditis in the BB rat is associated with lymphopenia but occurs independently of diabetes. Journal of Autoimmunity*, 8(4), 493–505. PMID: 7492346.
103. De Sanctis, G.T., Merchant, M., Beier, D.R., Dredge, R.D., Grobholz, J.K., Martin, T.R., Lander, E.S., & Drazen, J.M. (1995). *Quantitative locus analyses of airway hyperresponsiveness in A/J and C57BL/6J mice. Nature Genetics*, 11(2), 150–154. PMID: 7550342.
104. Chumakov, I.M., Rigault, P., LeGall, I., Bellannechantelot, C., Billault, A., Guillou, S., Soularue P., Guasconi G., Poullier E., Gros I., Belova, M., Sambucy, J., Susini, L., Gervy, P., Glibert, F., Beaufils, S., Bui, H., Massart, C., De Tand, M., Dukasz, F., Lecoulant, S., Ougen, P., Perrot, V., Saumier, M., Soravito, C., Bahouayila, R., Cohen-Akenin, A., Barillot, E., Bertrant, S., Codani, J., Caterina, D., Georges, I., Lacroix, B., Lucotte, G., Sahbatou, M., Schmit, C., Sangouard, M., Tubacher, E., Dib, C., Fauré, S., Fizames, C., Gyapay, G., Millasseau, P., Nguyen, S., Muselet, D., Vignal, A., Morrisette, J., Menninger, J., Lieman, J., Desai, T., Banks, A., Bray-Ward, P., Ward, D., Hudson, T., Gerety, S., Foote, S., Stein, L., Page, D.C., Lander, E.S., Weissenbach, J., Le Paslier, D., & Cohen, D. (1995). *A YAC contig map of the human genome. Nature*, 377(6547 Suppl), 175–297. PMID: 7566096.
105. Schork, N.J., Krieger, J.E., Trollet, M.R., Franchini, K.G., Koike, G., Krieger, E.M., Lander, E.S., Dzau, V.J., & Jacob, H.J. (1995). *A biometrical genome search in rats reveals the multigenic basis of blood pressure variation. Genome Research*, 5(2), 164–172. PMID: 9132270.
106. Dietrich, W.F., Copeland, N.G., Gilbert, D.J., Miller, J.C., Jenkins, N.A., & Lander, E.S. (1995). *Mapping the mouse genome: current status and future prospects. Proceedings of the National Academy of Sciences USA*, 92(24), 10849–10853. PMID: 7479896; PMCID: PMC40528.
107. Lander, E.S., & Kruglyak, L. (1995). *Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. Nature Genetics*, 11(3), 241–247. PMID: 7581446.
108. Parangi, S., Dietrich, W., Christofori, G., Lander, E.S., & Hanahan, D. (1995). *Tumor suppressor loci on mouse chromosomes 9 and 16 are lost at distinct stages of tumorigenesis in a transgenic model of islet cell carcinoma. Cancer Research*, 55(24), 6071–6076. PMID: 8521395.
109. Hudson, T.J., Stein, L.D., Gerety, S.S., Ma, J., Castle, A.B., Silva, J., Slonim, D.K., Baptista, R., Kruglyak, L., Xu, S.H., Hu, X., Colbert, A.M., Rosenberg, C., Reeve-Daly, M.P., Rozen, S., Hui, L., Wu, X., Vestergaard, C., Wilson, K.M., Bae, J.S., Maitra, S., Ganiatsas, S., Evans, C.A., DeAngelis, M.M., Ingalls, K.A., Nahf, R.W., Horton, L.T., Anderson, M.O., Collymore, A.J., Ye, W., Kouyoumjian, V., Zemsteva, I.S., Tam, J., Devine, R., Courtney, D.F., Renaud, M.T., Nguyen, H., O'Connor, T.J., Fizames, C., Fauré, S., Gyapay, G., Dib, C., Morrisette, J., Orlin, J.B., Birren, B.W., Goodman, N., Weissenbach, J., Hawkins, T.L., Foote, S., Page, D.C., & Lander, E.S. (1995). *An STS-based map of the human genome. Science*, 270(5244), 1945–1954. PMID: 8533086.
110. Superti-Furga, A., Hästbacka, J., Wilcox, W.R., Cohn, D.H., van der Harten, H.J., Rossi, A., Blau, N., Rimoin, D.L., Steinmann, B., Lander, E.S., & Gitzelmann, R. (1996). *Achondrogenesis type IB is caused by mutations in the diastrophic dysplasia sulphate transporter gene. Nature Genetics*, 12(1), 100–102. PMID: 8528239.
111. Brown, D.M., Provoost, A.P., Daly, M.J., Lander, E.S., & Jacob, H.J. (1996). *Renal disease susceptibility and hypertension are under independent genetic control in the fawn-hooded rat. Nature Genetics*, 12(1), 44–51. PMID: 8528250.
112. Jacob, H.J., Krieger, J.E., Dzau, V.J., & Lander, E.S. (1996). *Genetic dissection of hypertension in experimental animal models. Fundamental and Clinical Cardiology*, 26, 293–320.
113. Miller, J.C., Dietrich, W.F., Steen, R.G., Joyce, D.C., Merchant, M.A., Wessel, M.T., Damron D.M., Nahf, R.W., Stein, L.D., Dredge, R.D., Marquis, A.L., Daly, M.J., Reeve, M.P., Goodman, N., Lord, C.J., Montague, C.T., Prins, J.B., Todd, J.A., & Lander, E.S. (1996). *SSLP/microsatellite genetic linkage map of the mouse. In: M.F. Lyon, S. Rastan, & S.D.M. Brown (Eds.), Genetic Variants and Strains of the Laboratory Mouse (pp. 1671–1755). Oxford: Oxford University Press.*
114. Galli, J., Li, L.S., Glaser, A., Ostenson, C.G., Jiao, H., Fakhrai-Rad, H., Jacob, H.J., Lander, E.S., & Luthman, H. (1996). *Genetic analysis of non-insulin de-*

- pendent diabetes mellitus in the GK rat. *Nature Genetics*, 12(1), 31–37. PMID: 8528247.
115. Hästbacka, J., Superti-Furga, A., Wilcox, W.R., Rimoin, D.L., Cohn, D.H., & Lander, E.S. (1996). *Atelosteogenesis type II is caused by mutations in the diastrophic dysplasia sulfate-transporter gene (DTDST): evidence for a phenotypic series involving three chondrodysplasias*. *American Journal of Human Genetics*, 58(2), 255–262. PMID: 8571951; PMCID: PMC1914552.
116. Dietrich, W.F., Miller, J., Steen, R., Merchant, M.A., Damron-Boles, D., Husain, Z., Dredge R., Daly M.J., Ingalls K.A., O'Connor, T.J., Evans, C.A., DeAngelis, M.M., Levinson, D.M., Kruglyak, L., Goodman N., Copeland N.G., Jenkins, N.A., Hawkins, T.L., Stein, L., Page, D.C., & Lander, E.S. (1996). *A comprehensive genetic map of the mouse genome*. *Nature*, 380(6570), 149–152. PMID: 8600386.
117. Hamilton, B.A., Frankel, W.N., Kerrebrock, A.W., Hawkins, T.L., FitzHugh, W., Kusumi, K., Russell, L.B., Mueller, K.L., van Berkel, V., Birren, B.W., Kruglyak, L., & Lander, E.S. (1996). *Disruption of the nuclear hormone receptor ROR α in staggerer mice*. *Nature*, 379(6567), 736–739. PMID: 8602221.
118. Kruglyak, L., & Lander, E.S. (1996). *Limits on fine mapping of complex traits*. *American Journal of Human Genetics*, 58(5), 1092–1093. PMID: 8651271; PMCID: PMC1914627.
119. Kruglyak, L., Daly, M.J., Reeve-Daly, M.P., & Lander, E.S. (1996). *Parametric and nonparametric linkage analysis: a unified multipoint approach*. *American Journal of Human Genetics*, 58(6), 1347–1363. PMID: 8651312; PMCID: PMC1915045.
120. Yi, T. M., & Lander, E.S. (1996). *Iterative template refinement: Protein-fold prediction using iterative search and hybrid sequence/structure templates*. *Methods in Enzymology*, 266, 322–339. PMID: 8743692.
121. Kurooka, H., Segre, J.A., Hirano, Y., Nemhauser, J.L., Nishimura, H., Yoneda, K., Lander, E.S., & Honjo, T. (1996). *Rescue of the hairless phenotype in nude mice by transgenic insertion of the wild-type Hfh11 genomic locus*. *International Immunology*, 8(6), 961–966. PMID: 8671685.
122. Superti-Furga, A., Hästbacka, J., Rossi, A., van der Harten, J.J., Wilcox, W.R., Cohn, D.H., Rimoin, D.L., Steinmann, B., Lander, E.S., & Gitzelmann, R. (1996). *A family of chondrodysplasias caused by mutations in the diastrophic dysplasia sulfate transporter gene and associated with impaired sulfation of proteoglycans*. *Annals of the New York Academy of Sciences*, 785, 195–201. PMID: 8702127.
123. Gschwend, M., Levran, O., Kruglyak, L., Ranade, K., Verlander, P.C., Shen, S., Faure, S., Weissenbach, J., Altay, C., Lander, E.S., Auerbach, A.D., & Botstein, D. (1996). *A locus for Fanconi anemia on 16q determined by homozygosity mapping*. *American Journal of Human Genetics*, 59(2), 377–384. PMID: 8755924; PMCID: PMC1914713.
124. Mahtani, M.M., Widén, E., Lehto, M., Thomas, J., McCarthy, M., Brayer, J., Bryant, B., Chan, G., Daly, M.J., Forsblom, C., Kanninen, T., Kirby, A., Kruglyak, L., Munnely, K., Parkkonen, M., Reeve-Daly, M.P., Weaver, A., Brettin, T., Duyk, G., Lander, E.S., & Groop, L.C. (1996). *Mapping of a gene for type 2 diabetes associated with an insulin secretion defect by a genome scan in Finnish families*. *Nature Genetics*, 14(1), 90–94. PMID: 8782826.
125. Navin, A., Prekeris, R., Lisitsyn, N.A., Sonti, M.M., Grieco, D.A., Narayanswami, S., Lander, E.S., & Simpson, E.M. (1996). *Mouse Y-specific repeats isolated by whole chromosome representational difference analysis*. *Genomics*, 36(2), 349–353. PMID: 8812464.
126. Daly, M.J., & Lander, E.S. (1996). *The importance of being independent: sib pair analysis in diabetes*. *Nature Genetics*, 14(2), 131–132. PMID: 8841179.
127. Lander, E.S. (1996). *The new genomics: global views of biology*. *Science*, 274(5287), 536–539. PMID: 8928008.
128. Schuler, G.D., Boguski, M.S., Stewart, E.A., Stein, L.D., Gyapay, G., Rice, K., White, R.E., Rodriguez-Tome, P., Aggarwal, A., Bajorek, E., Bentolila, S., Birren, B.W., Butler, A., Castle, A.B., Chiannilkulchai, N., Chu, A., Clee, C., Cowles, S., Day, P.J.R., Dibling, T., Drouot, N., Dunham, I., Duprat, S., East, C., Edwards, C., Fan, J.B., Fang, N., Fizes, C., Garrett, C., Green, L., Hadley, D., Harris, M., Harrison, P., Brady, S., Hicks, A., Holloway, E., Hui, L., Hussaine, S., Louis-Dit-Sully, C., Ma, J., MacGilvery, A., Mader, C., Maratukulam, A., Matise, T.C., McKusick, K.B., Morissette, J., Mungall, A., Muselet, D., Nusbaum, H.C., Page, D.C., Peck, A., Perkins, S., Piercy, M., Qin, F., Quackenbush, J., Ranby, S., Reif, T., Rozen, S., Sanders, C., She, X., Silva, J., Slonim, D.K., Soderlund, C., Sun, W.L., Tabar, P., Thangarajah, T., Vega-Czarny, N., Vollrath, D., Voyticky, S., Wilmer, T., Wu, X., Adams, M.D., Auffray, C., Berry, R., Brandon, R., Dehejia, A., Goodfellow, P.N.,

- Houlgatte, R., Hudson, J.R., Ide, S.E., Iorio, K.R., Lee, W.Y., Seki, N., Nagase, T., Ishikawa, K., Nomura, N., Phillips, C., Polymeropoulos, M.H., Sandusky, M., Schmitt, K., Sikela, J.M., Swanson, K., Torres, R., Venter, J.C., Walter, N.A.R., Beckmann, J.S., Weissenbach, J., Myers, R.M., Cox, D.R., James, M.R., Bentley, D., Deloukas, P., Lander, E.S., & Hudson, T.J. (1996). *A gene map of the human genome*. *Science*, 274(5287), 540.
129. Haldi, M.L., Strickland, C., Lim, P., VanBerkel, V., Chen, X.N., Noya, D., Korenberg, J.R., Husain, Z., Miller, J., & Lander, E.S. (1996). *A comprehensive large-insert yeast artificial chromosome library for physical mapping of the mouse genome*. *Mammalian Genome*, 7(10), 767–769. PMID: 8854865.
130. Gould, K.A., Dietrich, W.F., Borenstein, N., Lander, E.S., & Dove, W.F. (1996). *Mom1 is a semi-dominant modifier of intestinal adenoma size and multiplicity in Min/+ mice*. *Genetics*, 144(4), 1769–1776. PMID: 8978062; PMCID: PMC1207726.
131. Gould, K.A., Luongo, C., Moser, A.R., McNeley, M.K., Borenstein, N., Shedlovsky, A., Dove, W.F., Hong, K., Dietrich, W.F., & Lander, E.S. (1996). *Genetic evaluation of candidate genes for the Mom1 modifier of intestinal neoplasia in mice*. *Genetics*, 144(4), 1777–1785. PMID: 8978063; PMCID: PMC1207727.
132. Slonim, D.K., Kruglyak, L., Stein, L., & Lander, E.S. (1997). *Building human genome maps with radiation hybrids*. *Proceedings of the First Annual International Conference on Computational Biology (RECOMB '97)*. New York: ACM Press.
133. Hamilton, B.A., Smith, D.J., Mueller, K.L., Kerrebrock, A.W., Bronson, R.T., van Berkel, V., Daly, M.J., Kruglyak, L., Reeve, M.P., Nemhauser, J.L., Hawkins, T.L., Rubin, E.M., & Lander, E.S. (1997). *The vibrator mutation causes neurodegeneration via reduced expression of P1TP α ;: positional complementation cloning and extragenic suppression*. *Neuron*, 18(5), 711–722. PMID: 9182797.
134. Kuokkanen, S., Gschwend, M., Rioux, J.D., Daly, M.J., Terwilliger, J.D., Tienari, P.J., Wikström, J., Palo, J., Stein, L.D., Hudson, T.J., Lander, E.S., & Peltonen, L. (1997). *Genomewide scan of multiple sclerosis in Finnish multiplex families*. *The American Journal of Human Genetics*, 61(6), 1379–1387. PMID: 9399895; PMCID: PMC1716063.
135. Hawkins, T.L., McKernan, K.J., Jacotot, L.B., MacKenzie, J.B., Richardson, P.M., & Lander, E.S. (1997). *A magnetic attraction to high-throughput genomics*. *Science*, 276(5320), 1887–1889. PMID: 9206843.
136. Cormier, R.T., Hong, K.H., Halberg, R.B., Hawkins, T.L., Richardson, P., Mulherkar, R., Dove, W.F., & Lander, E.S. (1997). *Secretory phospholipase Pla2g2a confers resistance to intestinal tumorigenesis*. *Nature Genetics*, 17(1), 88–91. PMID: 9288104.
137. Haldi, M.L., Lim, P., Kaphingst, K., Akella, U., Whang, J., & Lander, E.S. (1997). *Construction of a large-insert yeast artificial chromosome library of the rat genome*. *Mammalian Genome*, 8(6), 460. PMID: 9166603.
138. Sidow, A., Bulotsky, M.S., Kerrebrock, A.W., Bronson, R.T., Daly, M.J., Reeve, M.P., Hawkins, T.L., Birren, B.W., Jaenisch, R., & Lander, E.S. (1997). *Serrate2 is disrupted in the mouse limb-development mutant syndactylism*. *Nature*, 389(6652), 722–725. PMID: 9338782.
139. Shi, Y.P., Mohapatra, G., Miller, J., Hanahan, D., Lander, E.S., Gold, P., Pinkel, D., & Gray, J. (1997). *FISH probes for mouse chromosome identification*. *Genomics*, 45(1), 42–47. PMID: 9339359.
140. Laitinen, T., Kauppi, P., Ignatius, J., Ruotsalainen, T., Daly, M.J., Kääriäinen, H., Kruglyak, L., Laitinen, H., de la Chapelle, A., Lander, E.S., Laitinen, L.A., & Kere, J. (1997). *Genetic control of serum IgE levels and asthma: linkage and linkage disequilibrium studies in an isolated population*. *Human Molecular Genetics*, 6(12), 2069–2076. PMID: 9328470.
141. Lehto, M., Tuomi, T., Mahtani, M.M., Widén, E., Forsblom, C., Sarelin, L., Gullström, M., Isomaa, B., Lehtovirta, M., Hyrkkö, A., Kanninen, T., Orho, M., Manley, S., Turner, R.C., Brettn, T., Kirby, A., Thomas, J., Duyk, G., Lander, E.S., Taskinen, M.R., & Groop, L. (1997). *Characterization of the MODY3 phenotype. Early-onset diabetes caused by an insulin secretion defect*. *Journal of Clinical Investigation*, 99(4), 582–591. PMID: 9045858; PMCID: PMC507838.
142. Slonim, D., Kruglyak, L., Stein, L., & Lander, E.S. (1997). *Building human genome maps with radiation hybrids*. *Journal of Computational Biology*, 4(4), 487–504. PMID: 9385541.
143. Fazeli, A., Steen, R.G., Dickinson, S.L., Bautista, D., Dietrich, W.F., Bronson, R.T., Bresalier, R.S., Lander, E.S., Costa, J., & Weinberg, R.A. (1997). *Effects of p53 mutations on apoptosis in mouse intestinal and human colonic adenomas*. *Proceedings of the National Academy of Sciences USA*, 94(19), 10199–10204. PMID: 9294187; PMCID: PMC23339.

144. Radany, E.H., Hong, K., Keshavarzi, S., Lander, E.S., & Bishop, J.M. (1997). *Mouse mammary tumor virus/v-Ha-ras transgene-induced mammary tumors exhibit strain-specific allelic loss on mouse chromosome 4. Proceedings of the National Academy of Sciences USA*, 94(16), 8664–8669. PMID: 9238034; PMCID: PMC23068.
145. Kruglyak, L., & Lander, E.S. (1998). *Faster multipoint linkage analysis using Fourier transforms. Journal of Computational Biology*, 5(1), 1–7. PMID: 9541867.
146. Zhong, T.P., Kaphingst, K., Akella, U., Haldi, M., Lander, E.S., & Fishman, M.C. (1998). *Zebrafish genomic library in yeast artificial chromosomes. Genomics*, 48(1), 136–138. PMID: 9514818.
147. Bieg, S., Koike, G., Jiang, J., Klaff, L., Pettersson, A., MacMurray, A.J., Jacob, H.J., Lander, E.S., & Lernmark, A. (1998). *Genetic isolation of iddm 1 on chromosome 4 in the biobreeding (BB) rat. Mammalian Genome*, 9(4), 324–326. PMID: 9530633.
148. Wang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hsie, L., Topalogolu, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M., & Lander, E.S. (1998). *Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome. Science*, 280(5366), 1077–1082. PMID: 9582121.
149. Altshuler, D., Kruglyak, L., & Lander, E.S. (1998). *Genetic polymorphisms and disease. New England Journal of Medicine*, 338(22), 1626. PMID: 9606122.
150. Kusumi, K., Sun, E.S., Kerrebrock, A.W., Bronson, R.T., Chi, D.C., Bulotsky, M.S., Spencer, J.B., Birren, B.W., Frankel, W.N., & Lander, E.S. (1998). *The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries. Nature Genetics*, 19(3), 274–278. PMID: 9662403.
151. McCarthy, M.I., Kruglyak, L., & Lander, E.S. (1998). *Sib-pair collection strategies for complex diseases. Genetic Epidemiology*, 15(4), 317–340. PMID: 9671984.
152. Savukoski, M., Klockars, T., Holmberg, V., Santavuori, P., Lander, E.S., & Peltonen, L. (1998). *CLN5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid lipofuscinosis. Nature Genetics*, 19(3), 286–288. PMID: 9662406.
153. Ober, C., Cox, N.J., Abney, M., Di Rienzo, A., Lander, E.S., Changyaleket, B., Gidley, H., Kurtz, B., Lee, J., Nance, M., Pettersson, A., Prescott, J., Richardson, A., Schlenker, E., Summerhill, E., Willadsen, S., Parry R., & Collaborative Study on the Genetics of Asthma. (1998). *Genome-wide search for asthma susceptibility loci in a founder population. Human Molecular Genetics*, 7(9), 1393–1398. PMID: 9700192.
154. Szpirer, C., Szpirer, J., Van Vooren, P., Tissir, F., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (1998). *Gene-based anchoring of the rat genetic linkage and cytogenetic maps: new regional localizations, orientation of the linkage groups, and insights into mammalian chromosome evolution. Mammalian Genome*, 9(9), 721–734. PMID: 9716657.
155. Deloukas, P., Schuler, G.D., Gyapay, G., Beasley, E.M., Soderlund, C., Rodriguez-Tome, P., Hui, L., Matisse, T.C., McKusick, K.B., Beckmann, J.S., Bentolila, S., Bihoreau, M.T., Birren, B.W., Browne, J., Butler, A., Castle, A.B., Chiannikulchai, N., Clee, C., Day, P.J.R., Dehejia, A., Dibling, T., Drouot, N., Duprat, S., Fizames, C., Fox, S., Gelling, S., Green, L., Harrison, P., Hocking, R., Holloway, E., Hunt, S., Keil, S., Lijnzaad, P., Louis-Dit-Sully, C., Ma, J., Mendis, A., Miller, J., Morissette, J., Muselet, D., Nusbaum, H.C., Peck, A., Rozen, S., Simon, D., Slonim, D.K., Staples, R., Stein, L.D., Stewart, E.A., Suchard, M.A., Thangarajah, T., Vega-Czarny, N., Webber, C., Wu, X., Auffray, C., Nomura, N., Sikela, J.M., Polymeropoulos, M.H., James, M.R., Lander, E.S., Hudson, T.J., Myers, R.M., Cox, D.R., Weissenbach, J., Boguski, M.S., & Bentley, D.R. (1998). *A physical map of 30,000 human genes. Science*, 282(5389), 744–746. PMID: 9784132.
156. Rioux, J.D., Daly, M.J., Green, T., Stone, V., Lander, E.S., Hudson, T.J., Steinhart A.H., Bull, S., Cohen, Z., Greenberg, G., Griffiths, A., McLeod, R., Silverberg, M., Williams, C.N., & Siminovitch, K.A. (1998). *Absence of linkage between inflammatory bowel disease and selected loci on chromosomes 3, 7, 12, and 16. Gastroenterology*, 115(5), 1062–1065. PMID: 9797358.
157. Rioux, J.D., Stone, V.A., Daly, M.J., Cargill, M., Green, T., Nguyen, H., Nutman, T., Zimmerman, P.A., Tucker, M.A., Hudson, T., Goldstein, A.M., Lander, E.S., & Lin, A.Y. (1998). *Familial eosinophilia maps to the cytokine gene cluster on human chromosomal region 5q31-q33. The American Journal of Human Genetics*, 63(4), 1086–1094. PMID: 9758611; PMCID: PMC1377485.
158. Lander, E.S., & Ellis, J.J. (1998). *Founding father. Nature*, 396(6706), 13–14. PMID: 9817195.

159. Holstege, F.C., Jennings, E.G., Wyrick, J.J., Lee, T.I., Hengartner, C.J., Green, M.R., Golub, T.R., Lander, E.S., & Young, R.A. (1998). *Dissecting the regulatory circuitry of a eukaryotic genome*. *Cell*, 95(5), 717–728. PMID: 9845373.
160. Lander, E.S. (1998). *Scientific commentary: the scientific foundations and medical and social prospects of the Human Genome Project*. *The Journal of Law, Medicine & Ethics*, 26(3), 184–188. PMID: 11066875.
161. Szpirer, C., Szpirer, J., Van Vooren, P., Tissir, F., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (1998). *Gene-based anchoring of the rat genetic linkage and cytogenetic maps: new regional localizations, orientation of the linkage groups, and insights into mammalian chromosome evolution*. *Mammalian Genome*, 9(9), 721–734. PMID: 9716657.
162. Brown, D.M., Matise, T.C., Koike, G., Simon, J.S., Winer, E.S., Zangen, S., McLaughlin, M.G., Shiozawa, M., Atkinson, O.S., Hudson, J.R., Chakravarti, A., Lander, E.S., & Jacob, H.J. (1998). *An integrated genetic linkage map of the laboratory rat*. *Mammalian Genome*, 9(7), 521–530. PMID: 9657848.
163. Batzoglou, S., Berger, B., Kleitman, D.J., Lander, E.S., & Pachter, L. (1998). *Recent developments in computational gene recognition*. *Documenta Mathematica*, 649–658.
164. Lander, E.S. (1999). *Array of hope*. *Nature Genetics*, 21(1 Suppl), 3–4. PMID: 9915492.
165. Tamayo, P., Slonim, D., Mesirov, J., Zhu, Q., Kitareewan, S., Dmitrovsky, E., Lander, E.S., & Golub, T.R. (1999). *Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation*. *Proceedings of the National Academy of Sciences USA*, 96(6), 2907–2912. PMID: 10077610; PMCID: PMC15868.
166. Pardes, H., Manton, K.G., Lander, E.S., Tolley, H.D., Ullian, A.D., & Palmer, H. (1999). *Effects of medical research on health care and the economy*. *Science*, 283(5398), 36–37. PMID: 9917262.
167. Lander E.S. (1999). *Genetics in the 21st century*. *Human Genome News* 10, 1–2.
168. Cargill, M., Altshuler, D., Ireland, J., Sklar, P., Ardlie, K., Patil, N., Lane, C.R., Lim, E.P., Kalyanaraman, N., Nemesh, J., Ziaugra, L., Friedland, L., Rolfe, A., Warrington, J., Lipshutz, R., Daley, G.Q., & Lander, E.S. (1999). *Characterization of single-nucleotide polymorphisms in coding regions of human genes*. *Nature Genetics*, 22(3), 231–238. PMID: 10391209.
169. Fambrough, D., McClure, K., Kazlauskas, A., & Lander, E.S. (1999). *Diverse signaling pathways activated by growth factor receptors induce broadly overlapping, rather than independent, sets of genes*. *Cell*, 97(6), 727–741. PMID: 10380925.
170. Steen, R.G., Kwitek-Black, A.E., Glenn, C., Gullings-Handley, J., Van Etten, W., Atkinson, O.S., Appel, D., Twigger, S., Muir, M., Mull, T., Granados, M., Kissebah, M., Russo, K., Crane, R., Popp, M., Peden, M., Matise, T., Brown, D.M., Lu, J., Kingsmore, S., Tonellato, P.J., Rozen, S., Slonim, D., Young, P., Knoblauch, M., Provoost, A., Ganten, D., Colman, S.D., Rothberg, J., Lander, E.S., & Jacob, H.J. (1999). *A high-density integrated genetic linkage and radiation hybrid map of the laboratory rat*. *Genome Research*, 9(6), AP1–AP8. PMID: 10400928.
171. Pachter, L., Batzoglou, S., Spitkovsky, V.I., Banks, E., Lander, E.S., Kleitman, D.J., & Berger, B. (1999). *A dictionary-based approach for gene annotation*. *Journal of Computational Biology*, 6(3–4), 419–430. PMID: 10582576.
172. Hacia, J.G., Fan, J.B., Ryder, O., Jin, L., Edgemon, K., Ghandour, G., Mayer, R.A., Sun, B., Hsie, L., Robbins, C.M., Brody, L.C., Wang, D., Lander, E.S., Lipshutz, R., Fodor, S.P.A., & Collins, F.S. (1999). *Determination of ancestral alleles for human single-nucleotide polymorphisms using high-density oligonucleotide arrays*. *Nature Genetics*, 22(2), 164–167. PMID: 10369258.
173. Galitski, T., Saldanha, A.J., Styles, C.A., Lander, E.S., & Fink, G.R. (1999). *Ploidy regulation of gene expression*. *Science*, 285(5425), 251–254. PMID: 10398601.
174. Van Etten, W.J., Steen, R.G., Nguyen, H., Castle, A.B., Slonim, D.K., Ge, B., Nusbaum, C., Schuler, G.D., Lander, E.S., & Hudson, T.J. (1999). *Radiation hybrid map of the mouse genome*. *Nature Genetics*, 22(4), 384–387. PMID: 10431245.
175. Pfeifer, D., Kist, R., Dewar, K., Devon, K., Lander, E.S., Birren, B., Komiszewski, L., Back, E., & Scherer, G. (1999). *Campomelic dysplasia translocation breakpoints are scattered over 1 Mb proximal to SOX9: evidence for an extended control region*. *The American Journal of Human Genetics*, 65(1), 111–124. PMID: 10364523; PMCID: PMC1378081.
176. Nusbaum, C., Slonim, D.K., Harris, K.L., Birren, B.W., Steen, R.G., Stein, L.D., Miller, J., Dietrich, W.F., Nahf, R., Wang, V., Merport, O., Castle, A.B., Husain, Z., Farino, G., Gray, D., Anderson, M.O., Devine, R., Horton, L.T., Ye, W., Wu, X., Kouyoumjian, V., Zemsteva, I.S., Wu, Y., Collymore, A.J., Courtney, D.F., Tam, J., Cadman, M., Haynes, A.R., Heuston, C., Marsland, T., Southwell, A.,

- Trickett, P., Strivens, M.A., Ross, M.T., Makalowski, W., Xu, Y., Boguski, M.S., Carter, N.P., Denny, P., Brown, S.D.M., Hudson, T.J., & Lander, E.S. (1999). A YAC-based physical map of the mouse genome. *Nature Genetics*, 22(4), 388–393. PMID: 10431246.
177. Sidow, A., Bulotsky, M.S., Kerrebrock, A.W., Birren, B.W., Altshuler, D., Jaenisch, R., Johnson, K.R., & Lander, E.S. (1999). A novel member of the *F-box/WD40* gene family, encoding dactylin, is disrupted in the mouse dactylaplasia mutant. *Nature Genetics*, 23(1), 104–107. PMID: 10471509.
178. Hastbacka, J., Kerrebrock, A., Mekkala, K., Clines, G., Lovett, M., Kaitila, I., de la Chapelle, A., & Lander, E.S. (1999). Identification of the Finnish founder mutation for diastrophic dysplasia (DTD). *European Journal of Human Genetics*, 7(6), 664–670. PMID: 10482955.
179. Klaff, L.S., Koike, G., Jiang, J., Wang, Y., Bieg, S., Pettersson, A., Lander, E.S., Jacob, H., & Lernmark, A. (1999). *BB* rat diabetes susceptibility and body weight regulation genes colocalize on chromosome 2. *Mammalian Genome*, 10(9), 883–887. PMID: 10441739.
180. Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, J.P., Coller, H., Loh, M.L., Downing, J.R., Caligiuri, M.A., Bloomfield, C.D., & Lander, E.S. (1999). Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science*, 286(5439), 531–537. PMID: 10521349.
181. Wyrick, J.J., Holstege, F.C., Jennings, E.G., Causton, H.C., Shore, D., Grunstein, M., Lander, E.S., & Young, R.A. (1999). Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast. *Nature*, 402(6760), 418–421. PMID: 10586882.
182. De Sanctis, G.T., Singer, J.B., Jiao, A., Yandava, C.N., Lee, Y.H., Haynes, T.C., Lander, E.S., Beier, D.R., & Drazen, J.M. (1999). Quantitative trait locus mapping of airway responsiveness to chromosomes 6 and 7 in inbred mice. *American Journal of Physiology*, 277(6 Pt 1), L1118–L1123. PMID: 10600881.
183. Batzoglou, S., Berger, B., Mesirov, J., & Lander, E.S. (1999). Sequencing a genome by walking with clone-end sequences: a mathematical analysis. *Genome Research*, 9(12), 1163–1174. PMID: 10613838.
184. Klockars, T., Holmberg, V., Savukoski, M., Lander, E.S., & Peltonen, L. (1999). Transcript identification on the *CLN5* region on chromosome 13q22. *Human Genetics*, 105(1–2), 51–56. PMID: 10480355.
185. Madhani, H.D., Galitski, T., Lander, E.S., & Fink, G.R. (1999). Effectors of a developmental mitogen-activated protein kinase cascade revealed by expression signatures of signaling mutants. *Proceedings of the National Academy of Sciences USA*, 96(22), 12530–12535. PMID: 10535956; PMCID: PMC22972.
186. Lander, E.S., & Weinberg, R.A. (2000). *Genomics: Journey to the center of biology*. *Science*, 287(5459), 1777–1782. PMID: 10755930.
187. Engert, J.C., Bérubé, P., Mercier, J., Doré, C., Lepage, P., Ge, B., Bouchard, J.P., Mathieu, J., Mançon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J., & Richter, A. (2000). ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF. *Nature Genetics*, 24(2), 120–125. PMID: 10655055.
188. Nadeau, J.H., Singer, J.B., Matin, A., & Lander, E.S. (2000). Analysing complex genetic traits with chromosome substitution strains. *Nature Genetics*, 24(3), 221–225. PMID: 10700173.
189. Lindblad-Toh, K., Winchester, E., Daly, M.J., Wang, D.G., Hirschhorn, J.N., Laviolette, J.P., Ardlie, K., Reich, D.E., Robinson, E., Sklar, P., Shah, N., Thomas, D., Fan, J.B., Gingeras, T., Warrington, J., Patil, N., Hudson, T.J., & Lander, E.S. (2000). Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. *Nature Genetics*, 24(4), 381–386. PMID: 10742102.
190. Coller, H.A., Grandori, C., Tamayo, P., Colbert, T., Lander, E.S., Eisenman, R.N., & Golub, T.R. (2000). Expression analysis with oligonucleotide microarrays reveals that MYC regulates genes involved in growth, cell cycle, signaling, and adhesion. *Proceedings of the National Academy of Sciences USA*, 97(7), 3260–3265. PMID: 10737792; PMCID: PMC16226.
191. Szpirer, C., Szpirer, J., Vanvooren, P., Tissir, F., Kela, J., Lallemand, F., Hoebee, B., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (2000). The rat genetic and cytogenetic maps. *Journal of Experimental Animal Science*, 41(1), 38–39.
192. Bulman, M.P., Kusumi, K., Frayling, T.M., McKeown, C., Garrett, C., Lander, E.S., Krumlauf, R., Hattersley, A.T., Ellard, S., & Turnpenny, P.D. (2000). Mutations in the human delta homologue, *DLL3*, cause axial skeletal defects in spondylocostal dysostosis. *Nature Genetics*, 24(4), 438–441. PMID: 10742114.

193. Pajukanta, P., Cargill, M., Viitanen, L., Nuotio, I., Kareinen, A., Perola, M., Terwilliger, J.D., Kempas, E., Daly, M.J., Lilja, H., Rioux, J.D., Brettin, T., Viikari, J.S.A., Rönnemaa, T., Laakso, M., Lander, E.S., & Peltonen, L. (2000). *Two loci on chromosomes 2 and X for premature coronary heart disease identified in early- and late-settlement populations of Finland. The American Journal of Human Genetics*, 67(6), 1481–1493. PMID: 11078477; PMCID: PMC1287925.
194. Batzoglou, S., Pachter, L., Mesirov, J.P., Berger, B., & Lander, E.S. (2000). *Human and mouse gene structure: comparative analysis and application to exon prediction. Genome Research*, 10(7), 950–958. PMID: 10899144; PMCID: PMC310911.
195. Cormier, R.T., Bilger, A., Lillich, A.J., Halberg, R.B., Hong, K.H., Gould, K.A., Borenstein, N., Lander, E.S., & Dove, W.F. (2000). *The Mom1AKR intestinal tumor resistance region consists of Pla2g2a and a locus distal to D4Mit64. Oncogene*, 19(28), 3182–3192. PMID: 10918573.
196. Clark, E.A., Golub, T.R., Lander, E.S., & Hynes, R.O. (2000). *Genomic analysis of metastasis reveals an essential role for RhoC. Nature*, 406(6795), 532–535. PMID: 10952316.
197. Rioux, J.D., Silverberg, M.S., Daly, M.J., Steinhart, A.H., McLeod, R.S., Griffiths, A.M., Green, T., Brettin, T.S., Stone, V., Bull, S.B., Bitton, A., Williams, C.N., Greenberg, G.R., Cohen, Z., Lander, E.S., Hudson, T.J., & Siminovitch, K.A. (2000). *Genome-wide search in Canadian families with inflammatory bowel disease reveals two novel susceptibility loci. The American Journal of Human Genetics*, 66(6), 1863–1870. PMID: 10777714; PMCID: PMC1378042.
198. Altshuler, D., Hirschhorn, J.N., Klannemark, M., Lindgren, C.M., Vohl, M.C., Nemesh, J., Lane, C.R., Schaffner, S.F., Bolk, S., Brewer, C., Tuomi, T., Gaudet, D., Hudson, T.J., Daly, M.J., Groop, L., & Lander, E.S. (2000). *The common PPAR γ polymorphism is associated with decreased risk of type 2 diabetes. Nature Genetics*, 26(1), 76–80. PMID: 10973253.
199. Lindblad-Toh, K., Tanenbaum, D.M., Daly, M.J., Winchester, E., Lui, W.O., Villapakkam, A., Stanton, S.E., Larsson, C., Hudson, T.J., Johnson, B.E., Lander, E.S., & Meyerson, M. (2000). *Loss-of-heterozygosity analysis of small-cell lung carcinomas using single-nucleotide polymorphism arrays. Nature Biotechnology*, 18(9), 1001–1005. PMID: 10973224.
200. Hirschhorn, J.N., Sklar, P., Lindblad-Toh, K., Lim, Y.M., Ruiz-Gutierrez, M., Bolk, S., Langhorst, B., Schaffner, S., Winchester, E., & Lander, E.S. (2000). *SBE-TAGS: an array-based method for efficient single-nucleotide polymorphism genotyping. Proceedings of the National Academy of Sciences USA*, 97(22), 12164–12169. PMID: 11035790; PMCID: PMC17312.
201. Lander, E.S. (2000). *Genomics: launching a revolution in medicine. The Journal of Law, Medicine & Ethics*, 28(4-Suppl), 3–14. PMID: 11244841.
202. Altshuler, D., Pollara, V.J., Cowles, C.R., Van Etten, W.J., Baldwin, J., Linton, L., & Lander, E.S. (2000). *An SNP map of the human genome generated by reduced representation shotgun sequencing. Nature*, 407(6803), 513–516. PMID: 11029002.
203. Lander, E.S., Linton, L.M., Birren, B., Nusbaum, C., Zody, M.C., Baldwin, J., Devon, K., Dewar, K., Doyle, M., FitzHugh, H., Funke, R., Gage, D., Harris, K., Heaford, A., Howland, J., Kann, L., Lehoczky, J., LeVine, R., McEwan, P., McKernan, K., Meldrim, J., Mesirov, J.P., Miranda, C., Morris, W., Naylor, J., Raymond, C., Rosetti, M., Santos, R., Sheridan, A., Sougnez, C., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Wyman, D., Rogers, J., Sulston, J., Ainscough, R., Beck, S., Bentley, D., Burton, J., Clee, C., Carter, N., Coulson, A., Deadman, R., Deloukas, P., Dunham, A., Dunham, I., Durbin, R., French, L., Grafham, D., Gregory, S., Hubbard, T., Humphray, S., Hunt, A., Jones, M., Lloyd, C., McMurray, A., Matthews, L., Mercer, S., Milne, S., Mullikin, J.C., Mungall, A., Plumb, R., Ross, M., Shownkeen, R., Sims, S., Waterston, R.H., Wilson, R.K., Hillier, L.W., McPherson, J.D., Marra, M.A., Mardis, E.R., Fulton, L.A., Chinwalla, A.T., Pepin, K.H., Gish, W.R., Chissoe, S.L., Wendl, M.C., Delehaanty, K.D., Miner, T.L., Delehaanty, A., Kramer, J.B., Cook, L.L., Fulton, R.S., Johnson, D.L., Minx, P.J., Clifton, S.W., Hawkins, T., Branscomb, E., Predki, P., Richardson, P., Wenning, S., Slezak, T., Doggett, N., Cheng, J.F., Olsen, A., Lucas, S., Elkin, C., Uberbacher, E., Frazier, M., Gibbs, R., Muzny, D.M., Scherer, S.E., Bouck, J.B., Sodergren, E.J., Worley, K.C., Rives, C.M., Gorrell, J.H., Metzker, M.L., Naylor, S.L., Kucherlapati, R.S., Nelson, D.L., Weinstock, G.M., Sakaki, Y., Fujiyama, A., Hattori, M., Yada, T., Toyoda, A., Itoh, T., Kawagoe, C., Watanabe, H., Totoki, Y., Taylor, T., Weissbach, J., Heilig, R., Saurin, W., Artiguenave, F., Brothier, P., Bruls, T., Pelletier, E., Robert, C., Wincker, P., Smith, D.R., Doucette-Stamm, L., Rubenfield, M., Weinstock, K., Lee, H.M., Dubois, J., Rosenthal, A., Platzer, M., Nyakatura, G., Taudien, S., Rump, A., Yang, H., Yu, J., Wang, J., Huang, G., Gu, J., Hood, L., Rowen, L., Madan, A., Qin, S., Davis, R.W., Federspiel, N.A., Abola, A.P., Proctor, M.J., Myers, R.M., Schmutz,

- J., Dickson, M., Grimwood, J., Cox, D.R., Olson, M.V., Kaul, R., Raymond, C., Shimizu, N., Kawasaki, K., Minoshima, S., Evans, G.A., Athanasiou, M., Schultz, R., Roe, B.A., Chen, F., Pan, H., Ramser, J., Lehrach, H., Reinhardt, R., McCombie, W.R., de la Bastide, M., Dedhia, N., Blocker, H., Hornischer, K., Nordsiek, G., Agarwala, R., Aravind, L., Bailey, J.A., Bateman, A., Batzoglu, S., Birney, E., Bork, P., Brown, D.G., Burge, C.B., Cerutti, L., Chen, H.C., Church, D., Clamp, M., Copley, R.R., Doerks, T., Eddy, S.R., Eichler, E.E., Furey, T.S., Galagan, J., Gilbert, J.G., Harmon, C., Hayashizaki, Y., Haussler, D., Hermjakob, H., Hokamp, K., Jang, W., Johnson, J.S., Jones, T.A., Kasif, S., Kasprzyk, A., Kennedy, S., Kent, W.J., Kitts, P., Koonin, E.V., Korf, I., Kulp, D., Lancet, D., Lowe, T.M., McLysaght, A., Mikkelsen, T., Moran, J.V., Mulder, N., Pollara, V.J., Ponting, C.P., Schuler, G., Schultz, J., Slater, G., Smit, A.F., Stupka, E., Thierry-Mieg, D., Thierry-Mieg, J., Wagner, L., Wallis, J., Wheeler, R., Williams, A., Wolf, Y.I., Wolfe, K.H., Yang, S.P., Yeh, R.F., Collins, F., Guyer, M.S., Peterson, J., Felsenfeld, A., Wetterstrand, K.A., Patrinos, A., Morgan, M.J., de Jong, P., Catanese, J.J., Osoegawa, K., Shizuya, H., Choi, S., Chen, Y.J., Szustakowski, J., & International Human Genome Sequencing Consortium. (2001). *Initial sequencing and analysis of the human genome*. *Nature*, 409(6822), 860–921. PMID: 11237011.
204. Lee, N., Daly, M.J., Delmonte, T., Lander, E.S., Xu, F., Hudson, T.J., Mitchell, G.A., Morin, C.C., Robinson, B.H., & Rioux, J.D. (2001). A *genome-wide linkage-disequilibrium scan localizes the Saguenay-Lac-Saint-Jean cytochrome oxidase deficiency to 2p16*. *The American Journal of Human Genetics*, 68(2), 397–409. PMID: 11156535; PMCID: PMC1235273.
205. Cavanaugh, J., & IBD International Genetics Consortium. (2001). *International collaboration provides convincing linkage replication in complex disease through analysis of a large pooled data set: Crohn disease and chromosome 16*. *The American Journal of Human Genetics*, 68(5), 1165–1171. PMID: 11309682; PMCID: PMC1226097.
206. Bartoloni, L., Blouin, J.L., Maiti, A.K., Sainsbury, A., Rossier, C., Gehrig, C., She, J.X., Marron, M.P., Lander, E.S., Meeks, M., Chung, E., Armengot, M., Jorissen, M., Scott, H.S., Delozier-Blanchet, C.D., Gardiner, R.M., & Antonarakis, S.E. (2001). *Axonemal beta heavy chain dynein DNAH9: cDNA sequence, genomic structure, and investigation of its role in primary ciliary dyskinesia*. *Genomics*, 72(1), 21–33. PMID: 11247663.
207. Sachidanandam, R., Weissman, D., Schmidt, S.C., Kakol, J.M., Stein, L.D., Marth, G., Sherry, S., Mullikin, J.C., Mortimore, B.J., Willey, D., Hunt, S.E., Cole, C.G., Coggill, P.C., Rice, C.M., Ning, Z., Rogers, J., Bentley, D.R., Kwok, P.Y., Mardis, E.R., Yeh, R.T., Schultz, B., Cook, L., Davenport, R., Dante, M., Fulton, L., Hillier, L., Waterston, R.H., McPherson, J.D., Gilman, B., Schaffner, S., Van Etten, W.J., Reich, D., Higgins, J., Blumenstiel, B., Baldwin, J., Stange-Thomann, N., Zody, M.C., Linton, L., Lander, E.S., Altshuler, D., & International SNP Map Working Group. (2001). *A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms*. *Nature*, 409(6822), 928–933. PMID: 11237013.
208. Hong, K.H., Bonventre, J.C., O'Leary, E., Bonventre, J.V., & Lander, E.S. (2001). *Deletion of cytosolic phospholipase A2 suppresses ApcMin-induced tumorigenesis*. *Proceedings of the National Academy of Sciences USA*, 98(7), 3935–3939. PMID: 11274413; PMCID: PMC31157.
209. Jackson-Grusby, L., Beard, C., Possemato, R., Tudor, M., Fambrough, D., Csankovszki, G., Dausman, J., Lee, P., Wilson, C., Lander, E.S., & Jaenisch, R. (2001). *Loss of genomic methylation causes p53-dependent apoptosis and epigenetic deregulation*. *Nature Genetics*, 27(1), 31–39. PMID: 11137995.
210. Causton, H.C., Ren, B., Koh, S.S., Harbison, C.T., Kanin, E., Jennings, E.G., Lee, T.I., True, H.L., Lander, E.S., & Young, R.A. (2001). *Remodeling of yeast genome expression in response to environmental changes*. *Molecular Biology of the Cell*, 12(2), 323–337. PMID: 11179418; PMCID: PMC30946.
211. Yeang, C.H., Ramaswamy, S., Tamayo, P., Mukherjee, S., Rifkin, R.M., Angelo, M., Reich, M., Lander, E.S., Mesirov, J., & Golub, T.R. (2001). *Molecular classification of multiple tumor types*. *Bioinformatics*, 17(Suppl 1), S316–S322. PMID: 11473023.
212. Laitinen, T., Daly, M.J., Rioux, J.D., Kauppi, P., Laprise, C., Petäys, T., Green, T., Cargill, M., Haahtela, T., Lander, E.S., Laitinen, L.A., Hudson, T.J., & Kere, J. (2001). *A susceptibility locus for asthma-related traits on chromosome 7 revealed by genome-wide scan in a founder population*. *Nature Genetics*, 28(1), 87–91. PMID: 11326283.
213. Reich, D.E., Cargill, M., Bolk, S., Ireland, J., Sabeti, P.C., Richter, D.J., Lavery, T., Kouyoumjian, R., Farhadian, S.F., Ward, R., & Lander, E.S. (2001). *Linkage disequilibrium in the human genome*. *Nature*, 411(6834), 199–204. PMID: 11346797.

214. Hirschhorn, J.N., Lindgren, C.M., Daly, M.J., Kirby, A., Schaffner, S.F., Burt, N.P., Altshuler, D., Parker, A., Rioux, J.D., Platko, J., Gaudet, D., Hudson, T.J., Groop, L.C., & Lander, E.S. (2001). *Genomewide linkage analysis of stature in multiple populations reveals several regions with evidence of linkage to adult height. The American Journal of Human Genetics*, 69(1), 106–116. PMID: 11410839; PMCID: PMC1226025.
215. Barclay, J., Balaguero, N., Mione, M., Ackerman, S.L., Letts, V.A., Brodbeck, J., Canti, C., Meir, A., Page, K.M., Kusumi, K., Perez-Reyes, E., Lander, E.S., Frankel, W.N., Gardiner, R.M., Dolphin, A.C., & Rees, M. (2001). *Ducky mouse phenotype of epilepsy and ataxia is associated with mutations in the Cacna2d2 gene and decreased calcium channel current in cerebellar Purkinje cells. The Journal of Neuroscience*, 21(16), 6095–6104. PMID: 11487633.
216. Sklar, P., Schwab, S.G., Williams, N.M., Daly, M., Schaffner, S., Maier, W., Albus, M., Trixler, M., Eichhammer, P., Lerer, B., Hallmayer, J., Norton, N., Williams, H., Zammit, S., Cardno, A.G., Jones, S., McCarthy, G., Milanova, V., Kirov, G., O'Donovan, M.C., Lander, E.S., Owen, M.J., & Wildenauer, D.B. (2001). *Association analysis of NOTCH4 loci in schizophrenia using family and population-based controls. Nature Genetics*, 28(2), 126–128. PMID: 11381257.
217. Inoue, K., Dewar, K., Katsanis, N., Reiter, L.T., Lander, E.S., Devon, K.L., Wyman, D.W., Lupski, J.R., & Birren, B. (2001). *The 1.4-Mb CMT1A duplication/HNPP deletion genomic region reveals unique genome architectural features and provides insights into the recent evolution of new genes. Genome Research*, 11(6), 1018–1033. PMID: 11381029; PMCID: PMC311111.
218. Ardlie, K., Liu-Cordero, S.N., Eberle, M.A., Daly, M.J., Barrett, J., Winchester, E., Lander, E.S., & Kruglyak, L. (2001). *Lower-than-expected linkage disequilibrium between tightly linked markers in humans suggests a role for gene conversion. The American Journal of Human Genetics*, 69(3), 582–589. PMID: 11473344; PMCID: PMC1235487.
219. Reich, D.E., & Lander, E.S. (2001). *On the allelic spectrum of human disease. TRENDS in Genetics*, 17(9), 502–510. PMID: 11525833.
220. Hudson, T.J., Church, D.M., Greenaway, S., Nguyen, H., Cook, A., Steen, R.G., Van Etten, W.J., Castle, A.B., Strivens, M.A., Trickett, P., Heuston, C., Davison, C., Southwell, A., Hardisty, R., Varela-Carver, A., Haynes, A.R., Rodriguez-Tome, P., Doi, H., Ko, M.S.H., Pontius, J., Schriml, L., Wagner, L., Maglott, D., Brown, S.D.M., Lander, E.S., Schuler, G., & Denny, P. (2001). *A radiation hybrid map of mouse genes. Nature Genetics*, 29(2), 201–205. PMID: 11586302.
221. Rioux, J.D., Daly, M.J., Silverberg, M.S., Lindblad-Toh, K., Steinhart, H., Cohen, Z., Delmonte, T., Kocher, K., Miller, K., Guschwan, S., Kulbokas, E.J., O'Leary, S., Winchester, E., Dewar, K., Green, T., Stone, V., Chow, C., Cohen, A., Langelier, D., Lapointe, G., Gaudet, D., Faith, J., Branco, N., Bull, S.B., McLeod, R.S., Griffiths, A.M., Bitton, A., Greenberg, G.R., Lander, E.S., Siminovitch, K.A., & Hudson, T.J. (2001). *Genetic variation in the 5q31 cytokine gene cluster confers susceptibility to Crohn disease. Nature Genetics*, 29(2), 223–228. PMID: 11586304.
222. Daly, M.J., Rioux, J.D., Schaffner, S.F., Hudson, T.J., & Lander, E.S. (2001). *High-resolution haplotype structure in the human genome. Nature Genetics*, 29(2), 229–232. PMID: 11586305.
223. Huang, Q., Liu, D., Majewski, P., Schulte, L.C., Korn, J.M., Young, R.A., Lander, E.S., & Hacohen, N. (2001). *The plasticity of dendritic cell responses to pathogens and their components. Science*, 294(5543), 870–875. PMID: 11679675.
224. Staunton, J.E., Slonim, D.K., Coller, H.A., Tamayo, P., Angelo, M.J., Park, J., Scherf, U., Lee, J.K., Reinhold, W.O., Weinstein, J.N., Mesirov, J.P., Lander, E.S., & Golub, T.R. (2001). *Chemosensitivity prediction by transcriptional profiling. Proceedings of the National Academy of Sciences USA*, 98(19), 10787–10792. PMID: 11553813; PMCID: PMC58553.
225. Sweeney, C., Fambrough, D., Huard, C., Diamonti, A.J., Lander, E.S., Cantley, L.C., & Carraway, K.L. (2001). *Growth factor-specific signaling pathway stimulation and gene expression mediated by ErbB receptors. Journal of Biological Chemistry*, 276(25), 22685–22698. PMID: 11297548.
226. Ramaswamy, S., Tamayo, P., Rifkin, R., Mukherjee, S., Yeang, C.H., Angelo, M., Ladd, C., Reich, M., Latulippe, E., Mesirov, J.P., Poggio, T., Gerald, W., Loda, M., Lander, E.S., & Golub, T.R. (2001). *Multiclass cancer diagnosis using tumor gene expression signatures. Proceedings of the National Academy of Sciences USA*, 98(26), 15149–15154. PMID: 11742071; PMCID: PMC64998.
227. Lindblad-Toh, K., Lander, E.S., McPherson, J.D., Waterston, R.H., Rodgers, J., & Birney, E. (2001). *Progress in sequencing the mouse genome. Genesis*, 31(4), 137–141. PMID: 11783003.
228. Bhattacharjee, A., Richards, W.G., Staunton, J., Li, C., Monti, S., Vasa, P., Ladd, C., Beheshti, J., Bueno, R., Gillette, M., Loda, M., Weber, G., Mark, E.J.,

- Lander, E.S., Wong, W., Johnson, B.E., Golub, T.R., Sugarbaker, D.J., & Meyerson, M. (2001). *Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses. Proceedings of the National Academy of Sciences USA*, 98(24), 13790–13795. PMID: 11707567; PMCID: PMC61120.
229. Shipp, M.A., Ross, K.N., Tamayo, P., Weng, A.P., Kutok, J.L., Aguiar, R.C., Gaasenbeek, M., Angelo, M., Reich, M., Pinkus, G.S., Ray, T.S., Koval, M.A., Last, K.W., Norton, A., Lister, T.A., Mesirov, J., Neuberg, D.S., Lander, E.S., Aster, J.C., & Golub, T.R. (2002). *Diffuse large B-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning. Nature Medicine*, 8(1), 68–74. PMID: 11786909.
230. Armstrong, S.A., Staunton, J.E., Silverman, L.B., Pieters, R., den Boer, M.L., Minden, M.D., Sallan, S.E., Lander, E.S., Golub, T.R., & Korsmeyer, S.J. (2002). *MLL translocations specify a distinct gene expression profile that distinguishes a unique leukemia. Nature Genetics*, 30(1), 41–47. PMID: 11731795.
231. Pomeroy, S.L., Tamayo, P., Gaasenbeek, M., Sturla, L.M., Angelo, M., McLaughlin, M.E., Kim, J.Y., Goumnerova, L.C., Black, P.M., Lau, C., Allen, J.C., Zagzag, D., Olson, J.M., Curran, T., Wetmore, C., Biegel, J.A., Poggio, T., Mukherjee, S., Rifkin, R., Califano, A., Stolovitzky, G., Louis, D.N., Mesirov, J.P., Lander, E.S., & Golub, T.R. (2002). *Prediction of central nervous system embryonal tumour outcome based on gene expression. Nature*, 415(6870), 436–442. PMID: 11807556.
232. Lindgren, C.M., Mahtani, M.M., Widen, E., McCarthy, M.I., Daly, M.J., Kirby, A., Reeve, M.P., Kruglyak, L., Parker, A., Meyer, J., Almgren, P., Lehto, M., Kanninen, T., Tuomi, T., Groop, L.C., & Lander, E.S. (2002). *Genomewide search for type 2 diabetes mellitus susceptibility loci in Finnish families: the Botnia study. The American Journal of Human Genetics*, 70(2), 509–516. PMID: 11791216; PMCID: PMC384923.
233. Batzoglou, S., Jaffe, D.B., Stanley, K., Butler, J., Gnerre, S., Mauceli, E., Berger, B., Mesirov, J.P., & Lander, E.S. (2002). *ARACHNE: a whole-genome shotgun assembler. Genome Research*, 12(1), 177–189. PMID: 11779843; PMCID: PMC155255.
234. Nau, G.J., Richmond, J.F., Schlesinger, A., Jennings, E.G., Lander, E.S., & Young, R.A. (2002). *Human macrophage activation programs induced by bacterial pathogens. Proceedings of the National Academy of Sciences USA*, 99(3), 1503–1508. PMID: 11805289; PMCID: PMC122220.
235. Waterston, R.H., Lander, E.S., & Sulston, J.E. (2002). *On the sequencing of the human genome. Proceedings of the National Academy of Sciences USA*, 99(6), 3712–3716. PMID: 11880605; PMCID: PMC122589.
236. Singh, D., Febbo, P.G., Ross, K., Jackson, D.G., Manola, J., Ladd, C., Tamayo, P., Renshaw, A.A., D'Amico, A.V., Richie, J.P., Lander, E.S., Loda, M., Kantoff, P.W., Golub, T.R., & Sellers, W.R. (2002). *Gene expression correlates of clinical prostate cancer behavior. Cancer Cell*, 1(2), 203–209. PMID: 12086878.
237. Galagan, J.E., Nusbaum, C., Roy, A., Endrizzi, M.G., Macdonald, P., FitzHugh, W., Calvo, S., Engels, R., Smirnov, S., Atnoor, D., Brown, A., Allen, N., Naylor, J., Stange-Thomann, N., DeArellano, K., Johnson, R., Linton, L., McEwan, P., McKernan, K., Talamas, J., Tirrell, A., Ye, W., Zimmer, A., Barber, R.D., Cann, I., Graham, D.E., Grahame, D., Guss, A.M., Hedderich, R., Ingram-Smith, C., Kuettner, H.C., Krzycki, J., Leigh, J.A., Li, W., Liu, J., Mukhopadhyay, B., Reeve, J.N., Smith, K., Springer, T., Umayam, L.A., White, O., White, R.H., de Macario, E.C., Ferry, J.G., Jarrell, K.F., Jing, H., Macario, A.J.L., Paulsen, I., Pritchett, M., Sowers, K.R., Swanson, R.V., Zinder, S.H., Lander, E.S., Metcalf, W.W., & Birren, B.W. (2002). *The genome of M. acetivorans reveals extensive metabolic and physiological diversity. Genome Research*, 12(4), 532–542. PMID: 11932238; PMCID: PMC187521.
238. Gabriel, S.B., Schaffner, S.F., Nguyen, H., Moore, J.M., Roy, J., Blumenstiel, B., Higgins, J., DeFelice, M., Lochner, A., Faggart, M., Liu-Cordero, S.N., Rotimi, C., Adeyemo, A., Cooper, R., Ward, R., Lander, E.S., Daly, M.J., & Altshuler, D. (2002). *The structure of haplotype blocks in the human genome. Science*, 296(5576), 2225–2229. PMID: 12029063.
239. Ferrando, A.A., Neuberg, D.S., Staunton, J., Loh, M.L., Huard, C., Raimondi, S.C., Behm, F.G., Pui, C.H., Downing, J.R., Gilliland, D.G., Lander, E.S., Golub, T.R., & Look, A.T. (2002). *Gene expression signatures define novel oncogenic pathways in T cell acute lymphoblastic leukemia. Cancer Cell*, 1(1), 75–87. PMID: 12086890.
240. MacMurray, A.J., Moralejo, D.H., Kwitek, A.E., Rutledge, E.A., Van Yserloo, B., Gohlke, P., Speros, S.J., Snyder, B., Schaefer, J., Bieg, S., Jiang, J., Ettinger, R.A., Fuller, J., Daniels, T.L., Pettersson, A., Orlebeke, K., Birren, B.W., Jacob, H.J., Lander, E.S., & Lernmark, A. (2002). *Lymphopenia in the BB rat model of type 1*

diabetes is due to a mutation in a novel immune-associated nucleotide (Ian)-related gene. Genome Research, 12(7), 1029–1039. PMID: 12097339; PMCID: PMC186618.

241. Reich, D.E., Schaffner, S.F., Daly, M.J., McVean, G., Mullikin, J.C., Higgins, J.M., Richter, D.J., Lander, E.S., & Altshuler, D. (2002). *Human genome sequence variation and the influence of gene history, mutation and recombination. Nature Genetics, 32(1), 135–142. PMID: 12161752.*

242. Humpherys, D., Eggan, K., Akutsu, H., Friedman, A., Hochedlinger, K., Yanagimachi, R., Lander, E.S., Golub, T.R., & Jaenisch, R. (2002). *Abnormal gene expression in cloned mice derived from embryonic stem cell and cumulus cell nuclei. Proceedings of the National Academy of Sciences USA, 99(20), 12889–12894. PMID: 12235366; PMCID: PMC130555.*

243. Sabeti, P.C., Reich, D.E., Higgins, J.M., Levine, H.Z., Richter, D.J., Schaffner, S.F., Gabriel, S.B., Platko, J.V., Patterson, N.J., McDonald, G.J., Ackerman, H.C., Campbell, S.J., Altshuler, D., Cooper, R., Kwiatkowski, D., Ward, R., & Lander, E.S. (2002). *Detecting recent positive selection in the human genome from haplotype structure. Nature, 419(6909), 832–837. PMID: 12397357.*

244. Sklar, P., Gabriel, S.B., McInnis, M.G., Bennett, P., Lim, Y., Tsan, G., Schaffner, S., Kirov, G., Jones, I., Owen, M., Craddock, N., DePaulo, J.R., & Lander, E.S. (2002). *Family-based association study of 76 candidate genes in bipolar disorder: BDNF is a potential risk locus. Brain-derived neurotrophic factor. Molecular Psychiatry, 7(6), 579–593. PMID: 12140781.*

245. Cowles, C.R., Hirschhorn, J.N., Altshuler, D., & Lander, E.S. (2002). *Detection of regulatory variation in mouse genes. Nature Genetics, 32(3), 432–437. PMID: 12410233.*

246. Mouse Genome Sequencing Consortium, Waterston, R.H., Lindblad-Toh, K., Birney, E., Rogers, J., Abril, J.F., Agarwal, P., Agarwala, R., Ainscough, R., Alexandersson, M., An, P., Antonarakis, S.E., Attwood, J., Baertsch, R., Bailey, J., Barlow, K., Beck, S., Berry, E., Birren, B., Bloom, T., Bork, P., Botcherby, M., Bray, N., Brent, M.R., Brown, D.G., Brown, S.D., Bult, C., Burton, J., Butler, J., Campbell, R.D., Carninci, P., Cawley, S., Chiaromonte, F., Chinwalla, A.T., Church, D.M., Clamp, M., Clee, C., Collins, F.S., Cook, L.L., Copley, R.R., Coulson, A., Couronne, O., Cuff, J., Curwen, V., Cutts, T., Daly, M., David, R., Davies, J., Delehaunty, K.D., Deri, J., Dermitzakis, E.T., Dewey, C., Dickens, N.J., Diekhans, M., Dodge, S., Dubchak, I., Dunn, D.M., Eddy, S.R., Elnitski, L., Emes, R.D., Eswara, P., Eyras, E., Felsenfeld, A., Fewell, G.A., Flicek, P., Foley, K., Frankel, W.N., Fulton, L.A., Fulton, R.S., Furey, T.S., Gage, D., Gibbs, R.A., Glusman, G., Gnerre, S., Goldman, N., Goodstadt, L., Graffham, D., Graves, T.A., Green, E.D., Gregory, S., Guigó, R., Guyer, M., Hardison, R.C., Haussler, D., Hayashizaki, Y., Hillier, L.W., Hinrichs, A., Hlavina, W., Holzer, T., Hsu, F., Hua, A., Hubbard, T., Hunt, A., Jackson, I., Jaffe, D.B., Johnson, L.S., Jones, M., Jones, T.A., Joy, A., Kamal, M., Karlsson, E.K., Karolchik, D., Kasprzyk, A., Kawai, J., Keibler, E., Kells, C., Kent, W.J., Kirby, A., Kolbe, D.L., Korf, I., Kucherlapati, R.S., Kulbokas, E.J., Kulp, D., Landers, T., Leger, J.P., Leonard, S., Letunic, I., Levine, R., Li, J., Li, M., Lloyd, C., Lucas, S., Ma, B., Maglott, D.R., Mardis, E.R., Matthews, L., Mauceli, E., Mayer, J.H., McCarthy, M., McCombie, W.R., McLaren, S., McLay, K., McPherson, J.D., Meldrum, J., Meredith, B., Mesirov, J.P., Miller, W., Miner, T.L., Mongin, E., Montgomery, K.T., Morgan, M., Mott, R., Mullikin, J.C., Muzny, D.M., Nash, W.E., Nelson, J.O., Nhan, M.N., Nicol, R., Ning, Z., Nusbaum, C., O'Connor, M.J., Okazaki, Y., Oliver, K., Overton-Larty, E., Pachter, L., Parra, G., Pepin, K.H., Peterson, J., Pevzner, P., Plumb, R., Pohl, C.S., Poliakov, A., Ponce, T.C., Ponting, C.P., Potter, S., Quail, M., Reymond, A., Roe, B.A., Roskin, K.M., Rubin, E.M., Rust, A.G., Santos, R., Sapojnikov, V., Schultz, B., Schultz, J., Schwartz, M.S., Schwartz, S., Scott, C., Seaman, S., Searle, S., Sharpe, T., Sheridan, A., Shownkeen, R., Sims, S., Singer, J.B., Slater, G., Smit, A., Smith, D.R., Spencer, B., Stabenau, A., Stange-Thomann, N., Sugnet, C., Suyama, M., Tesler, G., Thompson, J., Torrents, D., Trevaskis, E., Tromp, J., Ucla, C., Ureta-Vidal, A., Vinson, J.P., Von Niederhausern, A.C., Wade, C.M., Wall, M., Weber, R.J., Weiss, R.B., Wendt, M.C., West, A.P., Wetterstrand, K., Wheeler, R., Whelan, S., Wierzbowski, J., Willey, D., Williams, S., Wilson, R.K., Winter, E., Worley, K.C., Wyman, D., Yang, S., Yang, S.P., Zdobnov, E.M., Zody, M.C., & Lander, E.S. (2002). *Initial sequencing and comparative analysis of the mouse genome. Nature, 420(6915), 520–562. PMID: 12466850.*

247. Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusica, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J.,

- Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., Hayashizaki, Y., FANTOM Consortium, & RIKEN Genome Exploration Research Group Phase I & II Team. (2002). *Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs*. *Nature*, 420(6915), 563–573. PMID: 12466851.
248. Wade, C.M., Kulbokas, E.J., Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K., & Daly, M.J. (2002). *The mosaic structure of variation in the laboratory mouse genome*. *Nature*, 420(6915), 563–573. PMID: 12466852.
249. Williams, C.N., Kocher, K., Lander, E.S., Daly, M.J., & Rioux, J.D. (2002). *Using a genome-wide scan and meta-analysis to identify a novel IBD locus and confirm previously identified IBD loci*. *Inflammatory Bowel Diseases*, 8(6), 375–381. PMID: 12454612.
250. Chen, C.Z., Li, M., de Graaf, D., Monti, S., Götting, B., Sanchez, M.J., Lander, E.S., Golub, T.R., Green, A.R., & Lodish, H.F. (2002). *Identification of endoglin as a functional marker that defines long-term repopulating hematopoietic stem cells*. *Proceedings of the National Academy of Sciences USA*, 99(24), 15468–15473. PMID: 12438646; PMCID: PMC137740.
251. Ramaswamy, S., Ross, K.N., Lander, E.S., & Golub, T.R. (2003). *A molecular signature of metastasis in primary solid tumors*. *Nature Genetics*, 33(1), 49–54. PMID: 12469122.
252. Lohmueller, K.E., Pearce, C.L., Pike, M., Lander, E.S., & Hirschhorn, J.N. (2003). *Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease*. *Nature Genetics*, 33(2), 177–182. PMID: 12524541.
253. Jaffe, D.B., Butler, J., Gnerre, S., Mauceli, E., Lindblad-Toh, K., Mesirov, J.P., Zody, M.C., & Lander, E.S. (2003). *Whole-genome sequence assembly for mammalian genomes: Arachne 2*. *Genome Research*, 13(1), 91–96. PMID: 12529310; PMCID: PMC430950.
254. Mootha, V.K., Lepage, P., Miller, K., Bunkinborg, J., Reich, M., Hjerrild, M., Delmonte, T., Villeneuve, A., Sladek, R., Xu, F., Mitchell, G.A., Morin, C., Mann, M., Hudson, T.J., Robinson, B., Rioux, J.D., & Lander, E.S. (2003). *Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics*. *Proceedings of the National Academy of Sciences USA*, 100(2), 605–610. PMID: 12529507; PMCID: PMC141043.
255. Waterston, R.H., Lander, E.S., & Sulston, J.E. (2003). *More on the sequencing of the human genome*. *Proceedings of the National Academy of Sciences USA*, 100(6), 3022–3024. PMID: 12631699; PMCID: PMC152236.
256. Xu, Y., Stange-Thomann, N., Weber, G., Bo, R., Dodge, S., David, R.G., Foley, K., Beheshti, J., Harris, N.L., Birren, B.W., Lander, E.S., & Meyerson, M. (2003). *Pathogen discovery from human tissue by sequence-based computational subtraction*. *Genomics*, 81(3), 329–335. PMID: 12659816.
257. Kamvysselis, M., Patterson, N., Birren, B., Berger, B., & Lander, E.S. (2003). *Whole-genome comparative annotation and regulatory motif discovery in multiple yeast species*. In *Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology* (pp. 157–166).
258. Chiang, D.Y., Moses, A.M., Kellis, M., Lander, E.S., & Eisen, M.B. (2003). *Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts*. *Genome Biology*, 4(7), R43. PMID: 12844359; PMCID: PMC193630.
259. Galagan, J.E., Calvo, S.E., Borkovich, K.A., Selker, E.U., Read, N.D., Jaffe, D., FitzHugh, W., Ma, L.J., Smirnov, S., Purcell, S., Rehman, B., Elkins, T., Engels, R., Wang, S., Nielsen, C.B., Butler, J., Endrizzi, M., Qui, D., Ianakiev, P., Bell-Pedersen, D., Nelson, M.A., Werner-Washburne, M., Selitrennikoff, C.P., Kinsey, J.A., Braun, E.L., Zelter, A., Schulte, U., Kothe, G.O., Jedd, G., Mewes, W., Staben, C., Marcotte, E., Greenberg, D., Roy, A., Foley, K., Naylor, J., Stange-Thomann, N., Barrett, R., Gnerre, S., Kamal, M., Kamvysselis, M., Mauceli, E., Bielke, C., Rudd,

- S., Frishman, D., Krystofova, S., Rasmussen, C., Metzenberg, R.L., Perkins, D.D., Kroken, S., Cogoni, C., Macino, G., Catcheside, D., Li, W., Pratt, R.J., Osmani, S.A., DeSouza, C.P., Glass, L., Orbach, M.J., Berglund, J.A., Voelker, R., Yarden, O., Plamann, M., Seiler, S., Dunlap, J., Radford, A., Aramayo, R., Natvig, D.O., Alex, L.A., Mannhaupt, G., Ebbola, D.J., Freitag, M., Paulsen, I., Sachs, M.S., Lander, E.S., Nusbaum, C., & Birren, B.W. (2003). *The genome sequence of the filamentous fungus Neurospora crassa*. *Nature*, 422(6934), 859–868. PMID: 12712197.
260. Kellis, M., Patterson, N., Endrizzi, M., Birren, B.W., & Lander, E.S. (2003). *Sequencing and comparison of yeast species to identify genes and regulatory elements*. *Nature*, 423(6937), 241–254. PMID: 12748633.
261. Giallourakis, C., Stoll, M., Miller, K., Hampe, J., Lander, E.S., Daly, M.J., Schreiber, S., & Rioux, J.D. (2003). *IBD5 is a general risk factor for inflammatory bowel disease: replication of association with Crohn disease and identification of a novel association with ulcerative colitis*. *The American Journal of Human Genetics*, 73(1), 205–211. PMID: 12776251; PMCID: PMC1180582.
262. Giallourakis, C., Stoll, M., Miller, K., Hampe, J., Lander, E.S., Daly, M.J., Schreiber, S., & Rioux, J.D. (2003). *PGC-1 α -responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes*. *Nature Genetics*, 34(3), 267–273. PMID: 12808457.
263. Lowe, C.J., Wu, M., Salic, A., Evans, L., Lander, E.S., Stange-Thomann, N., Gruber, C.E., Gerhart, J., & Kirschner, M. (2003). *Anteroposterior patterning in hemichordates and the origins of the chordate nervous system*. *Cell*, 113(7), 853–865. PMID: 12837244.
264. Rifkin, R., Mukherjee, S., Tamayo, P., Ramaswamy, S., Yeang, C.H., Angelo, M., Reich, M., Poggio, T., Lander, E.S., Golub, T.R., & Mesirov, J.P. (2003). *An analytical method for multiclass molecular cancer classification*. *Siam Review*, 45(4), 706–723.
265. Walsh, E.C., Mather, K.A., Schaffner, S.F., Farwell, L., Daly, M.J., Patterson, N., Cullen, M., Carrington, M., Bugawan, T.L., Erlich, H., Campbell, J., Barrett, J., Miller, K., Thomson, G., Lander, E.S., & Rioux, J.D. (2003). *An integrated haplotype map of the human major histocompatibility complex*. *The American Journal of Human Genetics*, 73(3), 580–590. PMID: 12920676; PMCID: PMC1180682.
266. Moses, A.M., Chiang, D.Y., Kellis, M., Lander, E.S., & Eisen, M.B. (2003). *Position specific variation in the rate of evolution in transcription factor binding sites*. *BMC Evolutionary Biology*, 3, 19. PMID: 12946282; PMCID: PMC212491.
267. Moralejo, D.H., Park, H.A., Speros, S.J., MacMurray, A.J., Kwitek, A.E., Jacob, H.J., Lander, E.S., & Lernmark, A. (2003). *Genetic dissection of lymphopenia from autoimmunity by introgression of mutated *Ian5* gene onto the F344 rat*. *Journal of Autoimmunity*, 21(4), 315–324. PMID: 14624755.
268. Mootha, V.K., Bunkenborg, J., Olsen, J.V., Hjerrild, M., Wisniewski, J.R., Stahl, E., Bolouri, M.S., Ray, H.N., Sihag, S., Kamal, M., Patterson, N., Lander, E.S., & Mann, M. (2003). *Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria*. *Cell*, 115(5), 629–640. PMID: 14651853.
269. International HapMap Consortium. (2003). *The International HapMap Project*. *Nature* 426, 789–796.
270. Sklar, P., Pato, M.T., Kirby, A., Petryshen, T.L., Medeiros, H., Carvalho, C., Macedo, A., Dourado, A., Coelho, I., Valente, J., Soares, M.J., Ferreira, C.P., Lei, M., Verner, A., Hudson, T.J., Morley, C.P., Kennedy, J.L., Azevedo, M.H., Lander, E.S., Daly, M.J., & Pato, C.N. (2004). *Genome-wide scan in Portuguese Island families identifies 5q31–5q35 as a susceptibility locus for schizophrenia and psychosis*. *Molecular Psychiatry*, 9(2), 213–218. PMID: 14699422.
271. Kellis, M., Birren, B.W., & Lander, E.S. (2004). *Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae**. *Nature*, 428(6983), 617–624. PMID: 15004568.
272. Singer, J.B., Hill, A.E., Burrage, L.C., Olszens, K.R., Song, J., Justice, M., O'Brien, W.E., Conti, D.V., Witte, J.S., Lander, E.S., & Nadeau, J.H. (2004). *Genetic dissection of complex traits with chromosome substitution strains of mice*. *Science*, 304(5669), 445–448. PMID: 15031436.
273. Freedman, M.L., Reich, D., Penney, K.L., McDonald, G.J., Mignault, A.A., Patterson, N., Gabriel, S.B., Topol, E.J., Smoller, J.W., Pato, C.N., Pato, M.T., Petryshen, T.L., Kolonel, L.N., Lander, E.S., Sklar, P., Henderson, B., Hirschhorn, J.N., & Altshuler, D. (2004). *Assessing the impact of population stratification on genetic association studies*. *Nature Genetics*, 36(4), 388–393. PMID: 15052270.
274. Mootha, V.K., Handschin, C., Arlow, D., Xie, X., St. Pierre, J., Sihag, S., Yang, W., Altshuler, D., Puigserver, P., Patterson, N., Willy, P.J., Schulman, I.G., Heyman, R.A., Lander, E.S., & Spiegelman, B.M. (2004). *Erralpha and Gabpa/b specify PGC-1 α -dependent oxidative phosphorylation gene expression that is altered*

in diabetic muscle. *Proceedings of the National Academy of Sciences USA*, 101(17), 6570-6575. PMID: 15100410; PMCID: PMC404086.

275. Tantisira, K.G., Lake, S., Silverman, E.S., Palmer, L.J., Lazarus, R., Silverman, E.K., Liggett, S.B., Gelfand, E.W., Rosenwasser, L.J., Richter, B., Israel, E., Wechsler, M., Gabriel, S., Altshuler, D., Lander, E.S., Drazen, J., & Weiss, S.T. (2004). *Corticosteroid pharmacogenetics: association of sequence variants in CRHR1 with improved lung function in asthmatics treated with inhaled corticosteroids. Human Molecular Genetics*, 13(13), 1353-1359. PMID: 15128701.

276. Sawcer, S.J., Maranian, M., Singlehurst, S., Yeo, T., Compston, A., Daly, M.J., De Jager, P.L., Gabriel, S., Hafler, D.A., Ivinson, A.J., Lander, E.S., Rioux, J.D., Walsh, E., Gregory, S.G., Schmidt, S., Pericak-Vance, M.A., Barcellos, L., Hauser, S.L., Oksenberg, J.R., Kenealy, S.J., & Haines, J.L. (2004). *Enhancing linkage analysis of complex disorders: an evaluation of high-density genotyping. Human Molecular Genetics*, 13(17), 1943-1949. PMID: 15238506.

277. Kellis, M., Patterson, N., Birren, B.W., Berger, B., & Lander, E.S. (2004). *Methods in comparative genomics: genome correspondence, gene identification and regulatory motif discovery. Journal of Computational Biology*, 11(2-3), 319-355. PMID: 15285895.

278. Krewson, T.D., Supelak, P.J., Hill, A.E., Singer, J.B., Lander, E.S., Nadeau, J.H., & Palmert, M.R. (2004). *Chromosomes 6 and 13 harbor genes that regulate pubertal timing in mouse chromosome substitution strains. Endocrinology*, 145(10), 4447-4451. PMID: 15284200.

279. Michalkiewicz, M., Michalkiewicz, T., Ettinger, R.A., Rutledge, E.A., Fuller, J.M., Moralejo, D.H., Van Yserloo, B., MacMurray, A.J., Kwitek, A.E., Jacob, H.J., Lander, E.S., & Lernmark, A. (2004). *Transgenic rescue demonstrates involvement of the *Ian5* gene in T cell development in the rat. Physiological Genomics*, 19(2), 228-232. PMID: 15328390.

280. Harbison, C.T., Gordon, D.B., Lee, T.I., Rinaldi, N.J., Macisaac, K.D., Danford, T.W., Hannett, N.M., Tagne, J.B., Reynolds, D.B., Yoo, J., Jennings, E.G., Zeitlinger, J., Pokholok, D.K., Kellis, M., Rolfe, P.A., Takusagawa, K.T., Lander, E.S., Gifford, D.K., Fraenkel, E., & Young, R.A. (2004). *Transcriptional regulatory code of a eukaryotic genome. Nature*, 431(7004), 99-104. PMID: 15343339; PMCID: PMC3006441.

281. Rioux, J.D., Karinen, H., Kocher, K., McMahon, S.G., Kärkkäinen, P., Janatuinen, E., Heikkinen, M., Julkunen, R., Pihlajamäki, J., Naukkarinen, A., Kosma, V.M., Daly, M.J., Lander, E.S., & Laakso, M. (2004). *Genomewide search and association studies in a Finnish celiac disease population: Identification of a novel locus and replication of the HLA and CTLA4 loci. American Journal of Medical Genetics Part A*, 130(4), 345-350. PMID: 15386476.

282. International Human Genome Sequencing Consortium. (2004). *Finishing the euchromatic sequence of the human genome. Nature*, 431(7011), 931-945. PMID: 15496913.

283. Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biémont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigó, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B.W., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quétier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J., & Roest Crolius, H. (2004). *Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature*, 431(7011), 946-957. PMID: 15496914.

284. Poirier, C., Qin, Y., Adams, C.P., Anaya, Y., Singer, J.B., Hill, A.E., Lander, E.S., Nadeau, J.H., & Bishop, C.E. (2004). *A complex interaction of imprinted and maternal-effect genes modifies sex determination in Odd Sex (Ods) mice. Genetics*, 168(3), 1557-1562. PMID: 15579706; PMCID: PMC1448764.

285. Singer, J.B., Hill, A.E., Nadeau, J.H., & Lander, E.S. (2005). *Mapping quantitative trait loci for anxiety in chromosome substitution strains of mice. Genetics*, 169(2), 855-862. PMID: 15371360; PMCID: PMC1449086.

286. Bernstein, B.E., Kamal, M., Lindblad-Toh, K., Bekiranov, S., Bailey, D.K., Huebert, D.J., McMahon, S., Karlsson, E.K., Kulbokas, E.J., Gingeras, T.R., Schreiber, S.L., & Lander, E.S. (2005). *Genomic maps and comparative analysis of histone modifications in human and mouse. Cell*, 120(2), 169-181. PMID: 15680324.

287. International HapMap Consortium. (2005). *A haplotype map of the human genome. Nature*, 437(7063), 1299-320. PMCID: PMC1880871.

288. Coordinating Committee of the Global HIV/AIDS Vaccine Enterprise. (2005). The Global HIV/AIDS Vaccine Enterprise: Scientific Strategic Plan. *PLoS Medicine*, 2(2), e25. PMID: 15740411; PMCID:PMC544553.
289. Ackerman, K.G., Huang, H., Grasemann, H., Puma, C., Singer, J.B., Hill, A.E., Lander, E.S., Nadeau, J.H., Churchill, G.A., Drazen, J.M., & Beier, D.R. (2005). *Interacting genetic loci cause airway hyperresponsiveness. Physiological Genomics*, 21(1), 105–111. PMID: 15657107.
290. Xie, X., Lu, J., Kulbokas, E.J., Golub, T.R., Mootha, V., Lindblad-Toh, K., Lander, E.S., & Kellis, M. (2005). *Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammals. Nature*, 434(7031), 338–345. PMID: 15735639; PMCID: PMC2923337.
291. Miretti, M.M., Walsh, E.C., Ke, X., Delgado, M., Griffiths, M., Hunt, S., Morrison, J., Whittaker, P., Lander, E.S., Cardon, L.R., Bentley, D.R., Rioux, J.D., Beck, S., & Deloukas, P. (2005). *A high-resolution linkage-disequilibrium map of the human major histocompatibility complex and first generation of tag single-nucleotide polymorphisms. The American Journal of Human Genetics*, 76(4), 634–646. PMID: 15747258; PMCID: PMC1199300.
292. Margulies, E.H., Vinson, J.P., NISC Comparative Sequencing Program, Miller, W., Jaffe, D.B., Lindblad-Toh, K., Chang, J.L., Green, E.D., Lander, E.S., Mullikin, J.C., & Clamp, M. (2005). *An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. Proceedings of the National Academy of Sciences USA*, 102(13), 4795–4800. PMID: 15778292; PMCID: PMC555705.
293. Vinson, J.P., Jaffe, D.B., O'Neill, K., Karlsson, E.K., Stange-Thomann, N., Anderson, S., Mesirov, J.P., Satoh, N., Satou, Y., Nusbaum, C., Birren, B.W., Galagan, J.E., & Lander, E.S. (2005). *Assembly of polymorphic genomes: algorithms and application to Ciona savignyi. Genome Research*, 15(8), 1127–1135. PMID: 16077012; PMCID: PMC1182225.
294. Sawcer, S., Ban, M., Maranian, M., Yeo, T.W., Compston, A., Kirby, A., Daly, M.J., De Jager, P.L., Walsh, E., Lander, E.S., Rioux, J.D., Hafler, D.A., Ivinson, A., Rimmler, J., Gregory, S.G., Schmidt, S., Pericak-Vance, M.A., Akesson, E., Hillert, J., Datta, P., Oturai, A., Ryder, L.P., Harbo, H.F., Spurkland, A., Myhr, K.M., Laaksonen, M., Booth, D., Heard, R., Stewart, G., Lincoln, R., Barcellos, L.F., Hauser, S.L., Oksenberg, J.R., Kenealy, S.J., Haines, J.L., International Multiple Sclerosis Consortium. (2005). *A high-density screen for linkage in multiple sclerosis. The American Journal of Human Genetics*, 77(3), 454–467. PMID: 16080120; PMCID: PMC1226210.
295. Chimpanzee Sequencing and Analysis Consortium. (2005). *Initial sequence of the chimpanzee genome and comparison with the human genome. Nature*, 437(7055), 69–87. PMID: 16136131.
296. Nusbaum, C., Zody, M.C., Borowsky, M.L., Kamal, M., Kodira, C.D., Taylor, T.D., Whittaker, C.A., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Yang, X., Abouelleil, A., Allen, N.R., Anderson, S., Bloom, T., Bugalter, B., Butler, J., Cook, A., DeCaprio, D., Engels, R., Garber, M., Gnirke, A., Hafez, N., Hall, J.L., Norman, C.H., Itoh, T., Jaffe, D.B., Kuroki, Y., Lehoczy, J., Lui, A., Macdonald, P., Mauceli, E., Mikkelsen, T.S., Naylor, J.W., Nicol, R., Nguyen, C., Noguchi, H., O'Leary, S.B., O'Neill, K., Pizani, B., Smith, C.L., Talamas, J.A., Topham, K., Totoki, Y., Toyoda, A., Wain, H.M., Young, S.K., Zeng, Q., Zimmer, A.R., Fujiyama, A., Hattori, M., Birren, B.W., Sakaki, Y., & Lander, E.S. (2005). *DNA sequence and analysis of human chromosome 18. Nature*, 437(7058), 551–555. PMID: 16177791.
297. Subramanian, A., Tamayo, P., Mootha, V.K., Mukherjee, S., Ebert, B.L., Gillette, M.A., Paulovich, A., Pomeroy, S.L., Golub, T.R., Lander, E.S., & Mesirov, J.P. (2005). *Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proceedings of the National Academy of Sciences USA*, 102(43), 15545–15550. PMID: 16199517; PMCID: PMC1239896.
298. Meissner, A., Gnirke, A., Bell, G.W., Ramsahoye, B., Lander, E.S., & Jaenisch, R. (2005). *Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis. Nucleic Acids Research*, 33(18), 5868–5877. PMID: 16224102; PMCID: PMC1258174.
299. Sabeti, P.C., Walsh, E., Schaffner, S.F., Varilly, P., Fry, B., Cullen, M., Mikkelsen, T.S., Roy, J., Patterson, N., Cooper, R., Altshuler, D., & Lander, E.S. (2005). *The case for selection of CCR5-delta32. PloS Biology*, 3(11): e378. PMID: 16248677; PMCID: PMC1275522.
300. Lindblad-Toh, K., Wade, C.M., Mikkelsen, T.S., Karlsson, E.K., Jaffe, D.B., Kamal, M., Clamp, M., Chang, J.L., Kulbokas, E.J., Zody, M.C., Mauceli, E., Xie, X., Breen, M., Wayne, R.K., Ostrander, E.A., Ponting, C.P., Galibert, F., Smith, D.R., DeJong, P.J., Kirkness, E., Alvarez, P., Biagi, T., Brockman, W., Butler, J., Chin, C.W., Cook, A., Cuff, J., Daly, M.J., DeCaprio, D., Gnerre, S., Grabherr, M.,

- Kellis, M., Kleber, M., Bardeleben, C., Goodstadt, L., Heger, A., Hitte, C., Kim, L., Koepfli, K.P., Parker, H.G., Pollinger, J.P., Searle, S.M., Sutter, N.B., Thomas, R., Webber, C., Baldwin, J., Abebe, A., Abouelleil, A., Aftuck, L., Ait-Zahra, M., Aldredge, T., Allen, N., An, P., Anderson, S., Antoine, C., Arachchi, H., Aslam, A., Ayotte, L., Bachantsang, P., Barry, A., Bayul, T., Benamara, M., Berlin, A., Bessette, D., Blitshteyn, B., Bloom, T., Blye, J., Boguslavskiy, L., Bonnet, C., Boukhgalter, B., Brown, A., Cahill, P., Calixte, N., Camarata, J., Cheshatsang, Y., Chu, J., Citroen, M., Collymore, A., Cooke, P., Dawoe, T., Daza, R., Decktor, K., DeGray, S., Dhargay, N., Dooley, K., Dooley, K., Dorje, P., Dorjee, K., Dorris, L., Duffey, N., Dupes, A., Egbiremolen, O., Elong, R., Falk, J., Farina, A., Faro, S., Ferguson, D., Ferreira, P., Fisher, S., FitzGerald, M., Foley, K., Foley, C., Franke, A., Friedrich, D., Gage, D., Garber, M., Gearin, G., Giannoukos, G., Goode, T., Goyette, A., Graham, J., Grandbois, E., Gyaltzen, K., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Healy, C., Hegarty, R., Honan, T., Horn, A., Houde, N., Hughes, L., Hunnicutt, L., Husby, M., Jester, B., Jones, C., Kamat, A., Kanga, B., Kells, C., Khazanovich, D., Kieu, A.C., Kisner, P., Kumar, M., Lance, K., Landers, T., Lara, M., Lee, W., Leger, J.P., Lennon, N., Leuper, L., LeVine, S., Liu, J., Liu, X., Lokyitsang, Y., Lokyitsang, T., Lui, A., Macdonald, J., Major, J., Marabella, R., Maru, K., Matthews, C., McDonough, S., Mehta, T., Meldrim, J., Melnikov, A., Meneus, L., Mihalev, A., Mihova, T., Miller, K., Mittelman, R., Mlenga, V., Mulrain, L., Munson, G., Navidi, A., Naylor, J., Nguyen, T., Nguyen, N., Nguyen, C., Nguyen, T., Nicol, R., Norbu, N., Norbu, C., Novod, N., Nyima, T., Olandt, P., O'Neill, B., O'Neill, K., Osman, S., Oyono, L., Patti, C., Perrin, D., Phunkhang, P., Pierre, F., Priest, M., Rachupka, A., Raghuraman, S., Rameau, R., Ray, V., Raymond, C., Rege, F., Rise, C., Rogers, J., Rogov, P., Sahalie, J., Settipalli, S., Sharpe, T., Shea, T., Sheehan, M., Sherpa, N., Shi, J., Shih, D., Sloan, J., Smith, C., Sparrow, T., Stalker, J., Stange-Thomann, N., Stavropoulos, S., Stone, C., Stone, S., Sykes, S., Tchuinga, P., Tenzing, P., Tesfaye, S., Thoulutsang, D., Thoulutsang, Y., Topham, K., Topping, I., Tsamla, T., Vassiliev, H., Venkataraman, V., Vo, A., Wangchuk, T., Wangdi, T., Weiland, M., Wilkinson, J., Wilson, A., Yadav, S., Yang, S., Yang, X., Young, G., Yu, Q., Zainoun, J., Zembek, L., Zimmer, A., & Lander, E.S. (2005). *Genome sequence, comparative analysis and haplotype structure of the domestic dog*. *Nature*, 438(7069), 803–819. PMID: 16341006.
301. Nusbaum, C., Mikkelsen, T.S., Zody, M.C., Asakawa, S., Taudien, S., Garber, M., Kodira, C.D., Schueler, M.G., Shimizu, A., Whittaker, C.A., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Yang, X., Allen, N.R., Anderson, S., Asakawa, T., Blechschmidt, K., Bloom, T., Borowsky, M.L., Butler, J., Cook, A., Corum, B., DeArellano, K., DeCaprio, D., Dooley, K.T., Dorris, L., Engels, R., Glöckner, G., Hafez, N., Hagopian, D.S., Hall, J.L., Ishikawa, S.K., Jaffe, D.B., Kamat, A., Kudoh, J., Lehmann, R., Lokitsang, T., Macdonald, P., Major, J.E., Matthews, C.D., Mauceli, E., Menzel, U., Mihalev, A.H., Minoshima, S., Murayama, Y., Naylor, J.W., Nicol, R., Nguyen, C., O'Leary, S.B., O'Neill, K., Parker, S.C., Polley, A., Raymond, C.K., Reichwald, K., Rodriguez, J., Sasaki, T., Schilhabel, M., Siddiqui, R., Smith, C.L., Sneddon, T.P., Talamas, J.A., Tenzin, P., Topham, K., Venkataraman, V., Wen, G., Yamazaki, S., Young, S.K., Zeng, Q., Zimmer, A.R., Rosenthal, A., Birren, B.W., Platzer, M., Shimizu, N., & Lander, E.S. (2006). *DNA sequence and analysis of human chromosome 8*. *Nature*, 439(7074), 331–335. PMID: 16421571.
302. Walsh, E.C., Sabeti, P., Hutcheson, H.B., Fry, B., Schaffner, S.F., de Bakker, P.I., Varilly, P., Palma, A.A., Roy, J., Cooper, R., Winkler, C., Zeng, Y., de The, G., Lander, E.S., O'Brien, S., & Altshuler, D. (2006). *Searching for signals of evolutionary selection in 168 genes related to immune function*. *Human Genetics*, 119(1–2), 92–102. PMID: 16362345.
303. Hill, A.E., Lander, E.S., & Nadeau, J.H. (2006). *Chromosome substitution strains: a new way to study genetically complex traits*. *Methods in Molecular Medicine*, 128, 153–172. PMID: 17071995.
304. Taylor, T.D., Noguchi, H., Totoki, Y., Toyoda, A., Kuroki, Y., Dewar, K., Lloyd, C., Itoh, T., Takeda, T., Kim, D.W., She, X., Barlow, K.F., Bloom, T., Bruford, E., Chang, J.L., Cuomo, C.A., Eichler, E., FitzGerald, M.G., Jaffe, D.B., LaButti, K., Nicol, R., Park, H.S., Seaman, C., Sougnez, C., Yang, X., Zimmer, A.R., Zody, M.C., Birren, B.W., Nusbaum, C., Fujiyama, A., Hattori, M., Rogers, J., Lander, E.S., & Sasaki, Y. (2006). *Human chromosome 11 DNA sequence and analysis including novel gene identification*. *Nature*, 440(7083), 497–500. PMID: 16477033; PMCID: PMC1413850.
305. Kamal, M., Xie, X., & Lander, E.S. (2006). *A large family of ancient repeat elements in the human genome is under strong selection*. *Proceedings of the National Academy of Sciences USA*, 103(8), 2740–2745.
306. Moffat, J., Grueneberg, D.A., Yang, X., Kim, S.Y., Kloepper, A.M., Hinkle, G., Piquani, B., Eisenhaure, T.M., Luo, B., Grenier, J.K., Carpenter, A.E., Foo, S.Y.,

- Stewart, S.A., Stockwell, B.R., Hacohen, N., Hahn, W.C., Lander, E.S., Sabatini, D.M., & Root, D.E. (2006). A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen. *Cell*, 124(6), 1283–1298. PMID: 16564017.
307. Zody, M.C., Garber, M., Sharpe, T., Young, S.K., Rowen, L., O'Neill, K., Whitaker, C.A., Kamal, M., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Kodira, C.D., Madan, A., Qin, S., Yang, X., Abbasi, N., Abouelleil, A., Arachchi, H.M., Baradarani, L., Birditt, B., Bloom, S., Bloom, T., Borowsky, M.L., Burke, J., Butler, J., Cook, A., DeArellano, K., DeCaprio, D., Dorris, L., Dors, M., Eichler, E.E., Engels, R., Fahey, J., Fleetwood, P., Friedman, C., Gearin, G., Hall, J.L., Hensley, G., Johnson, E., Jones, C., Kamat, A., Kaur, A., Locke, D.P., Madan, A., Munson, G., Jaffe, D.B., Lui, A., Macdonald, P., Mauceli, E., Naylor, J.W., Nesbitt, R., Nicol, R., O'Leary, S.B., Ratcliffe, A., Rounsley, S., She, X., Sneddon, K.M., Stewart, S., Sougnez, C., Stone, S.M., Topham, K., Vincent, D., Wang, S., Zimmer, A.R., Birren, B.W., Hood, L., Lander, E.S., & Nusbaum, C. (2006). Analysis of the DNA sequence and duplication history of human chromosome 15. *Nature*, 440(7084), 671–675. PMID: 16572171.
308. Tello-Ruiz, M.K., Curley, C., DelMonte, T., Giallourakis, C., Kirby, A., Miller, K., Wild, G., Cohen, A., Langelier, D., Latiano, A., Wedemeyer, N., Lander, E.S., Schreiber, S., Annesse, V., Daly, M.J., & Rioux, J.D. (2006). Haplotype-based association analysis of 56 functional candidate genes in the IBD6 locus on chromosome 19. *European Journal of Human Genetics*, 14(6), 780–790. PMID: 16570073.
309. Kamal, M., Xie, X., & Lander, E.S. (2006). A large family of ancient repeat elements in the human genome is under strong selection. *Proceedings of the National Academy of Sciences USA*, 103(8), 2740–2745. PMID: 16477033; PMCID: PMC1413850.
310. Root, D.E., Hacohen, N., Hahn, W.C., Lander, E.S., & Sabatini, D.M. (2006). Genome-scale loss-of-function screening with a lentiviral RNAi library. *Nature Methods*, 3(9), 715–719. PMID: 16929317.
311. Houstis, N., Rosen, E.D., & Lander, E.S. (2006). Reactive oxygen species have a causal role in multiple forms of insulin resistance. *Nature*, 440(7086), 944–948. PMID: 16612386.
312. Zody, M.C., Garber, M., Adams, D.J., Sharpe, T., Harrow, J., Lupski, J.R., Nicholson, C., Searle, S.M., Wilming, L., Young, S.K., Abouelleil, A., Allen, N.R., Bi, W., Bloom, T., Borowsky, M.L., Bugalter, B.E., Butler, J., Chang, J.L., Chen, C.K., Cook, A., Corum, B., Cuomo, C.A., de Jong, P.J., DeCaprio, D., Dewar, K., FitzGerald, M., Gilbert, J., Gibson, R., Gnerre, S., Goldstein, S., Grafham, D.V., Grocock, R., Hafez, N., Hagopian, D.S., Hart, E., Norman, C.H., Humphray, S., Jaffe, D.B., Jones, M., Kamal, M., Khodiyar, V.K., LaButti, K., Laird, G., Lehoczy, J., Liu, X., Lokyitsang, T., Loveland, J., Lui, A., Macdonald, P., Major, J.E., Matthews, L., Mauceli, E., McCarroll, S.A., Mihalev, A.H., Mudge, J., Nguyen, C., Nicol, R., O'Leary, S.B., Osoegawa, K., Schwartz, D.C., Shaw-Smith, C., Stankiewicz, P., Stewart, C., Swarbreck, D., Venkataraman, V., Whittaker, C.A., Yang, X., Zimmer, A.R., Bradley, A., Hubbard, T., Birren, B.W., Rogers, J., Lander, E.S., & Nusbaum, C. (2006). DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. *Nature*, 440(7087), 1045–1049. PMID: 16625196; PMCID: PMC2610434.
313. Bernstein, B.E., Mikkelsen, T.S., Xie, X., Kamal, M., Huebert, D.J., Cuff, J., Fry, B., Meissner, A., Wernig, M., Plath, K., Jaenisch, R., Wagschal, A., Feil, R., Schreiber, S.L., & Lander, E.S. (2006). A bivalent chromatin structure marks key developmental genes in embryonic stem cells. *Cell*, 125(2), 315–326. PMID: 16630819.
314. Pedersen, J.S., Bejerano, G., Siepel, A., Rosenbloom, K., Lindblad-Toh, K., Lander, E.S., Kent, J., Miller, W., & Haussler, D. (2006). Identification and classification of conserved RNA secondary structures in the human genome. *PLoS Computational Biology*, 2(4), e33. PMID: 16628248; PMCID: PMC1440920.
315. Patterson, N., Richter, D.J., Gnerre, S., Lander, E.S., & Reich, D. (2006). Genetic evidence for complex speciation of humans and chimpanzees. *Nature*, 441(7097), 1103–1108. PMID: 16710306.
316. Sabeti, P.C., Schaffner, S.F., Fry, B., Lohmueller, J., Varilly, P., Shamovsky, O., Palma, A., Mikkelsen, T.S., Altshuler, D., & Lander, E.S. (2006). Positive natural selection in the human lineage. *Science*, 312(5780), 1614–1620. PMID: 16778047.
317. Xie, X., Kamal, M., & Lander, E.S. (2006). A family of conserved noncoding elements derived from an ancient transposable element. *Proceedings of the National Academy of Sciences USA*, 103(31), 11659–11664. PMID: 16864796; PMCID: PMC1518811.
318. Lowe, C.J., Terasaki, M., Wu, M., Freeman, R.M., Runft, L., Kwan, K., Haigo, S., Aronowicz, J., Lander, E.S., Gruber, C., Smith, M., Kirschner, M., & Gerhart, J. (2006). Dorsoventral patterning in hemichordates: insights into early

- chordate evolution. *PLoS Biology*, 4(9), e291. PMID: 16933975; PMCID: PMC1551926.
319. Lamb, J., Crawford, E.D., Peck, D., Modell, J.W., Blat, I.C., Wrobel, M.J., Lerner, J., Brunet, J.P., Subramanian, A., Ross, K.N., Reich, M., Hieronymus, H., Wei, G., Armstrong, S.A., Haggarty, S.J., Clemons, P.A., Wei, R., Carr, S.A., Lander, E.S., & Golub, T.R. (2006). *The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease*. *Science*, 313(5795), 1929–1935. PMID: 17008526.
320. Wei, B.Q., Mikkelsen, T.S., McKinney, M.K., Lander, E.S., & Cravatt, B. F. (2006). *A second fatty acid amide hydrolase with variable distribution among placental mammals*. *Journal of Biological Chemistry*, 281(48), 36569–36578. PMID: 17015445.
321. Bourlat, S.J., Juliusdottir, T., Lowe, C.J., Freeman, R., Aronowicz, J., Kirschner, M., Lander, E.S., Thorndyke, M., Nakano, H., Kohn, A.B., Heyland, A., Moroz, L.L., Copley, R.R., & Telford, M.J. (2006). *Deuterostome phylogeny reveals monophyletic chordates and the new phylum Xenoturbellida*. *Nature*, 444(7115), 85–88. PMID: 17051155.
322. Hill, A.E., Lander, E.S., & Nadeau, J.H. (2006). *Chromosome substitution strains: A new way to study genetically complex traits*. *Methods in Molecular Medicine*, 128, 153–172. PMID: 17071995.
323. Volkman, S.K., Sabeti, P.C., DeCaprio, D., Neafsey, D.E., Schaffner, S.F., Milner, D.A., Daily, J.P., Sarr, O., Ndiaye, D., Ndir, O., Mboup, S., Duraisingh, M.T., Lukens, A., Derr, A., Stange-Thomann, N., Waggoner, S., Onofrio, R., Ziaugra, L., Mauceli, E., Gnerre, S., Jaffe, D.B., Zainoun, J., Wiegand, R.C., Birren, B.W., Hartl, D.L., Galagan, J.E., Lander, E.S., & Wirth, D.F. (2007). *A genome-wide map of diversity in Plasmodium falciparum*. *Nature Genetics*, 39(1), 113–119. PMID: 17159979.
324. Yeo, T.W., De Jager, P.L., Gregory, S.G., Barcellos, L.F., Walton, A., Goris, A., Fenoglio, C., Ban, M., Taylor, C.J., Goodman, R.S., Walsh, E., Wolfish, C.S., Horton, R., Traherne, J., Beck, S., Trowsdale, J., Caillier, S.J., Ivinson, A.J., Green, T., Pobywajlo, S., Lander, E.S., Pericak-Vance, M.A., Haines, J.L., Daly, M.J., Oksenberg, J.R., Hauser, S.L., Compston, A., Hafler, D.A., Rioux, J.D., & Sawcer, S. (2007). *A second major histocompatibility complex susceptibility locus for multiple sclerosis*. *Annals of Neurology*, 61(3), 228–236. PMID: 17252545; PMCID: PMC2737610.
325. Bernstein, B.E., Meissner, A., & Lander, E.S. (2007). *The mammalian epigenome*. *Cell*, 128(4), 669–681. PMID: 17320505.
326. Strohl, K.P., Gallagher, L., Lynn, A., Friedman, L., Hill, A., Singer, J.B., Lander, E.S., & Nadeau, J. (2007). *Sleep-related epilepsy in the A/J mouse*. *Sleep*, 30(2), 169–176. PMID: 17326542.
327. Xie, X., Mikkelsen, T.S., Gnirke, A., Lindblad-Toh, K., Kellis, M., & Lander, E.S. (2007). *Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites*. *Proceedings of the National Academy of Sciences USA*, 104(17), 7145–7150. PMID: 17442748; PMCID: PMC1852749.
328. Mikkelsen, T.S., Wakefield, M.J., Aken, B., Amemiya, C.T., Chang, J.L., Duke, S., Garber, M., Gentles, A.J., Goodstadt, L., Heger, A., Jurka, J., Kamal, M., Mauceli, E., Searle, S.M., Sharpe, T., Baker, M.L., Batzer, M.A., Benos, P.V., Belov, K., Clamp, M., Cook, A., Cuff, J., Das, R., Davidow, L., Deakin, J.E., Fazzari, M.J., Glass, J.L., Grabherr, M., Greal, J.M., Gu, W., Hore, T.A., Huttley, G.A., Kleber, M., Jirtle, R.L., Koina, E., Lee, J.T., Mahony, S., Marra, M.A., Miller, R.D., Nicholls, R.D., Oda, M., Papenfuss, A.T., Parra, Z.E., Pollock, D.D., Ray, D.A., Schein, J.E., Speed, T.P., Thompson, K., VandeBerg, J.L., Wade, C.M., Walker, J.A., Waters, P.D., Webber, C., Weidman, J.R., Xie, X., Zody, M.C., Broad Institute Genome Sequencing Platform, Broad Institute Whole Genome Assembly Team, Graves, J.A., Ponting, C.P., Breen, M., Samollow, P.B., Lander, E.S., & Lindblad-Toh, K. (2007). *Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences*. *Nature*, 447(7141), 167–177. PMID: 17495919.
329. Margulies, E.H., Cooper, G.M., Asimenos, G., Thomas, D.J., Dewey, C.N., Siepel, A., Birney, E., Keefe, D., Schwartz, A.S., Hou, M., Taylor, J., Nikolaev, S., Montoya-Burgos, J.I., Löytynoja, A., Whelan, S., Pardi, F., Massingham, T., Brown, J.B., Bickel, P., Holmes, I., Mullikin, J.C., Ureta-Vidal, A., Paten, B., Stone, E.A., Rosenbloom, K.R., Kent, W.J., Bouffard, G.G., Guan, X., Hansen, N.F., Idol, J.R., Maduro, V.V., Maskeri, B., McDowell, J.C., Park, M., Thomas, P.J., Young, A.C., Blakesley, R.W., Muzny, D.M., Sodergren, E., Wheeler, D.A., Worley, K.C., Jiang, H., Weinstock, G.M., Gibbs, R.A., Graves, T., Fulton, R., Mardis, E.R., Wilson, R.K., Clamp, M., Cuff, J., Gnerre, S., Jaffe, D.B., Chang, J.L., Lindblad-Toh, K., Lander, E.S., Hinrichs, A., Trumbower, H., Clawson, H., Zweig, A., Kuhn, R.M., Barber, G.,

- Harte, R., Karolchik, D., Field, M.A., Moore, R.A., Matthewson, C.A., Schein, J.E., Marra, M.A., Antonarakis, S.E., Batzoglu, S., Goldman, N., Hardison, R., Haussler, D., Miller, W., Pachter, L., Green, E.D., & Sidow, A. (2007). *Analyses of deep mammalian sequence alignments and constraint predictions for 1 percent of the human genome*. *Genome Research*, 17(6), 760–774. PMID: 17567995; PMCID: PMC1891336.
330. ENCODE Project Consortium. (2007). *Identification and analysis of functional elements in 1 percent of the human genome by the ENCODE pilot project*. *Nature*, 447(7146), 799–816. PMID: 17571346; PMCID: PMC2212820.
331. Boehm, J.S., Zhao, J.J., Yao, J., Kim, S.Y., Firestein, R., Dunn, I.F., Sjostrom, S.K., Garraway, L.A., Weremowicz, S., Richardson, A.L., Greulich, H., Stewart, C.J., Mulvey, L.A., Shen, R.R., Ambrogio, L., Hirozane-Kishikawa, T., Hill, D.E., Vidal, M., Meyerson, M., Grenier, J.K., Hinkle, G., Root, D.E., Roberts, T.M., Lander, E.S., Polyak, K., & Hahn, W.C. (2007). *Integrative genomic approaches identify IKKBE as a breast cancer oncogene*. *Cell*, 129(6), 1065–1079. PMID: 17574021.
332. Mikkelsen, T.S., Ku, M., Jaffe, D.B., Issac, B., Lieberman, E., Giannoukos, G., Alvarez, P., Brockman, W., Kim, T.K., Koche, R.P., Lee, W., Mendenhall, E., O'Donovan, A., Presser, A., Russ, C., Xie, X., Meissner, A., Wernig, M., Jaenisch, R., Nusbaum, C., Lander, E.S., & Bernstein, B.E. (2007). *Genome-wide maps of chromatin state in pluripotent and lineage-committed cells*. *Nature*, 448(7153), 553–560. PMID: 17603471; PMCID: PMC2921165.
333. International Multiple Sclerosis Genetics Consortium, Hafler, D.A., Compston, A., Sawcer, S., Lander, E.S., Daly, M.J., De Jager, P.L., de Bakker, P.I., Gabriel, S.B., Mirel, D.B., Ivinson, A.J., Pericak-Vance, M.A., Gregory, S.G., Rioux, J.D., McCauley, J.L., Haines, J.L., Barcellos, L.F., Cree, B., Oksenberg, J.R., & Hauser, S.L. (2007). *Risk alleles for multiple sclerosis identified by a genomewide study*. *New England Journal of Medicine*, 357(9), 851–862. PMID: 17660530.
334. Sabeti, P.C., Varilly, P., Fry, B., Lohmueller, J., Hostetter, E., Cotsapas, C., Xie, X., Byrne, E.H., McCarroll, S.A., Gaudet, R., Schaffner, S.F., Lander, E.S., International HapMap Consortium, Frazer, K.A., Ballinger, D.G., Cox, D.R., Hinds, D.A., Stuve, L.L., Gibbs, R.A., Belmont, J.W., Boudreau, A., Hardenbol, P., Leal, S.M., Pasternak, S., Wheeler, D.A., Willis, T.D., Yu, F., Yang, H., Zeng, C., Gao, Y., Hu, H., Hu, W., Li, C., Lin, W., Liu, S., Pan, H., Tang, X., Wang, J., Wang, W., Yu, J., Zhang, B., Zhang, Q., Zhao, H., Zhou, J., Gabriel, S.B., Barry, R., Blumenstiel, B., Camargo, A., Defelice, M., Faggart, M., Goyette, M., Gupta, S., Moore, J., Nguyen, H., Onofrio, R.C., Parkin, M., Roy, J., Stahl, E., Winchester, E., Ziaugra, L., Altshuler, D., Shen, Y., Yao, Z., Huang, W., Chu, X., He, Y., Jin, L., Liu, Y., Shen, Y., Sun, W., Wang, H., Wang, Y., Wang, Y., Xiong, X., Xu, L., Wayne, M.M., Tsui, S.K., Xue, H., Wong, J.T., Galver, L.M., Fan, J.B., Gunderson, K., Murray, S.S., Oliphant, A.R., Chee, M.S., Montpetit, A., Chagnon, F., Ferretti, V., Leboeuf, M., Olivier, J.F., Phillips, M.S., Roumy, S., Sallée, C., Verner, A., Hudson, T.J., Kwok, P.Y., Cai, D., Koboldt, D.C., Miller, R.D., Pawlikowska, L., Taillon-Miller, P., Xiao, M., Tsui, L.C., Mak, W., Song, Y.Q., Tam, P.K., Nakamura, Y., Kawaguchi, T., Kitamoto, T., Morizono, T., Nagashima, A., Ohnishi, Y., Sekine, A., Tanaka, T., Tsunoda, T., Deloukas, P., Bird, C.P., Delgado, M., Dermitzakis, E.T., Gwilliam, R., Hunt, S., Morrison, J., Powell, D., Stranger, B.E., Whittaker, P., Bentley, D.R., Daly, M.J., de Bakker, P.I., Barrett, J., Chretien, Y.R., Maller, J., McCarroll, S., Patterson, N., Pe'er, I., Price, A., Purcell, S., Richter, D.J., Sabeti, P., Saxena, R., Schaffner, S.F., Sham, P.C., Varilly, P., Altshuler, D., Stein, L.D., Krishnan, L., Smith, A.V., Tello-Ruiz, M.K., Thorisson, G.A., Chakravarti, A., Chen, P.E., Cutler, D.J., Kashuk, C.S., Lin, S., Abecasis, G.R., Guan, W., Li, Y., Munro, H.M., Qin, Z.S., Thomas, D.J., McVean, G., Auton, A., Bottolo, L., Cardin, N., Eyheramendy, S., Freeman, C., Marchini, J., Myers, S., Spencer, C., Stephens, M., Donnelly, P., Cardon, L.R., Clarke, G., Evans, D.M., Morris, A.P., Weir, B.S., Tsunoda, T., Johnson, T.A., Mullikin, J.C., Sherry, S.T., Feolo, M., Skol, A., Zhang, H., Zeng, C., Zhao, H., Matsuda, I., Fukushima, Y., Macer, D.R., Suda, E., Rotimi, C.N., Adebamowo, C.A., Ajayi, I., Aniagwu, T., Marshall, P.A., Nkwodimmah, C., Royal, C.D., Leppert, M.F., Dixon, M., Peiffer, A., Qiu, R., Kent, A., Kato, K., Niikawa, N., Adewole, I.F., Knoppers, B.M., Foster, M.W., Clayton, E.W., Watkin, J., Gibbs, R.A., Belmont, J.W., Muzny, D., Nazareth, L., Sodergren, E., Weinstock, G.M., Wheeler, D.A., Yakub, I., Gabriel, S.B., Onofrio, R.C., Richter, D.J., Ziaugra, L., Birren, B.W., Daly, M.J., Altshuler, D., Wilson, R.K., Fulton, L.L., Rogers, J., Burton, J., Carter, N.P., Clee, C.M., Griffiths, M., Jones, M.C., McLay, K., Plumb, R.W., Ross, M.T., Sims, S.K., Willey, D.L., Chen, Z., Han, H., Kang, L., Godbout, M., Wallenburg, J.C., L'Archevêque, P., Bellemare, G., Saeki, K., Wang, H., An, D., Fu, H., Li, Q., Wang, Z., Wang, R., Holden, A.L., Brooks, L.D., McEwen, J.E., Guyer, M.S., Wang, V.O., Peterson, J.L., Shi, M., Spiegel, J., Sung, L.M., Zacharia, L.F., Collins, F.S., Kennedy, K., Jamieson, R., & Stewart, J. (2007). *Genome-wide detec-*

tion and characterization of positive selection in human populations. *Nature*, 449(7164), 913–918. PMID: 17943131; PMCID: PMC2687721.

335. GAIN Collaborative Research Group, Manolio, T.A., Rodriguez, L.L., Brooks, L., Abecasis, G., Collaborative Association Study of Psoriasis, Ballinger, D., Daly, M., Donnelly, P., Faraone, S.V., International Multi-Center ADHD Genetics Project, Frazer, K., Gabriel, S., Gejman, P., Molecular Genetics of Schizophrenia Collaboration, Guttmacher, A., Harris, E.L., Insel, T., Kelsoe, J.R., Bipolar Genome Study, Lander, E.S., McCowin, N., Mailman, M.D., Nabel, E., Ostell, J., Pugh, E., Sherry, S., Sullivan, P.F., Major Depression Stage 1 Genomewide Association in Population-Based Samples Study, Thompson, J.F., Warram, J., Genetics of Kidneys in Diabetes (GoKinD) Study, Wholley, D., Milos, P.M., & Collins, F.S. (2007). *New models of collaboration in genome-wide association studies: the Genetic Association Information Network*. *Nature Genetics*, 39(9), 1045–1051. PMID: 17728769.

336. Getz, G., Hofling, H., Mesirov, J.P., Golub, T.R., Meyerson, M., Tibshirani, R., & Lander E.S. (2007). *The consensus coding sequences of human breast and colorectal cancers [Comment]*. *Science* 317(5844), 1500. PMID: 17872428.

337. Karlsson, E.K., Baranowska, I., Wade, C.M., Salmon Hillbertz, N.H., Zody, M.C., Anderson, N., Biagi, T.M., Patterson, N., Pielberg, G.R., Kulbokas, E.J., Comstock, K.E., Keller, E.T., Mesirov, J.P., von Euler, H., Kämpe, O., Hedhammar, A., Lander, E.S., Andersson, G., Andersson, L., & Lindblad-Toh, K. (2007). *Efficient mapping of mendelian traits in dogs through genome-wide association*. *Nature Genetics*, 39(11), 1321–1328. PMID: 17906626.

338. Weir, B.A., Woo, M.S., Getz, G., Perner, S., Ding, L., Beroukhi, R., Lin, W.M., Province, M.A., Kraja, A., Johnson, L.A., Shah, K., Sato, M., Thomas, R.K., Barletta, J.A., Borecki, I.B., Broderick, S., Chang, A.C., Chiang, D.Y., Chirieac, L.R., Cho, J., Fujii, Y., Gazdar, A.F., Giordano, T., Greulich, H., Hanna, M., Johnson, B.E., Kris, M.G., Lash, A., Lin, L., Lindeman, N., Mardis, E.R., McPherson, J.D., Minna, J.D., Morgan, M.B., Nadel, M., Orringer, M.B., Osborne, J.R., Ozenberger, B., Ramos, A.H., Robinson, J., Roth, J.A., Rusch, V., Sasaki, H., Shepherd, F., Sougnez, C., Spitz, M.R., Tsao, M.S., Twomey, D., Verhaak, R.G., Weinstock, G.M., Wheeler, D.A., Winckler, W., Yoshizawa, A., Yu, S., Zakowski, M.F., Zhang, Q., Beer, D.G., Wistuba, I.I., Watson, M.A., Garraway, L.A., Ladanyi, M., Travis, W.D., Pao, W., Rubin, M.A., Gabriel, S.B., Gibbs, R.A., Varmus, H.E., Wilson, R.K., Lander, E.S., & Meyerson, M. (2007). *Characterizing the cancer genome in lung adenocarcinoma*. *Nature*, 450(7171), 893–898. PMID: 17982442; PMCID: PMC2538683.

339. Miller, W., Rosenbloom, K., Hardison, R.C., Hou, M., Taylor, J., Raney, B., Burhans, R., King, D.C., Baertsch, R., Blankenberg, D., Kosakovsky Pond, S.L., Nekrutenko, A., Giardine, B., Harris, R.S., Tyekucheva, S., Diekhans, M., Pringle, T.H., Murphy, W.J., Lesk, A., Weinstock, G.M., Lindblad-Toh, K., Gibbs, R.A., Lander, E.S., Siepel, A., Haussler, D., & Kent, W.J. (2007). *28-way vertebrate alignment and conservation track in the UCSC Genome Browser*. *Genome Research*, 17(12), 1797–1808. PMID: 17984227; PMCID: PMC2099589.

340. Drosophila 12 Genomes Consortium, Clark, A.G., Eisen, M.B., Smith, D.R., Bergman, C.M., Oliver, B., Markow, T.A., Kaufman, T.C., Kellis, M., Gelbart, W., Iyer, V.N., Pollard, D.A., Sackton, T.B., Larracuent, A.M., Singh, N.D., Abad, J.P., Abt, D.N., Adryan, B., Aguade, M., Akashi, H., Anderson, W.W., Aquadro, C.F., Ardell, D.H., Arguello, R., Artieri, C.G., Barbash, D.A., Barker, D., Barsanti, P., Batterham, P., Batzoglou, S., Begun, D., Bhutkar, A., Blanco, E., Bosak, S.A., Bradley, R.K., Brand, A.D., Brent, M.R., Brooks, A.N., Brown, R.H., Butlin, R.K., Caggese, C., Calvi, B.R., Bernardo de Carvalho, A., Caspi, A., Castrezana, S., Celniker, S.E., Chang, J.L., Chapple, C., Chatterji, S., Chinwalla, A., Civetta, A., Clifton, S.W., Comeron, J.M., Costello, J.C., Coyne, J.A., Daub, J., David, R.G., Delcher, A.L., Delehaunty, K., Do, C.B., Ebling, H., Edwards, K., Eickbush, T., Evans, J.D., Filipinski, A., Findeiss, S., Freyhult, E., Fulton, L., Fulton, R., Garcia, A.C., Gardiner, A., Garfield, D.A., Garvin, B.E., Gibson, G., Gilbert, D., Gnerre, S., Godfrey, J., Good, R., Gotea, V., Gravely, B., Greenberg, A.J., Griffiths-Jones, S., Gross, S., Guigo, R., Gustafson, E.A., Haerty, W., Hahn, M.W., Halligan, D.L., Halpern, A.L., Halter, G.M., Han, M.V., Heger, A., Hillier, L., Hinrichs, A.S., Holmes, I., Hoskins, R.A., Hubisz, M.J., Hultmark, D., Huntley, M.A., Jaffe, D.B., Jagadeeshan, S., Jeck, W.R., Johnson, J., Jones, C.D., Jordan, W.C., Karpen, G.H., Kataoka, E., Keightley, P.D., Kheradpour, P., Kirkness, E.F., Koerich, L.B., Kristiansen, K., Kudrna, D., Kulathinal, R.J., Kumar, S., Kwok, R., Lander, E.S., Langley, C.H., Lapoint, R., Lazzaro, B.P., Lee, S.J., Levesque, L., Li, R., Lin, C.F., Lin, M.F., Lindblad-Toh, K., Llopart, A., Long, M., Low, L., Lozovsky, E., Lu, J., Luo, M., Machado, C.A., Makalowski, W., Marzo, M., Matsuda, M., Matzkin, L., McAllister, B., McBride, C.S., McKernan, B., McKernan, K., Mendez-Lago, M., Minx, P., Mollenhauer, M.U., Montooth, K., Mount, S.M., Mu, X., Myers, E., Negre, B., Newfeld, S., Nielsen, R., Noor, M.A., O'Grady, P., Pachter, L., Papacit, M., Parisi,

- M.J., Parisi, M., Parts, L., Pedersen, J.S., Pesole, G., Phillippy, A.M., Ponting, C.P., Pop, M., Porcelli, D., Powell, J.R., Prohaska, S., Pruitt, K., Puig, M., Quesneville, H., Ram, K.R., Rand, D., Rasmussen, M.D., Reed, L.K., Reenan, R., Reily, A., Remington, K.A., Rieger, T.T., Ritchie, M.G., Robin, C., Rogers, Y.H., Rohde, C., Rozas, J., Rubenfield, M.J., Ruiz, A., Russo, S., Salzberg, S.L., Sanchez-Gracia, A., Saranga, D.J., Sato, H., Schaeffer, S.W., Schatz, M.C., Schlenke, T., Schwartz, R., Segarra, C., Singh, R.S., Sirot, L., Sirota, M., Sisneros, N.B., Smith, C.D., Smith, T.F., Spieth, J., Stage, D.E., Stark, A., Stephan, W., Strausberg, R.L., Strempel, S., Sturgill, D., Sutton, G., Sutton, G.G., Tao, W., Teichmann, S., Tobar, Y.N., Tomimura, Y., Tsolas, J.M., Valente, V.L., Venter, E., Venter, J.C., Vicario, S., Vieira, F.G., Vilella, A.J., Villasante, A., Walenz, B., Wang, J., Wasserman, M., Watts, T., Wilson, D., Wilson, R.K., Wing, R.A., Wolfner, M.F., Wong, A., Wong, G.K., Wu, C.I., Wu, G., Yamamoto, D., Yang, H.P., Yang, S.P., Yorke, J.A., Yoshida, K., Zdobnov, E., Zhang, P., Zhang, Y., Zimin, A.V., Baldwin, J., Abdouelleil, A., Abdulkadir, J., Abebe, A., Abera, B., Abreu, J., Acer, S.C., Aftuck, L., Alexander, A., An, P., Anderson, E., Anderson, S., Arachi, H., Azer, M., Bachantsang, P., Barry, A., Bayul, T., Berlin, A., Bessette, D., Bloom, T., Blye, J., Boguslavskiy, L., Bonnet, C., Boukhgalter, B., Bourzgui, I., Brown, A., Cahill, P., Channer, S., Cheshatsang, Y., Chuda, L., Citroen, M., Collymore, A., Cooke, P., Costello, M., D'Aco, K., Daza, R., De Haan, G., DeGray, S., DeMaso, C., Dhargay, N., Dooley, K., Dooley, E., Doricent, M., Dorje, P., Dorjee, K., Dupes, A., Elong, R., Falk, J., Farina, A., Faro, S., Ferguson, D., Fisher, S., Foley, C.D., Franke, A., Friedrich, D., Gadbois, L., Gearin, G., Gearin, C.R., Giannoukos, G., Goode, T., Graham, J., Grandbois, E., Grewal, S., Gyaltzen, K., Hafez, N., Hagos, B., Hall, J., Henson, C., Hollinger, A., Honan, T., Huard, M.D., Hughes, L., Hurhula, B., Husby, M.E., Kamat, A., Kanga, B., Kashin, S., Khazanovich, D., Kisner, P., Lance, K., Lara, M., Lee, W., Lennon, N., Letendre, F., LeVine, R., Lipovsky, A., Liu, X., Liu, J., Liu, S., Lokyitsang, T., Lokyitsang, Y., Lubonja, R., Lui, A., MacDonald, P., Magnisalis, V., Maru, K., Matthews, C., McCusker, W., McDonough, S., Mehta, T., Meldrim, J., Meneus, L., Mihai, O., Mihalev, A., Mihova, T., Mittelman, R., Mlenga, V., Montmayeur, A., Mulrain, L., Navidi, A., Naylor, J., Negash, T., Nguyen, T., Nguyen, N., Nicol, R., Norbu, C., Norbu, N., Novod, N., O'Neill, B., Osman, S., Markiewicz, E., Oyono, O.L., Patti, C., Phunkhang, P., Pierre, F., Priest, M., Raghuraman, S., Rege, F., Reyes, R., Rise, C., Rogov, P., Ross, K., Ryan, E., Settipalli, S., Shea, T., Sherpa, N., Shi, L., Shih, D., Sparrow, T., Spaulding, J., Stalker, J., Stange-Thomann, N., Stavropoulos, S., Stone, C., Strader, C., Tesfaye, S., Thomson, T., Thoulutsang, Y., Thoulutsang, D., Topham, K., Topping, I., Tsamla, T., Vassiliev, H., Vo, A., Wangchuk, T., Wangdi, T., Weiland, M., Wilkinson, J., Wilson, A., Yadav, S., Young, G., Yu, Q., Zembek, L., Zhong, D., Zimmer, A., Zwirko, Z., Jaffe, D.B., Alvarez, P., Brockman, W., Butler, J., Chin, C., Gnerre, S., Grabherr, M., Kleber, M., Mauceli, E., & MacCallum, I. (2007). *Evolution of genes and genomes on the Drosophila phylogeny*. *Nature*, 450(7167), 203–218. PMID: 17994087.
341. Clamp, M., Fry, B., Kamal, M., Xie, X., Cuff, J., Lin, M.F., Kellis, M., Lindblad-Toh, K., & Lander, E.S. (2007). *Distinguishing protein-coding and non-coding genes in the human genome*. *Proceedings of the National Academy of Sciences USA*, 104(49), 19428–19433. PMID: 18040051; PMCID: PMC2148306.
342. Beroukhi, R., Getz, G., Nghiemphu, L., Barretina, J., Hsueh, T., Linhart, D., Vivanco, I., Lee, J.C., Huang, J.H., Alexander, S., Du, J., Kau, T., Thomas, R.K., Shah, K., Soto, H., Perner, S., Prensner, J., DeBiasi, R.M., Demichelis, F., Hatton, C., Rubin, M.A., Garraway, L.A., Nelson, S.F., Liau, L., Mischel, P.S., Cloughesy, T.F., Meyerson, M., Golub, T.A., Lander, E.S., Mellinghoff, I.K., & Sellers, W.R. (2007). *Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma*. *Proceedings of the National Academy of Sciences USA*, 104(50), 20007–20012. PMID: 18077431; PMCID: PMC2148413.
343. Daily, J.P., Scandell, D., Pochet, N., Le Roch, K., Plouffe, D., Kamal, M., Sarr, O., Mboup, S., Ndir, O., Wypij, D., Levasseur, K., Thomas, E., Tamayo, P., Dong, C., Zhou, Y., Lander, E.S., Ndiaye, D., Wirth, D., Winzler, E.A., Mesirov, J.P., & Regev, A. (2007). *Distinct physiological states of Plasmodium falciparum in malaria-infected patients*. *Nature*, 450(7172), 1091–1095. PMID: 18046333.
344. Brockman, W., Alvarez, P., Young, S., Garber, M., Giannoukos, G., Lee, W.L., Russ, C., Lander, E.S., Nusbaum, C., & Jaffe, D.B. (2008). *Quality scores and SNP detection in sequencing-by-synthesis systems*. *Genome Research*, 18(5), 763–770. PMID: 18212088; PMCID: PMC2336812.
345. Butler, J., MacCallum, I., Kleber, M., Shlyakhter, I.A., Belmonte, M.K., Lander, E.S., Nusbaum, C., & Jaffe, D.B. (2008). *ALLPATHS: de novo assembly of whole-genome shotgun microreads*. *Genome Research*, 18(5), 810–820. PMID: 18340039; PMCID: PMC2336810.

346. Onder, T.T., Gupta, P.B., Mani, S.A., Yang, J., Lander, E.S., & Weinberg, R.A. (2008). *Loss of E-cadherin promotes metastasis via multiple downstream transcriptional pathways*. *Cancer Research*, 68(10), 3645–3654. PMID: 18483246.
347. Freeman, R.M., Wu, M., Cordonnier-Pratt, M.M., Pratt, L.H., Gruber, C.E., Smith, M., Lander, E.S., Stange-Thomann, N., Lowe, C.J., Gerhart, J., & Kirschner, M. (2008). *cDNA sequences for transcription factors and signaling proteins of the hemichordate Saccoglossus kowalevskii: efficacy of the expressed sequence tag (EST) approach for evolutionary and developmental studies of a new organism*. *The Biological Bulletin*, 214(3), 284–302. PMID: 18574105.
348. Mikkelsen, T.S., Hanna, J., Zhang, X., Ku, M., Wernig, M., Schorderet, P., Bernstein, B.E., Jaenisch, R., Lander, E.S., & Meissner, A. (2008). *Dissecting direct reprogramming through integrative genomic analysis*. *Nature*, 454(7200), 49–55. PMID: 18509334; PMCID: PMC2754827.
349. Meissner, A., Mikkelsen, T.S., Gu, H., Wernig, M., Hanna, J., Sivachenko, A., Zhang, X., Bernstein, B.E., Nusbaum, C., Jaffe, D.B., Gnirke, A., Jaenisch, R., & Lander, E.S. (2008). *Genome-scale DNA methylation maps of pluripotent and differentiated cells*. *Nature*, 454(7205), 766–770. PMID: 18600261; PMCID: PMC2896277.
350. Cancer Genome Atlas Research Network. (2008). *Comprehensive genomic characterization defines human glioblastoma genes and core pathways*. *Nature*, 455(7216), 1061–1068. PMID: 18772890; PMCID: PMC2671642.
351. Ku, M., Koche, R.P., Rheinbay, E., Mendenhall, E.M., Endoh, M., Mikkelsen, T.S., Presser, A., Nusbaum, C., Xie, X., Chi, A.S., Adli, M., Kasif, S., Ptaszek, L.M., Cowan, C.A., Lander, E.S., Koseki, H., & Bernstein, B.E. (2008). *Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains*. *PLoS Genetics*, 4(10), e1000242. PMID: 18974828; PMCID: PMC2567431.
352. Ding, L., Getz, G., Wheeler, D.A., Mardis, E.R., McLellan, M.D., Cibulskis, K., Sougnez, C., Greulich, H., Muzny, D.M., Morgan, M.B., Fulton, L., Fulton, R.S., Zhang, Q., Wendl, M.C., Lawrence, M.S., Larson, D.E., Chen, K., Dooling, D.J., Sabo, A., Hawes, A.C., Shen, H., Jhangiani, S.N., Lewis, L.R., Hall, O., Zhu, Y., Mathew, T., Ren, Y., Yao, J., Scherer, S.E., Clerc, K., Metcalf, G.A., Ng, B., Milosavljevic, A., Gonzalez-Garay, M.L., Osborne, J.R., Meyer, R., Shi, X., Tang, Y., Koboldt, D.C., Lin, L., Abbott, R., Miner, T.L., Pohl, C., Fewell, G., Haipke, C., Schmidt, H., Dunford-Shore, B.H., Kraja, A., Crosby, S.D., Sawyer, C.S., Vickery, T., Sander, S., Robinson, J., Winkler, W., Baldwin, J., Chirieac, L.R., Dutt, A., Fennell, T., Hanna, M., Johnson, B.E., Onofrio, R.C., Thomas, R.K., Tonon, G., Weir, B.A., Zhao, X., Ziaugra, L., Zody, M.C., Giordano, T., Orringer, M.B., Roth, J.A., Spitz, M.R., Wistuba, I.I., Ozenberger, B., Good, P.J., Chang, A.C., Beer, D.G., Watson, M.A., Ladanyi, M., Broderick, S., Yoshizawa, A., Travis, W.D., Pao, W., Province, M.A., Weinstock, G.M., Varmus, H.E., Gabriel, S.B., Lander, E.S., Gibbs, R.A., Meyerson, M., & Wilson, R.K. (2008). *Somatic mutations affect key pathways in lung adenocarcinoma*. *Nature*, 455(7216), 1069–1075. PMID: 18948947; PMCID: PMC2694412.
353. Altshuler, D., Daly, M.J., & Lander, E.S. (2008). *Genetic mapping in human disease*. *Science*, 322(5903), 881–888. PMID: 18988837; PMCID: PMC2694957.
354. Miller, W., Drautz, D.I., Ratan, A., Pusey, B., Qi, J., Lesk, A.M., Tomsho, L.P., Packard, M.D., Zhao, F., Sher, A., Tikhonov, A., Raney, B., Patterson, N., Lindblad-Toh, K., Lander, E.S., Knight, J.R., Irzyk, G.P., Fredrikson, K.M., Harkins, T.T., Sheridan, S., Pringle, T., & Schuster, S.C. (2008). *Sequencing the nuclear genome of the extinct woolly mammoth*. *Nature*, 456(7220), 387–390. PMID: 19020620.
355. Shao, H., Burrage, L.C., Sinasac, D.S., Hill, A.E., Ernest, S.R., O'Brien, W., Courtland, H.W., Jepsen, K.J., Kirby, A., Kulbokas, E.J., Daly, M.J., Broman, K.W., Lander, E.S., & Nadeau, J.H. (2008). *Genetic architecture of complex traits: large phenotypic effects and pervasive epistasis*. *Proceedings of the National Academy of Sciences USA*, 105(50), 19910–19914. PMID: 19066216; PMCID: PMC2604967.
356. Luo, B., Cheung, H.W., Subramanian, A., Sharifnia, T., Okamoto, M., Yang, X., Hinkle, G., Boehm, J.S., Beroukhi, R., Weir, B.A., Mermel, C., Barbie, D.A., Awad, T., Zhou, X., Nguyen, T., Piqui, B., Li, C., Golub, T.R., Meyerson, M., Hacohen, N., Hahn, W.C., Lander, E.S., Sabatini, D.M., & Root, D.E. (2008). *Highly parallel identification of essential genes in cancer cells*. *Proceedings of the National Academy of Sciences USA*, 105(51), 20380–20385. PMID: 19091943; PMCID: PMC2629277.
357. Chiang, D.Y., Getz, G., Jaffe, D.B., O'Kelly, M.J., Zhao, X., Carter, S.L., Russ, C., Nusbaum, C., Meyerson, M., & Lander, E.S. (2009). *High-resolution mapping of copy-number alterations with massively parallel sequencing*. *Nature Methods*, 6(1), 99–103. PMID: 19043412; PMCID: PMC2630795.
358. Nusbaum, C., Ohsumi, T.K., Gomez, J., Aquadro, J., Victor, T.C., Warren, R.M., Hung, D.T., Birren, B.W., Lander, E.S., & Jaffe, D.B. (2009). *Sensitive, specific*

- polymorphism discovery in bacteria using massively parallel sequencing. Nature Methods*, 6(1), 67–69. PMID: 19079253; PMCID: PMC2613166.
359. Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E.M., Brockman, W., Fennell, T., Giannoukos, G., Fisher, S., Russ, C., Gabriel, S., Jaffe, D.B., Lander, E.S., & Nusbaum, C. (2009). *Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. Nature Biotechnology*, 27(2), 182–189. PMID: 19182786; PMCID: PMC2663421.
360. Guttman, M., Amit, I., Garber, M., French, C., Lin, M.F., Feldser, D., Huarte, M., Zuk, O., Carey, B.W., Cassady, J.P., Cabili, M.N., Jaenisch, R., Mikkelsen, T.S., Jacks, T., Hacohen, N., Bernstein, B.E., Kellis, M., Regev, A., Rinn, J.L., & Lander, E.S. (2009). *Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature*, 458(7235), 223–227. PMID: 19182780; PMCID: PMC2754849.
361. Vasudevan, K.M., Barbie, D.A., Davies, M.A., Rabinovsky, R., McNear, C.J., Kim, J.J., Hennessy, B.T., Tseng, H., Pochanard, P., Kim, S.Y., Dunn, I.F., Schinzel, A.C., Sandy, P., Hoersch, S., Sheng, Q., Gupta, P.B., Boehm, J.S., Reiling, J.H., Silver, S., Lu, Y., Stemke-Hale, K., Dutta, B., Joy, C., Sahin, A.A., Gonzalez-Angulo, A.M., Lluch, A., Rameh, L.E., Jacks, T., Root, D.E., Lander, E.S., Mills, G.B., Hahn, W.C., Sellers, W.R., & Garraway, L.A. (2009). *AKT-independent signaling downstream of oncogenic PIK3CA mutations in human cancer. Cancer Cell*, 16(1), 21–32. PMID: 19573809; PMCID: PMC2752826.
362. Khalil, A.M., Guttman, M., Huarte, M., Garber, M., Raj, A., Rivea Morales, D., Thomas, K., Presser, A., Bernstein, B.E., van Oudenaarden, A., Regev, A., Lander, E.S., & Rinn, J.L. (2009). *Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences USA*, 106(28), 11667–11672. PMID: 19571010; PMCID: PMC2704857.
363. Gupta, P.B., Onder, T.T., Jiang, G., Tao, K., Kuperwasser, C., Weinberg, R.A., & Lander, E.S. (2009). *Identification of selective inhibitors of cancer stem cells by high-throughput screening. Cell*, 138(4), 645–659. PMID: 19682730; PMCID: PMC4892125.
364. Gnerre, S., Lander, E.S., Lindblad-Toh, K., & Jaffe, D.B. (2009). *Assisted assembly: how to improve a de novo genome assembly by using related species. Genome Biology*, 10(8), R88. PMID: 19712469; PMCID: PMC2745769.
365. Lieberman-Aiden, E., van Berkum, N.L., Williams, L., Imakaev, M., Ragoczy, T., Telling, A., Amit, I., Lajoie, B.R., Sabo, P.J., Dorschner, M.O., Sandstrom, R., Bernstein, B., Bender, M.A., Groudine, M., Gnirke, A., Stamatoyannopoulos, J., Mirny, L.A., Lander, E.S., & Dekker, J. (2009). *Comprehensive mapping of long-range interactions reveals folding principles of the human genome. Science*, 326(5950), 289–293. PMID: 19815776; PMCID: PMC2858594.
366. Barbie, D.A., Tamayo, P., Boehm, J.S., Kim, S.Y., Moody, S.E., Dunn, I.F., Schinzel, A.C., Sandy, P., Meylan, E., Scholl, C., Fröhling, S., Chan, E.M., Sos, M.L., Michel, K., Mermel, C., Silver, S.J., Weir, B.A., Reiling, J.H., Sheng, Q., Gupta, P.B., Wadlow, R.C., Le, H., Hoersch, S., Wittner, B.S., Ramaswamy, S., Livingston, D.M., Sabatini, D.M., Meyerson, M., Thomas, R.K., Lander, E.S., Mesirov, J.P., Root, D.E., Gilliland, D.G., Jacks, T., & Hahn, W.C. (2009). *Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. Nature*, 462(7269), 108–112. PMID: 19847166; PMCID: PMC2783335.
367. Wade, C.M., Giulotto, E., Sigurdsson, S., Zoli, M., Gnerre, S., Imsland, F., Lear, T.L., Adelson, D.L., Bailey, E., Bellone, R.R., Blöcker, H., Distl, O., Edgar, R.C., Garber, M., Leeb, T., Mauceli, E., MacLeod, J.N., Penedo, M.C., Raison, J.M., Sharpe, T., Vogel, J., Andersson, L., Antczak, D.F., Biagi, T., Binns, M.M., Chowdhary, B.P., Coleman, S.J., Della Valle, G., Fryc, S., Guérin, G., Hasegawa, T., Hill, E.W., Jurka, J., Kiialainen, A., Lindgren, G., Liu, J., Magnani, E., Mickelson, J.R., Murray, J., Nergadze, S.G., Onofrio, R., Pedroni, S., Piras, M.F., Raudsepp, T., Rocchi, M., Røslund, K.H., Ryder, O.A., Searle, S., Skow, L., Swinburne, J.E., Syvänen, A.C., Tozaki, T., Valberg, S.J., Vaudin, M., White, J.R., Zody, M.C., Broad Institute Genome Sequencing Platform, Broad Institute Whole Genome Assembly Team, Lander, E.S., & Lindblad-Toh, K. (2009). *Genome sequence, comparative analysis, and population genetics of the domestic horse. Science*, 326(5954), 865–867. PMID: 19892987; PMCID: PMC3785132.
368. Markljung, E., Jiang, L., Jaffe, J.D., Mikkelsen, T.S., Wallerman, O., Larhammar, M., Zhang, X., Wang, L., Saenz-Vash, V., Gnirke, A., Lindroth, A.M., Barrés, R., Yan, J., Strömberg, S., De, S., Pontén, F., Lander, E.S., Carr, S.A., Zierath, J.R., Kullander, K., Wadelius, C., Lindblad-Toh, K., Andersson, G., Hjälm, G., & Andersson, L. (2009). *ZBED6, a novel transcription factor derived from a domesticated DNA transposon regulates IGF2 expression and muscle growth. PLoS Biology*, 7(12), e1000256. PMID: 20016685; PMCID: PMC2780926.

369. Lander, E.S., Jiang, G., & Tao, K. (2009). *Taking aim at aggressive cancer cells. Cancer Biology & Therapy*, 8(16), ii. PMID: 19830887.
370. Grossman, S.R., Shlyakhter, I., Karlsson, E.K., Byrne, E.H., Morales, S., Frieden, G., Hostetter, E., Angelino, E., Garber, M., Zuk, O., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2010). *A composite of multiple signals distinguishes causal variants in regions of positive selection. Science*, 327(5967), 883–886. PMID: 20056855.
371. Gu, H., Bock, C., Mikkelsen, T.S., Jäger, N., Smith, Z.D., Tomazou, E., Gnirke, A., Lander, E.S., & Meissner, A. (2010). *Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. Nature Methods*, 7(2), 133–136. PMID: 20062050; PMCID: PMC2860480.
372. Kim, S.Y., Dunn, I.F., Firestein, R., Gupta, P., Wardwell, L., Repich, K., Schinzel, A.C., Wittner, B., Silver, S.J., Root, D.E., Boehm, J.S., Ramaswamy, S., Lander, E.S., & Hahn, W.C. (2010). *CK1 ϵ is required for breast cancers dependent on β -catenin activity. PLoS One*, 5(2), e8979. PMID: 20126544; PMCID: PMC2813871.
373. Grossman, S.R., Shlyakhter, I., Karlsson, E.K., Byrne, E.H., Morales, S., Frieden, G., Hostetter, E., Angelino, E., Garber, M., Zuk, O., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2010). *A composite of multiple signals distinguishes causal variants in regions of positive selection. Science*, 327(5967), 883–886. PMID: 20056855.
374. Burrage, L.C., Baskin-Hill, A.E., Sinasac, D.S., Singer, J.B., Croniger, C.M., Kirby, A., Kulbokas, E.J., Daly, M.J., Lander, E.S., Broman, K.W., & Nadeau, J.H. (2010). *Genetic resistance to diet-induced obesity in chromosome substitution strains of mice. Mammalian Genome*, 21(3–4), 115–129. PMID: 20127486; PMCID: PMC3831885.
375. Beroukhi, R., Mermel, C.H., Porter, D., Wei, G., Raychaudhuri, S., Donovan, J., Barretina, J., Boehm, J.S., Dobson, J., Urashima, M., Mc Henry, K.T., Pinchback, R.M., Ligon, A.H., Cho, Y.J., Haery, L., Greulich, H., Reich, M., Winckler, W., Lawrence, M.S., Weir, B.A., Tanaka, K.E., Chiang, D.Y., Bass, A.J., Loo, A., Hoffman, C., Prensner, J., Liefeld, T., Gao, Q., Yecies, D., Signoretti, S., Maher, E., Kaye, F.J., Sasaki, H., Tepper, J.E., Fletcher, J.A., Tabernero, J., Baselga, J., Tsao, M.S., Demichelis, F., Rubin, M.A., Janne, P.A., Daly, M.J., Nucera, C., Levine, R.L., Ebert, B.L., Gabriel, S., Rustgi, A.K., Antonescu, C.R., Ladanyi, M., Letai, A., Garraway, L.A., Loda, M., Beer, D.G., True, L.D., Okamoto, A., Pomeroy, S.L., Singer, S., Golub, T.R., Lander, E.S., Getz, G., Sellers, W.R., & Meyerson, M. (2010). *The landscape of somatic copy-number alteration across human cancers. Nature*, 463(7283), 899–905. PMID: 20164920; PMCID: PMC2826709.
376. Berger, M.F., Levin, J.Z., Vijayendran, K., Sivachenko, A., Adiconis, X., Maguire, J., Johnson, L.A., Robinson, J., Verhaak, R.G., Sougnez, C., Onofrio, R.C., Ziaugra, L., Cibulskis, K., Laine, E., Barretina, J., Winckler, W., Fisher, D.E., Getz, G., Meyerson, M., Jaffe, D.B., Gabriel, S.B., Lander, E.S., Dummer, R., Gnirke, A., Nusbaum, C., & Garraway, L.A. (2010). *Integrative analysis of the melanoma transcriptome. Genome Research*, 20(4), 413–427. PMID: 20179022; PMCID: PMC2847744.
377. Guttman, M., Garber, M., Levin, J.Z., Donaghey, J., Robinson, J., Adiconis, X., Fan, L., Koziol, M.J., Gnirke, A., Nusbaum, C., Rinn, J.L., Lander, E.S., & Regev, A. (2010). *Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology*, 28(5), 503–510. PMID: 20436462; PMCID: PMC2868100.
378. International Cancer Genome Consortium, Hudson, T.J., Anderson, W., Artez, A., Barker, A.D., Bell, C., Bernabé, R.R., Bhan, M.K., Calvo, F., Eerola, I., Gerhard, D.S., Gutmacher, A., Guyer, M., Hemsley, F.M., Jennings, J.L., Kerr, D., Klatt, P., Kolar, P., Kusada, J., Lane, D.P., Laplace, F., Youyong, L., Nettekoven, G., Ozenberger, B., Peterson, J., Rao, T.S., Remacle, J., Schafer, A.J., Shibata, T., Stratton, M.R., Vockley, J.G., Watanabe, K., Yang, H., Yuen, M.M., Knoppers, B.M., Bobrow, M., Cambon-Thomsen, A., Dressler, L.G., Dyke, S.O., Joly, Y., Kato, K., Kennedy, K.L., Nicolás, P., Parker, M.J., Rial-Sebbag, E., Romeo-Casabona, C.M., Shaw, K.M., Wallace, S., Wiesner, G.L., Zeps, N., Lichter, P., Biankin, A.V., Chabannon, C., Chin, L., Clément, B., de Alava, E., Degos, F., Ferguson, M.L., Geary, P., Hayes, D.N., Hudson, T.J., Johns, A.L., Kasprzyk, A., Nakagawa, H., Penny, R., Piris, M.A., Sarin, R., Scarpa, A., Shibata, T., van de Vijver, M., Futreal, P.A., Aburatani, H., Bayés, M., Botwell, D.D., Campbell, P.J., Estivill, X., Gerhard, D.S., Grimmond, S.M., Gut, I., Hirst, M., López-Otin, C., Majumder, P., Marra, M., McPherson, J.D., Nakagawa, H., Ning, Z., Puente, X.S., Ruan, Y., Shibata, T., Stratton, M.R., Stunnenberg, H.G., Swerdlow, H., Velculescu, V.E., Wilson, R.K., Xue, H.H., Yang, L., Spellman, P.T., Bader, G.D., Boutros, P.C., Campbell, P.J., Flicek, P., Getz, G., Guigó, R., Guo, G., Haussler, D., Heath, S., Hubbard, T.J., Jiang, T.,

- Jones, S.M., Li, Q., López-Bigas, N., Luo, R., Muthuswamy, L., Ouellette, B.F., Pearson, J.V., Puente, X.S., Quesada, V., Raphael, B.J., Sander, C., Shibata, T., Speed, T.P., Stein, L.D., Stuart, J.M., Teague, J.W., Totoki, Y., Tsunoda, T., Valencia, A., Wheeler, D.A., Wu, H., Zhao, S., Zhou, G., Stein, L.D., Guigó, R., Hubbard, T.J., Joly, Y., Jones, S.M., Kasprzyk, A., Lathrop, M., López-Bigas, N., Ouellette, B.F., Spellman, P.T., Teague, J.W., Thomas, G., Valencia, A., Yoshida, T., Kennedy, K.L., Axton, M., Dyke, S.O., Futreal, P.A., Gerhard, D.S., Gunter, C., Guyer, M., Hudson, T.J., McPherson, J.D., Miller, L.J., Ozenberger, B., Shaw, K.M., Kasprzyk, A., Stein, L.D., Zhang, J., Haider, S.A., Wang, J., Yung, C.K., Cros, A., Liang, Y., Gnaneshan, S., Guberman, J., Hsu, J., Bobrow, M., Chalmers, D.R., Hasel, K.W., Joly, Y., Kaan, T.S., Kennedy, K.L., Knoppers, B.M., Lowrance, W.W., Masui, T., Nicolas, P., Rial-Sebbag, E., Rodriguez, L.L., Vergely, C., Yoshida, T., Grimmond, S.M., Biankin, A.V., Bowtell, D.D., Cloonan, N., deFazio, A., Eshleman, J.R., Etemadmoghadam, D., Gardiner, B.B., Kench, J.G., Scarpa, A., Sutherland, R.L., Tempero, M.A., Waddell, N.J., Wilson, P.J., McPherson, J.D., Gallinger, S., Tsao, M.S., Shaw, P.A., Petersen, G.M., Mukhopadhyay, D., Chin, L., DePinho, R.A., Thayer, S., Muthuswamy, L., Shazand, K., Beck, T., Sam, M., Timms, L., Ballin, V., Lu, Y., Ji, J., Zhang, X., Chen, F., Hu, X., Zhou, G., Yang, Q., Tian, G., Zhang, L., Xing, X., Li, X., Zhu, Z., Yu, Y., Yu, J., Yang, H., Lathrop, M., Tost, J., Brennan, P., Holcatova, I., Zaridze, D., Brazma, A., Egevard, L., Prokhortchouk, E., Banks, R.E., Uhlén, M., Cambon-Thomsen, A., Viksna, J., Ponten, F., Skryabin, K., Stratton, M.R., Futreal, P.A., Birney, E., Borg, A., Børesen-Dale, A.L., Caldas, C., Foekens, J.A., Martin, S., Reis-Filho, J.S., Richardson, A.L., Sotiriou, C., Stunnenberg, H.G., Thoms, G., van de Vijver, M., van't Veer, L., Calvo, F., Birnbaum, D., Blanche, H., Boucher, P., Boyault, S., Chabannon, C., Gut, I., Masson-Jacquemier, J.D., Lathrop, M., Pauporte, I., Pivot, X., Vincent-Salomon, A., Tabone, E., Theillet, C., Thomas, G., Tost, J., Treilleux, I., Calvo, F., Bioulac-Sage, P., Clément, B., Decaens, T., Degos, F., Franco, D., Gut, I., Gut, M., Heath, S., Lathrop, M., Samuel, D., Thomas, G., Zucman-Rossi, J., Lichter, P., Eils, R., Brors, B., Korbel, J.O., Korshunov, A., Landgraf, P., Lehrach, H., Pfister, S., Radlwimmer, B., Reifemberger, G., Taylor, M.D., von Kalle, C., Majumder, P.P., Sarin, R., Rao, T.S., Bhan, M.K., Scarpa, A., Pederzoli, P., Lawlor, R.A., Delledonne, M., Bardelli, A., Biankin, A.V., Grimmond, S.M., Gress, T., Klimstra, D., Zamboni, G., Shibata, T., Nakamura, Y., Nakagawa, H., Kusada, J., Tsunoda, T., Miyano, S., Aburatani, H., Kato, K., Fujimoto, A., Yoshida, T., Campo, E., López-Otin, C., Estivill, X., Guigó, R., de Sanjose, S., Piris, M.A., Montserrat, E., González-Díaz, M., Puente, X.S., Jares, P., Valencia, A., Himmelbauer, H., Quesada, V., Bea, S., Stratton, M.R., Futreal, P.A., Campbell, P.J., Vincent-Salomon, A., Richardson, A.L., Reis-Filho, J.S., van de Vijver, M., Thomas, G., Masson-Jacquemier, J.D., Aparicio, S., Borg, A., Børesen-Dale, A.L., Caldas, C., Foekens, J.A., Stunnenberg, H.G., van't Veer, L., Easton, D.F., Spellman, P.T., Martin, S., Barker, A.D., Chin, L., Collins, F.S., Compton, C.C., Ferguson, M.L., Gerhard, D.S., Getz, G., Gunter, C., Gutmacher, A., Guyer, M., Hayes, D.N., Lander, E.S., Ozenberger, B., Penny, R., Peterson, J., Sander, C., Shaw, K.M., Speed, T.P., Spellman, P.T., Vockley, J.G., Wheeler, D.A., Wilson, R.K., Hudson, T.J., Chin, L., Knoppers, B.M., Lander, E.S., Lichter, P., Stein, L.D., Stratton, M.R., Anderson, W., Barker, A.D., Bell, C., Bobrow, M., Burke, W., Collins, F.S., Compton, C.C., DePinho, R.A., Easton, D.F., Futreal, P.A., Gerhard, D.S., Green, A.R., Guyer, M., Hamilton, S.R., Hubbard, T.J., Kallioniemi, O.P., Kennedy, K.L., Ley, T.J., Liu, E.T., Lu, Y., Majumder, P., Marra, M., Ozenberger, B., Peterson, J., Schafer, A.J., Spellman, P.T., Stunnenberg, H.G., Wainwright, B.J., Wilson, R.K., & Yang, H. (2010). *International network of cancer genome projects. Nature*, 464(7291), 993–998. PMID: 20393554; PMCID: PMC2902243.
379. Green, R.E., Krause, J., Briggs, A.W., Maricic, T., Stenzel, U., Kircher, M., Patterson, N., Li, H., Zhai, W., Fritz, M.H., Hansen, N.F., Durand, E.Y., Malaspinas, A.S., Jensen, J.D., Marques-Bonet, T., Alkan, C., Prüfer, K., Meyer, M., Burbano, H.A., Good, J.M., Schultz, R., Aximu-Petri, A., Butthof, A., Höber, B., Höffner, B., Siegemund, M., Weihmann, A., Nusbaum, C., Lander, E.S., Russ, C., Novod, N., Affourtit, J., Egholm, M., Verna, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Doronichev, V.B., Golovanova, L.V., Lalueza-Fox, C., de la Rasilla, M., Fortea, J., Rosas, A., Schmitz, R.W., Johnson, P.L., Eichler, E.E., Falush, D., Birney, E., Mullikin, J.C., Slatkin, M., Nielsen, R., Kelso, J., Lachmann, M., Reich, D., & Pääbo, S. (2010). *A draft sequence of the Neandertal genome. Science*, 328(5979), 710–722. PMID: 20448178.
380. van Berkum, N.L., Lieberman-Aiden, E., Williams, L., Imakaev, M., Gnirke, A., Mirny, L.A., Dekker, J., & Lander, E.S. (2010). *Hi-C: a method to study the three-dimensional architecture of genomes. Journal of Visualized Experiments*, (39), e1869-e1869. PMID: 20461051; PMCID: PMC3149993.

381. Aiden, A.P., Rivera, M.N., Rheinbay, E., Ku, M., Coffman, E.J., Truong, T.T., Vargas, S.O., Lander, E.S., Haber, D.A., & Bernstein, B.E. (2010). *Wilms tumor chromatin profiles highlight stem cell properties and a renal developmental network*. *Cell Stem Cell*, 6(6), 591–602. PMID: 20569696; PMCID: PMC2897075.
382. Barretina, J., Taylor, B.S., Banerji, S., Ramos, A.H., Lagos-Quintana, M., Decarolis, P.L., Shah, K., Socci, N.D., Weir, B.A., Ho, A., Chiang, D.Y., Reva, B., Mermel, C.H., Getz, G., Antipin, Y., Beroukhi, R., Major, J.E., Hatton, C., Nicoletti, R., Hanna, M., Sharpe, T., Fennell, T.J., Cibulskis, K., Onofrio, R.C., Saito, T., Shukla, N., Lau, C., Nelander, S., Silver, S.J., Sougnez, C., Viale, A., Winckler, W., Maki, R.G., Garraway, L.A., Lash, A., Greulich, H., Root, D.E., Sellers, W.R., Schwartz, G.K., Antonescu, C.R., Lander, E.S., Varmus, H.E., Ladanyi, M., Sander, C., Meyerson, M., & Singer, S. (2010). *Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy*. *Nature Genetics*, 42(8), 715–721. PMID: 20601955; PMCID: PMC2911503.
383. Huarte, M., Guttman, M., Feldser, D., Garber, M., Koziol, M.J., Kenzelmann-Broz, D., Khalil, A.M., Zuk, O., Amit, I., Rabani, M., Attardi, L.D., Regev, A., Lander, E.S., Jacks, T., & Rinn, J.L. (2010). *A large intergenic noncoding RNA induced by p53 mediates global gene repression in the p53 response*. *Cell*, 142(3), 409–419. PMID: 20673990; PMCID: PMC2956184.
384. Taube, J.H., Herschkowitz, J.I., Komurov, K., Zhou, A.Y., Gupta, S., Yang, J., Hartwell, K., Onder, T.T., Gupta, P.B., Evans, K.W., Hollier, B.G., Ram, P.T., Lander, E.S., Rosen, J.M., Weinberg, R.A., & Mani, S.A. (2010). *Core epithelial-to-mesenchymal transition interactome gene-expression signature is associated with claudin-low and metaplastic breast cancer subtypes*. *Proceedings of the National Academy of Sciences USA*, 107(35), 15449–15454. PMID: 20713713; PMCID: PMC2932589.
385. Bernstein, B.E., Stamatoyannopoulos, J.A., Costello, J.F., Ren, B., Milosavljevic, A., Meissner, A., Kellis, M., Marra, M.A., Beaudet, A.L., Ecker, J.R., Farnham, P.J., Hirst, M., Lander, E.S., Mikkelsen, T.S., & Thomson, J.A. (2010). *The NIH roadmap epigenomics mapping consortium*. *Nature Biotechnology*, 28(10), 1045–1048. PMID: 20944595; PMCID: PMC3607281.
386. Mikkelsen, T.S., Xu, Z., Zhang, X., Wang, L., Gimble, J.M., Lander, E.S., & Rosen, E.D. (2010). *Comparative epigenomic analysis of murine and human adipogenesis*. *Cell*, 143(1), 156–169. PMID: 20887899; PMCID: PMC2950833.
387. Lander, E.S., & Gates, S.J. (2010). *Prepare and inspire*. *Science*, 330(6001), 151. PMID: 20929738.
388. Neafsey, D.E., Lawnczak, M.K., Park, D.J., Redmond, S.N., Coulibaly, M.B., Traore, S.F., Sagnon, N., Costantini, C., Johnson, C., Wiegand, R.C., Collins, F.H., Lander, E.S., Wirth, D.F., Kafatos, F.C., Besansky, N.J., Christophides, G.K., & Muskavitch, M.A. (2010). *SNP genotyping defines complex gene-flow boundaries among African malaria vector mosquitoes*. *Science*, 330(6003), 514–517. PMID: 20966254; PMCID: PMC4811326.
389. Loewer, S., Cabili, M.N., Guttman, M., Loh, Y.H., Thomas, K., Park, I.H., Garber, M., Curran, M., Onder, T., Agarwal, S., Manos, P.D., Datta, S., Lander, E.S., Schlaeger, T.M., Daley, G.Q., & Rinn, J.L. (2010). *Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells*. *Nature Genetics*, 42(12), 1113–1117. PMID: 21057500; PMCID: PMC3040650.
390. Fillmore, C.M., Gupta, P.B., Rudnick, J.A., Caballero, S., Keller, P.J., Lander, E.S., & Kuperwasser, C. (2010). *Estrogen expands breast cancer stem-like cells through paracrine FGF/Tbx3 signaling*. *Proceedings of the National Academy of Sciences USA*, 107(50), 21737–21742. PMID: 21098263; PMCID: PMC3003123.
391. Gnerre, S., Maccallum, I., Przybylski, D., Ribeiro, F.J., Burton, J.N., Walker, B.J., Sharpe, T., Hall, G., Shea, T.P., Sykes, S., Berlin, A.M., Aird, D., Costello, M., Daza, R., Williams, L., Nicol, R., Gnirke, A., Nusbaum, C., Lander, E.S., & Jaffe, D.B. (2011). *High-quality draft assemblies of mammalian genomes from massively parallel sequence data*. *Proceedings of the National Academy of Sciences USA*, 108(4), 1513–1518. PMID: 21187386; PMCID: PMC3029755.
392. Robinson, J.T., Thorvaldsdóttir, H., Winckler, W., Guttman, M., Lander, E.S., Getz, G., & Mesirov, J.P. (2011). *Integrative genomics viewer*. *Nature Biotechnology*, 29(1), 24–26. PMID: 21221095; PMCID: PMC3346182.
393. Sankaran, V.G., Menne, T.F., Scepanovic, D., Vergilio, J.A., Ji, P., Kim, J., Thiru, P., Orkin, S.H., Lander, E.S., & Lodish H.F. (2011). *MicroRNA-15a and -16-1 act via MYB to elevate fetal hemoglobin expression in human trisomy 13*. *Proceedings of the National Academy of Sciences USA*, 108(4), 1519–1524. PMID: 21205891; PMCID: PMC3029749.
394. Mills, R.E., Walter, K., Stewart, C., Handsaker, R.E., Chen, K., Alkan, C., Abyzov, A., Yoon, S.C., Ye, K., Cheetham, R.K., Chinwalla, A., Conrad, D.F., Fu, Y., Grubert, F., Hajirasouliha, I., Hormozdiari, F., Iakoucheva, L.M., Iqbal, Z., Kang,

- S., Kidd, J.M., Konkel, M.K., Korn, J., Khurana, E., Kural, D., Lam, H.Y., Leng, J., Li, R., Li, Y., Lin, C.Y., Luo, R., Mu, X.J., Nemesh, J., Peckham, H.E., Rausch, T., Scally, A., Shi, X., Stromberg, M.P., Stütz, A.M., Urban, A.E., Walker, J.A., Wu, J., Zhang, Y., Zhang, Z.D., Batzer, M.A., Ding, L., Marth, G.T., McVean, G., Sebat, J., Snyder, M., Wang, J., Ye, K., Eichler, E.E., Gerstein, M.B., Hurles, M.E., Lee, C., McCarroll, S.A., Korb, J.O., & 1000 Genomes Project. (2011). *Mapping copy number variation by population-scale genome sequencing. Nature*, 470(7332), 59–65. PMID: 21293372; PMCID: PMC3077050.
395. Proia, T.A., Keller, P.J., Gupta, P.B., Klebba, I., Jones, A.D., Sedic, M., Gilmore, H., Tung, N., Naber, S.P., Schnitt, S., Lander, E.S., & Kuperwasser, C. (2011). *Genetic predisposition directs breast cancer phenotype by dictating progenitor cell fate. Cell Stem Cell*, 8(2), 149–163. PMID: 21295272; PMCID: PMC3050563.
396. Lander, E.S. (2011). *Initial impact of the sequencing of the human genome. Nature*, 470(7333), 187–197. PMID: 21307931.
397. Berger, M.F., Lawrence, M.S., Demichelis, F., Drier, Y., Cibulskis, K., Sivachenko, A.Y., Sboner, A., Esgueva, R., Pflueger, D., Sougnez, C., Onofrio, R., Carter, S.L., Park, K., Habegger, L., Ambrogio, L., Fennell, T., Parkin, M., Saksena, G., Voet, D., Ramos, A.H., Pugh, T.J., Wilkinson, J., Fisher, S., Winckler, W., Mahan, S., Ardlie, K., Baldwin, J., Simons, J.W., Kitabayashi, N., MacDonald, T.Y., Kantoff, P.W., Chin, L., Gabriel, S.B., Gerstein, M.B., Golub, T.R., Meyerson, M., Tewari, A., Lander, E.S., Getz, G., Rubin, M.A., & Garraway, L.A. (2011). *The genomic complexity of primary human prostate cancer. Nature*, 470(7333), 214–220. PMID: 21307934; PMCID: PMC3075885.
398. Reshef, D.N., Reshef, Y.A., Finucane, H.K., Grossman, S.R., McVean, G., Turnbaugh, P.J., Lander, E.S., Mitzenmacher, M., & Sabeti, P.C. (2011). *Detecting novel associations in large data sets. Science*, 334(6062), 1518–1524. PMID: 22174245; PMCID: PMC3325791.
399. Wang, L., Lawrence, M.S., Wan, Y., Stojanov, P., Sougnez, C., Stevenson, K., Werner, L., Sivachenko, A., DeLuca, D.S., Zhang, L., Zhang, W., Vartanov, A.R., Fernandes, S.M., Goldstein, N.R., Folco, E.G., Cibulskis, K., Tesar, B., Sievers, Q.L., Shefler, E., Gabriel, S., Hacohen, N., Reed, R., Meyerson, M., Golub, T.R., Lander, E.S., Neuber, D., Brown, J.R., Getz, G., & Wu, C.J. (2011). *SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. New England Journal of Medicine*, 365(26), 2497–2506. PMID: 22150006; PMCID: PMC3685413.
400. Lander, E.S. (2011). *Genome-sequencing. The accelerator. Science* 331:1024.
401. Chapman, M.A., Lawrence, M.S., Keats, J.J., Cibulskis, K., Sougnez, C., Schinzel, A.C., Harview, C.L., Brunet, J.P., Ahmann, G.J., Adli, M., Anderson, K.C., Ardlie, K.G., Auclair, D., Baker, A., Bergsagel, P.L., Bernstein, B.E., Drier, Y., Fonseca, R., Gabriel, S.B., Hofmeister, C.C., Jagannath, S., Jakubowiak, A.J., Krishnan, A., Levy, J., Liefeld, T., Lonial, S., Mahan, S., Mfuko, B., Monti, S., Perkins, L.M., Onofrio, R., Pugh, T.J., Rajkumar, S.V., Ramos, A.H., Siegel, D.S., Sivachenko, A., Stewart, A.K., Trudel, S., Vij, R., Voet, D., Winckler, W., Zimmerman, T., Carpten, J., Trent, J., Hahn, W.C., Garraway, L.A., Meyerson, M., Lander, E.S., Getz, G., & Golub, T.R. (2011). *Initial genome sequencing and analysis of multiple myeloma. Nature*, 471(7339), 467–472. PMID: 21430775; PMCID: PMC3560292.
402. Van Tyne, D., Park, D.J., Schaffner, S.F., Neafsey, D.E., Angelino, E., Cortese, J.F., Barnes, K.G., Rosen, D.M., Lukens, A.K., Daniels, R.F., Milner, D.A., Johnson, C.A., Shlyakhter, I., Grossman, S.R., Becker, J.S., Yamins, D., Karlsson, E.K., Ndiaye, D., Sarr, O., Mboup, S., Happi, C., Furlotte, N.A., Eskin, E., Kang, H.M., Hartl, D.L., Birren, B.W., Wiegand, R.C., Lander, E.S., Wirth, D.F., Volkman, S.K., & Sabeti, P.C. (2011). *Identification and functional validation of the novel antimalarial resistance locus PF10_0355 in Plasmodium falciparum. PLoS Genetics*, 7(4), e1001383. PMID: 21533027; PMCID: PMC3080868.
403. Conrad, D.F., Keebler, J.E., DePristo, M.A., Lindsay, S.J., Zhang, Y., Casals, F., Idaghdour, Y., Hartl, C.L., Torroja, C., Garimella, K.V., Zilversmit, M., Cartwright, R., Rouleau, G.A., Daly, M., Stone, E.A., Hurles, M.E., Awadalla, P., & 1000 Genomes Project. (2011). *Variation in genome-wide mutation rates within and between human families. Nature Genetics*, 43(7), 712–714. PMID: 21666693; PMCID: PMC3322360.
404. Cheung, H.W., Cowley, G.S., Weir, B.A., Boehm, J.S., Rusin, S., Scott, J.A., East, A., Ali, L.D., Lizotte, P.H., Wong, T.C., Jiang, G., Hsiao, J., Mermel, C.H., Getz, G., Barretina, J., Gopal, S., Tamayo, P., Gould, J., Tsherniak, A., Stransky, N., Luo, B., Ren, Y., Drapkin, R., Bhatia, S.N., Mesirov, J.P., Garraway, L.A., Meyerson, M., Lander, E.S., Root, D.E., & Hahn, W.C. (2011). *Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. Proceedings of the National Academy of Sciences USA*, 108(30), 12372–12377. PMID: 21746896; PMCID: PMC3145679.

405. Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., McVean, G., Durbin, R., & 1000 Genomes Project Analysis Group. (2011). *The variant call format and VCFtools*. *Bioinformatics*, 27(15), 2156–2158. PMID: 21653522; PMCID: PMC3137218 .
406. Gupta, P.B., Fillmore, C.M., Jiang, G., Shapira, S.D., Tao, K., Kuperwasser, C., & Lander, E.S. (2011). *Stochastic state transitions give rise to phenotypic equilibrium in populations of cancer cells*. *Cell*, 146(4), 633–644. PMID: 21854987.
407. Stransky, N., Egloff, A.M., Tward, A.D., Kostic, A.D., Cibulskis, K., Sivachenko, A., Kryukov, G.V., Lawrence, M.S., Sougnez, C., McKenna, A., Shefler, E., Ramos, A.H., Stojanov, P., Carter, S.L., Voet, D., Cortés, M.L., Auclair, D., Berger, M.F., Saksena, G., Guiducci, C., Onofrio, R.C., Parkin, M., Romkes, M., Weissfeld, J.L., Seethala, R.R., Wang, L., Rangel-Escareño, C., Fernandez-Lopez, J.C., Hidalgo-Miranda, A., Melendez-Zajgla, J., Winckler, W., Ardlie, K., Gabriel, S.B., Meyerson, M., Lander, E.S., Getz, G., Golub, T.R., Garraway, L.A., & Grandis, J.R. (2011). *The mutational landscape of head and neck squamous cell carcinoma*. *Science*, 333(6046), 1157–1160. PMID: 21798893; PMCID: PMC3415217.
408. Guttman, M., Donaghey, J., Carey, B.W., Garber, M., Grenier, J.K., Munson, G., Young, G., Lucas, A.B., Ach, R., Bruhn, L., Yang, X., Amit, I., Meissner, A., Regev, A., Rinn, J.L., Root, D.E., & Lander, E.S. (2011). *lincRNAs act in the circuitry controlling pluripotency and differentiation*. *Nature*, 477(7364), 295–300. PMID: 21874018; PMCID: PMC3175327.
409. Alföldi, J., Di Palma, F., Grabherr, M., Williams, C., Kong, L., Mauceli, E., Russell, P., Lowe, C.B., Glor, R.E., Jaffe, J.D., Ray, D.A., Boissinot, S., Shedlock, A.M., Botka, C., Castoe, T.A., Colbourne, J.K., Fujita, M.K., Moreno, R.G., ten Hallers, B.F., Haussler, D., Heger, A., Heiman, D., Janes, D.E., Johnson, J., de Jong, P.J., Koriabine, M.Y., Lara, M., Novick, P.A., Organ, C.L., Peach, S.E., Poe, S., Pollock, D.D., de Queiroz, K., Sanger, T., Searle, S., Smith, J.D., Smith, Z., Swofford, R., Turner-Maier, J., Wade, J., Young, S., Zadissa, A., Edwards, S.V., Glenn, T.C., Schneider, C.J., Losos, J.B., Lander, E.S., Breen, M., Ponting, C.P., & Lindblad-Toh, K. (2011). *The genome of the green anole lizard and a comparative analysis with birds and mammals*. *Nature*, 477(7366), 587–591. PMID: 21881562; PMCID: PMC3184186.
410. Bass, A.J., Lawrence, M.S., Brace, L.E., Ramos, A.H., Drier, Y., Cibulskis, K., Sougnez, C., Voet, D., Saksena, G., Sivachenko, A., Jing, R., Parkin, M., Pugh, T., Verhaak, R.G., Stransky, N., Boutin, A.T., Barretina, J., Solit, D.B., Vakiani, E., Shao, W., Mishina, Y., Warmuth, M., Jimenez, J., Chiang, D.Y., Signoretti, S., Kaelin, W.G., Spardy, N., Hahn, W.C., Hoshida, Y., Ogino, S., Depinho, R.A., Chin, L., Garraway, L.A., Fuchs, C.S., Baselga, J., Tabernero, J., Gabriel, S., Lander, E.S., Getz, G., & Meyerson, M. (2011). *Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion*. *Nature Genetics*, 43(10), 964–968. PMID: 21892161; PMCID: PMC3802528.
411. Lindblad-Toh, K., Garber, M., Zuk, O., Lin, M.F., Parker, B.J., Washietl, S., Kheradpour, P., Ernst, J., Jordan, G., Mauceli, E., Ward, L.D., Lowe, C.B., Holloway, A.K., Clamp, M., Gnerre, S., Alföldi, J., Beal, K., Chang, J., Clawson, H., Cuff, J., Di Palma, F., Fitzgerald, S., Flicek, P., Guttman, M., Hubisz, M.J., Jaffe, D.B., Jungreis, I., Kent, W.J., Kostka, D., Lara, M., Martins, A.L., Massingham, T., Moltke, I., Raney, B.J., Rasmussen, M.D., Robinson, J., Stark, A., Vilella, A.J., Wen, J., Xie, X., Zody, M.C., Broad Institute Sequencing Platform and Whole Genome Assembly Team, Baldwin, J., Bloom, T., Chin, C.W., Heiman, D., Nicol, R., Nusbaum, C., Young, S., Wilkinson, J., Worley, K.C., Kovar, C.L., Muzny, D.M., Gibbs, R.A., Baylor College of Medicine Human Genome Sequencing Center Sequencing Team, Cree, A., Dihn, H.H., Fowler, G., Jhangiani, S., Joshi, V., Lee, S., Lewis, L.R., Nazareth, L.V., Okwuonu, G., Santibanez, J., Warren, W.C., Mardis, E.R., Weinstock, G.M., Wilson, R.K., Genome Institute at Washington University, Delehaunty, K., Dooling, D., Fronik, C., Fulton, L., Fulton, B., Graves, T., Minx, P., Sodergren, E., Birney, E., Margulies, E.H., Herrero, J., Green, E.D., Haussler, D., Siepel, A., Goldman, N., Pollard, K.S., Pedersen, J.S., Lander, E.S., & Kellis, M. (2011). *A high-resolution map of human evolutionary constraint using 29 mammals*. *Nature*, 478(7370), 476–482. PMID: 21993624; PMCID: PMC3207357.
412. Zuk, O., Hechter, E., Sunyaev, S.R., & Lander, E.S. (2012). *The mystery of missing heritability: Genetic interactions create phantom heritability*. *Proceedings of the National Academy of Sciences USA*, 109(4), 1193–1198. PMID: 22223662; PMCID: PMC3268279.
413. Grad, Y.H., Lipsitch, M., Feldgarden, M., Arachchi, H.M., Cerqueira, G.C., Fitzgerald, M., Godfrey, P., Haas, B.J., Murphy, C.I., Russ, C., Sykes, S., Walker, B.J., Wortman, J.R., Young, S., Zeng, Q., Abouelleil, A., Bochicchio, J., Chauvin, S., Desmet, T., Gujja, S., McCowan, C., Montmayeur, A., Steelman, S., Frimodt-

- Mosher, J., Petersen, A.M., Struve, C., Krogfelt, K.A., Bingen, E., Weill, F.X., Lander, E.S., Nusbaum, C., Birren, B.W., Hung, D.T., & Hanage, W.P. (2012). *Genomic epidemiology of the Escherichia coli O104: H4 outbreaks in Europe, 2011. Proceedings of the National Academy of Sciences USA*, 109(8), 3065–3070. PMID: 22315421; PMCID: PMC3286951.
414. Lohr, J.G., Stojanov, P., Lawrence, M.S., Auclair, D., Chapuy, B., Sougnez, C., Cruz-Gordillo, P., Knoechel, B., Asmann, Y.W., Slager, S.L., Novak, A.J., Dogan, A., Ansell, S.M., Link, B.K., Zou, L., Gould, J., Saksena, G., Stransky, N., Rangel-Escareño, C., Fernandez-Lopez, J.C., Hidalgo-Miranda, A., Melendez-Zajgla, J., Hernández-Lemus, E., Schwarz-Cruz y Celis, A., Imaz-Rosshandler, I., Ojesina, A.I., Jung, J., Pedamallu, C.S., Lander, E.S., Habermann, T.M., Cerhan, J.R., Shipp, M.A., Getz, G., & Golub, T.R. (2012). *Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. Proceedings of the National Academy of Sciences USA*, 109(10), 3879–3884. PMID: 22343534; PMCID: PMC3309757.
415. Melnikov, A., Murugan, A., Zhang, X., Tesileanu, T., Wang, L., Rogov, P., Feizi, S., Gnirke, A., Callan, C.G., Kinney, J.B., Kellis, M., Lander, E.S., & Mikkelsen, T.S. (2012). *Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. Nature Biotechnology*, 30(3), 271–277. PMID: 22371084; PMCID: PMC3297981.
416. Onder, T.T., Kara, N., Cherry, A., Sinha, A.U., Zhu, N., Bernt, K.M., Cahan, P., Marcarci, B.O., Unternaehrer, J., Gupta, P.B., Lander, E.S., Armstrong, S.A., & Daley, G.Q. (2012). *Chromatin-modifying enzymes as modulators of reprogramming. Nature*, 483(7391), 598–602. PMID: 22388813; PMCID: PMC3501145.
417. Jones, F.C., Grabherr, M.G., Chan, Y.F., Russell, P., Mauceli, E., Johnson, J., Swofford, R., Pirun, M., Zody, M.C., White, S., Birney, E., Searle, S., Schmutz, J., Grimwood, J., Dickson, M.C., Myers, R.M., Miller, C.T., Summers, B.R., Knecht, A.K., Brady, S.D., Zhang, H., Pollen, A.A., Howes, T., Amemiya, C., Broad Institute Genome Sequencing Platform & Whole Genome Assembly Team, Baldwin, J., Bloom, T., Jaffe, D.B., Nicol, R., Wilkinson, J., Lander, E.S., Di Palma, F., Lindblad-Toh, K., & Kingsley, D.M. (2012). *The genomic basis of adaptive evolution in threespine sticklebacks. Nature*, 484(7392), 55–61. PMID: 22481358; PMCID: PMC3322419.
418. Cancer Genome Atlas Research Network. (2012). *Comprehensive genomic characterization of squamous cell lung cancers. Nature*, 489(7417), 519–525. PMID: 22960745; PMCID: PMC3466113.
419. Carter, S.L., Cibulskis, K., Helman, E., McKenna, A., Shen, H., Zack, T., Laird, P.W., Onofrio, R.C., Winckler, W., Weir, B.A., Beroukhi, R., Pellman, D., Levine, D.A., Lander, E.S., Meyerson, M., & Getz, G. (2012). *Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology*, 30(5), 413–421. PMID: 22544022; PMCID: PMC4383288.
420. Berger, M.F., Hodis, E., Heffernan, T.P., Deribe, Y.L., Lawrence, M.S., Protopopov, A., Ivanova, E., Watson, I.R., Nickerson, E., Ghosh, P., Zhang, H., Zeit, R., Ren, X., Cibulskis, K., Sivachenko, A.Y., Wagle, N., Sucker, A., Sougnez, C., Onofrio, R., Ambrogio, L., Auclair, D., Fennell, T., Carter, S.L., Drier, Y., Stojanov, P., Singer, M.A., Voet, D., Jing, R., Saksena, G., Barretina, J., Ramos, A.H., Pugh, T.J., Stransky, N., Parkin, M., Winckler, W., Mahan, S., Ardlie, K., Baldwin, J., Wargo, J., Schadendorf, D., Meyerson, M., Gabriel, S.B., Golub, T.R., Wagner, S.N., Lander, E.S., Getz, G., Chin, L., & Garraway, L.A. (2012). *Melanoma genome sequencing reveals frequent PREX2 mutations. Nature*, 485(7399), 502–506. PMID: 22622578; PMCID: PMC3367798.
421. Germain, A.R., Carmody, L.C., Morgan, B., Fernandez, C., Forbeck, E., Lewis, T.A., Nag, P.P., Ting, A., VerPlank, L., Feng, Y., Perez, J.R., Dandapani, S., Palmer, M., Lander, E.S., Gupta, P.B., Schreiber, S.L., & Munoz, B. (2012). *Identification of a selective small molecule inhibitor of breast cancer stem cells. Bioorganic & Medicinal Chemistry Letters*, 22(10), 3571–3574. PMID: 22503247.
422. Barbieri, C.E., Baca, S.C., Lawrence, M.S., Demichelis, F., Blattner, M., Theurillat, J.P., White, T.A., Stojanov, P., Van Allen, E., Stransky, N., Nickerson, E., Chae, S.S., Boysen, G., Auclair, D., Onofrio, R.C., Park, K., Kitabayashi, N., MacDonald, T.Y., Sheikh, K., Vuong, T., Guiducci, C., Cibulskis, K., Sivachenko, A., Carter, S.L., Saksena, G., Voet, D., Hussain, W.M., Ramos, A.H., Winckler, W., Redman, M.C., Ardlie, K., Tewari, A.K., Mosquera, J.M., Rupp, N., Wild, P.J., Moch, H., Morrissey, C., Nelson, P.S., Kantoff, P.W., Gabriel, S.B., Golub, T.R., Meyerson, M., Lander, E.S., Getz, G., Rubin, M.A., & Garraway, L.A. (2012). *Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics*, 44(6), 685–689. PMID: 22610119; PMCID: PMC3673022.
423. Banerji, S., Cibulskis, K., Rangel-Escareno, C., Brown, K.K., Carter, S.L., Frederick, A.M., Lawrence, M.S., Sivachenko, A.Y., Sougnez, C., Zou, L., Cortes,

M.L., Fernandez-Lopez, J.C., Peng, S., Ardlie, K.G., Auclair, D., Bautista-Piña, V., Duke, F., Francis, J., Jung, J., Maffuz-Aziz, A., Onofrio, R.C., Parkin, M., Pho, N.H., Quintanar-Jurado, V., Ramos, A.H., Rebollar-Vega, R., Rodriguez-Cuevas, S., Romero-Cordoba, S.L., Schumacher, S.E., Stransky, N., Thompson, K.M., Uribe-Figueroa, L., Baselga, J., Beroukhir, R., Polyak, K., Sgroi, D.C., Richardson, A.L., Jimenez-Sanchez, G., Lander, E.S., Gabriel, S.B., Garraway, L.A., Golub, T.R., Melendez-Zajgla, J., Toker, A., Getz, G., Hidalgo-Miranda, A., & Meyerson, M. (2012). *Sequence analysis of mutations and translocations across breast cancer subtypes*. *Nature*, 486(7403), 405–409. PMID: 22722202; PMCID: PMC4148686.

424. Sankaran, V.G., Ghazvinian, R., Do, R., Thiru, P., Vergilio, J.A., Beggs, A.H., Sieff, C.A., Orkin, S.H., Nathan, D.G., Lander, E.S., & Gazda, H.T. (2012). *Exome sequencing identifies GATA1 mutations resulting in Diamond-Blackfan anemia*. *The Journal of Clinical Investigation*, 122(7), 2439–2443. PMID: 22706301; PMCID: PMC3386831.

425. Hodis, E., Watson, I.R., Kryukov, G.V., Arold, S.T., Imielinski, M., Theurillat, J.P., Nickerson, E., Auclair, D., Li, L., Place, C., Dicara, D., Ramos, A.H., Lawrence, M.S., Cibulskis, K., Sivachenko, A., Voet, D., Saksena, G., Stransky, N., Onofrio, R.C., Winckler, W., Ardlie, K., Wagle, N., Wargo, J., Chong, K., Morton, D.L., Stenke-Hale, K., Chen, G., Noble, M., Meyerson, M., Ladbury, J.E., Davies, M.A., Gershenwald, J.E., Wagner, S.N., Hoon, D.S., Schadendorf, D., Lander, E.S., Gabriel, S.B., Getz, G., Garraway, L.A., & Chin, L. (2012). *A landscape of driver mutations in melanoma*. *Cell*, 150(2), 251–263. PMID: 22817889; PMCID: PMC3600117.

426. Imielinski, M., Berger, A.H., Hammerman, P.S., Hernandez, B., Pugh, T.J., Hodis, E., Cho, J., Suh, J., Capelletti, M., Sivachenko, A., Sougnez, C., Auclair, D., Lawrence, M.S., Stojanov, P., Cibulskis, K., Choi, K., de Waal, L., Sharifnia, T., Brooks, A., Greulich, H., Banerji, S., Zander, T., Seidel, D., Leenders, F., Ansen, S., Ludwig, C., Engel-Riedel, W., Stoelben, E., Wolf, J., Goparaju, C., Thompson, K., Winckler, W., Kwiakowski, D., Johnson, B.E., Jänne, P.A., Miller, V.A., Pao, W., Travis, W.D., Pass, H.I., Gabriel, S.B., Lander, E.S., Thomas, R.K., Garraway, L.A., Getz, G., & Meyerson, M. (2012). *Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing*. *Cell*, 150(6), 1107–1120. PMID: 22980975; PMCID: PMC3557932.

427. Sankaran, V.G., Ludwig, L.S., Sicinska, E., Xu, J., Bauer, D.E., Eng, J.C., Patterson, H.C., Metcalf, R.A., Natkunam, Y., Orkin, S.H., Sicinski, P., Lander, E.S., & Lodish, H.F. (2012). *Cyclin D3 coordinates the cell cycle during differentiation to regulate erythrocyte size and number*. *Genes & Development*, 26(18), 2075–2087. PMID: 22929040; PMCID: PMC3444733.

428. Gire, S.K., Stremlau, M., Andersen, K.G., Schaffner, S.F., Bjornson, Z., Rubins, K., Hensley, L., McCormick, J.B., Lander, E.S., Garry, R.F., Hapji, C., & Sabeti, P.C. (2012). *Epidemiology. Emerging disease or diagnosis?*. *Science*, 338(6108), 750–752. PMID: 23139320.

429. Drier, Y., Lawrence, M.S., Carter, S.L., Stewart, C., Gabriel, S.B., Lander, E.S., Meyerson, M., Beroukhir, R., & Getz, G. (2013). *Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability*. *Genome Research*, 23(2), 228–235. PMID: 23124520; PMCID: PMC3561864.

430. Pugh, T.J., Morozova, O., Attiyeh, E.F., Asgharzadeh, S., Wei, J.S., Auclair, D.D., Carter, S.L., Cibulskis, K., Hanna, M., Kiezun, A., Kim, J., Lawrence, M.S., Lichtenstein, L., McKenna, A., Pedamallu, C.S., Ramos, A.H., Shefler, E., Sivachenko, A., Sougnez, C., Stewart, C., Ally, A., Birol, I., Chiu, R., Corbett, R.D., Hirst, M., Jackman, S.D., Kamoh, B., Khodabakshi, A.H., Krzywinski, M., Lo, A., Moore, R.A., Mungall, K.L., Qian, J., Tam, A., Thiessen, N., Zhao, Y., Cole, K.A., Diamond, M., Diskin, S.J., Mosse, Y.P., Wood, A.C., Ji, L., Sposto, R., Badgett, T., London, W.B., Moyer, Y., Gastier-Foster, J.M., Smith, M.A., Auvil, J.M., Gerhard, D.S., Hogarty, M.D., Jones, S.J., Lander, E.S., Gabriel, S.B., Getz, G., Seeger, R.C., Khan, J., Marra, M.A., Meyerson, M., & Maris, J.M. (2013). *The genetic landscape of high-risk neuroblastoma*. *Nature Genetics*, 45(3), 279–284. PMID: 23334666; PMCID: PMC3682833.

431. Costello, M., Pugh, T.J., Fennell, T.J., Stewart, C., Lichtenstein, L., Meldrim, J.C., Fostel, J.L., Friedrich, D.C., Perrin, D., Dionne, D., Kim, S., Gabriel, S.B., Lander, E.S., Fisher, S., & Getz, G. (2013). *Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation*. *Nucleic Acids Research*, 41(6), e67. PMID: 23303777; PMCID: PMC3616734.

432. Drier, Y., Lawrence, M.S., Carter, S.L., Stewart, C., Gabriel, S.B., Lander, E.S., Meyerson, M., Beroukhir, R., & Getz, G. (2013). *Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and*

- rearrangement-induced hypermutability. *Genome Research*, 23(2), 228–235. PMID: 23124520; PMCID: PMC3561864.
433. Engreitz, J.M., Pandya-Jones, A., McDonel, P., Shishkin, A., Sirokman, K., Surka, C., Kadri, S., Xing, J., Goren, A., Lander, E.S., Plath, K., & Guttman, M. (2013). *The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome*. *Science*, 341(6147), 1237973. PMID: 23828888; PMCID: PMC3778663.
434. Cibulskis, K., Lawrence, M.S., Carter, S.L., Sivachenko, A., Jaffe, D., Sougnez, C., Gabriel, S., Meyerson, M., Lander, E.S., & Getz, G. (2013). *Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples*. *Nature Biotechnology*, 31(3), 213–219. PMID: 23396013; PMCID: PMC3833702.
435. Grossman, S.R., Andersen, K.G., Shlyakhter, I., Tabrizi, S., Winnicki, S., Yen, A., Park, D.J., Griesemer, D., Karlsson, E.K., Wong, S.H., Cabili, M., Adegbola, R.A., Bamezai, R.N., Hill, A.V., Vannberg, F.O., Rinn, J.L., 1000 Genomes Project, Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2013). *Identifying recent adaptations in large-scale genomic data*. *Cell*, 152(4), 703–713. PMID: 23415221; PMCID: PMC3674781.
436. Cancer Genome Atlas Research Network. (2013). *Comprehensive molecular characterization of clear cell renal cell carcinoma*. *Nature*, 499(7456), 43–49. PMID: 23792563; PMCID: PMC3771322.
437. Gifford, C.A., Ziller, M.J., Gu, H., Trapnell, C., Donaghey, J., Tsankov, A., Shalek, A.K., Kelley, D.R., Shishkin, A.A., Issner, R., Zhang, X., Coyne, M., Fostel, J.L., Holmes, L., Meldrim, J., Guttman, M., Epstein, C., Park, H., Kohlbacher, O., Rinn, J., Gnirke, A., Lander, E.S., Bernstein, B.E., & Meissner, A. (2013). *Transcriptional and epigenetic dynamics during specification of human embryonic stem cells*. *Cell*, 153(5), 1149–1163. PMID: 23664763; PMCID: PMC3709577.
438. Dulak, A.M., Stojanov, P., Peng, S., Lawrence, M.S., Fox, C., Stewart, C., Bandla, S., Imamura, Y., Schumacher, S.E., Shefler, E., McKenna, A., Carter, S.L., Cibulskis, K., Sivachenko, A., Saksena, G., Voet, D., Ramos, A.H., Auclair, D., Thompson, K., Sougnez, C., Onofrio, R.C., Guiducci, C., Beroukhi, R., Zhou, Z., Lin, L., Lin, J., Reddy, R., Chang, A., Landrenau, R., Pennathur, A., Ogino, S., Luketich, J.D., Golub, T.R., Gabriel, S.B., Lander, E.S., Beer, D.G., Godfrey, T.E., Getz, G., & Bass, A.J. (2013). *Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity*. *Nature Genetics*, 45(5), 478–486. PMID: 23525077; PMCID: PMC3678719.
439. Baca, S.C., Prandi, D., Lawrence, M.S., Mosquera, J.M., Romanel, A., Drier, Y., Park, K., Kitabayashi, N., MacDonald, T.Y., Ghandi, M., Van Allen, E., Kryukov, G.V., Sboner, A., Theurillat, J.P., Soong, T.D., Nickerson, E., Auclair, D., Tewari, A., Beltran, H., Onofrio, R.C., Boysen, G., Guiducci, C., Barbieri, C.E., Cibulskis, K., Sivachenko, A., Carter, S.L., Saksena, G., Voet, D., Ramos, A.H., Winckler, W., Cipicchio, M., Ardlie, K., Kantoff, P.W., Berger, M.F., Gabriel, S.B., Golub, T.R., Meyerson, M., Lander, E.S., Elemento, O., Getz, G., Demicheli, F., Rubin, M.A., & Garraway, L.A. (2013). *Punctuated evolution of prostate cancer genomes*. *Cell*, 153(3), 666–677. PMID: 23622249; PMCID: PMC3690918.
440. Garraway, L.A., & Lander, E.S. (2013). *Lessons from the cancer genome*. *Cell*, 153(1), 17–37. PMID: 23540688.
441. Germain, A.R., Carmody, L.C., Nag, P.P., Morgan, B., Verplank, L., Fernandez, C., Donckele, E., Feng, Y., Perez, J.R., Dandapani, S., Palmer, M., Lander, E.S., Gupta, P.B., Schreiber, S.L., & Munoz, B. (2013). *Cinnamides as selective small-molecule inhibitors of a cellular model of breast cancer stem cells*. *Bioorganic & Medicinal Chemistry Letters*, 23(6), 1834–1838. PMID: 23403082.
442. Kirby, A., Gnirke, A., Jaffe, D.B., Barešová, V., Pochet, N., Blumenstiel, B., Ye, C., Aird, D., Stevens, C., Robinson, J.T., Cabili, M.N., Gat-Viks, I., Kelliher, E., Daza, R., DeFelice, M., Hůlková, H., Sovová, J., Vylet'al, P., Antignac, C., Guttman, M., Handsaker, R.E., Perrin, D., Steelman, S., Sigurdsson, S., Scheinman, S.J., Sougnez, C., Cibulskis, K., Parkin, M., Green, T., Rossin, E., Zody, M.C., Xavier, R.J., Pollak, M.R., Alper, S.L., Lindblad-Toh, K., Gabriel, S., Hart, P.S., Regev, A., Nusbaum, C., Knoch, S., Bleyer, A.J., Lander, E.S., & Daly, M.J. (2013). *Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing*. *Nature Genetics*, 45(3), 299–303. PMID: 23396133; PMCID: PMC3901305.
443. Landau, D.A., Carter, S.L., Stojanov, P., McKenna, A., Stevenson, K., Lawrence, M.S., Sougnez, C., Stewart, C., Sivachenko, A., Wang, L., Wan, Y., Zhang, W., Shukla, S.A., Vartanov, A., Fernandes, S.M., Saksena, G., Cibulskis, K., Tesar, B., Gabriel, S., Hacohen, N., Meyerson, M., Lander, E.S., Neuberg, D., Brown, J.R., Getz, G., & Wu, C.J. (2013). *Evolution and impact of subclonal mutations in chronic lymphocytic leukemia*. *Cell*, 152(4), 714–726. PMID: 23415222; PMCID: PMC3575604.

444. Guttman, M., Russell, P., Ingolia, N.T., Weissman, J.S., & Lander, E.S. (2013). *Ribosome profiling provides evidence that large noncoding RNAs do not encode proteins*. *Cell*, 154(1), 240–251. PMID: 23810193; PMCID: PMC3756563.
445. Hacohen, N., Fritsch, E.F., Carter, T.A., Lander, E.S., & Wu, C.J. (2013). *Getting personal with neoantigen-based therapeutic cancer vaccines*. *Cancer Immunology Research*, 1(1), 11–15. PMID: 24777245; PMCID: PMC4033902.
446. Lawrence, M.S., Stojanov, P., Polak, P., Kryukov, G.V., Cibulskis, K., Sivachenko, A., Carter, S.L., Stewart, C., Mermel, C.H., Roberts, S.A., Kiezun, A., Hammerman, P.S., McKenna, A., Drier, Y., Zou, L., Ramos, A.H., Pugh, T.J., Stransky, N., Helman, E., Kim, J., Sougnez, C., Ambrogio, L., Nickerson, E., Shefler, E., Cortés, M.L., Auclair, D., Saksena, G., Voet, D., Noble, M., DiCara, D., Lin, P., Lichtenstein, L., Heiman, D.I., Fennell, T., Imielinski, M., Hernandez, B., Hodis, E., Baca, S., Dulak, A.M., Lohr, J., Landau, D.A., Wu, C.J., Melendez-Zajgla, J., Hidalgo-Miranda, A., Koren, A., McCarroll, S.A., Mora, J., Lee, R.S., Crompton, B., Onofrio, R., Parkin, M., Winckler, W., Ardlie, K., Gabriel, S.B., Roberts, C.W., Biegel, J.A., Stegmaier, K., Bass, A.J., Garraway, L.A., Meyerson, M., Golub, T.R., Gordenin, D.A., Sunyaev, S., Lander, E.S., & Getz, G. (2013). *Mutational heterogeneity in cancer and the search for new cancer-associated genes*. *Nature*, 499(7457), 214–218. PMID: 23770567; PMCID: PMC3919509.
447. Farhat, M.R., Shapiro, B.J., Kieser, K.J., Sultana, R., Jacobson, K.R., Victor, T.C., Warren, R.M., Streicher, E.M., Calver, A., Sloutsky, A., Kaur, D., Posey, J.E., Plikaytis, B., Oggioni, M.R., Gardy, J.L., Johnston, J.C., Rodrigues, M., Tang, P.K., Kato-Maeda, M., Borowsky, M.L., Muddukrishna, B., Kreiswirth, B.N., Kurepina, N., Galagan, J., Gagneux, S., Birren, B., Rubin, E.J., Lander, E.S., Sabeti, P.C., & Murray, M. (2013). *Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis*. *Nature Genetics*, 45(10), 1183–1189. PMID: 23995135; PMCID: PMC3887553.
448. Schwartz, S., Agarwala, S.D., Mumbach, M.R., Jovanovic, M., Mertins, P., Shishkin, A., Tabach, Y., Mikkelsen, T.S., Satija, R., Ruvkun, G., Carr, S.A., Lander, E.S., Fink, G.R., & Regev, A. (2013). *High-resolution mapping reveals a conserved, widespread, dynamic mRNA methylation program in yeast meiosis*. *Cell*, 155(6), 1409–1421. PMID: 24269006; PMCID: PMC3956118.
449. Karlsson, E.K., Sigurdsson, S., Ivansson, E., Thomas, R., Elvers, I., Wright, J., Howald, C., Tonomura, N., Perloski, M., Swofford, R., Biagi, T., Fryc, S., Anderson, N., Courtay-Cahen, C., Youell, L., Ricketts, S.L., Mandlebaum, S., Rivera, P., von Euler, H., Kisseberth, W.C., London, C.A., Lander, E.S., Couto, G., Comstock, K., Starkey, M.P., Modiano, J.F., Breen, M., & Lindblad-Toh, K. (2013). *Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B*. *Genome Biology*, 14(12), R132. PMID: 24330828; PMCID: PMC4053774.
450. Wang, T., Wei, J.J., Sabatini, D.M., & Lander, E.S. (2014). *Genetic screens in human cells using the CRISPR-Cas9 system*. *Science*, 343(6166), 80–84. PMID: 24336569; PMCID: PMC3972032.
451. Lawrence, M.S., Stojanov, P., Mermel, C.H., Robinson, J.T., Garraway, L.A., Golub, T.R., Meyerson, M., Gabriel, S.B., Lander, E.S., & Getz, G. (2014). *Discovery and saturation analysis of cancer genes across 21 tumour types*. *Nature*, 505(7484), 495–501. PMID: 24390350; PMCID: PMC4048962.
452. Zuk, O., Schaffner, S.F., Samocha, K., Do, R., Hechter, E., Kathiresan, S., Daly, M.J., Neale, B.M., Sunyaev, S.R., & Lander, E.S. (2014). *Searching for missing heritability: designing rare variant association studies*. *Proceedings of the National Academy of Sciences USA*, 111(4), E455–E464. PMID: 24443550; PMCID: PMC3910587.
453. Hacisuleyman, E., Goff, L.A., Trapnell, C., Williams, A., Henao-Mejia, J., Sun, L., McClanahan, P., Hendrickson, D.G., Sauvageau, M., Kelley, D.R., Morse, M., Engreitz, J., Lander, E.S., Guttman, M., Lodish, H.F., Flavell, R., Raj, A., & Rinn, J.L. (2014). *Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre*. *Nature Structural & Molecular Biology*, 21(2), 198–206. PMID: 24463464; PMCID: PMC3950333.
454. Purcell, S.M., Moran, J.L., Fromer, M., Ruderfer, D., Solovieff, N., Roussos, P., O'Dushlaine, C., Chambert, K., Bergen, S.E., Kähler, A., Duncan, L., Stahl, E., Genovese, G., Fernández, E., Collins, M.O., Komiyama, N.H., Choudhary, J.S., Magnusson, P.K., Banks, E., Shakir, K., Garimella, K., Fennell, T., DePristo, M., Grant, S.G., Haggarty, S.J., Gabriel, S., Scolnick, E.M., Lander, E.S., Hultman, C.M., Sullivan, P.F., McCarroll, S.A., & Sklar, P. (2014). *A polygenic burden of rare disruptive mutations in schizophrenia*. *Nature*, 506(7487), 185–190. PMID: 24463508; PMCID: PMC4136494.
455. Hoepfner, M.P., Lundquist, A., Pirun, M., Meadows, J.R., Zamani, N., Johnson, J., Sundström, G., Cook, A., FitzGerald, M.G., Swofford, R., Mauceli, E.,

- Moghadam, B.T., Greka, A., Alföldi, J., Abouelleil, A., Aftuck, L., Bessette, D., Berlin, A., Brown, A., Gearin, G., Lui, A., Macdonald, J.P., Priest, M., Shea, T., Turner-Maier, J., Zimmer, A., Lander, E.S., di Palma, F., Lindblad-Toh, K., & Grabherr, M.G. (2014). *An improved canine genome and a comprehensive catalogue of coding genes and non-coding transcripts*. *PloS One*, 9(3), e91172. PMID: 24625832; PMCID: PMC3953330.
456. Wagle, N., Grabiner, B.C., Van Allen, E.M., Hodis, E., Jacobus, S., Supko, J.G., Stewart, M., Choueiri, T.K., Gandhi, L., Cleary, J.M., Elfiky, A.A., Taplin, M.E., Stack, E.C., Signoretti, S., Loda, M., Shapiro, G.I., Sabatini, D.M., Lander, E.S., Gabriel, S.B., Kantoff, P.W., Garraway, L.A., & Rosenberg, J.E. (2014). Activating mTOR mutations in a patient with an extraordinary response on a phase I trial of everolimus and pazopanib. *Cancer Discovery*, 4(5), 546–553. PMID: 24625776; PMCID: PMC4122326.
457. Van Allen, E.M., Wagle, N., Stojanov, P., Perrin, D.L., Cibulskis, K., Marlow, S., Jane-Valbuena, J., Friedrich, D.C., Kryukov, G., Carter, S.L., McKenna, A., Sivachenko, A., Rosenberg, M., Kiezun, A., Voet, D., Lawrence, M., Lichtenstein, L.T., Gentry, J.G., Huang, F.W., Fostel, J., Farlow, D., Barbie, D., Gandhi, L., Lander, E.S., Gray, S.W., Joffe, S., Janne, P., Garber, J., MacConaill, L., Lindeman, N., Rollins, B., Kantoff, P., Fisher, S.A., Gabriel, S., Getz, G., & Garraway, L.A. (2014). Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. *Nature Medicine*, 20(6), 682–688. PMID: 24836576; PMCID: PMC4048335.
458. Cho, J., Bass, A.J., Lawrence, M.S., Cibulskis, K., Cho, A., Lee, S.N., Yamauchi, M., Wagle, N., Pochanard, P., Kim, N., Park, A.K., Won, J., Hur, H.S., Greulich, H., Ogino, S., Sougnez, C., Voet, D., Tabernero, J., Jimenez, J., Baselga, J., Gabriel, S.B., Lander, E.S., Getz, G., Eck, M.J., Park, W.Y., & Meyerson, M. (2014). Colon cancer-derived oncogenic EGFR G724S mutant identified by whole genome sequence analysis is dependent on asymmetric dimerization and sensitive to cetuximab. *Molecular Cancer*, 13, 141. PMID: 24894453; PMCID: PMC4072491.
459. Hsu, P.D., Lander, E.S., & Zhang, F. (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell*, 157(6), 1262–1278. PMID: 24906146; PMCID: PMC4343198.
460. Wang, L., Shalek, A.K., Lawrence, M., Ding, R., Gaublot, J.T., Pochet, N., Stojanov, P., Sougnez, C., Shukla, S.A., Stevenson, K.E., Zhang, W., Wong, J., Sievers, Q.L., MacDonald, B.T., Vartanov, A.R., Goldstein, N.R., Neuber, D., He, X., Lander, E.S., Hacohen, N., Regev, A., Getz, G., Brown, J.R., Park, H., & Wu, C.J. (2014). Somatic mutation as a mechanism of Wnt/ β -catenin pathway activation in CLL. *Blood*, 124(7), 1089–1098. PMID: 24778153; PMCID: PMC4133483.
461. Rajasagi, M., Shukla, S.A., Fritsch, E.F., Keskin, D.B., DeLuca, D., Carmona, E., Zhang, W., Sougnez, C., Cibulskis, K., Sidney, J., Stevenson, K., Ritz, J., Neuber, D., Brusic, V., Gabriel, S., Lander, E.S., Getz, G., Hacohen, N., & Wu, C.J. (2014). Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, 124(3), 453–462. PMID: 24891321; PMCID: PMC4102716.
462. Ludwig, L.S., Gazda, H.T., Eng, J.C., Eichhorn, S.W., Thiru, P., Ghazvinian, R., George, T.I., Gotlib, J.R., Beggs, A.H., Sieff, C.A., Lodish, H.F., Lander, E.S., & Sankaran, V.G. (2014). Altered translation of GATA1 in Diamond-Blackfan anemia. *Nature Medicine*, 20(7), 748–753. PMID: 24952648; PMCID: PMC4087046.
463. Schwartz, S., Mumbach, M.R., Jovanovic, M., Wang, T., Maciag, K., Bushkin, G.G., Mertins, P., Ter-Ovanesyan, D., Habib, N., Cacchiarelli, D., Sanjana, N.E., Freinkman, E., Pacold, M.E., Satija, R., Mikkelsen, T.S., Hacohen, N., Zhang, F., Carr, S.A., Lander, E.S., & Regev, A. (2014). Perturbation of m6A writers reveals two distinct classes of mRNA methylation at internal and 5' sites. *Cell Reports*, 8(1), 284–296. PMID: 24981863; PMCID: PMC4142486.
464. Rajasagi, M., Shukla, S.A., Fritsch, E.F., Keskin, D.B., DeLuca, D., Carmona, E., Zhang, W., Sougnez, C., Cibulskis, K., Sidney, J., Stevenson, K., Ritz, J., Neuber, D., Brusic, V., Gabriel, S., Lander, E.S., Getz, G., Hacohen, N., & Wu, C.J. (2014). Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, 124(3), 453–462. PMID: 24891321; PMCID: PMC4102716.
465. Carneiro, M., Rubin, C.J., Di Palma, F., Albert, F.W., Alföldi, J., Barrio, A.M., Pielberg, G., Rafati, N., Sayyab, S., Turner-Maier, J., Younis, S., Afonso, S., Aken, B., Alves, J.M., Barrell, D., Bolet, G., Boucher, S., Burbano, H.A., Campos, R., Chang, J.L., Duranthon, V., Fontanesi, L., Garreau, H., Heiman, D., Johnson, J., Mage, R.G., Peng, Z., Queney, G., Rogel-Gaillard, C., Ruffier, M., Searle, S., Villafuerte, R., Xiong, A., Young, S., Forsberg-Nilsson, K., Good, J.M., Lander, E.S., Ferrand, N., Lindblad-Toh, K., & Andersson, L. (2014). Rabbit genome analysis re-

- veals a polygenic basis for phenotypic change during domestication. *Science*, 345(6200), 1074–1079. PMID: 25170157.
466. Gire, S.K., Goba, A., Andersen, K.G., Sealfon, R.S., Park, D.J., Kanneh, L., Jalloh, S., Momoh, M., Fullah, M., Dudas, G., Wohl, S., Moses, L.M., Yozwiak, N.L., Winnicki, S., Matranga, C.B., Malboeuf, C.M., Qu, J., Gladden, A.D., Schaffner, S.F., Yang, X., Jiang, P.P., Nekoui, M., Colubri, A., Coomber, M.R., Fonnies, M., Moigboi, A., Gbakie, M., Kamara, F.K., Tucker, V., Konuwa, E., Saffa, S., Sellu, J., Jalloh, A.A., Kovoma, A., Koninga, J., Mustapha, I., Kargbo, K., Foday, M., Yillah, M., Kanneh, F., Robert, W., Massally, J.L., Chapman, S.B., Bochicchio, J., Murphy, C., Nusbaum, C., Young, S., Birren, B.W., Grant, D.S., Scheffelin, J.S., Lander, E.S., Hapoi, C., Gevaio, S.M., Gnirke, A., Rambaut, A., Garry, R.F., Khan, S.H., & Sabeti, P.C. (2014). *Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak*. *Science*, 345(6202), 1369–1372. PMID: 25214632; PMCID: PMC4431643.
467. Brawand, D., Wagner, C.E., Li, Y.I., Malinsky, M., Keller, I., Fan, S., Simakov, O., Ng, A.Y., Lim, Z.W., Bezault, E., Turner-Maier, J., Johnson, J., Alcazar, R., Noh, H.J., Russell, P., Aken, B., Alföldi, J., Amemiya, C., Azzouzi, N., Baroiller, J.F., Barloy-Hubler, F., Berlin, A., Bloomquist, R., Carleton, K.L., Conte, M.A., D'Cotta, H., Eshel, O., Gaffney, L., Galibert, F., Gante, H.F., Gnerre, S., Greuter, L., Guyon, R., Haddad, N.S., Haerty, W., Harris, R.M., Hofmann, H.A., Hourlier, T., Hulata, G., Jaffe, D.B., Lara, M., Lee, A.P., MacCallum, I., Mwaiko, S., Nikaido, M., Nishihara, H., Ozouf-Costaz, C., Penman, D.J., Przybylski, D., Rakotomanga, M., Renn, S.C., Ribeiro, F.J., Ron, M., Salzburger, W., Sanchez-Pulido, L., Santos, M.E., Searle, S., Sharpe, T., Swofford, R., Tan, F.J., Williams, L., Young, S., Yin, S., Okada, N., Kocher, T.D., Miska, E.A., Lander, E.S., Venkatesh, B., Fernald, R.D., Meyer, A., Ponting, C.P., Streelman, J.T., Lindblad-Toh, K., Seehausen, O., & Di Palma, F. (2014). *The genomic substrate for adaptive radiation in African cichlid fish*. *Nature*, 513(7518), 375–381. PMID: 25186727; PMCID: PMC4353498.
468. Schwartz, S., Bernstein, D.A., Mumbach, M.R., Jovanovic, M., Herbst, R.H., León-Ricardo, B.X., Engreitz, J.M., Guttman, M., Satija, R., Lander, E.S., Fink, G., & Regev, A. (2014). *Transcriptome-wide mapping reveals widespread dynamic-regulated pseudouridylation of ncRNA and mRNA*. *Cell*, 159(1), 148–162. PMID: 25219674; PMCID: PMC4180118.
469. Engreitz, J.M., Sirokman, K., McDonel, P., Shishkin, A.A., Surka, C., Russell, P., Grossman, S.R., Chow, A.Y., Guttman, M., & Lander, E.S. (2014). *RNA–RNA interactions enable specific targeting of noncoding RNAs to nascent Pre-mRNAs and chromatin sites*. *Cell*, 159(1), 188–199. PMID: 25259926; PMCID: PMC4177037.
470. Myocardial Infarction Genetics Consortium Investigators. (2014). *Inactivating mutations in NPC1L1 and protection from coronary heart disease*. *New England Journal of Medicine*, 371(22), 2072–2082. PMID: 25390462; PMCID: PMC4335708.
471. Weisenfeld, N.I., Yin, S., Sharpe, T., Lau, B., Hegarty, R., Holmes, L., Sogoloff, B., Tabbaa, D., Williams, L., Russ, C., Nusbaum, C., Lander, E.S., MacCallum, I., & Jaffe, D.B. (2014). *Comprehensive variation discovery in single human genomes*. *Nature Genetics*, 46(12), 1350–1355. PMID: 25326702; PMCID: PMC4244235.
472. Giannakis, M., Hodis, E., Jasmine Mu, X., Yamauchi, M., Rosenbluh, J., Cibulskis, K., Saksena, G., Lawrence, M.S., Qian, Z.R., Nishihara, R., Van Allen, E.M., Hahn, W.C., Gabriel, S.B., Lander, E.S., Getz, G., Ogino, S., Fuchs, C.S., & Garraway, L.A. (2014). *RNF43 is frequently mutated in colorectal and endometrial cancers*. *Nature Genetics*, 46(12), 1264–1266. PMID: 25344691; PMCID: PMC4283570.
473. Landau, D.A., Clement, K., Ziller, M.J., Boyle, P., Fan, J., Gu, H., Stevenson, K., Sougnez, C., Wang, L., Li, S., Kotliar, D., Zhang, W., Ghandi, M., Garraway, L., Fernandes, S.M., Livak, K.J., Gabriel, S., Gnirke, A., Lander, E.S., Brown, J.R., Neuberg, D., Kharchenko, P.V., Hacohen, N., Getz, G., Meissner, A., & Wu, C.J. (2014). *Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia*. *Cancer Cell*, 26(6), 813–825. PMID: 25490447; PMCID: PMC4302418.
474. Golan, D., Lander, E.S., & Rosset, S. (2014). *Measuring missing heritability: inferring the contribution of common variants*. *Proceedings of the National Academy of Sciences USA*, 111(49), E5272–E5281. PMID: 25422463; PMCID: PMC4267399.
475. Rao, S.S., Huntley, M.H., Durand, N.C., Stamenova, E.K., Bochkov, I.D., Robinson, J.T., Sanborn, A.L., Machol, I., Omer, A.D., Lander, E.S., & Aiden, E.L. (2014). *A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping*. *Cell*, 159(7), 1665–1680. PMID: 25497547.
476. Perry, J.A., Kiezun, A., Tonzi, P., Van Allen, E.M., Carter, S.L., Baca, S.C., Cowley, G.S., Bhatt, A.S., Rheinbay, E., Pedamallu, C.S., Helman, E., Taylor-

- Weiner, A., McKenna, A., DeLuca, D.S., Lawrence, M.S., Ambrogio, L., Sougnez, C., Sivachenko, A., Walensky, L.D., Wagle, N., Mora, J., de Torres, C., Lavarino, C., Dos Santos Aguiar, S., Yunes, J.A., Brandalise, S.R., Mercado-Celis, G.E., Melendez-Zajgla, J., Cardenas-Cardós, R., Velasco-Hidalgo, L., Roberts, C.W., Garraway, L.A., Rodriguez-Galindo, C., Gabriel, S.B., Lander, E.S., Golub, T.R., Orkin, S.H., Getz, G., & Janeway, K.A. (2014). *Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences USA*, 111(51), E5564–E5573. PMID: 25512523; PMCID: PMC4280630.
477. Genovese, G., Kähler, A.K., Handsaker, R.E., Lindberg, J., Rose, S.A., Bakhroum, S.F., Chambert, K., Mick, E., Neale, B.M., Fromer, M., Purcell, S.M., Svantesson, O., Landén, M., Höglund, M., Lehmann, S., Gabriel, S.B., Moran, J.L., Lander, E.S., Sullivan, P.F., Sklar, P., Grönberg, H., Hultman, C.M., & McCarroll, S.A. (2014). *Clonal hematopoiesis and blood-cancer risk inferred from blood DNA sequence. New England Journal of Medicine*, 371(26), 2477–2487. PMID: 25426838; PMCID: PMC4290021.
478. Delaneau, O., Marchini, J., & 1000 Genomes Project Consortium. (2014). *Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications*, 5, 3934. PMID: 25653097; PMCID: PMC4338501.
479. Engreitz, J., Lander, E.S., & Guttman, M. (2015). *RNA antisense purification (RAP) for mapping RNA interactions with chromatin. Methods in Molecular Biology*, 1262, 183–197. PMID: 25555582.
480. Cancer Genome Atlas Research Network, Brat, D.J., Verhaak, R.G., Aldape, K.D., Yung, W.K., Salama, S.R., Cooper, L.A., Rheinbay, E., Miller, C.R., Vitucci, M., Morozova, O., Robertson, A.G., Noushmehr, H., Laird, P.W., Cherniack, A.D., Akbani, R., Huse, J.T., Ciriello, G., Poisson, L.M., Barnholtz-Sloan, J.S., Berger, M.S., Brennan, C., Colen, R.R., Colman, H., Flanders, A.E., Giannini, C., Grifford, M., Iavarone, A., Jain, R., Joseph, I., Kim, J., Kasaian, K., Mikkelsen, T., Murray, B.A., O'Neill, B.P., Pachter, L., Parsons, D.W., Sougnez, C., Sulman, E.P., Vandenberg, S.R., Van Meir, E.G., von Deimling, A., Zhang, H., Crain, D., Lau, K., Mallory, D., Morris, S., Paulauskis, J., Penny, R., Shelton, T., Sherman, M., Yena, P., Black, A., Bowen, J., Dicostanzo, K., Gastier-Foster, J., Leraas, K.M., Lichtenberg, T.M., Pierson, C.R., Ramirez, N.C., Taylor, C., Weaver, S., Wise, L., Zmuda, E., Davidsen, T., Demchok, J.A., Eley, G., Ferguson, M.L., Hutter, C.M., Mills Shaw, K.R., Ozenberger, B.A., Sheth, M., Sofia, H.J., Tarnuzzer, R., Wang, Z., Yang, L., Zenklusen, J.C., Ayala, B., Baboud, J., Chudamani, S., Jensen, M.A., Liu, J., Pihl, T., Raman, R., Wan, Y., Wu, Y., Ally, A., Auman, J.T., Balasundaram, M., Balu, S., Baylin, S.B., Beroukhi, R., Bootwalla, M.S., Bowlby, R., Bristow, C.A., Brooks, D., Butterfield, Y., Carlsen, R., Carter, S., Chin, L., Chu, A., Chuah, E., Cibulskis, K., Clarke, A., Coetzee, S.G., Dhalla, N., Fennell, T., Fisher, S., Gabriel, S., Getz, G., Gibbs, R., Guin, R., Hadjipanayis, A., Hayes, D.N., Hinoue, T., Hoadley, K., Holt, R.A., Hoyle, A.P., Jefferys, S.R., Jones, S., Jones, C.D., Kucherlapati, R., Lai, P.H., Lander, E.S., Lee, S., Lichtenstein, L., Ma, Y., Maglinte, D.T., Mahadeshwar, H.S., Marra, M.A., Mayo, M., Meng, S., Meyerson, M.L., Mieczkowski, P.A., Moore, R.A., Mose, L.E., Mungall, A.J., Pantazi, A., Parfenov, M., Park, P.J., Parker, J.S., Perou, C.M., Protopopov, A., Ren, X., Roach, J., Sabedot, T.S., Schein, J., Schumacher, S.E., Seidman, J.G., Seth, S., Shen, H., Simons, J.V., Sipahimalani, P., Soloway, M.G., Song, X., Sun, H., Tabak, B., Tam, A., Tan, D., Tang, J., Thiessen, N., Triche, T., Van Den Berg, D.J., Veluvolu, U., Waring, S., Weisenberger, D.J., Wilkerson, M.D., Wong, T., Wu, J., Xi, L., Xu, A.W., Yang, L., Zack, T.I., Zhang, J., Aksoy, B.A., Arachchi, H., Benz, C., Bernard, B., Carlin, D., Cho, J., DiCara, D., Frazer, S., Fuller, G.N., Gao, J., Gehlenborg, N., Haussler, D., Heiman, D.I., Iype, L., Jacobsen, A., Ju, Z., Katzman, S., Kim, H., Knijnenburg, T., Kreisberg, R.B., Lawrence, M.S., Lee, W., Leinonen, K., Lin, P., Ling, S., Liu, W., Liu, Y., Liu, Y., Lu, Y., Mills, G., Ng, S., Noble, M.S., Paull, E., Rao, A., Reynolds, S., Saksena, G., Sanborn, Z., Sander, C., Schultz, N., Senbabaoglu, Y., Shen, R., Shmulevich, I., Sinha, R., Stuart, J., Sumer, S.O., Sun, Y., Tasman, N., Taylor, B.S., Voet, D., Weinhold, N., Weinstein, J.N., Yang, D., Yoshihara, K., Zheng, S., Zhang, W., Zou, L., Abel, T., Sadeghi, S., Cohen, M.L., Eschbacher, J., Hattab, E.M., Raghunathan, A., Schniederjan, M.J., Aziz, D., Barnett, G., Barrett, W., Bigner, D.D., Boice, L., Brewer, C., Calatuzzolo, C., Campos, B., Carlotti, C.G., Chan, T.A., Cuppini, L., Curley, E., Cuzzubbo, S., Devine, K., DiMeco, F., Duell, R., Elder, J.B., Fehrenbach, A., Finocchiaro, G., Friedman, W., Fulop, J., Gardner, J., Hermes, B., Herold-Mende, C., Jungk, C., Kendler, A., Lehman, N.L., Lipp, E., Liu, O., Mandt, R., McGraw, M., McLendon, R., McPherson, C., Neder, L., Nguyen, P., Noss, A., Nunziata, R., Ostrom, Q.T., Palmer, C., Perin, A., Pollo, B., Potapov, A., Potapova, O., Rathmell, W.K., Rotin, D., Scarpace, L., Schilero, C., Senecal, K., Shimmel, K., Shurkhay, V., Sifri, S., Singh, R., Sloan,

- A.E., Smolenski, K., Staugaitis, S.M., Steele, R., Thorne, L., Tirapelli, D.P., Unterberg, A., Vallurupalli, M., Wang, Y., Warnick, R., Williams, F., Wolinsky, Y., Bell, S., Rosenberg, M., Stewart, C., Huang, F., Grimsby, J.L., Radenbaugh, A.J., & Zhang, J. (2015). *Comprehensive, integrative genomic analysis of diffuse lower-grade gliomas*. *New England Journal of Medicine*, 372(26), 2481–2498. PMID: 26061751; PMCID: PMC4530011.
481. Do, R., Stitzel, N.O., Won, H.H., Jørgensen, A.B., Duga, S., Angelica Merlini, P., Kiezun, A., Farrall, M., Goel, A., Zuk, O., Guella, I., Asselta, R., Lange, L.A., Peloso, G.M., Auer, P.L., NHLBI Exome Sequencing Project, Girelli, D., Martinelli, N., Farlow, D.N., DePristo, M.A., Roberts, R., Stewart, A.F., Saleheen, D., Danesh, J., Epstein, S.E., Sivapalaratnam, S., Hovingh, G.K., Kastelein, J.J., Samani, N.J., Schunkert, H., Erdmann, J., Shah, S.H., Kraus, W.E., Davies, R., Nikpay, M., Johansen, C.T., Wang, J., Hegele, R.A., Hechter, E., Marz, W., Kleber, M.E., Huang, J., Johnson, A.D., Li, M., Burke, G.L., Gross, M., Liu, Y., Assimes, T.L., Heiss, G., Lange, E.M., Folsom, A.R., Taylor, H.A., Olivieri, O., Hamsten, A., Clarke, R., Reilly, D.F., Yin, W., Rivas, M.A., Donnelly, P., Rossouw, J.E., Psaty, B.M., Herrington, D.M., Wilson, J.G., Rich, S.S., Bamshad, M.J., Tracy, R.P., Cupples, L.A., Rader, D.J., Reilly, M.P., Spertus, J.A., Cresci, S., Hartiala, J., Tang, W.H., Hazen, S.L., Allayee, H., Reiner, A.P., Carlson, C.S., Kooperberg, C., Jackson, R.D., Boerwinkle, E., Lander, E.S., Schwartz, S.M., Siscovick, D.S., McPherson, R., Tybjaerg-Hansen, A., Abecasis, G.R., Watkins, H., Nickerson, D.A., Ardisson, D., Sunyaev, S.R., O'Donnell, C.J., Altshuler, D., Gabriel, S., & Kathiresan, S. (2015). *Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction*. *Nature*, 518(7537), 102–106. PMID: 25487149; PMCID: PMC4319990.
482. Tonomura, N., Elvers, I., Thomas, R., Megquier, K., Turner-Maier, J., Howald, C., Sarver, A.L., Swofford, R., Frantz, A.M., Ito, D., Mauceli, E., Arendt, M., Noh, H.J., Koltookian, M., Biagi, T., Fryc, S., Williams, C., Avery, A.C., Kim, J.H., Barber, L., Burgess, K., Lander, E.S., Karlsson, E.K., Azuma, C., Modiano, J.F., Breen, M., & Lindblad-Toh, K. (2015). *Genome-wide association study identifies shared risk loci common to two malignancies in golden retrievers*. *PLoS Genetics*, 11(2), e1004922. PMID: 25642983; PMCID: PMC4333733.
483. Thormaehlen, A.S., Schuberth, C., Won, H.H., Blattmann, P., Joggerst-Thomalla, B., Theiss, S., Asselta, R., Duga, S., Merlini, P.A., Ardisson, D., Lander, E.S., Gabriel, S., Rader, D.J., Peloso, G.M., Pepperkok, R., Kathiresan, S., & Runz, H. (2015). *Systematic cell-based phenotyping of missense alleles empowers rare variant association studies: a case for LDLR and myocardial infarction*. *PLoS Genetics*, 11(2), e1004855. PMID: 25647241; PMCID: PMC4409815.
484. Kim, H., Zheng, S., Amini, S.S., Virk, S.M., Mikkelsen, T., Brat, D.J., Grimsby, J., Sougnez, C., Muller, F., Hu, J., Sloan, A.E., Cohen, M.L., Van Meir, E.G., Scarpacci, L., Laird, P.W., Weinstein, J.N., Lander, E.S., Gabriel, S., Getz, G., Meyerson, M., Chin, L., Barnholtz-Sloan, J.S., & Verhaak, R.G. (2015). *Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution*. *Genome Research*, 25(3), 316–327. PMID: 25650244; PMCID: PMC4352879.
485. Lander, E.S. (2015). *Cutting the Gordian helix—regulating genomic testing in the era of precision medicine*. *New England Journal of Medicine*, 372(13), 1185–1186. PMID: 25689017.
486. McHugh, C.A., Chen, C.K., Chow, A., Surka, C.F., Tran, C., McDonel, P., Pandya-Jones, A., Blanco, M., Burghard, C., Moradian, A., Sweredoski, M.J., Shishkin, A.A., Su, J., Lander, E.S., Hess, S., Plath, K., & Guttman, M. (2015). *The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3*. *Nature*, 521(7551), 232–236. PMID: 25915022; PMCID: PMC4516396.
487. Lander ES. (2015). *Brave New Genome*. *New England Journal of Medicine*, 373(1), 5–8. PMID: 26039524.
488. Cacchiarelli, D., Trapnell, C., Ziller, M.J., Soumillon, M., Cesana, M., Karnik, R., Donaghey, J., Smith, Z.D., Ratanasirintrawoot, S., Zhang, X., Ho Sui, S.J., Wu, Z., Akopian, V., Gifford, C.A., Doench, J., Rinn, J.L., Daley, G.Q., Meissner, A., Lander, E.S., & Mikkelsen, T.S. (2015). *Integrative analyses of human reprogramming reveal dynamic nature of induced pluripotency*. *Cell*, 162(2), 412–424. PMID: 26186193; PMCID: PMC4511597.
489. Stachler, M.D., Taylor-Weiner, A., Peng, S., McKenna, A., Agoston, A.T., Odze, R.D., Davison, J.M., Nason, K.S., Loda, M., Leshchiner, I., Stewart, C., Stojanov, P., Seepo, S., Lawrence, M.S., Ferrer-Torres, D., Lin, J., Chang, A.C., Gabriel, S.B., Lander, E.S., Beer, D.G., Getz, G., Carter, S.L., & Bass, A.J. (2015). *Paired exome analysis of Barrett's esophagus and adenocarcinoma*. *Nature Genetics*, 47(9), 1047–1055. PMID: 26192918; PMCID: PMC4552571.

490. Andersen, K.G., Shapiro, B.J., Matranga, C.B., Sealton, R., Lin, A.E., Moses, L.M., Folarin, O.A., Goba, A., Odia, I., Ehiane, P.E., Momoh, M., England, E.M., Winnicki, S., Branco, L.M., Gire, S.K., Phelan, E., Tariyal, R., Tewhey, R., Omoniwa, O., Fullah, M., Fonnies, R., Fonnies, M., Kanneh, L., Jalloh, S., Gbakie, M., Saffa, S., Karbo, K., Gladden, A.D., Qu, J., Stremlau, M., Nekoui, M., Finucane, H.K., Tabrizi, S., Vitti, J.J., Birren, B., Fitzgerald, M., McCowan, C., Ireland, A., Berlin, A.M., Bochicchio, J., Tazon-Vega, B., Lennon, N.J., Ryan, E.M., Bjornson, Z., Milner, D.A., Lukens, A.K., Broodie, N., Rowland, M., Heinrich, M., Akdag, M., Schieffelin, J.S., Levy, D., Akpan, H., Bausch, D.G., Rubins, K., McCormick, J.B., Lander, E.S., Günther, S., Hensley, L., Okogbenin, S., Viral Hemorrhagic Fever Consortium, Schaffner, S.F., Okokhere, P.O., Khan, S.H., Grant, D.S., Akpede, G.O., Asogun, D.A., Gnirke, A., Levin, J.Z., Happi, C.T., Garry, R.F., & Sabeti, P.C. (2015). *Clinical sequencing uncovers origins and evolution of Lassa virus*. *Cell*, 162(4), 738–750. PMID: 26276630; PMCID: PMC4537774.
491. Kamburov, A., Lawrence, M.S., Polak, P., Leshchiner, I., Lage, K., Golub, T.R., Lander, E.S., & Getz, G. (2015). *Comprehensive assessment of cancer missense mutation clustering in protein structures*. *Proceedings of the National Academy of Sciences USA*, 112(40), E5486–E5495. PMID: 26392535; PMCID: PMC4603469.
492. Brastianos, P.K., Carter, S.L., Santagata, S., Cahill, D.P., Taylor-Weiner, A., Jones, R.T., Van Allen, E.M., Lawrence, M.S., Horowitz, P.M., Cibulskis, K., Ligon, K.L., Tabernero, J., Seoane, J., Martinez-Saez, E., Curry, W.T., Dunn, I.F., Paek, S.H., Park, S.H., McKenna, A., Chevalier, A., Rosenberg, M., Barker, F.G., Gill, C.M., Van Hummelen, P., Thorner, A.R., Johnson, B.E., Hoang, M.P., Choueiri, T.K., Signoretti, S., Sougnez, C., Rabin, M.S., Lin, N.U., Winer, E.P., Stemmer-Rachamimov, A., Meyerson, M., Garraway, L., Gabriel, S., Lander, E.S., Beroukheim, R., Batchelor, T.T., Baselga, J., Louis, D.N., Getz, G., & Hahn, W.C. (2015). *Genomic characterization of brain metastases reveals branched evolution and potential therapeutic targets*. *Cancer Discovery*, 5(11), 1164–1177. PMID: 26410082; PMCID: PMC4916970.
493. Wang, T., Birsoy, K., Hughes, N.W., Krupczak, K.M., Post, Y., Wei, J.J., Lander, E.S., & Sabatini, D.M. (2015). *Identification and characterization of essential genes in the human genome*. *Science*, 350(6264), 1096–1101. PMID: 26472758; PMCID: PMC4662922.
494. Landau, D.A., Tausch, E., Taylor-Weiner, A.N., Stewart, C., Reiter, J.G., Bahlo, J., Kluth, S., Bozic, I., Lawrence, M., Böttcher, S., Carter, S.L., Cibulskis, K., Mertens, D., Sougnez, C.L., Rosenberg, M., Hess, J.M., Edelman, J., Kless, S., Kneba, M., Ritgen, M., Fink, A., Fischer, K., Gabriel, S., Lander, E.S., Nowak, M.A., Döhner, H., Hallek, M., Neuberg, D., Getz, G., Stilgenbauer, S., & Wu, C.J. (2015). *Mutations driving CLL and their evolution in progression and relapse*. *Nature*, 526(7574), 525–530. PMID: 26466571; PMCID: PMC4815041.
495. Golan, D., Rosset, S., & Lander, E.S. (2015). *Downward bias in heritability estimation is not due to simplified linkage equilibrium SNP simulation [Reply]*. *Proceedings of the National Academy of Sciences USA*, 112(40), E5452–E5453. PMID: 26417112; PMCID: PMC4603505.
496. Sanborn, A.L., Rao, S.S., Huang, S.C., Durand, N.C., Huntley, M.H., Jewett, A.I., Bochkov, I.D., Chinnappan, D., Cutkosky, A., Li, J., Geeting, K.P., Gnirke, A., Melnikov, A., McKenna, D., Stamenova, E.K., Lander, E.S., & Aiden, E.L. (2015). *Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes*. *Proceedings of the National Academy of Sciences USA*, 112(47), E6456–E6465. PMID: 26499245; PMCID: PMC4664323.
497. Kasar, S., Kim, J., Improgo, R., Tiao, G., Polak, P., Haradhvala, N., Lawrence, M.S., Kiezun, A., Fernandes, S.M., Bahl, S., Sougnez, C., Gabriel, S., Lander, E.S., Kim, H.T., Getz, G., & Brown, J.R. (2015). *Whole-genome sequencing reveals activation-induced cytidine deaminase signatures during indolent chronic lymphocytic leukaemia evolution*. *Nature Communications*, 6, 8866. PMID: 26638776; PMCID: PMC4686820.
498. Lander, E.S. (2016). *The Heroes of CRISPR*. *Cell*, 164(1–2), 18–28. PMID: 26771483.
499. Yassour, M., Lim, M.Y., Yun, H.S., Tickle, T.L., Sung, J., Song, Y.M., Lee, K., Franzosa, E.A., Morgan, X.C., Gevers, D., Lander, E.S., Xavier, R.J., Birren, B.W., Ko, G., & Huttenhower, C. (2016). *Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes*. *Genome Medicine*, 8(1), 17. PMID: 26884067; PMCID: PMC4756455.
500. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Single guide RNA library design and construction*. *Cold Spring Harbor Protocols*, 3, pdb.prot090803. PMID: 26933249; PMCID: PMC4804709.

501. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Viral packaging and cell culture for CRISPR-based screens. Cold Spring Harbor Protocols*, 3, pdb.prot090811. PMID: 26933250; PMCID: PMC4804706.
502. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Large-scale single guide RNA library construction and use for CRISPR-Cas9-based genetic screens. Cold Spring Harbor Protocols*, 3, pdb.top086892. PMID: 26933254; PMCID: PMC4804892.
503. Giannakis, M., Mu, X.J., Shukla, S.A., Qian, Z.R., Cohen, O., Nishihara, R., Bahl, S., Cao, Y., Amin-Mansour, A., Yamauchi, M., Sukawa, Y., Stewart, C., Rosenberg, M., Mima, K., Inamura, K., Noshio, K., Nowak, J.A., Lawrence, M.S., Giovannucci, E.L., Chan, A.T., Ng, K., Meyerhardt, J.A., Van Allen, E.M., Getz, G., Gabriel, S.B., Lander, E.S., Wu, C.J., Fuchs, C.S., Ogino, S., & Garraway, L.A. (2016). *Genomic correlates of immune-cell infiltrates in colorectal carcinoma. Cell Reports*, 15(4), 857–865. PMID: 27149842; PMCID: PMC4850357.
504. Blumenstiel, B., DeFelice, M., Birsoy, O., Bleyer, A.J., Kmoch, S., Carter, T.A., Gnirke, A., Kidd, K., Rehm, H.L., Ronco, L., Lander, E.S., Gabriel, S., & Lennon, N.J. (2016). *Development and validation of a mass spectrometry-based assay for the molecular diagnosis of Mucin-1 kidney disease. The Journal of Molecular Diagnostics*, 18(4), 566–571. PMID: 27157321.
505. Abudayyeh, O.O., Gootenberg, J.S., Konermann, S., Joung, J., Slaymaker, I.M., Cox, D.B., Shmakov, S., Makarova, K.S., Semenova, E., Minakhin, L., Severinov, K., Regev, A., Lander, E.S., Koonin, E.V., & Zhang, F. (2016). *C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science*, 353(6299), aaf5573. PMID: 27256883.
506. Tewhey, R., Kotliar, D., Park, D.S., Liu, B., Winnicki, S., Reilly, S.K., Andersen, K.G., Mikkelsen, T.S., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2016). *Direct identification of hundreds of expression-modulating variants using a multiplexed reporter assay. Cell*, 165(6), 1519–1529. PMID: 27259153; PMCID: PMC4957403.
507. Yassour, M., Vatanen, T., Siljander, H., Hämäläinen, A.M., Härkönen, T., Ryhänen, S.J., Franzosa, E.A., Vlamakis, H., Huttenhower, C., Gevers, D., Lander, E.S., Knip, M., DIABIMMUNE Study Group, & Xavier, R.J. (2016). *Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. Science Translational Medicine*, 8(343), 343ra81. PMID: 27306663; PMCID: PMC5032909.
508. Darrow, E.M., Huntley, M.H., Dudchenko, O., Stamenova, E.K., Durand, N.C., Sun, Z., Huang, S.C., Sanborn, A.L., Machol, I., Shamim, M., Seberg, A.P., Lander, E.S., Chadwick, B.P., & Aiden, E.L. (2016). *Deletion of DXZ4 on the human inactive X chromosome alters higher-order genome architecture. Proceedings of the National Academy of Sciences USA*, 113(31), E4504–E4512. PMID: 27432957; PMCID: PMC4978254.
509. Durand, N.C., Robinson, J.T., Shamim, M.S., Machol, I., Mesirov, J.P., Lander, E.S., & Aiden, E.L. (2016). *Juicebox provides a visualization system for Hi-C contact maps with unlimited zoom. Cell Systems*, 3(1), 99–101. PMID: 27467250.
510. Durand, N.C., Shamim, M.S., Machol, I., Rao, S.S., Huntley, M.H., Lander, E.S., & Aiden, E.L. (2016). *Juicer provides a one-click system for analyzing loop-resolution Hi-C experiments. Cell Systems*, 3(1), 95–98. PMID: 27467249.
511. Burger, J.A., Landau, D.A., Taylor-Weiner, A., Bozic, I., Zhang, H., Sarosiek, K., Wang, L., Stewart, C., Fan, J., Hoellenriegel, J., Sivina, M., Dubuc, A.M., Fraser, C., Han, Y., Li, S., Livak, K.J., Zou, L., Wan, Y., Konoplev, S., Sougnez, C., Brown, J.R., Abruzzo, L.V., Carter, S.L., Keating, M.J., Davids, M.S., Wierda, W.G., Cibulskis, K., Zenz, T., Werner, L., Dal Cin, P., Kharchenko, P., Neuberg, D., Kantarjian, H., Lander, E.S., Gabriel, S., O'Brien, S., Letai, A., Weitz, D.A., Nowak, M.A., Getz, G., & Wu, C.J. (2016). *Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications*, 20(7), 11589. PMID: 27199251; PMCID: PMC4876453.
512. Khera, A.V., Won, H.H., Peloso, G.M., Lawson, K.S., Bartz, T.M., Deng, X., van Leeuwen, E.M., Natarajan, P., Emdin, C.A., Bick, A.G., Morrison, A.C., Brody, J.A., Gupta, N., Nomura, A., Kessler, T., Duga, S., Bis, J.C., van Duijn, C.M., Cupples, L.A., Psaty, B., Rader, D.J., Danesh, J., Schunkert, H., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Wilson, J.G., Correa, A., Boerwinkle, E., Merlino, P.A., Ardissino, D., Saleheen, D., Gabriel, S., & Kathiresan, S. (2016). *Diagnostic yield and clinical utility of sequencing familial hypercholesterolemia genes in patients with severe hypercholesterolemia. Journal of the American College of Cardiology*, 67(22), 2578–2589. PMID: 27050191.
513. Engreitz, J.M., Haines, J.E., Perez, E.M., Munson, G., Chen, J., Kane, M., McDonel, P.E., Guttman, M., & Lander, E.S. (2016). *Local regulation of gene expression by lncRNA promoters, transcription and splicing. Nature* 539(7629), 452–455. PMID: 27783602

514. Dixit, A., Parnas, O., Li, B., Chen, J., Fulco, C.P., Jerby-Arnon, L., Marjanovic, N.D., Dionne, D., Burks, T., Raychowdhury, R., Adamson, B., Norman, T.M., Lander, E.S., Weissman, J.S., Friedman, N., & Regev, S. (2016). *Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens*. *Cell*, 167(7), 1853–1866.e1817.

515. Emdin, C.A., Khera, A.V., Natarajan, P., Klarin, D., Won, H.H., Peloso, G.M., Stitzel, N.O., Nomura, A., Zekavat, S.M., Bick, A.G., Gupta, N., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Willer, C., Abecasis, G.R., Felix, J.F., Vasan, R.S., Lander, E., Rader, D.J., Danesh, J., Ardissino, D., Gabriel, S., Saleheen, D., & Kathiresan, S. (2016). *Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels*. *Journal of the American College of Cardiology*, 68(25), 2761–2772.

516. Fuchsberger, C., Flannick, J., Teslovich, T.M., Mahajan, A., Agarwala, V., Gaulton, K.J., Ma, C., Fontanillas, P., Moutsianas, L., McCarthy, D.J., Rivas, M.A., Perry, J.R., Sim, X., Blackwell, T.W., Robertson, N.R., Rayner, N.W., Cingolani, P., Locke, A.E., Fernandez Tajos, J., Highland, H.M., Dupuis, J., Chines, P.S., Lindgren, C.M., Hartl, C., Jackson, A.U., Chen, H., Huyghe, J.R., van de Bunt, M., Pearson, R.D., Kumar, A., Muller-Nurasyid, M., Grarup, N., Stringham, H.M., Gamazon, E.R., Lee, J., Chen, Y., Scott, R.A., Below, J.E., Chen, P., Huang, J., Go, M.J., Stitzel, M.L., Pasko, D., Parker, S.C., Varga, T.V., Green, T., Beer, N.L., Day-Williams, A.G., Ferreira, T., Fingerlin, T., Horikoshi, M., Hu, C., Huh, I., Ikram, M.K., Kim, B.J., Kim, Y., Kim, Y.J., Kwon, M.S., Lee, J., Lee, S., Lin, K.H., Maxwell, T.J., Nagai, Y., Wang, X., Welch, R.P., Yoon, J., Zhang, W., Barzilai, N., Voight, B.F., Han, B.G., Jenkinson, C.P., Kuulasmaa, T., Kuusisto, J., Manning, A., Ng, M.C., Palmer, N.D., Balkau, B., Stancakova, A., Abboud, H.E., Boeing, H., Giedraitis, V., Prabhakaran, D., Gottesman, O., Scott, J., Carey, J., Kwan, P., Grant, G., Smith, J.D., Neale, B.M., Purcell, S., Butterworth, A.S., Howson, J.M., Lee, H.M., Lu, Y., Kwak, S.H., Zhao, W., Danesh, J., Lam, V.K., Park, K.S., Saleheen, D., So, W.Y., Tam, C.H., Afzal, U., Aguilar, D., Arya, R., Aung, T., Chan, E., Navarro, C., Cheng, C.Y., Palli, D., Correa, A., Curran, J.E., Rybin, D., Farook, V.S., Fowler, S.P., Freedman, B.I., Griswold, M., Hale, D.E., Hicks, P.J., Khor, C.C., Kumar, S., Lehne, B., Thuillier, D., Lim, W.Y., Liu, J., van der Schouw, Y.T., Loh, M., Musani, S.K., Puppala, S., Scott, W.R., Yengo, L., Tan, S.T., Taylor, H.A., Jr., Thameem, F., Wilson, G., Sr., Wong, T.Y., Njolstad, P.R., Levy, J.C., Mangino, M., Bonnycastle, L.L., Schwarzmayr, T., Fadista, J., Surdulescu, G.L., Herder, C., Groves, C.J., Wieland, T., Bork-Jensen, J., Brandslund, I., Christensen, C., Koistinen, H.A., Doney, A.S., Kinnunen, L., Esko, T., Farmer, A.J., Hakaste, L., Hodgkisson, D., Kravic, J., Lyssenko, V., Hollensted, M., Jorgensen, M.E., Jorgensen, T., Ladenvall, C., Justesen, J.M., Karajamaki, A., Kriebel, J., Rathmann, W., Lannfelt, L., Lauritzen, T., Narisu, N., Linneberg, A., Melander, O., Milani, L., Neville, M., Orho-Melander, M., Qi, L., Qi, Q., Roden, M., Rolandsson, O., Swift, A., Rosengren, A.H., Stirrups, K., Wood, A.R., Mihailov, E., Blancher, C., Carneiro, M.O., Maguire, J., Poplin, R., Shakir, K., Fennell, T., DePristo, M., Hrahe de Angelis, M., Deloukas, P., Gjesing, A.P., Jun, G., Nilsson, P., Murphy, J., Onofrio, R., Thorand, B., Hansen, T., Meisinger, C., Hu, F.B., Isomaa, B., Karpe, F., Liang, L., Peters, A., Huth, C., O'Rahilly, S.P., Palmer, C.N., Pedersen, O., Rauramaa, R., Tuomilehto, J., Salomaa, V., Watanabe, R.M., Syvanen, A.C., Bergman, R.N., Bharadwaj, D., Bottinger, E.P., Cho, Y.S., Chandak, G.R., Chan, J.C., Chia, K.S., Daly, M.J., Ebrahim, S.B., Langenberg, C., Elliott, P., Jablonski, K.A., Lehman, D.M., Jia, W., Ma, R.C., Pollin, T.I., Sandhu, M., Tandon, N., Froguel, P., Barroso, I., Teo, Y.Y., Zeggini, E., Loos, R.J., Small, K.S., Ried, J.S., DeFronzo, R.A., Grallert, H., Glaser, B., Metspalu, A., Wareham, N.J., Walker, M., Banks, E., Gieger, C., Ingelsson, E., Im, H.K., Illig, T., Franks, P.W., Buck, G., Trakalo, J., Buck, D., Prokopenko, I., Magi, R., Lind, L., Farjoun, Y., Owen, K.R., Gloyn, A.L., Strauch, K., Tuomi, T., Kooner, J.S., Lee, J.Y., Park, T., Donnelly, P., Morris, A.D., Hattersley, A.T., Bowden, D.W., Collins, F.S., Atzmon, G., Chambers, J.C., Spector, T.D., Laakso, M., Strom, T.M., Bell, G.I., Blangero, J., Duggirala, R., Tai, E.S., McVean, G., Hani, C.L., Wilson, J.G., Seielstad, M., Frayling, T.M., Meigs, J.B., Cox, N.J., Sladek, R., Lander, E.S., Gabriel, S., Burt, N.P., Mohlke, K.L., Meitinger, T., Groop, L., Abecasis, G., Florez, J.C., Scott, L.J., Morris, A.P., Kang, H.M., Boehnke, M., Altshuler, D., & McCarthy, M.I. (2016). *The genetic architecture of type 2 diabetes*. *Nature*, 536(7614), 41–47.

517. Fulco, C.P., Munschauer, M., Anyoha, R., Munson, G., Grossman, S.R., Perez, E.M., Kane, M., Cleary, B., Lander, E.S., & Engreitz, J.M. (2016). *Systematic mapping of functional enhancer-promoter connections with CRISPR interference*. *Science*, 354(6313), 769–773.

518. Park, R.J., Wang, T., Koundakjian, D., Hultquist, J.F., Lamothe-Molina, P., Monel, B., Schumann, K., Yu, H., Krupczak, K.M., Garcia-Beltran, W., Piechocka-Trocha, A., Krogan, N.J., Marson, A., Sabatini, D.M., Lander, E.S., Hacohen, N., & Walker, B.D. (2017). A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. *Nature Genetics*, 49(2), 193–203. doi: 10.1038/ng.3741.
519. Guo, M.H., Nandakumar, S.K., Ulirsch, J.C., Zekavat, S.M., Buenrostro, J.D., Natarajan, P., Salem, R.M., Chiarle, R., Mitt, M., Kals, M., Parn, K., Fischer, K., Milani, L., Magi, R., Palta, P., Gabriel, S.B., Metspalu, A., Lander, E.S., Kathiresan, S., Hirschhorn, J.N., Esko, T., & Sankaran, V.G. (2017). Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. *Proceedings of the National Academy of Sciences U S A*, 114(3), E327–e336.
520. The Cancer Genome Atlas Research Network (2017). Integrated genomic characterization of oesophageal carcinoma. *Nature*, 541(7636), 169–175.
521. Grossman, S.R., Zhang, X., Wang, L., Engreitz, J., Melnikov, A., Rogov, P., Tewhey, R., Isakova, A., Deplancke, B., Bernstein, B.E., Mikkelsen, T.S., & Lander, E.S. (2017). Systematic dissection of genomic features determining transcription factor binding and enhancer function. *Proceedings of the National Academy of Sciences U S A*, 114(7), E1291–e1300.
522. Khera, A.V., Won, H.H., Peloso, G.M., O'Dushlaine, C., Liu, D., Stitzel, N.O., Natarajan, P., Nomura, A., Emdin, C.A., Gupta, N., Borecki, I.B., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartzel, D.N., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Rader, D.J., Danesh, J., Ardisson, D., Gabriel, S., Willer, C., Abecasis, G.R., Saleheen, D., Dewey, F.E., & Kathiresan, S. (2017). Association of rare and common variation in the lipoprotein lipase gene with coronary artery disease. *Journal of the American Medical Association*, 317(9), 937–946.
523. Kim, A.R., Ulirsch, J.C., Wilmes, S., Unal, E., Moraga, I., Karakukcu, M., Yuan, D., Kazerounian, S., Abdulhay, N.J., King, D.S., Gupta, N., Gabriel, S.B., Lander, E.S., Patiroglu, T., Ozcan, A., Ozdemir, M.A., Garcia, K.C., Piehler, J., Gazda, H.T., Klein, D.E., & Sankaran, V.G. (2017). Functional selectivity in cytokine signaling revealed through a pathogenic EPO mutation. *Cell*, 168(6), 1053–1064.e1015.
524. Wang, T., Yu, H., Hughes, N.W., Liu, B., Kendirli, A., Klein, K., Chen, W.W., Lander, E.S., & Sabatini, D.M. (2017). Gene essentiality profiling reveals gene networks and synthetic lethal interactions with oncogenic Ras. *Cell*, 168(5), 890–903.e815.
525. Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., & Aiden, E.L. (2017). De novo assembly of the aedes aegypti genome using hi-c yields chromosome-length scaffolds. *Science*, 356(6333), 92–95.
526. Khera, A.V., Won, H.H., Peloso, G.M., O'Dushlaine, C., Liu, D., Stitzel, N.O., Natarajan, P., Nomura, A., Emdin, C.A., Gupta, N., Borecki, I.B., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartzel, D.N., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Rader, D.J., Danesh, J., Ardisson, D., Gabriel, S., Willer, C., Abecasis, G.R., Saleheen, D., Dewey, F.E., & Kathiresan, S. (2017). Association of rare and common variation in the lipoprotein lipase gene with coronary artery disease. *Journal of the American Medical Association*, 317(9), 937–946.
527. Kim, A.R., Ulirsch, J.C., Wilmes, S., Unal, E., Moraga, I., Karakukcu, M., Yuan, D., Kazerounian, S., Abdulhay, N.J., King, D.S., Gupta, N., Gabriel, S.B., Lander, E.S., Patiroglu, T., Ozcan, A., Ozdemir, M.A., Garcia, K.C., Piehler, J., Gazda, H.T., Klein, D.E., & Sankaran, V.G. (2017). Functional selectivity in cytokine signaling revealed through a pathogenic epo mutation. *Cell*, 168(6), 1053–1064.e1015.
528. Mitt, M., Kals, M., Parn, K., Gabriel, S.B., Lander, E.S., Palotie, A., Ripatti, S., Morris, A.P., Metspalu, A., Esko, T., Magi, R., & Palta, P. (2017). Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage wgs-based imputation reference panel. *European Journal of Human Genetics*, 25(7), 869–876.
529. Nomura, A., Won, H.H., Khera, A.V., Takeuchi, F., Ito, K., McCarthy, S., Emdin, C.A., Klarin, D., Natarajan, P., Zekavat, S.M., Gupta, N., Peloso, G.M., Borecki, I.B., Teslovich, T.M., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartze, D.N.,

- Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Juang, J.J., Hsiung, C.A., Lin, S.Y., Wang, J.S., Tada, H., Kawashiri, M.A., Inazu, A., Yamagishi, M., Katsuya, T., Nakashima, E., Nakatochi, M., Yamamoto, K., Yokota, M., Momozawa, Y., Rotter, J.I., Lander, E.S., Rader, D.J., Danesh, J., Ardisino, D., Gabriel, S., Willer, C.J., Abecasis, G.R., Saleheen, D., Kubo, M., Kato, N., Ida Chen, Y.D., Dewey, F.E., & Kathiresan, S. (2017). *Protein-truncating variants at the cholesteryl ester transfer protein gene and risk for coronary heart disease. Circulation Research*, 121(1), 81–88.
530. Ott, P.A., Hu, Z., Keskin, D.B., Shukla, S.A., Sun, J., Bozym, D.J., Zhang, W., Luoma, A., Giobbie-Hurder, A., Peter, L., Chen, C., Olive, O., Carter, T.A., Li, S., Lieb, D.J., Eisenhaure, T., Gjini, E., Stevens, J., Lane, W.J., Javeri, I., Nallaiappan, K., Salazar, A.M., Daley, H., Seaman, M., Buchbinder, E.I., Yoon, C.H., Harden, M., Lennon, N., Gabriel, S., Rodig, S.J., Barouch, D.H., Aster, J.C., Getz, G., Wucherpfennig, K., Neuberger, D., Ritz, J., Lander, E.S., Fritsch, E.F., Hacohen, N., & Wu, C.J. (2017). *An immunogenic personal neoantigen vaccine for patients with melanoma. Nature*, 547(7662), 217–221.
531. Rheinbay, E., Parasuraman, P., Grimsby, J., Tiao, G., Engreitz, J.M., Kim, J., Lawrence, M.S., Taylor-Weiner, A., Rodriguez-Cuevas, S., Rosenberg, M., Hess, J., Stewart, C., Maruvka, Y.E., Stojanov, P., Cortes, M.L., Seepo, S., Cibulskis, C., Tracy, A., Pugh, T.J., Lee, J., Zheng, Z., Ellisen, L.W., Iafrate, A.J., Boehm, J.S., Gabriel, S.B., Meyerson, M., Golub, T.R., Baselga, J., Hidalgo-Miranda, A., Shioda, T., Bernards, A., Lander, E.S., & Getz, G. (2017). *Recurrent and functional regulatory mutations in breast cancer. Nature*, 547(7661), 55–60.
532. Rusu, V., Hoch, E., Mercader, J.M., Tenen, D.E., Gymrek, M., Hartigan, C.R., DeRan, M., von Grotthuss, M., Fontanillas, P., Spooner, A., Guzman, G., Deik, A.A., Pierce, K.A., Dennis, C., Clish, C.B., Carr, S.A., Wagner, B.K., Schenone, M., Ng, M.C.Y., Chen, B.H., Centeno-Cruz, F., Zerrweck, C., Orozco, L., Altshuler, D.M., Schreiber, S.L., Florez, J.C., Jacobs, S.B.R., & Lander, E.S. (2017). *Type 2 diabetes variants disrupt function of slc16a11 through two distinct mechanisms. Cell*, 170(1), 199–212.e120.
533. Saleheen, D., Natarajan, P., Armean, I.M., Zhao, W., Rasheed, A., Khetarpal, S.A., Won, H.H., Karczewski, K.J., O'Donnell-Luria, A.H., Samocha, K.E., Weisburd, B., Gupta, N., Zaidi, M., Samuel, M., Imran, A., Abbas, S., Majeed, F., Ishaq, M., Akhtar, S., Trindade, K., Mucksavage, M., Qamar, N., Zaman, K.S., Yaqoob, Z., Saghir, T., Rizvi, S.N.H., Memon, A., Hayyat Mallick, N., Ishaq, M., Rasheed, S.Z., Memon, F.U., Mahmood, K., Ahmed, N., Do, R., Krauss, R.M., MacArthur, D.G., Gabriel, S., Lander, E.S., Daly, M.J., Frossard, P., Danesh, J., Rader, D.J., & Kathiresan, S. (2017). *Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature*, 544(7649), 235–239.
534. Stitzel, N.O., Khera, A.V., Wang, X., Bierhals, A.J., Vourakis, A.C., Sperry, A.E., Natarajan, P., Klarin, D., Emdin, C.A., Zekavat, S.M., Nomura, A., Erdmann, J., Schunkert, H., Samani, N.J., Kraus, W.E., Shah, S.H., Yu, B., Boerwinkle, E., Rader, D.J., Gupta, N., Frossard, P.M., Rasheed, A., Danesh, J., Lander, E.S., Gabriel, S., Saleheen, D., Musunuru, K., & Kathiresan, S. (2017). *Angptl3 deficiency and protection against coronary artery disease. J Am Coll Cardiol*, 69(16), 2054–2063.
535. Tiao, G., Improgo, M.R., Kasar, S., Poh, W., Kamburov, A., Landau, D.A., Tausch, E., Taylor-Weiner, A., Cibulskis, C., Bahl, S., Fernandes, S.M., Hoang, K., Rheinbay, E., Kim, H.T., Bahlo, J., Robrecht, S., Fischer, K., Hallek, M., Gabriel, S., Lander, E.S., Stilgenbauer, S., Wu, C.J., Kiezun, A., Getz, G., & Brown, J.R. (2017). *Rare germline variants in atm are associated with chronic lymphocytic leukemia. Leukemia* 31(10), 2244–2247.
536. Joung, J., Engreitz, J.M., Konermann, S., Abudayyeh, O.O., Verdine, V.K., Aguet, F., Gootenberg, J.S., Sanjana, N.E., Wright, J.B., Fulco, C.P., Tseng, Y.Y., Yoon, C.H., Boehm, J.S., Lander, E.S., & Zhang, F. (2017). *Genome-scale activation screen identifies a lncrna locus regulating a gene neighbourhood. Nature*, 548(7667), 343–346.
537. Polak, P., Kim, J., Braunstein, L.Z., Karlic, R., Haradhavala, N.J., Tiao, G., Rosebrock, D., Livitz, D., Kubler, K., Mouw, K.W., Kamburov, A., Maruvka, Y.E., Leshchiner, I., Lander, E.S., Golub, T.R., Zick, A., Orthwein, A., Lawrence, M.S., Batra, R.N., Caldas, C., Haber, D.A., Laird, P.W., Shen, H., Ellisen, L.W., D'Andrea, A.D., Chanock, S.J., Foulkes, W.D., & Getz, G. (2017). *A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics* 49(10), 1476–1486.
538. Abudayyeh, O.O., Gootenberg, J.S., Essletzbichler, P., Han, S., Joung, J., Belanto, J.J., Verdine, V., Cox, D.B.T., Kellner, M.J., Regev, A., Lander, E.S., Voytas, D.F., Ting, A.Y., & Zhang, F. (2017). *Rna targeting with crispr-cas13. Nature*, 550(7675), 280–284.

539. Rao, S.S.P., Huang, S.C., Glenn St Hilaire, B., Engreitz, J.M., Perez, E.M., Kieffer-Kwon, K.R., Sanborn, A.L., Johnstone, S.E., Bascom, G.D., Bochkov, I.D., Huang, X., Shamim, M.S., Shin, J., Turner, D., Ye, Z., Omer, A.D., Robinson, J.T., Schlick, T., Bernstein, B.E., Casellas, R., Lander, E.S., & Aiden, E.L. (2017). *Cohesin loss eliminates all loop domains*. *Cell*, 171(2), 305–320.e324.
540. Cleary, B., Cong, L., Cheung, A., Lander, E.S., & Regev, A. (2017). *Efficient generation of transcriptomic profiles by random composite measurements*. *Cell*, 171(6), 1424–1436.e1418.
541. Hall, A.B., Yassour, M., Sauk, J., Garner, A., Jiang, X., Arthur, T., Lagoudas, G.K., Vatanen, T., Fornelos, N., Wilson, R., Bertha, M., Cohen, M., Garber, J., Khalili, H., Gevers, D., Ananthakrishnan, A.N., Kugathasan, S., Lander, E.S., Blainey, P., Vlamakis, H., Xavier, R.J., & Huttenhower, C. (2017). *A novel ruminococcus gnavus clade enriched in inflammatory bowel disease patients*. *Genome Med*, 9(1), 103.
542. Flannick, J., Fuchsberger, C., Mahajan, A., Teslovich, T.M., Agarwala, V., Gaulton, K.J., Caulkins, L., Koesterer, R., Ma, C., Moutsianas, L., McCarthy, D.J., Rivas, M.A., Perry, J.R.B., Sim, X., Blackwell, T.W., Robertson, N.R., Rayner, N.W., Cingolani, P., Locke, A.E., Tajos, J.F., Highland, H.M., Dupuis, J., Chines, P.S., Lindgren, C.M., Hartl, C., Jackson, A.U., Chen, H., Huyghe, J.R., van de Bunt, M., Pearson, R.D., Kumar, A., Muller-Nurasyid, M., Grarup, N., Stringham, H.M., Gamazon, E.R., Lee, J., Chen, Y., Scott, R.A., Below, J.E., Chen, P., Huang, J., Go, M.J., Stitzel, M.L., Pasko, D., Parker, S.C.J., Varga, T.V., Green, T., Beer, N.L., Day-Williams, A.G., Ferreira, T., Fingerlin, T., Horikoshi, M., Hu, C., Huh, I., Ikram, M.K., Kim, B.J., Kim, Y., Kim, Y.J., Kwon, M.S., Lee, J., Lee, S., Lin, K.H., Maxwell, T.J., Nagai, Y., Wang, X., Welch, R.P., Yoon, J., Zhang, W., Barzilay, N., Voight, B.F., Han, B.G., Jenkinson, C.P., Kuulasmaa, T., Kuusisto, J., Manning, A., Ng, M.C.Y., Palmer, N.D., Balkau, B., Stancakova, A., Abboud, H.E., Boeing, H., Giedraitis, V., Prabhakaran, D., Gottesman, O., Scott, J., Carey, J., Kwan, P., Grant, G., Smith, J.D., Neale, B.M., Purcell, S., Butterworth, A.S., Howson, J.M.M., Lee, H.M., Lu, Y., Kwak, S.H., Zhao, W., Danesh, J., Lam, V.K.L., Park, K.S., Saleheen, D., So, W.Y., Tam, C.H.T., Afzal, U., Aguilar, D., Arya, R., Aung, T., Chan, E., Navarro, C., Cheng, C.Y., Palli, D., Correa, A., Curran, J.E., Rybin, D., Farook, V.S., Fowler, S.P., Freedman, B.I., Griswold, M., Hale, D.E., Hicks, P.J., Khor, C.C., Kumar, S., Lehne, B., Thuillier, D., Lim, W.Y., Liu, J., Loh, M., Musani, S.K., Puppala, S., Scott, W.R., Yengo, L., Tan, S.T., Taylor, H.A., Thameem, F., Wilson, G., Wong, T.Y., Njolstad, P.R., Levy, J.C., Mangino, M., Bonnycastle, L.L., Schwarzmayr, T., Fadista, J., Surdulescu, G.L., Herder, C., Groves, C.J., Wieland, T., Bork-Jensen, J., Brandslund, I., Christensen, C., Koistinen, H.A., Doney, A.S.F., Kinnunen, L., Esko, T., Farmer, A.J., Hakaste, L., Hodgkiss, D., Kravic, J., Lyssenko, V., Hollensted, M., Jorgensen, M.E., Jorgensen, T., Ladvall, C., Justesen, J.M., Karajamaki, A., Kriebel, J., Rathmann, W., Lannfelt, L., Lauritzen, T., Narisu, N., Linneberg, A., Melander, O., Milani, L., Neville, M., Orho-Melander, M., Qi, L., Qi, Q., Roden, M., Rolandsson, O., Swift, A., Rosengren, A.H., Stirrups, K., Wood, A.R., Mihailov, E., Blancher, C., Carneiro, M.O., Maguire, J., Poplin, R., Shakir, K., Fennell, T., DePristo, M., de Angelis, M.H., Deloukas, P., Gjesing, A.P., Jun, G., Nilsson, P., Murphy, J., Onofrio, R., Thorand, B., Hansen, T., Meisinger, C., Hu, F.B., Isomaa, B., Karpe, F., Liang, L., Peters, A., Huth, C., O'Rahilly, S.P., Palmer, C.N.A., Pedersen, O., Rauramaa, R., Tuomilehto, J., Salomaa, V., Watanabe, R.M., Syvanen, A.C., Bergman, R.N., Bharadwaj, D., Bottinger, E.P., Cho, Y.S., Chandak, G.R., Chan, J.C., Chia, K.S., Daly, M.J., Ebrahim, S.B., Langenberg, C., Elliott, P., Jablonski, K.A., Lehman, D.M., Jia, W., Ma, R.C.W., Pollin, T.I., Sandhu, M., Tandon, N., Froguel, P., Barroso, I., Teo, Y.Y., Zeggini, E., Loos, R.J.F., Small, K.S., Ried, J.S., DeFronzo, R.A., Grallert, H., Glaser, B., Metspalu, A., Wareham, N.J., Walker, M., Banks, E., Gieger, C., Ingelsson, E., Im, H.K., Illig, T., Franks, P.W., Buck, G., Trakalo, J., Buck, D., Prokopenko, I., Magi, R., Lind, L., Farjoun, Y., Owen, K.R., Gloyn, A.L., Strauch, K., Tuomi, T., Kooner, J.S., Lee, J.Y., Park, T., Donnelly, P., Morris, A.D., Hattersley, A.T., Bowden, D.W., Collins, F.S., Atzmon, G., Chambers, J.C., Spector, T.D., Laakso, M., Strom, T.M., Bell, G.I., Blangero, J., Duggirala, R., Tai, E.S., McVean, G., Hanis, C.L., Wilson, J.G., Seielstad, M., Frayling, T.M., Meigs, J.B., Cox, N.J., Sladek, R., Lander, E.S., Gabriel, S., Mohlke, K.L., Meitinger, T., Groop, L., Abecasis, G., Scott, L.J., Morris, A.P., Kang, H.M., Altshuler, D., Burt, N.P., Florez, J.C., Boehnke, M., & McCarthy, M.I. (2017). *Sequence data and association statistics from 12,940 type 2 diabetes cases and controls*. *Sci Data*, 4, 170–179.
543. Regev, A., Teichmann, S.A., Lander, E.S., Amit, I., Benoist, C., Birney, E., Bodenmiller, B., Campbell, P., Carninci, P., Clatworthy, M., Clevers, H., Deplancke, B., Dunham, I., Eberwine, J., Eils, R., Enard, W., Farmer, A., Fugger, L., Gottgens, B., Hacohen, N., Haniffa, M., Hemberg, M., Kim, S., Klenerman, P., Kriegstein, A.,

- Lein, E., Linnarsson, S., Lundberg, E., Lundeberg, J., Majumder, P., Marioni, J.C., Merad, M., Mhlanga, M., Nawijn, M., Netea, M., Nolan, G., Pe'er, D., Phillipakis, A., Ponting, C.P., Quake, S., Reik, W., Rozenblatt-Rosen, O., Sanes, J., Satija, R., Schumacher, T.N., Shalek, A., Shapiro, E., Sharma, P., Shin, J.W., Stegle, O., Stratton, M., Stubbington, M.J.T., Theis, F.J., Uhlen, M., van Oudenaarden, A., Wagner, A., Watt, F., Weissman, J., Wold, B., Xavier, R., & Yosef, N. (2017). *The human cell atlas*. *Elife*, 6.
544. Zhou, Y., Castonguay, P., Sidhom, E.H., Clark, A.R., Dvela-Levitt, M., Kim, S., Sieber, J., Wieder, N., Jung, J.Y., Andreeva, S., Reichardt, J., Dubois, F., Hoffmann, S.C., Basgen, J.M., Montesinos, M.S., Weins, A., Johnson, A.C., Lander, E.S., Garrett, M.R., Hopkins, C.R., & Greka, A. (2017). *A small-molecule inhibitor of trpc5 ion channels suppresses progressive kidney disease in animal models*. *Science*, 358(6368), 1332–1336.
545. Grasso, C.S., Giannakis, M., Wells, D.K., Hamada, T., Mu, X.J., Quist, M., Nowak, J.A., Nishihara, R., Qian, Z.R., Inamura, K., Morikawa, T., Noshio, K., Abril-Rodriguez, G., Connolly, C., Escuin-Ordinas, H., Geybels, M.S., Grady, W.M., Hsu, L., Hu-Lieskova, S., Huyghe, J.R., Kim, Y.J., Krystofinski, P.E., Leiserson, M.D., Montoya, D.J., Nadel, B.B., Pellegrini, M., Pritchard, C.C., Puig-Saus, C., Quist, E.H., Raphael, B.J., Salipante, S.J., Shin, D.S., Shinbrot, E., Shirts, B., Shukla, S., Stanford, J.L., Sun, W., Tsoi, J., Upfill-Brown, A., Wheeler, D.A., Wu, C.J., Yu, M., Zaidi, S.H., Zaretsky, J.M., Gabriel, S.B., Lander, E.S., Garraway, L.A., Hudson, T.J., Fuchs, C.S., Ribas, A., Ogino, S., & Peters, U. (2018). *Genetic mechanisms of immune evasion in colorectal cancer*. *Cancer Discovery*, 8(6):730–749.
546. Ott, P. A., Hu, Z., Keskin, D. B., Shukla, S. A., Sun, J., Bozym, D. J., Zhang, W., Luoma, A., Giobbie-Hurder, A., Peter, L., Chen, C., Olive, O., Carter, T. A., Li, S., Lieb, D. J., Eisenhaure, T., Gjini, E., Stevens, J., Lane, W. J., Javeri, I., Nallaiappan, K., Salazar, A. M., Daley, H., Seaman, M., Buchbinder, E. I., Yoon, C. H., Harden, M., Lennon, N., Gabriel, S., Rodig, S. J., Barouch, D. H., Aster, J. C., Getz, G., Wucherpfennig, K., Neuberg, D., Ritz, J., Lander, E. S., Fritsch, E. V., Hacohen, N. & Wu, C. J. (2018). *Corrigendum: An immunogenic personal neoantigen vaccine for patients with melanoma*. *Nature*, 555(7696): 402.
547. Khajuria, R.K., Munschauer, M., Ulirsch, J.C., Fiorini, C., Ludwig, L.S., McFarland, S.K., Abdulhay, N.J., Specht, H., Keshishian, H., Mani, D.R., Jovanovic, M., Ellis, S.R., Fulco, C.P., Engreitz, J.M., Schutz, S., Lian, J., Gripp, K.W., Weinberg, O.K., Pinkus, G.S., Gehrke, L., Regev, A., Lander, E.S., Gazda, H.T., Lee, W.Y., Panse, V.G., Carr, S.A., & Sankaran, V.G. (2018). *Ribosome levels selectively regulate translation and lineage commitment in human hematopoiesis*. *Cell*, 173(1):90–103.
548. Tewhey, R., Kotliar, D., Park, D.S., Liu, B., Winnicki, S., Reilly, S.K., Andersen, K.G., Mikkelsen, T.S., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2018). *Direct identification of hundreds of expression-modulating variants using a multiplexed reporter assay*. *Cell*, 172(5), 1132–1134.
549. Grossman, S.R., Engreitz, J., Ray, J.P., Nguyen, T.H., Hacohen, N., & Lander, E.S. (2018). *Positional specificity of different transcription factor classes within enhancers*. *Proceedings of the National Academy of Sciences U S A*, 115(30), E7222–E7230.
550. Yassour, M., Jason, E., Hogstrom, L.J., Arthur, T.D., Tripathi, S., Siljander, H., Selvenius, J., Oikarinen, S., Hyoty, H., Virtanen, S.M., Ilonen, J., Ferretti, P., Pasolli, E., Tett, A., Asnicar, F., Segata, N., Vlamakis, H., Lander, E.S., Huttenhower, C., Knip, M., & Xavier, R.J. (2018). *Strain-level analysis of mother-to-child bacterial transmission during the first few months of life*. *Cell Host Microbe*, 24(1), 146–154.e144.
551. Khera, A. V., Chaffin, M., Aragam, K. G., Haas, M. E., Roselli, C., Choi, S. H., Natarajan, P., Lander, E. S., Lubitz, S. A., Ellinor, P. T. & Kathiresan, S. (2018). *Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations*. *Nature Genetics*, 50(9): 1219–1224.
552. Bis, J. C., Jian, X., Kunkle, B. W., Chen, Y., Hamilton-Nelson, K. L., Bush, W. S., Salerno, W. J., Lancour, D., Ma, Y., Renton, A. E., Marcora, E., Farrell, J. J., Zhao, Y., Qu, L., Ahmad, S., Amin, N., Amouyel, P., Beecham, G. W., Below, J. E., Campion, D., Charbonnier, C., Chung, J., Crane, P. K., Cruchaga, C., Cupples, L. A., Dartigues, J. F., DeBette, S., Deleuze, J. F., Fulton, L., Gabriel, S. B., Genin, E., Gibbs, R. A., Goate, A., Grenier-Boley, B., Gupta, N., Haines, J. L., Havulinna, A. S., Helisalmi, S., Hiltunen, M., Howrigan, D. P., Ikram, M. A., Kaprio, J., Konrad, J., Kuzma, A., Lander, E. S., Lathrop, M., Lehtimäki, T., Lin, H., Mattila, K., Mayeux, R., Muzny, D. M., Nasser, W., Neale, B., Nho, K., Nicolas, G., Patel, D., Pericak-Vance, M. A., Perola, M., Psaty, B. M., Quenez, O., Rajabli, F., Redon, R., Reitz, C., Remes, A. M., Salomaa, V., Sarnowski, C., Schmidt, H., Schmidt, M., Schmidt, R., Soininen, H., Thornton, T. A., Tosto, G., Tzourio, C., van der Lee, S.

- J., van Duijn, C. M., Vardarajan, B., Wang, W., Wijsman, E., Wilson, R. K., Witten, D., Worley, K. C., Zhang, X., Bellenguez, C., Lambert, J. C., Kurki, M. I., Palotie, A., Daly, M., Boerwinkle, E., Lunetta, K. L., Destefano, A. L., Dupuis, J., Martin, E. R., Schellenberg, G. D., Seshadri, S., Naj, A. C., Fornage, M. & Farrer, L. A. (2018). *Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry*. [Epub ahead of print]
553. Natarajan, P., Peloso, G. M., Zekavat, S. M., Montasser, M., Ganna, A., Chaffin, M., Khera, A. V., Zhou, W., Bloom, J. M., Engreitz, J. M., Ernst, J., O'Connell, J. R., Ruotsalainen, S. E., Alver, M., Manichaikul, A., Johnson, W. C., Perry, J. A., Poterba, T., Seed, C., Surakka, I. L., Esko, T., Ripatti, S., Salomaa, V., Correa, A., Vasan, R. S., Kellis, M., Neale, B. M., Lander, E. S., Abecasis, G., Mitchell, B., Rich, S. S., Wilson, J. G., Cupples, L. A., Rotter, J. I., Willer, C. J. & Kathiresan, S. (2018). *Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications*, 9(1): 3391.
554. Munschauer, M., Nguyen, C. T., Sirokman, K., Hartigan, C. R., Hogstrom, L., Engreitz, J. M., Ulirsch, J. C., Fulco, C. P., Subramanian, V., Chen, J., Schenone, M., Guttman, M., Carr, S. A. & Lander, E. S. (2018). *The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. Nature*, 561(7721): 132–136.
555. Alver, M., Palover, M., Saar, A., Lall, K., Zekavat, S. M., Tonisson, N., Leitsalu, L., Reigo, A., Nikopensius, T., Ainla, T., Kals, M., Magi, R., Gabriel, S. B., Eha, J., Lander, E. S., Irs, A., Philippakis, A., Marandi, T., Natarajan, P., Metspalu, A., Kathiresan, S. & Esko, T. (2018). *Recall by genotype and cascade screening for familial hypercholesterolemia in a population-based biobank from Estonia. Genetics in Medicine*. [Epub ahead of print]
556. Ulirsch, J. C., Verboon, J. M., Kazerounian, S., Guo, M. H., Yuan, D., Ludwig, L. S., Handsaker, R. E., Abdulhay, N. J., Fiorini, C., Genovese, G., Lim, E. T., Cheng, A., Cummings, B. B., Chao, K. R., Beggs, A. H., Genetti, C. A., Sieff, C. A., Newburger, P. E., Niewiadomska, E., Matysiak, M., Vlachos, A., Lipton, J. M., Atsidaftos, E., Glader, B., Narla, A., Gleizes, P. E., O'Donohue, M. F., Montel-Lehry, N., Amor, D. J., McCarroll, S. A., O'Donnell-Luria, A. H., Gupta, N., Gabriel, S. B., MacArthur, D. G., Lander, E. S., Lek, M., Da Costa, L., Nathan, D. G., Korostelev, A. A., Do, R., Sankaran, V. G. & Gazda, H. T. (2018). *The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics*, 103(6): 930–947.
557. Hsu, J. Y., Fulco, C. P., Cole, M. A., Canver, M. C., Pellin, D., Sher, F., Farouni, R., Clement, K., Guo, J. A., Biasco, L., Orkin, S. H., Engreitz, J. M., Lander, E. S., Joung, J. K., Bauer, D. E. & Pinello, L. (2018). *CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods*, 15(12): 992–993.
558. Khera, A. V., Chaffin, M., Zekavat, S. M., Collins, R. L., Roselli, C., Natarajan, P., Lichtman, J. H., D'Onofrio, G., Mathera, J. A., Dreyer, R. P., Spertus, J. A., Taylor, K. D., Psaty, B. M., Rich, S. S., Post, W. S., Gupta, N., Gabriel, S., Lander, E., Chen, Y. I., Talkowski, M. E., Rotter, J. I., Krumholz, H. M., & Kathiresan, S. (2018). *Whole Genome Sequencing to Characterize Monogenic and Polygenic Contributions in Patients Hospitalized with Early-Onset Myocardial Infarction. Circulation*.
559. Adelman, C. H., Wang, T., Sabatini, D. M. & Lander, E. S. (2019). *Genome-Wide CRISPR/Cas9 Screening for Identification of Cancer Genes in Cell Lines. Methods in Molecular Biology*, 1907: 125–136.
560. Keskin, D. B., Anandappa, A. J., Sun, J., Tirosh, I., Mathewson, N. D., Li, S., Oliveira, G., Giobbie-Hurder, A., Felt, K., Gjini, E., Shukla, S. A., Hu, Z., Li, L., Le, P. M., Allesoe, R. L., Richman, A. R., Kowalczyk, M. S., Abdelrahman, S., Geduldig, J. E., Charbonneau, S., Pelton, K., Iorgulescu, J. B., Elagina, L., Zhang, W., Olive, O., McCluskey, C., Olsen, L. R., Stevens, J., Lane, W. J., Salazar, A. M., Daley, H., Wen, P. Y., Chiocca, E. A., Harden, M., Lennon, N. J., Gabriel, S., Getz, G., Lander, E. S., Regev, A., Ritz, J., Neuber, D., Rodig, S. J., Ligon, K. L., Suva, M. L., Wucherpennig, K. W., Hacohen, N., Fritsch, E. F., Livak, K. J., Ott, P. A., Wu, C. J. & Reardon, D. A. (2019). *Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. Nature*, 565(7738): 234–239.
561. Schiebinger, G., Shu, J., Tabaka, M., Cleary, B., Subramanian, V., Solomon, A., Gould, J., Liu, S., Lin, S., Berube, P., Lee, L., Chen, J., Brumbaugh, J., Rigollet, P., Hochedlinger, K., Jaenisch, R., Regev, A., & Lander, E. S. (2019). *Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. Cell*, 176(4): 928–943.e22.
562. Lander, E. S. (2019). *2018 William Allan Award: Discovering the Genes for Common Disease: From Families to Populations. Am J Hum Genet*, 104(3): 375–383.

563. Khera, A. V., Chaffin, M., Wade, K. H., Zahid, S., Brancale, J., Xia, R., Distefano, M., Senol-Cosar, O., Haas, M. E., Bick, A., Aragam, K. G., Lander, E. S., Smith, G. D., Mason-Suares, H., Fornage, M., Lebo, M., Timpson, N. J., Kaplan, L. M. & Kathiresan, S. (2019). *Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood*. *Cell*. 177: 587–596 e589.
564. Lander, E. S., Baylis, F., Zhang, F., Charpentier, E., Berg, P., Bourgain, C., Friedrich, B., Joung, J. K., Li, J., Liu, D., Naldini, L., Nie, J. B., Qiu, R., Schoene-Seifert, B., Shao, F., Terry, S., Wei, W. & Winnacker, E. L. (2019). *Adopt a moratorium on heritable genome editing*. *Nature*. 567: 165–168.
565. Poulsen, B. E., Yang, R., Clatworthy, A. E., White, T., Osmulski, S. J., Li, L., Penaranda, C., Lander, E. S., Shores, N. & Hung, D. T. (2019). *Defining the core essential genome of Pseudomonas aeruginosa*. *Proc Natl Acad Sci U S A*.
566. Ulirsch, J. C., Verboon, J. M., Kazerounian, S., Guo, M. H., Yuan, D., Ludwig, L. S., Handsaker, R. E., Abdulhay, N. J., Fiorini, C., Genovese, G., Lim, E. T., Cheng, A., Cummings, B. B., Chao, K. R., Beggs, A. H., Genetti, C. A., Sieff, C. A., Newburger, P. E., Niewiadomska, E., Matysiak, M., Vlachos, A., Lipton, J. M., Atsidaftos, E., Glader, B., Narla, A., Gleizes, P. E., O'Donohue, M. F., Montel-Lehry, N., Amor, D. J., McCarroll, S. A., O'Donnell-Luria, A. H., Gupta, N., Gabriel, S. B., MacArthur, D. G., Lander, E. S., Lek, M., Da Costa, L., Nathan, D. G., Korostelev, A. A., Do, R., Sankaran, V. G. & Gazda, H. T. (2019). *The Genetic Landscape of Diamond-Blackfan Anemia*. *Am J Hum Genet*. 104: 356.
567. Johnson, E. O., LaVerriere, E., Office, E., Stanley, M., Meyer, E., Kawate, T., Gomez, J. E., Audette, R.E., Bandyopadhyay, N., Betancourt, N., Delano, K., Da Silva, I., Davis, J., Gallo, C., Gardner, M., Golas, A. J., Guinn, K. M., Kennedy, S., Korn, R., McConnell, J. A., Moss, C. E., Murphy, K. C., Nietupski, R. M., Papavinasandaram, K. G., Pinkham, J. T., Pino, P. A., Proulx, M. K., Ruecker, N., Song, N., Thompson, M., Trujillo, C., Wakabayashi, S., Wallach, J. B., Watson, C., Ioerger, T. R., Lander, E. S., Hubbard, B. K., Serrano-Wu, M. H., Ehrst, S., Fitzgerald, M., Rubin, E. J., Sasseti C. M., Schnappinger, D., & Hung, D. T. (2019). *Large-scale chemical-genetics yields new M. tuberculosis inhibitor classes*. *Nature*. 571(7763): 72–78.
568. Feng, Y. A., Howrigan, D. P., Abbott, L. E., Tashman, K., Cerrato, F., Singh, T., Heyne, H., Byrnes, A., Churchhouse, C., Watts, N., Solomonson, M., Lal, D., Heinzen, E. L., Dhindsa, R. S., Stanley, K. E., Cavalleri, G. L., Hakonarson, H., Helbig, I., Krause, R., May, P., Weckhuysen, S., Petrovski, S., Kamalakaran, S., Sisodiya, S. M., Cossette, P., Cotsapas, C., De Jonghe, P., Dixon-Salazar, T., Guerrini, R., Kwan, P., Marson, A. G., Stewart, R., Depondt, C., Dlugos, D. J., Scheffer, I. E., Striano, P., Freyer, C., McKenna, K., Regan, B. M., Bellows, S. T., Leu, C., Bennett, C. A., Johns, E. M. C., Macdonald, A., Shilling, H., Burgess, R., Weckhuysen, D., Bahlo, M., O'Brien, T. J., Todaro, M., Stamberger, H., Andrade, D. M., Sadoway, T. R., Mo, K., Krestel, H., Gallati, S., Papacostas, S. S., Kousiappa, I., Tanteles, G. A., Štěrbová, K., Vlčková, M., Sedláčková, L., Lašuthová, P., Klein, K. M., Rosenow, F., Reif, P. S., Knake, S., Kunz, W. S., Zsurka, G., Elger, C. E., Bauer, J., Rademacher, M., Pendziwiat, M., Muhle, H., Rademacher, A., van Baalen, A., von Spiczak, S., Stephani, U., Afawi, Z., Korczyn, A. D., Kanaan, M., Canavati, C., Kurlmann, G., Müller-Schlüter, K., Kluger, G., Häusler, M., Blatt, I., Lemke, J. R., Krey, I., Weber, Y. G., Wolking, S., Becker, F., Hengsbach, C., Rau, S., Maisch, A. F., Steinhoff, B. J., Schulze-Bonhage, A., Schubert-Bast, S., Schreiber, H., Borggräfe, I., Schankin, C. J., Mayer, T., Korinthenberg, R., Brockmann, K., Kurlmann, G., Dennig, D., Madeleyn, R., Kälviäinen, R., Auvinen, P., Saarela, A., Linnankivi, T., Lehesjoki, A. E., Rees, M. I., Chung, S. K., Pickrell, W. O., Powell, R., Schneider, N., Balestrini, S., Zagaglia, S., Braatz, V., Johnson, M. R., Auce, P., Sills, G. J., Baum, L. W., Sham, P. C., Cherny, S. S., Lui, C. H. T., Barišić, N., Delanty, N., Doherty, C. P., Shukralla, A., McCormack, M., El-Naggar, H., Canafoglia, L., Franceschetti, S., Castellotti, B., Granata, T., Zara, F., Iacomino, M., Madaia, F., Vari, M. S., Mancardi, M. M., Salpietro, V., Bisulli, F., Tinuper, P., Licchetta, L., Pippucci, T., Stipa, C., Minardi, R., Gambardella, A., Labate, A., Annesi, G., Manna, L., Gagliardi, M., Parrini, E., Mei, D., Vetro, A., Bianchini, C., Montomoli, M., Doccini, V., Marini, C., Suzuki, T., Inoue, Y., Yamakawa, K., Tumiene, B., Sadleir, L. G., King, C., Mountier, E., Caglayan, S. H., Arslan, M., Yap & inodot; Z., Yis, U., Topaloglu, P., Kara, B., Turkdogan, B., Gundogdu-Eken, A., Bebek, N., Ugur & Idot;seri, S., Baykan, B., Salman, B., Haryanyan, G., Yücesan, E., Kesim, Y., Ozkara, Ç., Poduri, A., Shiedley, B. R., Shain, C., Buono, R. J., Ferraro, T. N., Sperling, M. R., Lo, W., Privitera, M., French, J. A., Schachter, S., Kuzniecky, R. I., Devinsky, O., Hegde, M., Khankhanian, P., Helbig, K. L., Ellis, C. A., Spalletta, G., Piras, F., Piras, F., Gili, T., Ciullo, V., Reif, A., McQuillin, A., Bass, N., McIntosh, A., Blackwood, D., Johnstone, M., Palotie, A., Pato, M. T., Pato, C. N., Bromet, E. J., Carvalho, C. B.,

- Achtyes, E. D., Azevedo, M. H., Kotov, R., Lehrer, D. S., Malaspina, D., Marder, S. R., Medeiros, H., Morley, C. P., Perkins, D. O., Sobell, J. L., Buckley, P. F., Macciardi, F., Rapaport, M. H., Knowles, J. A., Fanous, A. H., McCarroll, S. A., Gupta, N., Gabriel, S. B., Daly, M. J., Lander, E. S., Lowenstein, D. H., Goldstein, D. B., Lerche, H., Berkovic, S. F., & Neale, B. M. (2019). *Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals*. *Am J Hum Genet.* 105(2): 267–282.
569. Dvela-Levitt, M., Kost-Alimova, M., Emani, M., Kohnert, E., Thompson, R., Sidhom, E. H., Rivadeneira, A., Sahakian, N., Roignot, J., Papagregoriou, G., Montesinos, M. S., Clark, A. R., McKinney, D., Gutierrez, J., Roth, M., Ronco, L., Elonga, E., Carter, T. A., Gnirke, A., Melanson, M., Hartland, K., Wieder, N., Hsu, J. C., Deltas, C., Hughey, R., Bleyer, A. J., Kmoch, S., Zivná, M., Barešova, V., Kota, S., Schlondorff, J., Heiman, M., Alper, S. L., Wagner, F., Weins, A., Golub, T. R., Lander, E. S., & Greka, A. (2019). *Small Molecule Targets TMED9 and Promotes Lysosomal Degradation to Reverse Proteinopathy*. *Cell.* 178(3): 521–535 e23.
570. Albers, J., Aoun, J. E., Audia, J. E., Bailey, M. P., Barrett, P., Bartel, D., Bienamie, J. J., Blum, R. I., Boger, J., Bollenbacher, J., Bonney, M. W., Booth, B., Bradbury, D. M., Brandicourt, O., Braunwald, E., Carpenter, A. E., Chang, H. E., Cheruvu, P., Christensen, G., Church, G., Clayman, M. D., Cooney, C. L., Cox, G. F., Curley, S. J., Dahiyat, B., DePinho, R. A., Diekman, J., Doerfler, D., Dornbusch, D., Douglas, R. H., Dunsire, D., Ebright, R. H., Eskridge, W., Flesher, G. J., Fong, K., Formela, J. F., Foster-Cheek, K., Francois, C., Franken, M. P., Franklin, H., Fu, Y. X., Gage, L. P., Gardner, P., Gardner, J., Genead, M., Geraghty, J. A., Gerweck, L., Gill, S., Gillis, S., Goeddel, D. V., Goldsmith, M., Graves, K., Gray, M. A., Grayzel, D., Greene, B., Gregory, R. J., Greve-Philips, C. A., Gros, D. A., Hamburg, M. A., Hammerschmidt, M., Hao, Y., Hartounian, H., Hasnain, F., Hastings, P. J., Hawkins, E. S., He, W. W., He, W., Hirzel, A., Hong, Z., Hoppenot, H., Jia, W., Kaplan, J., Keiper, J., King, V., Kolchinsky, P., Koller, D., Laikind, P., Lander, E. S., Langer, R. S., LaVoie, D. L., Lawton, A., Lee, J. J., Leff, J. S., Lepore, J., Leschly, N., Li, Q., Liang, M. H., Lieberman, J., Lim, J., Lindenberg, M., Lippard, S. J., Liu, D. R., Liu, Y., Liu, S. L., Lodish, H., Loncar, B., Lopatin, U., Love, T. W., Lowe, D., Lowy, I., Lu, H., Luo, L., Mahanthappa, N. K., Martin, P. W. Jr., Martini, A., Martucci, W. E., McArthur, J., McCann, C. M., McCarthy, S., McLachlan, D., Mello, C., Mento, S. J., Meyers, J., Meyers, R., Mills, K., Moch, K. I., Moos, W. H., Narachi, M., Nashat, A., Newell, W. J., Nodelman, O., Olle, B., Osborn, J. E., Oyler, J. V., Pao, W., Patel, N., Perez, R., Peterkin, D., Pompino, A., Pruzanski, M., Dan Quinn, Qutub, A. A., Raab, M. G., Radaelli, M., Rakhit, A., Ramamoorthi, K., Rastetter, W., Reed, J. C., Reinhart, H., Rhodes, J. P., Rieflin, W. J., Rong, L., Rosan, D. E., Rosenblatt, M., Rutter, W. J., Samudio, I., Samuels, C., Sato, V. L., Saunders, B., Scadden, D., Scangos, G., Scarlett, J. A., Schegerin, M., Schimmel, P., Schreiber, S. L., Schubert, C. R., Schulman, A., Shaff, E., Shaffer, R., Sharp, P. A., Sheng, M., Sheng, G., Shenk, T., Shi, F., Silos-Santiago, A., Simonian, N., Slaterry, W., Smith, J. A., Stocks, C., Stoffel, M., Su, M., Su, L., Tandon, N., Tang, C. M., Taunton-Rigby, A., Tezapsidis, N., Theuer, C., Thornberry, N. A., Tolar, M., Topol, E., Tormos, W., Trask, A., Truex, S., Tuschl, T., Varmus, H. E., Vasconcelles, M. J., Vounatsos, M., Walbert, T. P., Walsh, C. T., Wang, J., Wang, J., Wang, N., Westphal, C., Wierenga, W., Williams, D. E., Williams, L. T., Winningham, R. E., Wirth, P., Witt, R., Wood, C., Woodhouse, D. J., Wright, R., Wu, Y., Xanthopoulos, K. G., Xiao, C., Xiao, T. S., Xie, J., Xu, Y., Xu, Z. C., Yakatan, G. J., Yuan, L., Yung, W. K. A., Zamore, P. D., Zaydman, M., Zeng, X. M., Zerhouni, E., Zhang, F., Zhang, Q., & Zhang, S. (2019). *Chinese scientists and U.S. leadership in the life sciences*. *Nat Biotechnol.* 37(11): 1261–1263.
571. Hoch, E., Florez, J. C., Lander, E. S., & Jacobs, S. B. R. (2019). *Gain-of-Function Claims for Type-2-Diabetes-Associated Coding Variants in SLC16A11 Are Not Supported by the Experimental Data*. *Cell Rep.* 29(3): 778–780.
572. Khera, A. V., Mason-Suares, H., Brockman, D., Wang, M., VanDenburgh, M. J., Senol-Cosar, O., Patterson, C., Newton-Cheh, C., Zekavat, S. M., Pester, J., Chasman, D. I., Kabrhel, C., Jensen, M. K., Manson, J. E., Gaziano, J. M., Taylor, K. D., Sotoodehnia, N., Post, W. S., Rich, S. S., Rotter, J. I., Lander, E. S., Rehm, H. L., Ng K., Philippakis, A., Lebo, M., Albert, CM, & Kathiresan, S. (2019). *Rare Genetic Variants Associated With Sudden Cardiac Death in Adults*. *J Am Coll Cardiol.* 74(21): 2623–2634.
573. Fulco, C. P., Nasser, J., Jones, T. R., Munson, G., Bergman, D. T., Subramanian, V., Grossman, S. R., Anyoha, R., Doughty, B. R., Patwardhan, T. A., Nguyen, T. H., Kane, M., Perez, E. M., Durand, N. C., Lareau, C. A., Stamenova, E. K., Aiden, E. L., Lander, E. S., & Engreitz, J. M. (2019). *Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations*. *Nat Genet.* 51(12): 1664–1669.

574. Basak, A., Munschauer, M., Lareau, C. A., Montbleau, K. E., Ulirsch, J. C., Hartigan, C. R., Schenone, M., Lian, J., Wang, Y., Huang, Y., Wu, X., Gehrke, L., Rice, C. M., An, X., Christou, H. A., Mohandas, N., Carr, S. A., Chen, J. J., Orkin, S. H., Lander, E. S. & Sankaran, V. G. (2020). *Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation*. *Nature genetics*. 52(2): 138–145.
575. Dietlein, F., Weghorn, D., Taylor-Weiner, A., Richters, A., Reardon, B., Liu, D., Lander, E. S., Van Allen, E. M. & Sunyaev, S. R. (2020). *Identification of cancer driver genes based on nucleotide context*. *Nature genetics*. 52(2): 208–218.
576. Painter, C. A., Jain, E., Tomson, B. N., Dunphy, M., Stoddard, R. E., Thomas, B. S., Damon, A. L., Shah, S., Kim, D., Gomez Tejeda Zanutto, J., Hornick, J. L., Chen, Y. L., Merriam, P., Raut, C. P., Demetri, G. D., Van Tine, B. A., Lander, E. S., Golub, T. R. & Wagle, N. (2020). *The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research*. *Nature medicine*. 26(2): 181–187.
577. Ray, J. P., de Boer, C. G., Fulco, C. P., Lareau, C. A., Kanai, M., Ulirsch, J. C., Tewhey, R., Ludwig, L. S., Reilly, S. K., Bergman, D. T., Engreitz, J. M., Issner, R., Finucane, H. K., Lander, E. S., Regev, A. & Hacohen, N. (2020). *Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features*. *Nature communications*. 11(1): 1237.
578. Vallabh, S. M., Minikel, E. V., Schreiber, S. L. & Lander, E. S. (2020). *Towards a treatment for genetic prion disease: trials and biomarkers*. *The Lancet. Neurology*. 19(4): 361–368.
579. Abel, H. J., Larson, D. E., Regier, A. A., Chiang, C., Das, I., Kanchi, K. L., Layer, R. M., Neale, B. M., Salerno, W. J., Reeves, C., Buyske, S., NHGRI Centers for Common Disease Genomics, Matise, T. C., Muzny, D. M., Zody, M. C., Lander, E. S., Dutcher, S. K., Stitzel N. O., & Hall I. M. (2020). *Mapping and characterization of structural variation in 17,795 human genomes*. *Nature*. 583(7814): 83–89.
580. Fahed, A. C., Wang, M., Homburger, J. R., Patel, A. P., Bick, A. G., Neben, C. L., Lai, C., Brockman, D., Philippakis, A., Ellinor, P. T., Cassa, C. A., Lebo, M., Ng, K., Lander, E. S., Zhou, A. Y., Kathiresan, S., & Khera, A. V. (2020). *Polygenic background modifies penetrance of monogenic variants for tier 1 genomic conditions*. *Nature communications*. 11(1): 3635.
581. Zoonomia Consortium. (2020). *A comparative genomics multitool for scientific discovery and conservation*. *Nature* 587(7833): 240–245.
582. Bick A.G., Weinstock J.S., Nandakumar S.K., Fulco C.P., Bao E.L., Zekavat S.M., Szeto M.D., Liao X., Leventhal M.J., Nasser J., Chang K., Laurie C., Burugula B.B., Gibson C.J., Lin A.E., Taub M.A., Aguet F., Ardlie K., Mitchell B.D., Barnes K.C., Moscati A., Fornage M., Redline S., Psaty B.M., Silverman E.K., Weiss S.T., Palmer N.D., Vasan R.S., Burchard E.G., Kardia S.L.R., He J., Kaplan R.C., Smith N.L., Arnett D.K., Schwartz D.A., Correa A., de Andrade M., Guo X., Konkole B.A., Custer B., Peralta J.M., Gui H., Meyers D.A., McGarvey S.T., Chen I.Y., Shoemaker M.B., Peyser P.A., Broome J.G., Gogarten S.M., Wang F.F., Wong Q., Montasser M.E., Daya M., Kenny E.E., North K.E., Launer L.J., Cade B.E., Bis J.C., Cho M.H., Lasky-Su J., Bowden D.W., Cupples L.A., Mak A.C.Y., Becker L.C., Smith J.A., Kelly T.N., Aslibekyan S., Heckbert S.R., Tiwari H.K., Yang I.V., Heit J.A., Lubitz S.A., Johnson J.M., Curran J.E., Wenzel S.E., Weeks D.E., Rao D.C., Darbar D., Moon J.Y., Tracy R.P., Buth E.J., Rafaels N., Loos R.J.F., Durda P., Liu Y., Hou L., Lee J., Kachroo P., Freedman B.I., Levy D., Bielak L.F., Hixson J.E., Floyd J.S., Whitsel E.A., Ellinor P.T., Irvin M.R., Fingerlin T.E., Raffield L.M., Armasu S.M., Wheeler M.M., Sabino E.C., Blangero J., Williams L.K., Levy B.D., Sheu W.H., Roden D.M., Boerwinkle E., Manson J.E., Mathias R.A., Desai P., Taylor K.D., Johnson A.D.; NHLBI Trans-Omics for Precision Medicine Consortium, Auer P.L., Kooperberg C., Laurie C.C., Blackwell T.W., Smith A.V., Zhao H., Lange E., Lange L., Rich S.S., Rotter J.I., Wilson J.G., Scheet P., Kitzman J.O., Lander E.S., Engreitz J.M., Ebert B.L., Reiner A.P., Jaiswal S., Abecasis G., Sankaran V.G., Kathiresan S., & Natarajan P. (2020). *Inherited causes of clonal haematopoiesis in 97,691 whole genomes*. *Nature*. 586(7831): 763–768.
583. Schmidt N., Lareau C.A., Keshishian H., Ganski S., Schneider C., Hennig T., Melanson R., Werner S., Wei Y., Zimmer M., Ade J., Kirschner L., Zielinski S., Dölken L., Lander E.S., Caliskan N., Fischer U., Vogel J., Carr S.A., Bodem J., & Munschauer M. (2020). *The SARS-CoV-2 RNA-protein interactome in infected human cells*. *Nature Microbiology*. Epub ahead of print.
584. Marshall J.L., Doughty B.R., Subramanian V., Guckelberger P., Wang Q., Chen L.M., Rodrigues S.G., Zhang K., Fulco C.P., Nasser J., Grinkevich E.J., Noel T., Mangiameli S., Bergman D.T., Greka A., Lander E.S., Chen F., & Engreitz J.M. *HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequenc-*

ing of DNA probes. (2020). *Proceedings of the National Academy of Sciences*. 117(52): 33404–33413.

585. Mitchell C.M., Mazzoni C., Hogstrom L., Bryant A., Bergerat A., Cher A., Pochan S., Herman P., Carrigan M., Sharp K., Huttenhower C., Lander E.S., Vlamakis H., Xavier R.J., & Yassour M. *Delivery Mode Affects Stability of Early Infant Gut Microbiota*. (2020). *Cell Reports Medicine*. 1(9): 100156.

586. Collins F.S., Doudna J.A., Lander E.S., Rotimi C.N. *Human Molecular Genetics and Genomics—Important Advances and Exciting Possibilities*. (2021). *New England Journal of Medicine*. Epub ahead of print.

587. Sinnott-Armstrong N., Sousa I.S., Laber S., Rendina-Ruedy E., Nitter Dankel S.E., Ferreira T., Mellgren G., Karasik D., Rivas M., Pritchard J., Guntur A.R., Cox R.D., Lindgren C.M., Hauner H., Sallari R., Rosen C.J., Hsu Y.H., Lander E.S., Kiel D.P., Claussnitzer M. *A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density*. (2021) *Cell Metab*. Epub ahead of print.

IV. OTHER PUBLICATIONS

I have also authored OpEds, PCAST reports during the Obama Administration, Ad Hoc working group reports, Supreme Court amicus briefs, and a law review article.

OpEds:

- Just when we need it most, science is in danger (Boston Globe): <https://www.bostonglobe.com/2020/10/08/opinion/just-when-we-need-it-most-science-is-danger/>
- Looking to the future of patient-centered cancer research and treatment (Boston Globe; with Reed Jobs): <https://www.bostonglobe.com/opinion/2018/10/18/looking-future-patient-centered-cancer-research-and-treatment/C7jJ2IV0Z0PjOHZOxv9oyJ/story.html>
- Will America yield its position as the world's leader in science and technology? (Boston Globe): <https://www.broadinstitute.org/files/sections/about/012918-BostonGlobe-LanderOpEd.pdf>
- America's 'Miracle Machine' is in desperate need of, well, a miracle (Washington Post; with Eric Schmidt): <https://www.broadinstitute.org/files/sections/about/050517-WashPost-OpEdMiracleMachine.pdf>
- Hype vs. hope in medical research (Boston Globe/Medium): <https://www.broadinstitute.org/files/sections/about/BostonGlobe-HypeVsHope-opinion.pdf> (Medium: https://medium.com/@eric_lander/hype-vs-hope-in-medical-research-3fbd8edf018d)
- Fix the Flaws in Forensic Science (New York Times): <https://www.nytimes.com/2015/04/21/opinion/fix-the-flaws-in-forensic-science.html>
- Private Money Pays Off For Medicine (Wall Street Journal; with Louis V. Gerstner, Jr.): <https://www.wsj.com/articles/eric-lander-and-louis-gerstner-private-money-pays-off-for-medicine-1407710070>
- The Accelerator (Science): <https://science.sciencemag.org/content/331/6020/1024.2.full>
- In Wake of Genetic Revolution, Questions About Its Meaning (New York Times): <https://www.nytimes.com/2000/09/12/science/essay-in-wake-of-genetic-revolution-questions-about-its-meaning.html>

Law Review Article:

- Fixing Rule 702: The PCAST Report and Steps to Ensure the Reliability of Forensic Feature-Comparison Methods in the Criminal Courts: https://www.broadinstitute.org/files/sections/about/PCAST/2018_percent20ensurin_g-reliability-forensic.pdf

Supreme Court Amicus Briefs:

- *Association of Molecular Pathology v. Myriad Genetics*: <https://www.broadinstitute.org/files/sections/about/12-398-ac-Lander.pdf>
- *Gill v. Whitford*: https://www.brennancenter.org/sites/default/files/legal-work/Gill_AmicusBrief_EricLander_InSupportofAppellees.pdf
- *Rucho v. Common Cause*: https://www.broadinstitute.org/files/sections/about/Gerrymandering_AmicusBrief_EricLander_Rucho.pdf

Reports

- *International Commission on the Clinical Use of Human Germline Genome Editing* Heritable Human Genome Editing report: <https://www.nap.edu/catalog/25665/heritable-human-genome-editing>
- *39 Reports of the President's Council of Advisors on Science and Technology (PCAST)*, which I co-chaired during the Obama Administration, 2009–2017 (one classified): <https://obamawhitehouse.archives.gov/administration/eop/ostp/pcast/docsreports>
- *OPCAST Ad Hoc Pandemic Response Group* (single document with all six reports): https://opcast.org/OPCAST_Compendium.pdf
- *On Human Gene Editing: International Summit Statement*: <https://www.nationalacademies.org/news/2015/12/on-human-gene-editing-international-summit-statement>
- *National Academy of Sciences Committee on DNA Technology in Forensic Science* report: <https://www.nap.edu/catalog/1866/dna-technology-in-forensic-science>

V. ONLINE MATERIALS

Online Courses:

Introduction to Biology—The Secret of Life (edX):
<https://www.edx.org/course/introduction-to-biology-the-secret-of-life-3>
 Fundamentals of Biology (MIT OpenCourseware):
<https://ocw.mit.edu/courses/biology/7-01sc-fundamentals-of-biology-fall-2011/>

Podcasts:

Brave New Planet (host):
<https://www.pushkin.fm/show/brave-new-planet/>
 Clear + Vivid (guest):
<https://podcasts.apple.com/us/podcast/eric-lander-decoding-life/id1400082430?i=1000506582017>
 Lovett or Leave It (guest):
<https://podcasts.apple.com/us/podcast/coup-clutz-clan/id1216346463?i=1000499693551>
 Deep Background with Noah Feldman (guest):
<https://podcasts.apple.com/us/podcast/the-big-data-revolution/id1460055316?i=1000501053706>
 Armchair Expert (guest):
<https://armchairexpert.simplecast.com/episodes/eric-lander-yfQOITJc>
 Stay Tuned with Preet (guest):
<https://cafe.com/stay-tuned/playing-god-with-eric-lander/>
 Theory and Practice (guest):
<https://podcasts.apple.com/us/podcast/eric-lander-broad-institute/id1480260459?i=1000459308356>
 Talking Machines podcast (guest):
<https://www.thetalkingmachines.com/episodes/eric-lander-and-restricted-boltzmann-machines>

Relevant Lectures and Talks:

Lecture 14: “Rapid research response in a pandemic” (MIT):
<https://www.youtube.com/watch?v=HLkuchTScn8>
 Klinsky Lecture on Science, Law and Policy (Harvard Law School):
<https://www.youtube.com/watch?v=2WOZJ-kn2Tc>
 Science, Technology, and the Future of America (HUBweek):
<https://www.youtube.com/watch?v=SfN7b79SSec>
 “Secrets of the Human Genome” (Killian Lecture):
<https://www.youtube.com/watch?t=8m21s&v=ztMBrL21bP4&feature=youtu.be>
 Precision Medicine: the Promise, the Journey, the Future (Public Health Grand Rounds at the Aspen Institute):
<https://www.youtube.com/watch?v=Rfh-0xIVCpo>
 Limits to our Understanding (International Summit on Human Gene Editing):
<https://vimeo.com/showcase/3703972/video/149192705>
 The Miracle Machine (National Math Festival):
<https://vimeo.com/133400574>

Aspen Ideas Festival Afternoon of Conversation:

<https://www.youtube.com/watch?v=ZoTuRTYuY14>

Future of U.S. Innovation (Brookings Institute):

<https://www.c-span.org/video/?300258-4/future-us-innovation#>

Save the Miracle Machine:

https://www.youtube.com/watch?v=BNqa8TWM_10

Millennium evenings at the White House, Information Meets Genomics:

<https://www.youtube.com/watch?v=5hnMi714CX0>

18. List digital platforms (including social media and other digital content sites) on which you currently or have formerly operated an account, regardless of whether or not the account was held in your name or an alias. Include the name of an “alias” or “handle” you have used on each of the named platforms. Indicate whether the account is active, deleted, or dormant. Include a link to each account if possible.

Twitter [Active]: https://twitter.com/eric_lander (A podcast that I hosted also has a Twitter account, <https://twitter.com/BravePlanetPod>, although I do not maintain that account.)

Instagram [Dormant]: <https://www.instagram.com/ericlander17/>

Facebook [Deleted]: I do not have a personal Facebook account. (An account was created in 2013, never used, and then deleted.)

Reddit [Dormant]: https://www.reddit.com/user/Eric_Lander

Medium [Dormant]: https://medium.com/@eric_lander

19. Please identify each instance in which you have testified orally or in writing before Congress in a governmental or non-governmental capacity and specify the date and subject matter of each testimony.

I have testified before such bodies on these two occasions:

1. United States Senate Committee on Commerce, Science, and Space: The Science and Standards of Forensics (March 28, 2012)
2. The House Appropriations Subcommittee on Labor, Health and Human Services, Education, and Related Agencies: FY 1996 budget for the National Institutes of Health (February 2, 1995)

To the best of my recollection, I have not testified on other occasions.

20. Given the current mission, major programs, and major operational objectives of the department/agency to which you have been nominated, what in your background or employment experience do you believe affirmatively qualifies you for appointment to the position for which you have been nominated, and why do you wish to serve in that position?

Affirmative qualifications for the Director of the Office of Science and Technology Policy (OSTP): I have worked as scientist for 35 years, including on major scientific projects such as the Human Genome Project; I have served on several bodies that provide advice concerning science and technology to the Federal government, including co-chairing for eight years the President's Council of Advisors on Science and Technology (which provides advice to the President and the White House) and serving for four years on the Defense Innovation Board (which provides advice to the Secretary of Defense and the DOD).

I wish to serve in this position because I believe that (i) U.S. science and technology will be crucial to our Nation's health, economic prosperity and national security in the decades ahead and (ii) sound Federal policies can promote U.S. science and technology.

21. What do you believe are your responsibilities, if confirmed, to ensure that the department/agency has proper management and accounting controls, and what experience do you have in managing a large organization?

Responsibilities to Ensure Proper Management and Accounting Controls: I recognize that as Director, I would be responsible for all issues of compliance at the agency including management and accounting responsibility. Working with appointed leadership, career staff and Congressional oversight, I will work to ensure that OSTP meets the highest standards of professionalism and compliance to serve the public good. This would include ensuring that the agency adhere to the OSTP Open Government Plan, promoting transparency, timely responses to Congressional and GAO inquiries and compliance with reporting requirements.

Experience Managing Large Organizations: Since 2004, I have served as the CEO, President and Founding Director of the Broad Institute of MIT and Harvard. Since 2009, the Broad Institute has been an 501(c)(3) non-profit organization, with a large scientific community (currently more than 4,500 people), many employees (currently more than 2,000 people) and a large budget (currently more than \$500 million/year).

22. What do you believe to be the top three challenges facing the department/agency, and why?

As the President has noted: In the aftermath of WWII, the United States adopted a wise science and technology strategy that has guided the Nation for 75 years, ensuring that the U.S. has been the world leader in scientific discovery and technological innovation and yielding enormous benefits for the Nation's health, economic prosperity and national security. However, much has changed over the past 75 years—making it now essential to “refresh and reinvigorate our national science and technology strategy to set us on a strong course for the *next* 75 years, so that our children and grandchildren may inhabit a healthier, safer, more just, peaceful, and prosperous world.”

The President posed five critical questions, and he is seeking answers in the form of policies—including strategies, activities and structures—to ensure our Nation's success in the decades ahead.

Consistent with the President's letter, I believe the top three challenges are to develop policies to:

- (1) *Ensure that we learn from the current pandemic in the broadest sense—about what **is** possible or what **should become** possible—to address the widest range of needs related to our public health.*

This work includes how we can: dramatically improve our ability to rapidly address threats from pathogens, including emerging pandemics, potential bioweapons, and antibiotic resistance; dramatically speed our ability to develop and conduct clinical trials of therapies for other types of diseases like cancer; enable the rapid sharing, with patient consent, of health information to build a smarter and more effective healthcare system; best use telemedicine to improve health for all Americans; and much more.

- (2) *Ensure that the United States will be the world leader in the technologies and industries of the future that will be critical to our economic prosperity and national security, especially in competition with China.*

New technologies are emerging with increasing rapidity that have the potential to transform our lives, increase our economic prosperity by creating new industries and jobs, and protect our national security. Examples of new or rapidly evolving technologies include artificial intelligence, synthetic biology, quantum computing, advanced energy technologies, advanced manufacturing, cybersecurity, semiconductors, telecommunications, and much more.

Over the past 75 years, America has consistently been a world leader in the development of all major technologies, with huge economic and national security benefits. Today, other countries—especially China—are making unprecedented investments and doing everything in their power to promote the growth of new industries and eclipse America's scientific and technological leadership. Our future depends on our ability to keep pace with our competitors and to lead in the fields that will define the economy of tomorrow.

We need to focus on: maintaining the right level of national investment; creating the structures, infrastructures, and policies needed to accelerate the path from research laboratories to development projects to the marketplace; strengthening and expanding the connections between academia, industry, and government, which have historically been crucial for advancing technology and protecting national security; and ensuring that technological advances create rather than diminish high-quality jobs.

In addition, we need to ensure the long-term health of science and technology in our Nation—from expanding the availability of high-quality STEM education for all students and addressing stresses on colleges and universities, to protecting scientific integrity within government and making government a premier destination for scientists and technologists to work.

- (3) *Ensure that the creation and rewards of science and technology are fully shared across America and among all Americans.*

Science and technology—including training, engagement, employment and the benefits—remain unevenly distributed across racial, gender, economic, and geographic lines in the US. We must ensure that Americans of all backgrounds are drawn into both the creation and the rewards of science and technology. We need to ensure that science and technology hubs flourish in every part of the country. And, we need to ensure that advances in medical science benefit the health of all Americans, including substantially reducing disparities across racial, socioeconomic and geographic disparities in health.

B. POTENTIAL CONFLICTS OF INTEREST

1. Describe all financial arrangements, deferred compensation agreements, and other continuing dealings with business associates, clients, or customers. Please include information related to retirement accounts.

I have no continuing financial arrangements, deferred compensation agreements, or other continuing dealings with business associates, clients, or customers. My retirement accounts consist of the following:

- a. The Broad Institute, Inc. 457(b) Plan (Fidelity Freedom 2025 K Shares)
- b. Broad Institute, Inc. 401k Retirement Plan (Fidelity Freedom 2025 Fund Class K Shares)
- c. Harvard University Tax-Deferred Annuity Plan (Vanguard Institutional Target Retirement 2020 Fund Institutional Class Shares)
- d. A Sep IRA, consisting of:
 - a) Old Westbury Fixed Income Fund
 - b) Old Westbury Credit Income Fund
 - c) Old Westbury Large Cap Strategies
 - d) Old Westbury Small & Mid Cap Strategies
 - e) Old Westbury All Cap Core Fund
 - f) Old Westbury Multi-Asset Opportunities Fund
- e. A Traditional IRA, consisting of:
 - a) Old Westbury Fixed Income Fund
 - b) Old Westbury Multi-Asset Opportunities Fund
 - c) Old Westbury Credit Income Fund
 - d) Old Westbury Large Cap Strategies
 - e) Old Westbury Small & Mid Cap Strategies
 - f) Old Westbury All Cap Core Fund
- f. Whitehead Institute for Biomedical Research, consisting of:
 - a) TIAA Traditional
 - b) CREF Stock
 - c) CREF Growth
 - d) CREF Equity Index
- g. Whitehead Institute for Biomedical Research 403(B), consisting of:
 - a) CREF Growth
 - b) CREF Bond Market
- h. Retirement Income Plan For Teaching Faculty of Harvard University, consisting of:
 - a) TIAA Traditional
 - b) CREF Stock R3

For the Broad Institute 457(b) and 401k plans, I will continue to participate in this defined contribution plan. The plan sponsor will not make contributions while I am on an unpaid leave of absence during my government service.

For the Harvard University Tax-Deferred Annuity Plan, I will continue to participate in this defined contribution plan. The plan sponsor will not make contributions while I am on an unpaid leave of absence during my government service.

For the Whitehead Institute for Biomedical Research retirement accounts, I will continue to participate in this defined contribution plan. The plan sponsor ceased making contributions upon my separation.

For the Retirement Income Plan for Teaching Faculty of Harvard University, I will continue to participate in this defined contribution plan. The plan sponsor will not make contributions while I am on an unpaid leave of absence during my government service.

2. Do you have any commitments or agreements, formal or informal, to maintain employment, affiliation, or practice with any business, association or other organization during your appointment? If so, please explain.

As described in my ethics agreement, I have been granted leaves of absence from my tenured faculty appointments at (i) MIT, (ii) Harvard and (iii) the Broad Insti-

tute of MIT and Harvard, pursuant to their leave of absence policies and will abide by the terms governing those leaves set forth in the ethics agreement.

3. Indicate any investments, obligations, liabilities, or other relationships which could involve potential conflicts of interest in the position to which you have been nominated. Explain how you will resolve each potential conflict of interest.

In connection with the nomination process, I have consulted with the Office of Government Ethics and the Designated Agency Ethics Official at the Office of Science Technology Policy to identify any potential conflict of interest. Any conflict of interest will be resolved according to the terms of an ethics agreement that I have entered into with OSTP's Designated Agency Ethics Official and that will be provided to this Committee. In the event that an actual or potential conflict of interest arises during my appointment, I will consult with OSTP's ethics counsel and take the measures necessary to resolve the conflict.

4. Describe any business relationship, dealing, or financial transaction which you have had during the last ten years, whether for yourself, on behalf of a client, or acting as an agent, that could in any way constitute or result in a possible conflict of interest in the position to which you have been nominated. Explain how you will resolve each potential conflict of interest.

In connection with the nomination process, I have consulted with the Office of Government Ethics and the Designated Agency Ethics Official at the Office of Science Technology Policy to identify any potential conflict of interest. Any conflict of interest will be resolved according to the terms of an ethics agreement that I have entered into with OSTP's Designated Agency Ethics Official and that will be provided to this Committee. In the event that an actual or potential conflict of interest arises during my appointment, I will consult with OSTP's ethics counsel and take the measures necessary to resolve the conflict.

5. Identify any other potential conflicts of interest, and explain how you will resolve each potential conflict of interest.

In connection with the nomination process, I have consulted with the Office of Government Ethics and the Designated Agency Ethics Official at the Office of Science Technology Policy to identify any potential conflict of interest. Any conflict of interest will be resolved according to the terms of an ethics agreement that I have entered into with OSTP's Designated Agency Ethics Official and that will be provided to this Committee. In the event that an actual or potential conflict of interest arises during my appointment, I will consult with OSTP's ethics counsel and take the measures necessary to resolve the conflict.

6. Describe any activity during the past ten years, including the names of clients represented, in which you have been engaged for the purpose of directly or indirectly influencing the passage, defeat, or modification of any legislation or affecting the administration and execution of law or public policy. None.

C. LEGAL MATTERS

1. Have you ever been disciplined or cited for a breach of ethics, professional misconduct, or retaliation by, or been the subject of a complaint to, any court, administrative agency, the Office of Special Counsel, professional association, disciplinary committee, or other professional group? If yes:

- a. Provide the name of agency, association, committee, or group;
- b. Provide the date the citation, disciplinary action, complaint, or personnel action was issued or initiated;
- c. Describe the citation, disciplinary action, complaint, or personnel action;
- d. Provide the results of the citation, disciplinary action, complaint, or personnel action.

No.

2. Have you ever been investigated, arrested, charged, or held by any Federal, State, or other law enforcement authority of any Federal, State, county, or municipal entity, other than for a minor traffic offense? If so, please explain.

No, (except for routine background investigations required for security clearance).

3. Have you or any business or nonprofit of which you are or were an officer ever been involved as a party in an administrative agency proceeding, criminal proceeding, or civil litigation? If so, please explain.

CRISPR Patent Litigation. The Broad Institute has been involved in various proceedings related to which party was the first to invent various aspects of the CRISPR genome-editing technology. These patent questions have been the subject of proceedings before the U.S. Patent and Trademark Office and the European Patent Office Board of Appeals, with one decision appealed to the U.S. Court of Appeals, Federal Circuit. The principal cases are listed below.

- *Regents of University of California v. The Broad Institute, Inc. (0:2017bca ag01907)*, U.S. Court of Appeals, Federal Circuit

In 2012, researchers from the University of California, University of Vienna, and Emmanuelle Charpentier (collectively, “UC”) published their use of CRISPR-Cas9 to precisely cut purified DNA in a test tube. Shortly thereafter, researchers from the Broad Institute, Inc., Massachusetts Institute of Technology, and the President and Fellows of Harvard College (collectively, “Broad”) published their use of CRISPR-Cas9 to edit DNA in living cells, including human cells. The Patent Trial and Appeal Board (“Board”) found that Broad’s invention was patentably *distinct* from UC’s. UC appealed, and the Federal Court of Appeals affirmed the Board’s decision.

- *Boards of Appeal of the European Patent Office*, Case Number: T 0844/18-3.308, Application Number: 13818570.7, Publication Number: 2771468

This appeal concerns European patent 2 771 468 having the title “ENGINEERING OF SYSTEMS, METHODS AND OPTIMIZED GUIDE COMPOSITIONS FOR SEQUENCE MANIPULATION” that is based upon European patent application No. 13 818 570.7 and the PCT application, PCT/US2013/074819 filed on 12 December 2013 (“PCT ’819”). European patent 2 771 468 and PCT ’819 claim priority from twelve U.S. provisional patent applications (referred to as P1 to P12 in the decision of the opposition division).

- *George W. Schlich v. The Broad Institute, Inc., Feng Zhang, Naomi Habib, and Le Cong (1:2016mc91278)*, U.S. Court of Appeals, First Circuit

European patent attorney representing genome editing company petitioned to obtain discovery from non-profit medical research organization in relation to opposition proceedings currently before the European Patent Office (EPO) in which the attorney challenged the validity of several of the organization’s European patents involving technology used in the programmable genome editing of mammalian cells. The United States District Court for the District of Massachusetts, *F. Dennis Saylor, IV, J., 2016 WL 7209565*, denied petition and subsequently, *2017 WL 1015005*, denied patent attorney’s motion for reconsideration. Patent attorney appealed.

- *Benson Hill Biosystems Inc v. The Broad Institute Inc.*, U.S. Patent and Trademark Office, Case PGR 2018–00072, U.S. Patent No. 9,790,490

Benson Hill Biosystems requested post grant review of U.S. Patent No 9,790,490, which was assigned to the Broad Institute, Presidents and Fellows of Harvard College, and MIT “patent owners”. This request was denied on 1/22/2019.

Other Litigation

- *Xiulin Liu v. The Broad Institute, Inc.(1:2017cv12045)*, Massachusetts District Court, filed 10/19/17, closed 11/13/17

In the Complaint, Plaintiff made allegations of wrongful termination and age discrimination. The Broad disputed Plaintiff’s claims. The Court dismissed Plaintiff’s Complaint on November 13, 2017. Liu made similar allegations in a complaint filed with the Massachusetts Commission Against Discrimination and the U.S. Equal Employment Opportunity Commission; the action was dismissed after investigation by the MCAD.

- *Natissa Enterprises Ltd v. Broad Institute (1:2019mc91124)*, filed 04/02/19, closed 05/02/19, Massachusetts District Court

Plaintiff filed a Motion to Compel and Enforce Subpoena as to the Broad in regard to a separate matter, *In re Illumina Inc. Securities Litigation*, No. CV-03044–L (S.D. Cal.). The Broad opposed Plaintiff’s motion to compel. Plaintiff agreed, by Stipulation dated and filed on April 30, 2019, to withdraw its motion to compel and dismiss the action against the Broad.

4. Have you ever been convicted (including pleas of guilty or *nolo contendere*) of any criminal violation other than a minor traffic offense? If so, please explain. No.

5. Have you ever been accused, formally or informally, of sexual harassment or discrimination on the basis of sex, race, religion, or any other basis? If so, please explain. No.

6. Please advise the Committee of any additional information, favorable or unfavorable, which you feel should be disclosed in connection with your nomination.

I am not aware of additional information relevant to this section.

D. RELATIONSHIP WITH COMMITTEE

1. Will you ensure that your department/agency complies with deadlines for information set by congressional committees, and that your department/agency endeavors to timely comply with requests for information from individual Members of Congress, including requests from members in the minority? Yes.

2. Will you ensure that your department/agency does whatever it can to protect congressional witnesses and whistle blowers from reprisal for their testimony and disclosures? Yes.

3. Will you cooperate in providing the Committee with requested witnesses, including technical experts and career employees, with firsthand knowledge of matters of interest to the Committee? Yes.

4. Are you willing to appear and testify before any duly constituted committee of the Congress on such occasions as you may be reasonably requested to do so? Yes.

ATTACHMENT A9: RÉSUMÉ OF ERIC STEVEN LANDER

TITLE

President & Founding Director, The Eli and Edythe L. Broad Institute of MIT and Harvard

Professor, Department of Biology, Massachusetts Institute of Technology

Professor, Department of Systems Biology, Harvard Medical School

OFFICE

Broad Institute
415 Main Street, Cambridge, MA 02142
617-714-7010 (phone)

HOME**DATE OF BIRTH**

February 3, 1957
Brooklyn, New York

CITIZENSHIP

United States

EDUCATION

Princeton University, Princeton, New Jersey, 1974–1978
A.B. with highest honors in Mathematics, June 1978
Oxford University, Oxford, England, 1978–1981
D. Phil. in Mathematics, January 1981

FACULTY APPOINTMENTS (CURRENT)

The Eli and Edythe L. Broad Institute of MIT and Harvard
President and Founding Director, 2003–present

Massachusetts Institute of Technology, Department of Biology
Professor, 1993–present
Associate Professor (with tenure), 1989–1993
Visiting Scientist, 1984–1989

Harvard Medical School, Department of Systems Biology
Professor, 2004–present

FACULTY APPOINTMENTS (PAST)

Whitehead Institute for Biomedical Research
Director, Whitehead/MIT Center for Genome Research, 1990–2003
Member, 1989–2008
Whitehead Fellow, 1986–1989

Harvard University, Graduate School of Business
Associate Professor, 1987–1990
Assistant Professor, 1981–1986

- Taught courses on mathematics, statistics and economics; developed new courses on bidding and bargaining; artificial intelligence; and science-based businesses.
- During this period learned molecular biology and genetics in laboratories of Peter Cherbas and William Gelbart at Harvard, and H. Robert Horvitz, David Botstein and David Page at MIT.

SUMMER COURSES

The Jackson Laboratory, Bar Harbor, Maine
Short Course in Medical and Mammalian Genetics,
Lecturer, Summer 1987, 1989, 1990

Cold Spring Harbor Laboratory, Cold Spring Harbor, New York
Genetic Approaches to Human Disease Using DNA Markers
Course Co-organizer, Summer 1989, 1990, 1991

Hampshire College Summer Studies in Mathematics, Amherst, Massachusetts
National Science Foundation program for exceptional high school students,
Faculty, Summer 1975, 1976, 1979

MENTORING

Mentored more than 100 scientists, many who have gone on to become faculty at leading universities, research centers, and hospitals (including Harvard, Caltech, Princeton, Massachusetts General Hospital, Brigham and Women's Hospital, Dana-Farber Cancer Institute, Boston Children's Hospital, Fred Hutchinson Cancer Institute, Baylor College of Medicine, Weizmann Institute, Hebrew University of Jerusalem, U.S. National Institutes of Health) and biotechnology and pharmaceutical companies.

HONORARY DOCTORATES

Charles University, Czech Republic, Honorary Doctorate, 2020
Ben-Gurion University of the Negev, Israel, Honorary Doctorate, 2017
Université catholique de Louvain, Belgium, Honorary Doctorate, 2017
Brandeis University, Honorary Doctorate, 2014
Worcester Polytechnic Institute, Honorary Doctorate and Commencement Speaker, 2013
Columbia University, Honorary Doctorate, 2008
Lund University, Sweden, Honorary Doctorate, 2007
Northeastern University, Honorary Doctorate and Commencement Speaker, 2005
University of Massachusetts at Lowell, Honorary Doctorate, 2005
Williams College, Honorary Doctorate and Commencement Speaker, 2003
Mount Sinai School of Medicine, Honorary Doctorate, 2001
Medical College of Wisconsin, Honorary Doctorate, 2001
Tel Aviv University, Honorary Doctorate, 2000

ELECTED ACADEMIES

Pontifical Academy of Sciences, 2020
Council on Foreign Relations, 2014
Royal Swedish Academy of Sciences, Class of Biosciences, 2013
European Molecular Biology Organization, 2012
Academy of Athens, 2009
U.S. Institute of Medicine, 1999
American Academy of Arts and Sciences, 1999
American Academy of Achievement, 1999
U.S. National Academy of Sciences, 1997

AWARDS AND PRIZES (Selected)

Association for Molecular Pathology (AMP) Award for Excellence in Molecular Diagnostics, 2016
Friends of Cancer Research Leadership Award, 2016
"for pioneering research unlocking the molecular origins of cancer, leadership guiding our Nation's scientific priorities, and dedication to empowering a new generation of researchers to accelerate biomedical advancements"
James R. Killian, Jr. Faculty Achievement Award, MIT, 2016
"for extraordinary professional achievements by an MIT faculty member"
Fellow, American Association for Cancer Research Academy, 2016
AAAS Philip Hauge Abelson Prize, 2015
"for signal contributions to the advancement of science in the United States"
Han-Mo Koo Memorial Award, Van Andel Institute, 2015

Time Magazine's 10 years of Influence, 2013

Block Memorial Award for Distinguished Achievement in Cancer Research, Ohio State University, 2013

Breakthrough Prize in Life Sciences, 2013
"For the discovery of general principles for identifying human disease genes, and enabling their application to medicine through the creation and analysis of genetic, physical and sequence maps of the human genome."

Harvey Prize for Human Health, Technion University, Israel, 2012
"In recognition of his significant contributions to the field of genomics, as the driving force behind most of the major advances in this field."

Dan David Prize, Genome Research, Tel Aviv University, Israel, 2012
"For the Future Dimension—Genome Research"

Dart/NYU Biotechnology Achievement Award, 2012

Albany Prize in Medicine and Biomedical Research, Albany Medical College, 2010

New York Academy of Medicine Medal for Distinguished Contribution in Biomedical Sciences, 2009

A. Clifford Barger Excellence in Mentoring Award, Harvard Medical School, 2008–2009

U.S. News & World Report "America's Best Leaders," 2006

Reenpaa Medal, Finnish Cultural Foundation, 2006

AAAS Award for Public Understanding of Science and Technology, 2004
"for his excellence in communicating complex scientific ideas, and their implications for society, to the general public and policy-makers, while actively engaged in a demanding and aggressive research program."

Research!America Award for Sustained Leadership at the National Level, 2004

Lila Gruber Cancer Award, American Academy of Dermatology, 2004

Time Magazine, List of "100 Most Influential People in the World Today," 2004

Josiah Willard Gibbs Prize Lecturer, American Mathematical Society, 2004

American Scientist of the Year Award, R&D Magazine, 2003

Scientist of the Year Award, National Disease Research Interchange, 2003

Alfred Benzon Foundation Prize, Denmark, 2002

Gairdner Foundation International Award, Canada, 2002
"for his major seminal contribution to the sequencing of the human and other genomes"

John von Neumann Award, Society for Industrial and Applied Mathematics, Philadelphia, 2002

Special Achievement Award, Miami Nature Biotechnology Winter Symposium, 2002

City of Medicine Award, 2001, with John Sulston and Robert Waterston

Max Delbruck Medal, Berlin, 2001

J. Allyn Taylor Prize, Canada, 2001

Novartis Drew Award in Biomedical Research, 2001

Distinguished Service Award, American College of Neuropsychopharmacology, 2001

Allen Award, American Society of Human Genetics, 2000
"to the community of scientists that carried out the Human Genome Project", accepted on behalf of community, together with Francis Collins and Craig Venter

Beckman Prize, American Association for Lab Automation, 2000

Millennium Lecturer, The White House, October 1999

Pasarow Prize in Cancer, Robert J. and Claire Pasarow Foundation, 1998

Chiron Prize for Biotechnology, American Society for Microbiology, 1998

Phi Beta Kappa Associates Award, 1998
"for outstanding work as a scientist"

Woodrow Wilson Award for Public Service, Princeton University, 1998
"the university's highest award to an alumnus of the undergraduate college"

American Academy of Microbiology, elected 1997

Dickson Prize in Medicine, University of Pittsburgh, 1997

Class of 1960 Fellows Award, Massachusetts Institute of Technology, 1996
"for outstanding teaching"

Kroc Distinguished Lecturer, University of Washington, Seattle, 1996

Rhoads Memorial Award, American Association for Cancer Research, 1995
"for excellence in cancer research"

Herman Beerman Lecturer, Society for Investigative Dermatology, 1995

Herbert Boyer Lecturer in Genetics, University of California at San Francisco, 1995

Gladstone Distinguished Lecturer, Gladstone Institute, 1994

Ralph R. Braund Distinguished Visiting Professor, University of Tennessee, 1994

Herbert W. Dickerman Award, New York Department of Health, 1993

Christian A. Herter Distinguished Lecturer, New York University, 1993

Baker Memorial Prize for Excellence in Undergraduate Teaching, MIT, 1992

Fellow, American Association for the Advancement of Science, 1990
"for research on the application of mathematical and statistical approaches to molecular genetics"

MacArthur Prize Fellow, *for research in human genetics and mathematics*, 1987–1992

Rhodes Scholar, 1978–1981

Johnson Memorial Bequest, Oxford University, *for best thesis in mathematics*, June 1981

Senior Prize, Oxford University, June 1981

Valedictorian, Princeton University, June 1978

Pyne Prize, Princeton University, February 1978
"the highest award the university confers upon an undergraduate"

Phi Beta Kappa Award, Princeton University, June 1978
"for highest academic achievement"

Class of 1863 Prize and Andrew Brown Prize in Mathematics, Princeton University, 1976, 1977

U.S. Mathematical Olympiad Team, Silver Medal, 16th International Mathematical Olympiad, Erfurt, East Germany, 1974

First Place, Westinghouse Science Talent Search, 1974

GOVERNMENT SERVICE (Selected)

Defense Innovation Board, Office of the Secretary of Defense: Member, 2016–2020

President's Council on Jobs and Competitiveness (President's Jobs Council), Executive Office of the President: Member, 2011–2012

President's Council of Advisors on Science and Technology (PCAST), Executive Office of the President: Co-Chair, 2009–2017

Presidential Commission on the National Medal of Science: Member, 1995–2000

National Institutes of Health: Member, Advisory Committee to the Director, 1995–2000

National Cancer Advisory Board: Member, 2003–2006

National Institute of Mental Health: Member, Genetics Working Group, 1997–1998

National Center for Human Genome Research (NIH): Chair, Genome Research Review Committee, 1990–1994

National Science Foundation: Member, Advisory Committee, Biological and Behavioral Sciences, 1989–1994

National Center for Human Genome Research (NIH): Chair, Ad Hoc Study Section on New Technologies for Genome Analysis, 1989

National Library of Medicine (NIH): Chair, Ad Hoc Study Section on Analysis of Molecular Biology Data, 1988

National Institutes of Health: Chair, Subcommittee on Genetic Information, Advisory Committee on Human Genome Project, 1988

National Heart Lung and Blood Institute (NIH): Member, Special Panel on Applications of Molecular Genetics to Hypertension and Atherosclerosis, 1988

Congressional Office of Technology Assessment: Member, Panel on DNA Forensics, 1989

NON-PROFIT AND ACADEMIC BOARDS (Selected)

Life Science Cares: Member, Board of Advisors, 2019–2021
 Society for Science & The Public: Member, Honorary Board, 2019–2021
 Biden Cancer Initiative: Member, Board of Directors, 2017–2021
 Harvard Kennedy School, Belfer Center for Science and International Affairs: Member, Board of Directors, 2017–2021
 Parker Institute for Cancer Immunotherapy: Member, Scientific Advisory Board, 2015–2021
 Global Alliance for Genomics and Health: Member, Strategic Advisory Board, 2014–2021
 Innocence Project: Member, Board of Directors, 2004–2021
 Ontario Institute for Cancer Research: Co-Chair, Scientific Advisory Board, 2009–2017
 Salk Institute for Biological Studies: Non-Resident Fellow, 2010–2018
 Ragon Institute: Member, Scientific Advisory Board, 2009–2021
 Massachusetts General Hospital: Member, Research Advisory Council, 2009–2012
 Boston University: Board of Trustees, 2008–2013
 International Cancer Genomics Consortium: Member, Scientific Planning Committee, 2007–2008
 Institute for Molecular Medicine, Finland: Member, Scientific Advisory Board, 2007–2015
 Memorial Sloan Kettering Cancer Center: Member, Board of Scientific Consultants, 2001–2008
 American Society of Human Genetics: Member, Board of Directors, 2001–2003
 Finnish Genome Center: Member, Scientific Advisory Board, 2000–2006
 The Jackson Laboratory: Member, Corporation, 1999–2004
 Massachusetts General Hospital: Member, Scientific Advisory Board, 1997–2001
 Task Force on Science, Health Care and the Economy: Member, 1997–present
 National Heart Lung and Blood Institute: Co-chair, Panel on Genetic Resources, 1996–1997
 National Cancer Institute: Co-chair, Developmental Diagnostics Working Group, 1996–1997
 Dana-Farber Cancer Institute: Member, Scientific Advisory Board, 1996–2001
 Joint Steering Committee for Public Policy: Chair, 1996–2001; Member, 1994–2001
 Genetics Society of America: Member, Board of Directors, 1992–1997
 The Jackson Laboratory: Member, Scientific Advisory Board, 1992–1997
 Human Genome Organization: Governing Council, 1992–1997
 National Academy of Sciences: Co-chair, Symposium on Molecular Biology and Computer Science, 1990
 National Academy of Sciences: Chair, Committee on Mathematics and Molecular Biology, 1989–1990
 National Academy of Sciences: Member, Committee on DNA Technology in Forensic Science, 1990–1993
 National Academy of Sciences: Member, Organizing Committee for Symposium on the Frontiers of Science, 1990
 Princeton University: Member, Board of Trustees, 1987–1991
 Princeton University: Member, Advisory Council, Department of Mathematics, 1981–1985

EDITORIAL BOARDS (Selected)

Functional and Integrative Genomics, Editorial Board, 1999–2009
Annual Review of Genomics and Human Genetics, Editor, 1999–2005
Physiological Genomics, Editorial Board, 1999–2003
Computational Biology, Editorial Board, 1994–2009

Genetic Analysis: Techniques and Applications, Editorial Board, 1994–1995
Human Mutation, Editorial Board, 1993–1995
Advances in Applied Mathematics, Editorial Board, 1993–1995
Genetic Epidemiology, Editorial Board, 1991–1996
PCR Methods and Applications, Editorial Board, 1991–1995
Current Opinion in Genetics and Development, Editorial Board, 1991–1995
Human Molecular Genetics, Editorial Board, 1991–1995
Mammalian Genome, Editorial Board, 1991–2009
Genomics, Editorial Board, 1986–1999
Theoretical Population Biology, Editorial Board, 1987–1991

CORPORATE BOARDS, CONSULTING AND OTHER (Selected)

Codiak Biosciences: Board of Directors, 2015–2021
 NEON Therapeutics: Board of Directors, 2015–2021
 F-Prime Capital (formerly Fidelity Biosciences): Scientific Advisory Board, 2010–2021
 Infinity Pharmaceuticals: Board of Directors, 2001–2016
 Third Rock Ventures: Scientific Advisory Board, 2007–2021
 Foundation Medicine, Founding Advisor, 2010–2014
 Millennium Pharmaceuticals: Board of Directors, 1993–2007
 Affymetrix: Scientific Advisory Board, 1995–2000
 Healthcare Ventures: Member, Scientific Advisory Board, 1990–1995
 Arris Pharmaceutical: Scientific Advisory Board, 1990–1997
 Medigene: Chair, Scientific Advisory Board, 1990–1994
 E. Dupont de Nemours: Consultant, 1988
 Thinking Machines Corporation: Consultant, 1990–1994
 Collaborative Research: Consultant, 1985–1987
 National Broadcasting Company: Consultant on statistics and economics, 1985
 Attorney General, State of Hawaii: Consultant on law and economics, 1985
 Wyche, Burgess, Freeman & Parham, Atlanta, Georgia: Consultant on bidding and law, 1982
 Bell Laboratories: Consultant on mathematics and statistics, 1981
 Business Week Magazine: Staff reporter (AAAS Mass Media Intern Fellowship for science journalism), 1977

PUBLICATIONS

Web of Science (as of 2020):
Total publications: 639
Citations: 223,166

H-index: 208
Google Scholar (as of 2020):
Citations: 486,772
H-index: 279

BOOK

1. Lander, E.S. (1983). *Symmetric designs: an algebraic approach (Vol. 74)*. New York, NY: Cambridge University Press.

EDITED BOOK

2. Lander, E.S., & Waterman, M.S. (Eds.). (1995). *Calculating the secrets of life: Contributions of the mathematical sciences to molecular biology*. Washington, DC: National Academy Press.

ARTICLES

Mathematics

3. Lander, E.S. (1981). *Symmetric designs and self-dual codes*. *Journal of the London Mathematical Society*, 2(2), 193–204.
4. Lander, E.S. (1981). *Characterization of biplanes by their automorphism groups*. In M. Aigner & D. Jungnickel. (Eds.), *Geometries and groups* (pp. 204–218). Berlin Heidelberg, Germany: Springer-Verlag.

5. Lander, E.S. (1988). *Characterizing symmetric designs by their symmetries*. *Journal of Algebra*, 113(1), 1–18.
6. Lander, E.S. (1988). *Restrictions upon multipliers of an abelian difference set*. *Archiv der Mathematik*, 50(3), 241–242.
7. Arratia, R., & Lander, E.S. (1990). *The distribution of clusters in random graphs*. *Advances in Applied Mathematics*, 11(1), 36–48.
8. Chernoff, H., & Lander, E.S. (1995). *Asymptotic distribution of the likelihood ratio test that a mixture of two binomials is a single binomial*. *Journal of Statistical Planning and Inference*, 43(1), 19–40.

Economics

9. Farrell, J., & Lander, E.S. (1989). *Competition between and within teams: The lifeboat principle*. *Economics Letters*, 29(3), 205–208.

Biology

10. Lander, E.S., & Botstein, D. (1986). *Consanguinity and heterogeneity: Cystic fibrosis need not be homogeneous in Italy*. *American Journal of Human Genetics*, 39(2), 282–283. PMID: 3752091; PMCID: PMC1683934.
11. Lander, E.S., & Botstein, D. (1986). *Strategies for studying heterogeneous genetic traits in humans by using a linkage map of restriction fragment length polymorphisms*. *Proceedings of the National Academy of Sciences*, 83(19), 7353–7357. PMID: 2876423; PMCID: PMC386715.
12. Lander, E.S., & Botstein, D. (1986). *Mapping complex genetic traits in humans: new methods using a complete RFLP linkage map*. *Cold Spring Harbor Symposia on Quantitative Biology*, 51(Pt 1), 49–62. PMID: 2884068.
13. Lander, E.S., & Green, P. (1987). *Construction of multilocus genetic linkage maps in humans*. *Proceedings of the National Academy of Sciences USA*, 84(8), 2363–2367. PMID: 3470801; PMCID: PMC304651.
14. Lander, E.S., & Botstein, D. (1987). *Homozygosity mapping: a way to map human recessive traits with the DNA of inbred children*. *Science*, 236(4808), 1567–1570. PMID: 2884728.
15. Green, P., Barker, D., Knowlton, R., Schumm, J., Lander, E.S., Oliphant, A., Willard, H., Akots, G., Brown, V., Gravius, T., Helms, C., Nelson, C., Parker, C., Rediker, K., Watt, D., Weiffenbach, B., & Donis-Keller, H. (1987). *A genetic linkage map of chromosome 7 including the cystic fibrosis region*. In: G. Mastella & P.M. Quinton (Eds.), *Cellular and Molecular Basis of Cystic Fibrosis*. San Francisco, CA: San Francisco Press.
16. Barker, D., Green, P., Knowlton, R., Schumm, J., Lander, E.S., Oliphant, A., Willard, H., Akots, G., Brown, V., Gravius, T., Helms, C., Nelson, C., Parker, C., Rediker, K., Rising, M., Watt, D., Weiffenbach, B., & Donis-Keller, H. (1987). *Genetic linkage map of human chromosome 7 with 63 DNA markers*. *Proceedings of the National Academy of Sciences USA*, 84(22), 8006–8010. PMID: 2891136; PMCID: PMC299465.
17. Lander, E.S., Green, P., Abrahamson, J., Barlow, A., Daly, M.J., Lincoln, S.E., & Newburg, L. (1987). *MAPMAKER: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations*. *Genomics*, 1(2), 174–181. PMID: 3692487.
18. Donis-Keller, H., Green, P., Helms, C., Cartinhour, S., Weiffenbach, B., Stephens, K., Keith, T.P., Bowden, D.W., Smith, D.R., Lander, E.S., Botstein, D., Akots, G., Rediker, K.S., Gravius, T., Brown, V.A., Rising, M.B., Parker, C., Powers, J.A., Watt, D.E., Kauffman, E.R., Bricker, A., Phipps, P., Muller-Kahle, H., Fulton, T.R., Ng, S., Schumm, J.W., Braman, J.C., Knowlton, R.G., Barker, D.F., Crooks, S.M., Lincoln, S., Daly, M.J., & Abrahamson, J. (1987). *A genetic linkage map of the human genome*. *Cell*, 51(2), 319–337. PMID: 3664638.
19. Lincoln, S.E., & Lander, E.S. (1987). *Constructing genetic linkage maps with MAPMAKER: A tutorial and reference manual*. *Whitehead Institute Technical Report*, 107.
20. Lander, E.S. (1987). *The new human genetics: Mapping inherited diseases*. *Princeton Alumni Weekly*, (March 25), 10–16.
21. Lander, E.S., & Waterman, M.S. (1988). *Genomic mapping by fingerprinting random clones: a mathematical analysis*. *Genomics*, 2(3), 231–239. PMID: 3294162.
22. Chang, C., Bowman, J.L., DeJohn, A.W., Lander, E.S., & Meyerowitz, E.M. (1988). *Restriction fragment length polymorphism linkage map for Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences USA*, 85(18), 6856–6860. PMID: 2901107; PMCID: PMC282077.
23. Dracopoli, N.C., Stanger, B.Z., Ito, C.Y., Call, K.M., Lincoln, S.E., Lander, E.S., Housman, D.E. (1988). *A genetic linkage map of 27 loci from PND to FY on*

- the short arm of human chromosome I. *American Journal of Human Genetics*, 43(4), 462–470. PMID: 2902785; PMCID: PMC1715484.
24. Lander, E.S., & Lincoln, S.E. (1988). *The appropriate threshold for declaring linkage when allowing sex-specific recombination rates*. *American Journal of Human Genetics*, 43(4), 396–400. PMID: 3177382; PMCID: PMC1715500.
25. Paterson, A.H., Lander, E.S., Hewitt, J.D., Peterson, S., Lincoln, S.E., & Tanksley, S.D. (1988). *Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms*. *Nature*, 335(6192), 721–726. PMID: 2902517.
26. Lander, E.S. (1988). *Splitting schizophrenia*. *Nature*, 336(6195), 105–106. PMID: 2903447.
27. Lander, E.S. (1988). *Mapping complex genetic traits in humans*. In: K. Davies (Ed.), *Genome analysis: A practical approach* (pp. 171–188). Oxford: IRL Press.
28. Lander, E.S. (1988). *Restriction fragments: Their properties and uses*. In: M. Waterman (Ed.), *Mathematical methods for DNA sequences* (pp. 35–52). Boca Raton, FL: CRC Press.
29. Hulbert, S.H., Ilott, T.W., Legg, E.J., Lincoln, S.E., Lander, E.S., & Michelmore, R.W. (1988). *Genetic analysis of the fungus, Bremia lactucae, using restriction fragment length polymorphisms*. *Genetics*, 120(4), 947–958. PMID: 2906309; PMCID: PMC1203586.
30. Lander, E.S., Mesirov, J.P., & Taylor, W.J. (1988). *Protein sequence comparison on a data parallel computer*. *Proceedings of the 1988 International Conference on Parallel Processing, August 15–19, 1988/sponsored by Department of Electrical Engineering, Penn State University*.
31. Lander, E.S., & Botstein, D. (1989). *Mapping mendelian factors underlying quantitative traits using RFLP linkage maps*. *Genetics*, 121(1), 185–199. PMID: 2563713; PMCID: PMC1203601.
32. Pato, C.N., Lander, E.S., & Schulz, S.C. (1989). *Prospects for the genetic analysis of schizophrenia*. *Schizophrenia Bulletin*, 15(3), 365–372. PMID: 2683037.
33. Lander, E.S. (1989). *DNA fingerprinting on trial*. *Nature*, 339(6225), 501–505. PMID: 2567496.
34. Lander, E.S. (1989). *Population genetic considerations in the forensic use of DNA typing*. *Banbury Report*, 32, 143–156.
35. Lander, E.S., & Daly, M.J. (1989). *Genetic mapping of the cystic fibrosis region: Multipoint linkage analysis in two-generation pedigrees*. In: R.C. Elston, M.A. Spence, S.E. Hodge, & J.W. MacCluer (Eds.), *Genetic Analysis Workshop 6: Multipoint Mapping and Linkage Based upon Affected Pedigree Members*. New York: Alan R. Liss.
36. Lander, E.S., Mesirov, J.P., & Taylor, W.J. (1989). *Study of protein sequence comparison metrics on the Connection Machine CM-2*. *The Journal of Supercomputing*, 3(4), 255–269.
37. Lander, E.S. (1989). *Genetic mapping of polygenic factors causing diabetes in inbred rodent strains*. In: *Nordisk Insulin Symposium No. 3: Genes and Gene Products in the Development of Diabetes Mellitus—Basic and Clinical Aspects*, Oslo, Norway. Amsterdam: Elsevier Publishers.
38. Accili, D., Frapier, C., Mosthaf, L., McKeon, C., Elbein, S.C., Permutt, M.A., Ramon, E., Lander, E.S., Ullrich, A., & Taylor, S.I. (1989). *A mutation in the insulin receptor gene that impairs transport of the receptor to the plasma membrane and causes insulin-resistant diabetes*. *The EMBO Journal*, 8(9), 2509–2517. PMID: 2573522; PMCID: PMC401244.
39. Lander E.S., & Botstein, D. (1989). *Accurate and efficient mapping of quantitative trait loci*. In: T. Helentjaris & B. Burr (Eds.), *Development and Application of Molecular Markers in Problems in Plant Genetics; Current Communications in Molecular Biology* (pp. 89–96). Cold Spring Harbor, NY: Cold Spring Harbor Press.
40. Jones, R., Taylor, W.J., Zhang, X., Mesirov, J.P., & Lander, E.S. (1990). *Protein sequence comparison on the Connection Machine CM-2*. In *Computers and DNA: Proceedings of the Interface Between Computation Science and Nucleic Acid Sequencing Workshop, Dec 12–16, 1988*. Redwood City, Calif.: Addison-Wesley Pub. Co.
41. Lander, E.S., & Lodish, H. (1990). *Mitochondrial diseases: gene mapping and gene therapy*. *Cell*, 61(6), 925–926. PMID: 2190693.
42. Chakravarti, A., & Lander, E.S. (1990). *Genetic approaches to the dissection of complex diseases*. *Banbury Report*, 33, 307–315.
43. Immerman, N., & Lander, E.S. (1990). *Describing graphs: A first-order approach to graph canonization*. In A.L. Selman (Ed.), *Complexity Theory Retrospective* (pp. 59–81). New York, NY: Springer-Verlag.
44. Paterson A.H., Lander, E.S., & Tanksley, S.D. (1990). *Mapping QTLs affecting agriculturally important traits: Some examples from the tomato*. In: J.E. Womack

(Ed.), *Mapping the Genomes of Agriculturally Important Animals*. Cold Spring Harbor, NY: Cold Spring Harbor Press.

45. MacMurray, A.J., Weaver, A., Shin, H.S., & Lander, E.S. (1991). *An automated method for DNA preparation from thousands of YAC clones*. *Nucleic Acids Research*, 19(2), 385–390. PMID: 2014175; PMCID: PMC333606.

46. Paterson, A.H., Damon, S., Hewitt, J.D., Zamir, D., Rabinowitch, H.D., Lincoln, S.E., Lander, E.S., & Tanksley, S.D. (1991). *Mendelian factors underlying quantitative traits in tomato: comparison across species, generations, and environments*. *Genetics*, 127(1), 181–197. PMID: 1673106; PMCID: PMC1204303.

47. Lander, E.S., & Green, P. (1991). *Counting algorithms for linkage: correction to Morton and Collins*. *Annals of Human Genetics*, 55(Pt. 1), 33–38. PMID: 2042933.

48. Lander, E.S. (1991). *Molecular Biology: The new frontier for computational science*. *Very Large Scale Computation in the 21st Century*, 25, 138.

49. Green, P., & Lander, E.S. (1991). *Forensic DNA tests and Hardy-Weinberg equilibrium*. *Science*, 253(5023), 1038–1039. PMID: 17775346.

50. Lander, E.S. (1991). *Research on DNA typing catching up with courtroom application*. *American Journal of Human Genetics*, 48(5), 819–823. PMID: 1760000; PMCID: PMC1683053.

51. Lander, E.S. (1991). *Research on DNA typing validated in the literature [Reply]*. *American Journal of Human Genetics* 49, 899–903.

52. Jacob, H.J., Lindpaintner, K., Lincoln, S.E., Kusumi, K., Bunker, R.K., Mao, Y.P., Ganten, D., Dzau, V.J., & Lander, E.S. (1991). *Genetic mapping of a gene causing hypertension in the stroke-prone spontaneously hypertensive rat*. *Cell*, 67(1), 213–224. PMID: 1655275.

53. Arratia, R., Lander, E.S., Tavaré, S., & Waterman, M.S. (1991). *Genomic mapping by anchoring random clones: A mathematical analysis*. *Genomics*, 11(4), 806–827. PMID: 1783390.

54. Lander, E.S., Langridge, R., & Saccocio, D.M. (1991). *Computing in molecular biology: mapping and interpreting biological information*. *Computer*, 24(11), 6–13.

55. Dietrich, W., Katz, H., Lincoln, S.E., Shin, H.S., Friedman, J., Dracopoli, N.C., & Lander, E.S. (1992). *A genetic map of the mouse suitable for typing intraspecific crosses*. *Genetics*, 131(2), 423–447. PMID: 1353738; PMCID: PMC1205016.

56. Stuber, C.W., Lincoln, S.E., Wolff, D.W., Helentjaris, T., & Lander, E.S. (1992). *Identification of genetic factors contributing to heterosis in a hybrid from two elite maize inbred lines using molecular markers*. *Genetics*, 132(3), 823–839. PMID: 1468633; PMCID: PMC1205218.

57. Jacob, H.J., Pettersson, A., Wilson, D., Mao, Y., Lernmark, A., & Lander, E.S. (1992). *Genetic dissection of autoimmune type I diabetes in the BB rat*. *Nature Genetics*, 2(1), 56–60. PMID: 1303251.

58. Lander, E.S. (1992). *DNA fingerprinting: Science, law, and the ultimate identifier*. In: D.J. Kevles & L. Hood (Eds.), *The Code of Codes: Scientific and Social Issues in the Human Genome Project* (pp. 191–210). Cambridge, MA: Harvard University Press.

59. Waterman, M.S., Eggert, M., & Lander, E.S. (1992). *Parametric sequence comparisons*. *Proceedings of the National Academy of Sciences USA*, 89(13), 6090–6093. PMID: 1631095; PMCID: PMC49443.

60. Groot, P.C., Moen, C.J., Dietrich, W., Stoye, J.P., Lander, E.S., & Demant, P. (1992). *The recombinant congenic strains for analysis of multigenic traits: genetic composition*. *The FASEB Journal*, 6(10), 2826–2835. PMID: 1634045.

61. Lincoln, S.E., & Lander, E.S. (1992). *Systematic detection of errors in genetic linkage data*. *Genomics*, 14(3), 604–610. PMID: 1427888.

62. Hästbacka, J., de la Chapelle, A., Kaitila, I., Sistonen, P., Weaver, A., & Lander, E.S. (1992). *Linkage disequilibrium mapping in isolated founder populations: diastrophic dysplasia in Finland*. *Nature Genetics*, 2(3), 204–211. PMID: 1345170.

63. Goff, D.J., Galvin, K., Katz, H., Westerfield, M., Lander, E.S., & Tabin, C.J. (1992). *Identification of polymorphic simple sequence repeats in the genome of the zebrafish*. *Genomics*, 14(1), 200–202. PMID: 1427829.

64. Luongo, C., Gould, K.A., Su, L.K., Kinzler, K.W., Vogelstein, B., Dietrich, W., Lander, E.S., & Moser, A.R. (1993). *Mapping of multiple intestinal neoplasia (Min) to proximal chromosome 18 of the mouse*. *Genomics*, 15(1), 3–8. PMID: 8094372.

65. Dietrich, W., Miller, J., Katz, H., Joyce, D., Steen, R., Lincoln, S., Daly, M., Reeve, M.P., Weaver, A., Goodman, N., Dracopoli, N., and Lander, E.S. (1993). *SSLP genetic map of the mouse (Mus musculus) 2N= 40*. *Genetic Maps*, 4–110.

66. Yi, T.M., & Lander, E.S. (1993). *Protein secondary structure prediction using nearest-neighbor methods*. *Journal of Molecular Biology*, 232(4), 1117–1129. PMID: 8371270.

67. Kusumi, K., Smith, J.S., Segre, J.A., Koos, D.S., & Lander, E.S. (1993). *Construction of a large-insert yeast artificial chromosome library of the mouse genome. Mammalian Genome*, 4(7), 391–392. PMID: 8358173.
68. Lander, E.S. (1993). *DNA fingerprinting: the NRC report. Science*, 260(5112), 1221. PMID: 8493559.
69. Lander, E.S. (1993). *Finding similarities and differences among genomes. Nature Genetics*, 4(1), 5–6. PMID: 8513322.
70. Lehesjoki, A.E., Koskineniemi, M., Norio, R., Tirrito, S., Sistonen, P., Lander, E.S., & de la Chapelle, A. (1993). *Localization of the EPM1 gene for progressive myoclonus epilepsy on chromosome 21: linkage disequilibrium allows high resolution mapping. Human Molecular Genetics*, 2(8), 1229–1234. PMID: 8104628.
71. Yi, T.M., & Lander, E.S. (1993). *Protein secondary structure prediction using nearest-neighbor methods. Journal of Molecular Biology*, 232(4), 1117–1129. PMID: 8371270.
72. Copeland, N.G., Jenkins, N.A., Gilbert, D.J., Eppig, J.T., Maltais, L.J., Miller, J.C., Dietrich, W.F., Weaver, A., Lincoln, S.E., Steen, R.G., Stein, L.D., Nadeau, J., & Lander, E.S. (1993). *A genetic linkage map of the mouse: current applications and future prospects. Science*, 262(5130), 57–66. PMID: 8211130.
73. Copeland, G., Gilbert, D.J., Jenkins, N.A., Nadeau, J.H., Eppig, J.T., Maltais, L., Miller, J.C., Dietrich, W.F., Steen, R.G., Lincoln, S.E., Weaver, A., Joyce, D.C., Merchant, M., Wessel, M., Katz, H., Stein, L.D., Reeve, M.P., Daly, M.C., Dredge, R.D., Marquis, A., Goodman, N., & Lander, E.S. (1993). *Genome map IV: The mouse. Science*, 262, 67–82.
74. Dietrich, W.F., Lander, E.S., Smith, J.S., Moser, A.R., Gould, K.A., Luongo, C., Borenstein, N., & Dove, W. (1993). *Genetic identification of Mom-1, a major modifier locus affecting Min-induced intestinal neoplasia in the mouse. Cell*, 75(4), 631–639. PMID: 8242739.
75. Lisitsyn, N.A., Segre, J.A., Kusumi, K., Lisitsyn, N.M., Nadeau, J.H., Frankel, W.N., Wigler, M., & Lander, E.S. (1994). *Direct isolation of polymorphic markers linked to a trait by genetically directed representational difference analysis. Nature Genetics*, 6(1), 57–63. PMID: 8136836.
76. Wiseman, R.W., Cochran, C., Dietrich, W., Lander, E.S., & Söderkvist, P. (1994). *Allelotyping of butadiene-induced lung and mammary adenocarcinomas of B6C3F1 mice: frequent losses of heterozygosity in regions homologous to human tumor-suppressor genes. Proceedings of the National Academy of Sciences USA*, 91(9), 3759–3763. PMID: 8170984; PMCID: PMC43661.
77. Dietrich, W.F., Miller, J.C., Steen, R.G., Merchant, M., Damron, D., Nahf, R., Gross A., Joyce, D.C., Wessel, M., Dredge, R.D., & Marquis, A. (1994). *A genetic map of the mouse with 4,006 simple sequence length polymorphisms. Nature Genetics*, 7(2 Spec No), 220–245. PMID: 7920646.
78. Hsu, L.C., Kennan, W.S., Shepel, L.A., Jacob, H.J., Szpirer, C., Szpirer, J., Lander, E.S., & Gould, M.N. (1994). *Genetic identification of Mcs-1, a rat mammary carcinoma suppressor gene. Cancer Research*, 54(10), 2765–2770. PMID: 8168109.
79. Yi, T.M., & Lander, E.S. (1994). *Recognition of related proteins by iterative template refinement (ITR). Protein Science*, 3(8), 1315–1328. PMID: 7987226; PMCID: PMC2142931.
80. Lander, E.S., & Schork, N.J. (1994). *Genetic dissection of complex traits. Science*, 265(5181), 2037–2048. PMID: 8091226.
81. Dietrich, W.F., Radany, E.H., Smith, J.S., Bishop, J.M., Hanahan, D., & Lander, E.S. (1994). *Genome-wide search for loss of heterozygosity in transgenic mouse tumors reveals candidate tumor suppressor genes on chromosomes 9 and 16. Proceedings of the National Academy of Sciences USA*, 91(20), 9451–9455. PMID: 7937788; PMCID: PMC44830.
82. Hästbacka, J., de la Chapelle, A., Mahtani, M.M., Clines, G., Reeve-Daly, M.P., Daly, M.J., Hamilton, B.A., Kusumi, K., Trivedi, B., Weaver, A., Coloma, A., Lovett, M., Buckler, A., Ilkka, K., & Lander, E.S. (1994). *The diastrophic dysplasia gene encodes a novel sulfate transporter: positional cloning by fine-structure linkage disequilibrium mapping. Cell*, 78(6), 1073–1087. PMID: 7923357.
83. Cox, D.R., Green, E.D., Lander, E.S., Cohen, D., & Myers, R.M. (1994). *Assessing mapping progress in the Human Genome Project. Science*, 265(5181), 2031–2032. PMID: 8091223.
84. Lander, E.S., & Budowle, B. (1994). *DNA fingerprinting dispute laid to rest. Nature*, 371(6500), 735–738. PMID: 7818670.
85. Hegi, M.E., Devereux, T.R., Dietrich, W.F., Cochran, C.J., Lander, E.S., Foley, J.F., Maronpot R.R., Anderson M.W., & Wiseman, R.W. (1994). *Allelotype analysis of mouse lung carcinomas reveals frequent allelic losses on chromosome 4 and an association between allelic imbalances on chromosome 6 and K-ras activation. Cancer Research*, 54(23), 6257–6264. PMID: 7954475.

86. Haldi, M., Perrot, V., Saumier, M., Desai, T., Cohen, D., Cherif, D., Ward, D., & Lander, E.S. (1994). *Large human YACs constructed in a rad52 strain show a reduced rate of chimerism*. *Genomics*, 24(3), 478–484. PMID: 7713499.
87. Truett, G.E., Jacob, H.J., Miller, J., Drouin, G., Bahary, N., Smoller, J.W., Lander, E.S., & Leibel, R.L. (1995). *Genetic map of rat chromosome 5 including the fatty (fa) locus*. *Mammalian Genome*, 6(1), 25–30. PMID: 7719022.
88. Lander, E.S., & Kruglyak, L. (1995). *Genetic dissection of complex traits*. *Nature Genetics*, 11(3), 241–247. PMID: 7581446.
89. Chernoff, H., & Lander, E.S. (1995). *Asymptotic distribution of the likelihood ratio test that a mixture of two binomials is a single binomial*. *Journal of Statistical Planning and Inference*, 43(1), 19–40.
90. Lander, E.S. (1995). *Mapping heredity: Using probabilistic models and algorithms to map genes and genomes*. In: E.S. Lander & M.S. Waterman (Eds.), *Calculating the Secrets of Life: Contributions of the Mathematical Sciences to Molecular Biology* (pp. 25–55). Washington, DC: National Academy Press.
91. Lander, E.S., & Waterman, M.S. (1995). *The Secrets of Life: A Mathematician's Introduction to Molecular Biology*. In: E.S. Lander & M.S. Waterman (Eds.), *Calculating the Secrets of Life: Contributions of the Mathematical Sciences to Molecular Biology* (pp. 25–55). Washington, DC: National Academy Press.
92. Kruglyak, L., Daly, M.J., & Lander, E.S. (1995). *Rapid multipoint linkage analysis of recessive traits in nuclear families, including homozygosity mapping*. *American Journal of Human Genetics*, 56(2), 519–527. PMID: 7847388; PMCID: PMC1801139.
93. Jacob, H.J., Brown, D.M., Bunker, R.K., Daly, M.J., Dzau, V.J., Goodman, A., Kren, V., Kurtz, T., Lernmark, A., Levan, G., Mao, Y.P., Pettersson, A., Pravenec, M., Simon, J.S., Szpirer, C., Szpirer, J., Trolliet, M.R., Winer, E.S., & Lander, E.S. (1995). *A genetic linkage map of the laboratory rat, Rattus norvegicus*. *Nature Genetics*, 9(1), 63–69. PMID: 7704027.
94. Kruglyak, L., & Lander, E.S. (1995). *A nonparametric approach for mapping quantitative trait loci*. *Genetics*, 139(3), 1421–1428. PMID: 7768449; PMCID: PMC1206467.
95. Lander, E.S. (1995). *Mapping heredity: Using probabilistic models and algorithms to map genes and genomes (Part I)*. *Notices of the AMS*, 42, 747–753.
96. Lander, E.S. (1995). *Mapping Heredity: Using probabilistic models and algorithms to map genes and genomes (Part II)*. *Notices of the AMS*, 42(8), 854–858.
97. Bell, C.J., Budarf, M.L., Nieuwenhuijsen, B.W., Barnoski, B.L., Buetow, K.H., Campbell, K., Colbert A., Collins J., Desjardins, P.R., DeZwaan, T., Eckman, B., Fischbeck, K.H., Foote, S., Hart, K., Hiester, K., Van Het Hoog, M.J., Hopper, E., McDermid, H.E., Overton, C., Reeve-Daly, M.P., Searls, D.B., Watson, E., Winston, R., Valmiki, V.H., Nussbaum, R.L., Lander, E.S., Emanuel, B.S., & Hudson, T.J. (1995). *Integration of physical, breakpoint and genetic maps of chromosome 22. Localization of 587 yeast artificial chromosomes with 238 mapped markers*. *Human Molecular Genetics*, 4(1), 59–69. PMID: 7711735.
98. Dietrich, W.F., Damron, D.M., Isberg, R.R., Lander, E.S., & Swanson, M.S. (1995). *Lgn1, a gene that determines susceptibility to Legionella pneumophila, maps to mouse chromosome 13*. *Genomics*, 26(3), 443–450. PMID: 7607666.
99. Kruglyak, L., & Lander, E.S. (1995). *High-resolution genetic mapping of complex traits*. *American Journal of Human Genetics*, 56(5), 1212–1223. PMID: 7726179; PMCID: PMC1801437.
100. Kruglyak, L., & Lander, E.S. (1995). *Complete multipoint sib-pair analysis of qualitative and quantitative traits*. *American Journal of Human Genetics*, 57(2), 439–454. PMID: 7668271; PMCID: PMC1801561.
101. Segre, J.A., Nemhauser, J.L., Taylor, B.A., Nadeau, J.H., & Lander, E.S. (1995). *Positional cloning of the nude locus: genetic, physical, and transcription maps of the region and mutations in the mouse and rat*. *Genomics*, 28(3), 549–559. PMID: 7490093.
102. Pettersson, A., Wilson, D., Daniels, T., Tobin, S., Jacob, H.J., Lander, E.S., & Lernmark, A. (1995). *Thyroiditis in the BB rat is associated with lymphopenia but occurs independently of diabetes*. *Journal of Autoimmunity*, 8(4), 493–505. PMID: 7492346.
103. De Sanctis, G.T., Merchant, M., Beier, D.R., Dredge, R.D., Grobholz, J.K., Martin, T.R., Lander, E.S., & Drazen, J.M. (1995). *Quantitative locus analyses of airway hyperresponsiveness in A/J and C57BL/6J mice*. *Nature Genetics*, 11(2), 150–154. PMID: 7550342.
104. Chumakov, I.M., Rigault, P., LeGall, I., Bellannechanelot, C., Billault, A., Guillou, S., Soularue P., Guasconi G., Poullier E., Gros I., Belova, M., Sambucy, J., Susini, L., Gervy, P., Glibert, F., Beaufils, S., Bui, H., Massart, C., De Tand, M., Dukasz, F., Lecoulant, S., Ougen, P., Perrot, V., Saumier, M., Soravito, C.,

- Bahouayila, R., Cohen-Akenin, A., Barillot, E., Bertrant, S., Codani, J., Caterina, D., Georges, I., Lacroix, B., Lucotte, G., Sahbatou, M., Schmit, C., Sangouard, M., Tubacher, E., Dib, C., Fauré, S., Fizames, C., Gyapay, G., Millasseau, P., Nguyen, S., Muselet, D., Vignal, A., Morrisette, J., Menninger, J., Lieman, J., Desai, T., Banks, A., Bray-Ward, P., Ward, D., Hudson, T., Gerety, S., Foote, S., Stein, L., Page, D.C., Lander, E.S., Weissenbach, J., Le Paslier, D., & Cohen, D. (1995). A YAC contig map of the human genome. *Nature*, 377(6547 Suppl), 175–297. PMID: 7566096.
105. Schork, N.J., Krieger, J.E., Trollet, M.R., Franchini, K.G., Koike, G., Krieger, E.M., Lander, E.S., Dzau, V.J., & Jacob, H.J. (1995). A biometrical genome search in rats reveals the multigenic basis of blood pressure variation. *Genome Research*, 5(2), 164–172. PMID: 9132270.
106. Dietrich, W.F., Copeland, N.G., Gilbert, D.J., Miller, J.C., Jenkins, N.A., & Lander, E.S. (1995). Mapping the mouse genome: current status and future prospects. *Proceedings of the National Academy of Sciences USA*, 92(24), 10849–10853. PMID: 7479896; PMCID: PMC40528.
107. Lander, E.S., & Kruglyak, L. (1995). Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. *Nature Genetics*, 11(3), 241–247. PMID: 7581446.
108. Parangi, S., Dietrich, W., Christofori, G., Lander, E.S., & Hanahan, D. (1995). Tumor suppressor loci on mouse chromosomes 9 and 16 are lost at distinct stages of tumorigenesis in a transgenic model of islet cell carcinoma. *Cancer Research*, 55(24), 6071–6076. PMID: 8521395.
109. Hudson, T.J., Stein, L.D., Gerety, S.S., Ma, J., Castle, A.B., Silva, J., Slonim, D.K., Baptista, R., Kruglyak, L., Xu, S.H., Hu, X., Colbert, A.M., Rosenberg, C., Reeve-Daly, M.P., Rozen, S., Hui, L., Wu, X., Vestergaard, C., Wilson, K.M., Bae, J.S., Maitra, S., Ganiatsas, S., Evans, C.A., DeAngelis, M.M., Ingalls, K.A., Nahf, R.W., Horton, L.T., Anderson, M.O., Collymore, A.J., Ye, W., Kouyoumjian, V., Zemsteva, I.S., Tam, J., Devine, R., Courtney, D.F., Renaud, M.T., Nguyen, H., O'Connor, T.J., Fizames, C., Fauré, S., Gyapay, G., Dib, C., Morrisette, J., Orlin, J.B., Birren, B.W., Goodman, N., Weissenbach, J., Hawkins, T.L., Foote, S., Page, D.C., & Lander, E.S. (1995). An STS-based map of the human genome. *Science*, 270(5244), 1945–1954. PMID: 8533086.
110. Superti-Furga, A., Hästbacka, J., Wilcox, W.R., Cohn, D.H., van der Harten, H.J., Rossi, A., Blau, N., Rimo, D.L., Steinmann, B., Lander, E.S., & Gitzelmann, R. (1996). Achondrogenesis type IB is caused by mutations in the diastrophic dysplasia sulphate transporter gene. *Nature Genetics*, 12(1), 100–102. PMID: 8528239.
111. Brown, D.M., Provoost, A.P., Daly, M.J., Lander, E.S., & Jacob, H.J. (1996). Renal disease susceptibility and hypertension are under independent genetic control in the fawn-hooded rat. *Nature Genetics*, 12(1), 44–51. PMID: 8528250.
112. Jacob, H.J., Krieger, J.E., Dzau, V.J., & Lander, E.S. (1996). Genetic dissection of hypertension in experimental animal models. *Fundamental and Clinical Cardiology*, 26, 293–320.
113. Miller, J.C., Dietrich, W.F., Steen, R.G., Joyce, D.C., Merchant, M.A., Wessel, M.T., Damron D.M., Nahf, R.W., Stein, L.D., Dredge, R.D., Marquis, A.L., Daly, M.J., Reeve, M.P., Goodman, N., Lord, C.J., Montague, C.T., Prins, J.B., Todd, J.A., & Lander, E.S. (1996). SSLP/microsatellite genetic linkage map of the mouse. In: M.F. Lyon, S. Rastan, & S.D.M. Brown (Eds.), *Genetic Variants and Strains of the Laboratory Mouse* (pp. 1671–1755). Oxford: Oxford University Press.
114. Galli, J., Li, L.S., Glaser, A., Ostenson, C.G., Jiao, H., Fakhrai-Rad, H., Jacob, H.J., Lander, E.S., & Luthman, H. (1996). Genetic analysis of non-insulin dependent diabetes mellitus in the GK rat. *Nature Genetics*, 12(1), 31–37. PMID: 8528247.
115. Hästbacka, J., Superti-Furga, A., Wilcox, W.R., Rimo, D.L., Cohn, D.H., & Lander, E.S. (1996). Atelosteogenesis type II is caused by mutations in the diastrophic dysplasia sulfate-transporter gene (DTDST): evidence for a phenotypic series involving three chondrodysplasias. *American Journal of Human Genetics*, 58(2), 255–262. PMID: 8571951; PMCID: PMC1914552.
116. Dietrich, W.F., Miller, J., Steen, R., Merchant, M.A., Damron-Boles, D., Husain, Z., Dredge, R., Daly, M.J., Ingalls, K.A., O'Connor, T.J., Evans, C.A., DeAngelis, M.M., Levinson, D.M., Kruglyak, L., Goodman, N., Copeland N.G., Jenkins, N.A., Hawkins, T.L., Stein, L., Page, D.C., & Lander, E.S. (1996). A comprehensive genetic map of the mouse genome. *Nature*, 380(6570), 149–152. PMID: 8600386.
117. Hamilton, B.A., Frankel, W.N., Kerrebrock, A.W., Hawkins, T.L., FitzHugh, W., Kusumi, K., Russell, L.B., Mueller, K.L., van Berkel, V., Birren, B.W., Kruglyak, L., & Lander, E.S. (1996). Disruption of the nuclear hormone receptor ROR α in staggerer mice. *Nature*, 379(6567), 736–739. PMID: 8602221.

118. Kruglyak, L., & Lander, E.S. (1996). *Limits on fine mapping of complex traits. American Journal of Human Genetics*, 58(5), 1092–1093. PMID: 8651271; PMCID: PMC1914627.
119. Kruglyak, L., Daly, M.J., Reeve-Daly, M.P., & Lander, E.S. (1996). *Parametric and nonparametric linkage analysis: a unified multipoint approach. American Journal of Human Genetics*, 58(6), 1347–1363. PMID: 8651312; PMCID: PMC1915045.
120. Yi, T. M., & Lander, E.S. (1996). *Iterative template refinement: Protein-fold prediction using iterative search and hybrid sequence/structure templates. Methods in Enzymology*, 266, 322–339. PMID: 8743692.
121. Kurooka, H., Segre, J.A., Hirano, Y., Nemhauser, J.L., Nishimura, H., Yoneda, K., Lander, E.S., & Honjo, T. (1996). *Rescue of the hairless phenotype in nude mice by transgenic insertion of the wild-type Hfh11 genomic locus. International Immunology*, 8(6), 961–966. PMID: 8671685.
122. Superti-Furga, A., Hästbacka, J., Rossi, A., van der Harten, J.J., Wilcox, W.R., Cohn, D.H., Rimoin, D.L., Steinmann, B., Lander, E.S., & Gitzelmann, R. (1996). *A family of chondrodysplasias caused by mutations in the diastrophic dysplasia sulfate transporter gene and associated with impaired sulfation of proteoglycans. Annals of the New York Academy of Sciences*, 785, 195–201. PMID: 8702127.
123. Gschwend, M., Levrán, O., Kruglyak, L., Ranade, K., Verlander, P.C., Shen, S., Faure, S., Weissenbach, J., Altay, C., Lander, E.S., Auerbach, A.D., & Botstein, D. (1996). *A locus for Fanconi anemia on 16q determined by homozygosity mapping. American Journal of Human Genetics*, 59(2), 377–384. PMID: 8755924; PMCID: PMC1914713.
124. Mahtani, M.M., Widén, E., Lehto, M., Thomas, J., McCarthy, M., Brayer, J., Bryant, B., Chan, G., Daly, M.J., Forsblom, C., Kanninen, T., Kirby, A., Kruglyak, L., Munnely, K., Parkkonen, M., Reeve-Daly, M.P., Weaver, A., Brettin, T., Duyk, G., Lander, E.S., & Groop, L.C. (1996). *Mapping of a gene for type 2 diabetes associated with an insulin secretion defect by a genome scan in Finnish families. Nature Genetics*, 14(1), 90–94. PMID: 8782826.
125. Navin, A., Prekeris, R., Lisitsyn, N.A., Sonti, M.M., Grieco, D.A., Narayanswami, S., Lander, E.S., & Simpson, E.M. (1996). *Mouse Y-specific repeats isolated by whole chromosome representational difference analysis. Genomics*, 36(2), 349–353. PMID: 8812464.
126. Daly, M.J., & Lander, E.S. (1996). *The importance of being independent: sib pair analysis in diabetes. Nature Genetics*, 14(2), 131–132. PMID: 8841179.
127. Lander, E.S. (1996). *The new genomics: global views of biology. Science*, 274(5287), 536–539. PMID: 8928008.
128. Schuler, G.D., Boguski, M.S., Stewart, E.A., Stein, L.D., Gyapay, G., Rice, K., White, R.E., Rodriguez-Tome, P., Aggarwal, A., Bajorek, E., Bentolila, S., Birren, B.W., Butler, A., Castle, A.B., Chiannilkulchai, N., Chu, A., Clee, C., Cowles, S., Day, P.J.R., Dibling, T., Drouot, N., Dunham, I., Duprat, S., East, C., Edwards, C., Fan, J.B., Fang, N., Fizames, C., Garrett, C., Green, L., Hadley, D., Harris, M., Harrison, P., Brady, S., Hicks, A., Holloway, E., Hui, L., Hussaine, S., Louis-Dit-Sully, C., Ma, J., MacGilvery, A., Mader, C., Maratukulam, A., Matise, T.C., McKusick, K.B., Morissette, J., Mungall, A., Muselet, D., Nusbaum, H.C., Page, D.C., Peck, A., Perkins, S., Piercy, M., Qin, F., Quackenbush, J., Ranby, S., Reif, T., Rozen, S., Sanders, C., She, X., Silva, J., Slonim, D.K., Soderlund, C., Sun, W.L., Tabar, P., Thangarajah, T., Vega-Czarny, N., Vollrath, D., Voyticky, S., Wilmer, T., Wu, X., Adams, M.D., Auffray, C., Berry, R., Brandon, R., Dehejia, A., Goodfellow, P.N., Houlgatte, R., Hudson, J.R., Ide, S.E., Iorio, K.R., Lee, W.Y., Seki, N., Nagase, T., Ishikawa, K., Nomura, N., Phillips, C., Polymeropoulos, M.H., Sandusky, M., Schmitt, K., Sikela, J.M., Swanson, K., Torres, R., Venter, J.C., Walter, N.A.R., Beckmann, J.S., Weissenbach, J., Myers, R.M., Cox, D.R., James, M.R., Bentley, D., Deloukas, P., Lander, E.S., & Hudson, T.J. (1996). *A gene map of the human genome. Science*, 274(5287), 540.
129. Haldi, M.L., Strickland, C., Lim, P., VanBerkel, V., Chen, X.N., Noya, D., Korenberg, J.R., Husain, Z., Miller, J., & Lander, E.S. (1996). *A comprehensive large-insert yeast artificial chromosome library for physical mapping of the mouse genome. Mammalian Genome*, 7(10), 767–769. PMID: 8854865.
130. Gould, K.A., Dietrich, W.F., Borenstein, N., Lander, E.S., & Dove, W.F. (1996). *Mom1 is a semi-dominant modifier of intestinal adenoma size and multiplicity in Min/+ mice. Genetics*, 144(4), 1769–1776. PMID: 8978062; PMCID: PMC1207726.
131. Gould, K.A., Luongo, C., Moser, A.R., McNeley, M.K., Borenstein, N., Shedlovsky, A., Dove, W.F., Hong, K., Dietrich, W.F., & Lander, E.S. (1996). *Genetic*

- evaluation of candidate genes for the *Mom1* modifier of intestinal neoplasia in mice. *Genetics*, 144(4), 1777–1785. PMID: 8978063; PMID: PMC1207727.
132. Slonim, D.K., Kruglyak, L., Stein, L., & Lander, E.S. (1997). *Building human genome maps with radiation hybrids. Proceedings of the First Annual International Conference on Computational Biology (RECOMB '97)*. New York: ACM Press.
133. Hamilton, B.A., Smith, D.J., Mueller, K.L., Kerrebrock, A.W., Bronson, R.T., van Berkel, V., Daly, M.J., Kruglyak, L., Reeve, M.P., Nemhauser, J.L., Hawkins, T.L., Rubin, E.M., & Lander, E.S. (1997). *The vibrator mutation causes neurodegeneration via reduced expression of PITP α ; positional complementation cloning and extragenic suppression*. *Neuron*, 18(5), 711–722. PMID: 9182797.
134. Kuokkanen, S., Gschwend, M., Rioux, J.D., Daly, M.J., Terwilliger, J.D., Tienari, P.J., Wikström, J., Palo, J., Stein, L.D., Hudson, T.J., Lander, E.S., & Peltonen, L. (1997). *Genome-wide scan of multiple sclerosis in Finnish multiplex families*. *The American Journal of Human Genetics*, 61(6), 1379–1387. PMID: 9399895; PMID: PMC1716063.
135. Hawkins, T.L., McKernan, K.J., Jacotot, L.B., MacKenzie, J.B., Richardson, P.M., & Lander, E.S. (1997). *A magnetic attraction to high-throughput genomics*. *Science*, 276(5320), 1887–1889. PMID: 9206843.
136. Cormier, R.T., Hong, K.H., Halberg, R.B., Hawkins, T.L., Richardson, P., Mulherkar, R., Dove, W.F., & Lander, E.S. (1997). *Secretory phospholipase *Pla2g2a* confers resistance to intestinal tumorigenesis*. *Nature Genetics*, 17(1), 88–91. PMID: 9288104.
137. Haldi, M.L., Lim, P., Kaphingst, K., Akella, U., Whang, J., & Lander, E.S. (1997). *Construction of a large-insert yeast artificial chromosome library of the rat genome*. *Mammalian Genome*, 8(6), 460. PMID: 9166603.
138. Sidow, A., Bulotsky, M.S., Kerrebrock, A.W., Bronson, R.T., Daly, M.J., Reeve, M.P., Hawkins, T.L., Birren, B.W., Jaenisch, R., & Lander, E.S. (1997). *Serrate2 is disrupted in the mouse limb-development mutant syndactylism*. *Nature*, 389(6652), 722–725. PMID: 9338782.
139. Shi, Y.P., Mohapatra, G., Miller, J., Hanahan, D., Lander, E.S., Gold, P., Pinkel, D., & Gray, J. (1997). *FISH probes for mouse chromosome identification*. *Genomics*, 45(1), 42–47. PMID: 9339359.
140. Laitinen, T., Kauppi, P., Ignatius, J., Ruotsalainen, T., Daly, M.J., Kääriäinen, H., Kruglyak, L., Laitinen, H., de la Chapelle, A., Lander, E.S., Laitinen, L.A., & Kere, J. (1997). *Genetic control of serum IgE levels and asthma: linkage and linkage disequilibrium studies in an isolated population*. *Human Molecular Genetics*, 6(12), 2069–2076. PMID: 9328470.
141. Lehto, M., Tuomi, T., Mahtani, M.M., Widén, E., Forsblom, C., Sarelin, L., Gullström, M., Isomaa, B., Lehtovirta, M., Hyrkkö, A., Kanninen, T., Orho, M., Manley, S., Turner, R.C., Brettn, T., Kirby, A., Thomas, J., Duyk, G., Lander, E.S., Taskinen, M.R., & Groop, L. (1997). *Characterization of the MODY3 phenotype. Early-onset diabetes caused by an insulin secretion defect*. *Journal of Clinical Investigation*, 99(4), 582–591. PMID: 9045858; PMID: PMC507838.
142. Slonim, D., Kruglyak, L., Stein, L., & Lander, E.S. (1997). *Building human genome maps with radiation hybrids*. *Journal of Computational Biology*, 4(4), 487–504. PMID: 9385541.
143. Fazeli, A., Steen, R.G., Dickinson, S.L., Bautista, D., Dietrich, W.F., Bronson, R.T., Bresalier, R.S., Lander, E.S., Costa, J., & Weinberg, R.A. (1997). *Effects of p53 mutations on apoptosis in mouse intestinal and human colonic adenomas*. *Proceedings of the National Academy of Sciences USA*, 94(19), 10199–10204. PMID: 9294187; PMID: PMC23339.
144. Radany, E.H., Hong, K., Keshavarzi, S., Lander, E.S., & Bishop, J.M. (1997). *Mouse mammary tumor virus/v-Ha-ras transgene-induced mammary tumors exhibit strain-specific allelic loss on mouse chromosome 4*. *Proceedings of the National Academy of Sciences USA*, 94(16), 8664–8669. PMID: 9238034; PMID: PMC23068.
145. Kruglyak, L., & Lander, E.S. (1998). *Faster multipoint linkage analysis using Fourier transforms*. *Journal of Computational Biology*, 5(1), 1–7. PMID: 9541867.
146. Zhong, T.P., Kaphingst, K., Akella, U., Haldi, M., Lander, E.S., & Fishman, M.C. (1998). *Zebrafish genomic library in yeast artificial chromosomes*. *Genomics*, 48(1), 136–138. PMID: 9514818.
147. Bieg, S., Koike, G., Jiang, J., Klaff, L., Pettersson, A., MacMurray, A.J., Jacob, H.J., Lander, E.S., & Lernmark, A. (1998). *Genetic isolation of iddm 1 on chromosome 4 in the biobreeding (BB) rat*. *Mammalian Genome*, 9(4), 324–326. PMID: 9530633.
148. Wang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hsie, L., Topaloglu, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N.,

- Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M., & Lander, E.S. (1998). *Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome*. *Science*, 280(5366), 1077–1082. PMID: 9582121.
149. Altshuler, D., Kruglyak, L., & Lander, E.S. (1998). *Genetic polymorphisms and disease*. *New England Journal of Medicine*, 338(22), 1626. PMID: 9606122.
150. Kusumi, K., Sun, E.S., Kerrebrock, A.W., Bronson, R.T., Chi, D.C., Bulotsky, M.S., Spencer, J.B., Birren, B.W., Frankel, W.N., & Lander, E.S. (1998). *The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation of early somite boundaries*. *Nature Genetics*, 19(3), 274–278. PMID: 9662403.
151. McCarthy, M.I., Kruglyak, L., & Lander, E.S. (1998). *Sib-pair collection strategies for complex diseases*. *Genetic Epidemiology*, 15(4), 317–340. PMID: 9671984.
152. Savukoski, M., Klockars, T., Holmberg, V., Santavuori, P., Lander, E.S., & Peltonen, L. (1998). *CLN5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid lipofuscinosis*. *Nature Genetics*, 19(3), 286–288. PMID: 9662406.
153. Ober, C., Cox, N.J., Abney, M., Di Rienzo, A., Lander, E.S., Changyaleket, B., Gidley, H., Kurtz, B., Lee, J., Nance, M., Pettersson, A., Prescott, J., Richardson, A., Schlenker, E., Summerhill, E., Willadsen, S., Parry R., & Collaborative Study on the Genetics of Asthma. (1998). *Genome-wide search for asthma susceptibility loci in a founder population*. *Human Molecular Genetics*, 7(9), 1393–1398. PMID: 9700192.
154. Szpirer, C., Szpirer, J., Van Vooren, P., Tissir, F., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (1998). *Gene-based anchoring of the rat genetic linkage and cytogenetic maps: new regional localizations, orientation of the linkage groups, and insights into mammalian chromosome evolution*. *Mammalian Genome*, 9(9), 721–734. PMID: 9716657.
155. Deloukas, P., Schuler, G.D., Gyapay, G., Beasley, E.M., Soderlund, C., Rodriguez-Tome, P., Hui, L., Matise, T.C., McKusick, K.B., Beckmann, J.S., Bentolila, S., Bihoreau, M.T., Birren, B.W., Browne, J., Butler, A., Castle, A.B., Chiannikulchai, N., Clee, C., Day, P.J.R., Dehejia, A., Dibling, T., Drouot, N., Duprat, S., Fizames, C., Fox, S., Gelling, S., Green, L., Harrison, P., Hocking, R., Holloway, E., Hunt, S., Keil, S., Lijnzaad, P., Louis-Dit-Sully, C., Ma, J., Mendis, A., Miller, J., Morissette, J., Muselet, D., Nusbaum, H.C., Peck, A., Rozen, S., Simon, D., Slonim, D.K., Staples, R., Stein, L.D., Stewart, E.A., Suchard, M.A., Thangarajah, T., Vega-Czarny, N., Webber, C., Wu, X., Auffray, C., Nomura, N., Sikela, J.M., Polymeropoulos, M.H., James, M.R., Lander, E.S., Hudson, T.J., Myers, R.M., Cox, D.R., Weissenbach, J., Boguski, M.S., & Bentley, D.R. (1998). *A physical map of 30,000 human genes*. *Science*, 282(5389), 744–746. PMID: 9784132.
156. Rioux, J.D., Daly, M.J., Green, T., Stone, V., Lander, E.S., Hudson, T.J., Steinhart A.H., Bull, S., Cohen, Z., Greenberg, G., Griffiths, A., McLeod, R., Silverberg, M., Williams, C.N., & Siminovitch, K.A. (1998). *Absence of linkage between inflammatory bowel disease and selected loci on chromosomes 3, 7, 12, and 16*. *Gastroenterology*, 115(5), 1062–1065. PMID: 9797358.
157. Rioux, J.D., Stone, V.A., Daly, M.J., Cargill, M., Green, T., Nguyen, H., Nutman, T., Zimmerman, P.A., Tucker, M.A., Hudson, T., Goldstein, A.M., Lander, E.S., & Lin, A.Y. (1998). *Familial eosinophilia maps to the cytokine gene cluster on human chromosomal region 5q31–q33*. *The American Journal of Human Genetics*, 63(4), 1086–1094. PMID: 9758611; PMCID: PMC1377485.
158. Lander, E.S., & Ellis, J.J. (1998). *Founding father*. *Nature*, 396(6706), 13–14. PMID: 9817195.
159. Holstege, F.C., Jennings, E.G., Wyrick, J.J., Lee, T.I., Hengartner, C.J., Green, M.R., Golub, T.R., Lander, E.S., & Young, R.A. (1998). *Dissecting the regulatory circuitry of a eukaryotic genome*. *Cell*, 95(5), 717–728. PMID: 9845373.
160. Lander, E.S. (1998). *Scientific commentary: the scientific foundations and medical and social prospects of the Human Genome Project*. *The Journal of Law, Medicine & Ethics*, 26(3), 184–188. PMID: 11066875.
161. Szpirer, C., Szpirer, J., Van Vooren, P., Tissir, F., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (1998). *Gene-based anchoring of the rat genetic linkage and cytogenetic maps: new regional localizations, orientation of the linkage groups, and insights into mammalian chromosome evolution*. *Mammalian Genome*, 9(9), 721–734. PMID: 9716657.
162. Brown, D.M., Matise, T.C., Koike, G., Simon, J.S., Winer, E.S., Zangen, S., McLaughlin, M.G., Shiozawa, M., Atkinson, O.S., Hudson, J.R., Chakravarti, A., Lander, E.S., & Jacob, H.J. (1998). *An integrated genetic linkage map of the laboratory rat*. *Mammalian Genome*, 9(7), 521–530. PMID: 9657848.

163. Batzoglu, S., Berger, B., Kleitman, D.J., Lander, E.S., & Pachter, L. (1998). *Recent developments in computational gene recognition. Documenta Mathematica*, 649–658.
164. Lander, E.S. (1999). *Array of hope. Nature Genetics*, 21(1 Suppl), 3–4. PMID: 9915492.
165. Tamayo, P., Slonim, D., Mesirov, J., Zhu, Q., Kitareewan, S., Dmitrovsky, E., Lander, E.S., & Golub, T.R. (1999). *Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation. Proceedings of the National Academy of Sciences USA*, 96(6), 2907–2912. PMID: 10077610; PMCID: PMC15868.
166. Pardes, H., Manton, K.G., Lander, E.S., Tolley, H.D., Ullian, A.D., & Palmer, H. (1999). *Effects of medical research on health care and the economy. Science*, 283(5398), 36–37. PMID: 9917262.
167. Lander E.S. (1999). *Genetics in the 21st century. Human Genome News* 10, 1–2.
168. Cargill, M., Altshuler, D., Ireland, J., Sklar, P., Ardlie, K., Patil, N., Lane, C.R., Lim, E.P., Kalyanaraman, N., Nemesh, J., Ziaugra, L., Friedland, L., Rolfe, A., Warrington, J., Lipshutz, R., Daley, G.Q., & Lander, E.S. (1999). *Characterization of single-nucleotide polymorphisms in coding regions of human genes. Nature Genetics*, 22(3), 231–238. PMID: 10391209.
169. Fambrough, D., McClure, K., Kazlauskas, A., & Lander, E.S. (1999). *Diverse signaling pathways activated by growth factor receptors induce broadly overlapping, rather than independent, sets of genes. Cell*, 97(6), 727–741. PMID: 10380925.
170. Steen, R.G., Kwitek-Black, A.E., Glenn, C., Gullings-Handley, J., Van Etten, W., Atkinson, O.S., Appel, D., Twigger, S., Muir, M., Mull, T., Granados, M., Kissebah, M., Russo, K., Crane, R., Popp, M., Peden, M., Matise, T., Brown, D.M., Lu, J., Kingsmore, S., Tonellato, P.J., Rozen, S., Slonim, D., Young, P., Knoblauch, M., Provoost, A., Ganten, D., Colman, S.D., Rothberg, J., Lander, E.S., & Jacob, H.J. (1999). *A high-density integrated genetic linkage and radiation hybrid map of the laboratory rat. Genome Research*, 9(6), AP1–AP8. PMID: 10400928.
171. Pachter, L., Batzoglu, S., Spitkovsky, V.I., Banks, E., Lander, E.S., Kleitman, D.J., & Berger, B. (1999). *A dictionary-based approach for gene annotation. Journal of Computational Biology*, 6(3–4), 419–430. PMID: 10582576.
172. Hacia, J.G., Fan, J.B., Ryder, O., Jin, L., Edgemon, K., Ghandour, G., Mayer, R.A., Sun, B., Hsie, L., Robbins, C.M., Brody, L.C., Wang, D., Lander, E.S., Lipshutz, R., Fodor, S.P.A., & Collins, F.S. (1999). *Determination of ancestral alleles for human single-nucleotide polymorphisms using high-density oligonucleotide arrays. Nature Genetics*, 22(2), 164–167. PMID: 10369258.
173. Galitski, T., Saldanha, A.J., Styles, C.A., Lander, E.S., & Fink, G.R. (1999). *Ploidy regulation of gene expression. Science*, 285(5425), 251–254. PMID: 10398601.
174. Van Etten, W.J., Steen, R.G., Nguyen, H., Castle, A.B., Slonim, D.K., Ge, B., Nusbaum, C., Schuler, G.D., Lander, E.S., & Hudson, T.J. (1999). *Radiation hybrid map of the mouse genome. Nature Genetics*, 22(4), 384–387. PMID: 10431245.
175. Pfeifer, D., Kist, R., Dewar, K., Devon, K., Lander, E.S., Birren, B., Komiszewski, L., Back, E., & Scherer, G. (1999). *Campomelic dysplasia translocation breakpoints are scattered over 1 Mb proximal to SOX9: evidence for an extended control region. The American Journal of Human Genetics*, 65(1), 111–124. PMID: 10364523; PMCID: PMC1378081.
176. Nusbaum, C., Slonim, D.K., Harris, K.L., Birren, B.W., Steen, R.G., Stein, L.D., Miller, J., Dietrich, W.F., Nahf, R., Wang, V., Merport, O., Castle, A.B., Husain, Z., Farino, G., Gray, D., Anderson, M.O., Devine, R., Horton, L.T., Ye, W., Wu, X., Kouyoumjian, V., Zemsteva, I.S., Wu, Y., Collymore, A.J., Courtney, D.F., Tam, J., Cadman, M., Haynes, A.R., Heuston, C., Marsland, T., Southwell, A., Trickett, P., Strivens, M.A., Ross, M.T., Makalowski, W., Xu, Y., Boguski, M.S., Carter, N.P., Denny, P., Brown, S.D.M., Hudson, T.J., & Lander, E.S. (1999). *A YAC-based physical map of the mouse genome. Nature Genetics*, 22(4), 388–393. PMID: 10431246.
177. Sidow, A., Bulotsky, M.S., Kerrebrock, A.W., Birren, B.W., Altshuler, D., Jaenisch, R., Johnson, K.R., & Lander, E.S. (1999). *A novel member of the F-box/WD40 gene family, encoding dactylin, is disrupted in the mouse dactylaplasia mutant. Nature Genetics*, 23(1), 104–107. PMID: 10471509.
178. Hastbacka, J., Kerrebrock, A., Makkala, K., Clines, G., Lovett, M., Kaitila, I., de la Chapelle, A., & Lander, E.S. (1999). *Identification of the Finnish founder mutation for diastrophic dysplasia (DTD). European Journal of Human Genetics*, 7(6), 664–670. PMID: 10482955.
179. Klaff, L.S., Koike, G., Jiang, J., Wang, Y., Bieg, S., Pettersson, A., Lander, E.S., Jacob, H., & Lernmark, A. (1999). *BB rat diabetes susceptibility and body*

- weight regulation genes colocalize on chromosome 2. *Mammalian Genome*, 10(9), 883–887. PMID: 10441739.
180. Golub, T.R., Slonim, D.K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, J.P., Coller, H., Loh, M.L., Downing, J.R., Caligiuri, M.A., Bloomfield, C.D., & Lander, E.S. (1999). *Molecular classification of cancer: class discovery and class prediction by gene expression monitoring*. *Science*, 286(5439), 531–537. PMID: 10521349.
181. Wyrick, J.J., Holstege, F.C., Jennings, E.G., Causton, H.C., Shore, D., Grunstein, M., Lander, E.S., & Young, R.A. (1999). *Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast*. *Nature*, 402(6760), 418–421. PMID: 10586882.
182. De Sanctis, G.T., Singer, J.B., Jiao, A., Yandava, C.N., Lee, Y.H., Haynes, T.C., Lander, E.S., Beier, D.R., & Drazen, J.M. (1999). *Quantitative trait locus mapping of airway responsiveness to chromosomes 6 and 7 in inbred mice*. *American Journal of Physiology*, 277(6 Pt 1), L1118–L1123. PMID: 10600881.
183. Batzoglou, S., Berger, B., Mesirov, J., & Lander, E.S. (1999). *Sequencing a genome by walking with clone-end sequences: a mathematical analysis*. *Genome Research*, 9(12), 1163–1174. PMID: 10613838.
184. Klockars, T., Holmberg, V., Savukoski, M., Lander, E.S., & Peltonen, L. (1999). *Transcript identification on the CLN5 region on chromosome 13q22*. *Human Genetics*, 105(1–2), 51–56. PMID: 10480355.
185. Madhani, H.D., Galitski, T., Lander, E.S., & Fink, G.R. (1999). *Effectors of a developmental mitogen-activated protein kinase cascade revealed by expression signatures of signaling mutants*. *Proceedings of the National Academy of Sciences USA*, 96(22), 12530–12535. PMID: 10535956; PMCID: PMC22972.
186. Lander, E.S., & Weinberg, R.A. (2000). *Genomics: Journey to the center of biology*. *Science*, 287(5459), 1777–1782. PMID: 10755930.
187. Engert, J.C., Bérubé, P., Mercier, J., Doré, C., Lepage, P., Ge, B., Bouchard, J.P., Mathieu, J., Mançon, S.B., Schalling, M., Lander, E.S., Morgan, K., Hudson, T.J., & Richter, A. (2000). *ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF*. *Nature Genetics*, 24(2), 120–125. PMID: 10655055.
188. Nadeau, J.H., Singer, J.B., Matin, A., & Lander, E.S. (2000). *Analysing complex genetic traits with chromosome substitution strains*. *Nature Genetics*, 24(3), 221–225. PMID: 10700173.
189. Lindblad-Toh, K., Winchester, E., Daly, M.J., Wang, D.G., Hirschhorn, J.N., Laviolette, J.P., Ardlie, K., Reich, D.E., Robinson, E., Sklar, P., Shah, N., Thomas, D., Fan, J.B., Gingeras, T., Warrington, J., Patil, N., Hudson, T.J., & Lander, E.S. (2000). *Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse*. *Nature Genetics*, 24(4), 381–386. PMID: 10742102.
190. Coller, H.A., Grandori, C., Tamayo, P., Colbert, T., Lander, E.S., Eisenman, R.N., & Golub, T.R. (2000). *Expression analysis with oligonucleotide microarrays reveals that MYC regulates genes involved in growth, cell cycle, signaling, and adhesion*. *Proceedings of the National Academy of Sciences USA*, 97(7), 3260–3265. PMID: 10737792; PMCID: PMC16226.
191. Szpirer, C., Szpirer, J., Vanvooren, P., Tissir, F., Kela, J., Lallemand, F., Hoebee, B., Simon, J.S., Koike, G., Jacob, H.J., Lander, E.S., Helou, K., Klinga-Levan, K., & Levan, G. (2000). *The rat genetic and cytogenetic maps*. *Journal of Experimental Animal Science*, 41(1), 38–39.
192. Bulman, M.P., Kusumi, K., Frayling, T.M., McKeown, C., Garrett, C., Lander, E.S., Krumlauf, R., Hattersley, A.T., Ellard, S., & Turnpenny, P.D. (2000). *Mutations in the human delta homologue, DLL3, cause axial skeletal defects in spondylocostal dysostosis*. *Nature Genetics*, 24(4), 438–441. PMID: 10742114.
193. Pajukanta, P., Cargill, M., Viitanen, L., Nuotio, I., Kareinen, A., Perola, M., Terwilliger, J.D., Kempas, E., Daly, M.J., Lilja, H., Rioux, J.D., Brettin, T., Viikari, J.S.A., Rönnemaa, T., Laakso, M., Lander, E.S., & Peltonen, L. (2000). *Two loci on chromosomes 2 and X for premature coronary heart disease identified in early-and late-settlement populations of Finland*. *The American Journal of Human Genetics*, 67(6), 1481–1493. PMID: 11078477; PMCID: PMC1287925.
194. Batzoglou, S., Pachter, L., Mesirov, J.P., Berger, B., & Lander, E.S. (2000). *Human and mouse gene structure: comparative analysis and application to exon prediction*. *Genome Research*, 10(7), 950–958. PMID: 10899144; PMCID: PMC310911.
195. Cormier, R.T., Bilger, A., Lillich, A.J., Halberg, R.B., Hong, K.H., Gould, K.A., Borenstein, N., Lander, E.S., & Dove, W.F. (2000). *The Mom1AKR intestinal tumor resistance region consists of Pla2g2a and a locus distal to D4Mit64*. *Oncogene*, 19(28), 3182–3192. PMID: 10918573.

196. Clark, E.A., Golub, T.R., Lander, E.S., & Hynes, R.O. (2000). *Genomic analysis of metastasis reveals an essential role for RhoC*. *Nature*, 406(6795), 532–535. PMID: 10952316.
197. Rioux, J.D., Silverberg, M.S., Daly, M.J., Steinhart, A.H., McLeod, R.S., Griffiths, A.M., Green, T., Brettin, T.S., Stone, V., Bull, S.B., Bitton, A., Williams, C.N., Greenberg, G.R., Cohen, Z., Lander, E.S., Hudson, T.J., & Siminovitch, K.A. (2000). *Genomewide search in Canadian families with inflammatory bowel disease reveals two novel susceptibility loci*. *The American Journal of Human Genetics*, 66(6), 1863–1870. PMID: 10777714; PMCID: PMC1378042.
198. Altshuler, D., Hirschhorn, J.N., Klannemark, M., Lindgren, C.M., Vohl, M.C., Nemesh, J., Lane, C.R., Schaffner, S.F., Bolk, S., Brewer, C., Tuomi, T., Gaudet, D., Hudson, T.J., Daly, M.J., Groop, L., & Lander, E.S. (2000). *The common PPAR γ ; Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes*. *Nature Genetics*, 26(1), 76–80. PMID: 10973253.
199. Lindblad-Toh, K., Tanenbaum, D.M., Daly, M.J., Winchester, E., Lui, W.O., Villapakkam, A., Stanton, S.E., Larsson, C., Hudson, T.J., Johnson, B.E., Lander, E.S., & Meyerson, M. (2000). *Loss-of-heterozygosity analysis of small-cell lung carcinomas using single-nucleotide polymorphism arrays*. *Nature Biotechnology*, 18(9), 1001–1005. PMID: 10973224.
200. Hirschhorn, J.N., Sklar, P., Lindblad-Toh, K., Lim, Y.M., Ruiz-Gutierrez, M., Bolk, S., Langhorst, B., Schaffner, S., Winchester, E., & Lander, E.S. (2000). *SBE-TAGS: an array-based method for efficient single-nucleotide polymorphism genotyping*. *Proceedings of the National Academy of Sciences USA*, 97(22), 12164–12169. PMID: 11035790; PMCID: PMC17312.
201. Lander, E.S. (2000). *Genomics: launching a revolution in medicine*. *The Journal of Law, Medicine & Ethics*, 28(4-Suppl), 3–14. PMID: 11244841.
202. Altshuler, D., Pollara, V.J., Cowles, C.R., Van Etten, W.J., Baldwin, J., Linton, L., & Lander, E.S. (2000). *An SNP map of the human genome generated by reduced representation shotgun sequencing*. *Nature*, 407(6803), 513–516. PMID: 11029002.
203. Lander, E.S., Linton, L.M., Birren, B., Nusbaum, C., Zody, M.C., Baldwin, J., Devon, K., Dewar, K., Doyle, M., FitzHugh, H., Funke, R., Gage, D., Harris, K., Heaford, A., Howland, J., Kann, L., LeHoczy, J., LeVine, R., McEwan, P., McKernan, K., Meldrim, J., Mesirov, J.P., Miranda, C., Morris, W., Naylor, J., Raymond, C., Rosetti, M., Santos, R., Sheridan, A., Sougnez, C., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Wyman, D., Rogers, J., Sulston, J., Ainscough, R., Beck, S., Bentley, D., Burton, J., Clee, C., Carter, N., Coulson, A., Deadman, R., Deloukas, P., Dunham, A., Dunham, I., Durbin, R., French, L., Grafham, D., Gregory, S., Hubbard, T., Humphray, S., Hunt, A., Jones, M., Lloyd, C., McMurray, A., Matthews, L., Mercer, S., Milne, S., Mullikin, J.C., Mungall, A., Plumb, R., Ross, M., Showkeen, R., Sims, S., Waterston, R.H., Wilson, R.K., Hillier, L.W., McPherson, J.D., Marra, M.A., Mardis, E.R., Fulton, L.A., Chinwalla, A.T., Pepin, K.H., Gish, W.R., Chissoe, S.L., Wendl, M.C., Delehaanty, K.D., Miner, T.L., Delehaanty, A., Kramer, J.B., Cook, L.L., Fulton, R.S., Johnson, D.L., Minx, P.J., Clifton, S.W., Hawkins, T., Branscomb, E., Predki, P., Richardson, P., Wenning, S., Slezak, T., Doggett, N., Cheng, J.F., Olsen, A., Lucas, S., Elkin, C., Uberbacher, E., Frazier, M., Gibbs, R., Muzny, D.M., Scherer, S.E., Bouck, J.B., Sodergren, E.J., Worley, K.C., Rives, C.M., Gorrell, J.H., Metzker, M.L., Naylor, S.L., Kucherlapati, R.S., Nelson, D.L., Weinstock, G.M., Sakaki, Y., Fujiyama, A., Hattori, M., Yada, T., Toyoda, A., Itoh, T., Kawagoe, C., Watanabe, H., Totoki, Y., Taylor, T., Weissenbach, J., Heilig, R., Saurin, W., Artiguenave, F., Brottier, P., Bruls, T., Pelletier, E., Robert, C., Wincker, P., Smith, D.R., Doucette-Stamm, L., Rubenfield, M., Weinstock, K., Lee, H.M., Dubois, J., Rosenthal, A., Platzer, M., Nyakatura, G., Taudien, S., Rump, A., Yang, H., Yu, J., Wang, J., Huang, G., Gu, J., Hood, L., Rowen, L., Madan, A., Qin, S., Davis, R.W., Federspiel, N.A., Abola, A.P., Proctor, M.J., Myers, R.M., Schmutz, J., Dickson, M., Grimwood, J., Cox, D.R., Olson, M.V., Kaul, R., Raymond, C., Shimizu, N., Kawasaki, K., Minoshima, S., Evans, G.A., Athanasiou, M., Schultz, R., Roe, B.A., Chen, F., Pan, H., Ramser, J., Lehrach, H., Reinhardt, R., McCombie, W.R., de la Bastide, M., Dedhia, N., Blocker, H., Hornischer, K., Nordsiek, G., Agarwala, R., Aravind, L., Bailey, J.A., Bateman, A., Batzoglu, S., Birney, E., Bork, P., Brown, D.G., Burge, C.B., Cerutti, L., Chen, H.C., Church, D., Clamp, M., Copley, R.R., Doerks, T., Eddy, S.R., Eichler, E.E., Furey, T.S., Galagan, J., Gilbert, J.G., Harmon, C., Hayashizaki, Y., Haussler, D., Hermjakob, H., Hokamp, K., Jang, W., Johnson, J.S., Jones, T.A., Kasif, S., Kasprzyk, A., Kennedy, S., Kent, W.J., Kitts, P., Koonin, E.V., Korf, I., Kulp, D., Lancet, D., Lowe, T.M., McLysaght, A., Mikkelsen, T., Moran, J.V., Mulder, N., Pollara, V.J., Ponting, C.P., Schuler, G., Schultz, J., Slater, G., Smit, A.F., Stupka, E., Thierry-Mieg, D., Thierry-Mieg, J., Wagner, L., Wallis, J., Wheeler, R., Williams, A., Wolf, Y.I., Wolfe, K.H., Yang, S.P.,

- Yeh, R.F., Collins, F., Guyer, M.S., Peterson, J., Felsenfeld, A., Wetterstrand, K.A., Patrinos, A., Morgan, M.J., de Jong, P., Catanese, J.J., Osoegawa, K., Shizuya, H., Choi, S., Chen, Y.J., Szustakowski, J., & International Human Genome Sequencing Consortium. (2001). *Initial sequencing and analysis of the human genome*. *Nature*, 409(6822), 860–921. PMID: 11237011.
204. Lee, N., Daly, M.J., Delmonte, T., Lander, E.S., Xu, F., Hudson, T.J., Mitchell, G.A., Morin, C.C., Robinson, B.H., & Rioux, J.D. (2001). A *genome-wide linkage disequilibrium scan localizes the Saguenay-Lac-Saint-Jean cytochrome oxidase deficiency to 2p16*. *The American Journal of Human Genetics*, 68(2), 397–409. PMID: 11156535; PMCID: PMC1235273.
205. Cavanaugh, J., & IBD International Genetics Consortium. (2001). *International collaboration provides convincing linkage replication in complex disease through analysis of a large pooled data set: Crohn disease and chromosome 16*. *The American Journal of Human Genetics*, 68(5), 1165–1171. PMID: 11309682; PMCID: PMC1226097.
206. Bartoloni, L., Blouin, J.L., Maiti, A.K., Sainsbury, A., Rossier, C., Gehrig, C., She, J.X., Marron, M.P., Lander, E.S., Meeks, M., Chung, E., Armengot, M., Jorissen, M., Scott, H.S., Delozier-Blanchet, C.D., Gardiner, R.M., & Antonarakis, S.E. (2001). *Axonemal beta heavy chain dynein DNAH9: cDNA sequence, genomic structure, and investigation of its role in primary ciliary dyskinesia*. *Genomics*, 72(1), 21–33. PMID: 11247663.
207. Sachidanandam, R., Weissman, D., Schmidt, S.C., Kakol, J.M., Stein, L.D., Marth, G., Sherry, S., Mullikin, J.C., Mortimore, B.J., Willey, D., Hunt, S.E., Cole, C.G., Coggill, P.C., Rice, C.M., Ning, Z., Rogers, J., Bentley, D.R., Kwok, P.Y., Mardis, E.R., Yeh, R.T., Schultz, B., Cook, L., Davenport, R., Dante, M., Fulton, L., Hillier, L., Waterston, R.H., McPherson, J.D., Gilman, B., Schaffner, S., Van Etten, W.J., Reich, D., Higgins, J., Blumenstiel, B., Baldwin, J., Stange-Thomann, N., Zody, M.C., Linton, L., Lander, E.S., Altshuler, D., & International SNP Map Working Group. (2001). *A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms*. *Nature*, 409(6822), 928–933. PMID: 11237013.
208. Hong, K.H., Bonventre, J.C., O'Leary, E., Bonventre, J.V., & Lander, E.S. (2001). *Deletion of cytosolic phospholipase A2 suppresses ApcMin-induced tumorigenesis*. *Proceedings of the National Academy of Sciences USA*, 98(7), 3935–3939. PMID: 11274413; PMCID: PMC31157.
209. Jackson-Grusby, L., Beard, C., Possemato, R., Tudor, M., Fambrough, D., Csankovszki, G., Dausman, J., Lee, P., Wilson, C., Lander, E.S., & Jaenisch, R. (2001). *Loss of genomic methylation causes p53-dependent apoptosis and epigenetic deregulation*. *Nature Genetics*, 27(1), 31–39. PMID: 11137995.
210. Causton, H.C., Ren, B., Koh, S.S., Harbison, C.T., Kanin, E., Jennings, E.G., Lee, T.I., True, H.L., Lander, E.S., & Young, R.A. (2001). *Remodeling of yeast genome expression in response to environmental changes*. *Molecular Biology of the Cell*, 12(2), 323–337. PMID: 11179418; PMCID: PMC30946.
211. Yeang, C.H., Ramaswamy, S., Tamayo, P., Mukherjee, S., Rifkin, R.M., Angelo, M., Reich, M., Lander, E.S., Mesirov, J., & Golub, T.R. (2001). *Molecular classification of multiple tumor types*. *Bioinformatics*, 17(Suppl 1), S316–S322. PMID: 11473023.
212. Laitinen, T., Daly, M.J., Rioux, J.D., Kauppi, P., Laprise, C., Petäys, T., Green, T., Cargill, M., Haahtela, T., Lander, E.S., Laitinen, L.A., Hudson, T.J., & Kere, J. (2001). *A susceptibility locus for asthma-related traits on chromosome 7 revealed by genome-wide scan in a founder population*. *Nature Genetics*, 28(1), 87–91. PMID: 11326283.
213. Reich, D.E., Cargill, M., Bolik, S., Ireland, J., Sabeti, P.C., Richter, D.J., Lavery, T., Kouyoumjian, R., Farhadian, S.F., Ward, R., & Lander, E.S. (2001). *Linkage disequilibrium in the human genome*. *Nature*, 411(6834), 199–204. PMID: 11346797.
214. Hirschhorn, J.N., Lindgren, C.M., Daly, M.J., Kirby, A., Schaffner, S.F., Burt, N.P., Altshuler, D., Parker, A., Rioux, J.D., Platko, J., Gaudet, D., Hudson, T.J., Groop, L.C., & Lander, E.S. (2001). *Genomewide linkage analysis of stature in multiple populations reveals several regions with evidence of linkage to adult height*. *The American Journal of Human Genetics*, 69(1), 106–116. PMID: 11410839; PMCID: PMC1226025.
215. Barclay, J., Balaguero, N., Mione, M., Ackerman, S.L., Letts, V.A., Brodbeck, J., Canti, C., Meir, A., Page, K.M., Kusumi, K., Perez-Reyes, E., Lander, E.S., Frankel, W.N., Gardiner, R.M., Dolphin, A.C., & Rees, M. (2001). *Ducky mouse phenotype of epilepsy and ataxia is associated with mutations in the Cacna2d2 gene and decreased calcium channel current in cerebellar Purkinje cells*. *The Journal of Neuroscience*, 21(16), 6095–6104. PMID: 11487633.

216. Sklar, P., Schwab, S.G., Williams, N.M., Daly, M., Schaffner, S., Maier, W., Albus, M., Trixler, M., Eichhammer, P., Lerer, B., Hallmayer, J., Norton, N., Williams, H., Zammit, S., Cardno, A.G., Jones, S., McCarthy, G., Milanova, V., Kirov, G., O'Donovan, M.C., Lander, E.S., Owen, M.J., & Wildenauer, D.B. (2001). *Association analysis of NOTCH4 loci in schizophrenia using family and population-based controls*. *Nature Genetics*, 28(2), 126–128. PMID: 11381257.
217. Inoue, K., Dewar, K., Katsanis, N., Reiter, L.T., Lander, E.S., Devon, K.L., Wyman, D.W., Lupski, J.R., & Birren, B. (2001). *The 1.4-Mb CMT1A duplication/HNPP deletion genomic region reveals unique genome architectural features and provides insights into the recent evolution of new genes*. *Genome Research*, 11(6), 1018–1033. PMID: 11381029; PMCID: PMC311111.
218. Ardlie, K., Liu-Cordero, S.N., Eberle, M.A., Daly, M.J., Barrett, J., Winchester, E., Lander, E.S., & Kruglyak, L. (2001). *Lower-than-expected linkage disequilibrium between tightly linked markers in humans suggests a role for gene conversion*. *The American Journal of Human Genetics*, 69(3), 582–589. PMID: 11473344; PMCID: PMC1235487.
219. Reich, D.E., & Lander, E.S. (2001). *On the allelic spectrum of human disease*. *TRENDS in Genetics*, 17(9), 502–510. PMID: 11525833.
220. Hudson, T.J., Church, D.M., Greenaway, S., Nguyen, H., Cook, A., Steen, R.G., Van Etten, W.J., Castle, A.B., Strivens, M.A., Trickett, P., Heuston, C., Davison, C., Southwell, A., Hardisty, R., Varela-Carver, A., Haynes, A.R., Rodriguez-Tome, P., Doi, H., Ko, M.S.H., Pontius, J., Schriml, L., Wagner, L., Maglott, D., Brown, S.D.M., Lander, E.S., Schuler, G., & Denny, P. (2001). *A radiation hybrid map of mouse genes*. *Nature Genetics*, 29(2), 201–205. PMID: 11586302.
221. Rioux, J.D., Daly, M.J., Silverberg, M.S., Lindblad-Toh, K., Steinhart, H., Cohen, Z., Delmonte, T., Kocher, K., Miller, K., Guschwan, S., Kulbokas, E.J., O'Leary, S., Winchester, E., Dewar, K., Green, T., Stone, V., Chow, C., Cohen, A., Langelier, D., Lapointe, G., Gaudet, D., Faith, J., Branco, N., Bull, S.B., McLeod, R.S., Griffiths, A.M., Bittou, A., Greenberg, G.R., Lander, E.S., Siminovitch, K.A., & Hudson, T.J. (2001). *Genetic variation in the 5q31 cytokine gene cluster confers susceptibility to Crohn disease*. *Nature Genetics*, 29(2), 223–228. PMID: 11586304.
222. Daly, M.J., Rioux, J.D., Schaffner, S.F., Hudson, T.J., & Lander, E.S. (2001). *High-resolution haplotype structure in the human genome*. *Nature Genetics*, 29(2), 229–232. PMID: 11586305.
223. Huang, Q., Liu, D., Majewski, P., Schulte, L.C., Korn, J.M., Young, R.A., Lander, E.S., & Hacohen, N. (2001). *The plasticity of dendritic cell responses to pathogens and their components*. *Science*, 294(5543), 870–875. PMID: 11679675.
224. Staunton, J.E., Slonim, D.K., Coller, H.A., Tamayo, P., Angelo, M.J., Park, J., Scherf, U., Lee, J.K., Reinhold, W.O., Weinstein, J.N., Mesirov, J.P., Lander, E.S., & Golub, T.R. (2001). *Chemosensitivity prediction by transcriptional profiling*. *Proceedings of the National Academy of Sciences USA*, 98(19), 10787–10792. PMID: 11553813; PMCID: PMC585553.
225. Sweeney, C., Fambrough, D., Huard, C., Diamonti, A.J., Lander, E.S., Cantley, L.C., & Carraway, K.L. (2001). *Growth factor-specific signaling pathway stimulation and gene expression mediated by ErbB receptors*. *Journal of Biological Chemistry*, 276(25), 22685–22698. PMID: 11297548.
226. Ramaswamy, S., Tamayo, P., Rifkin, R., Mukherjee, S., Yeang, C.H., Angelo, M., Ladd, C., Reich, M., Latulippe, E., Mesirov, J.P., Poggio, T., Gerald, W., Loda, M., Lander, E.S., & Golub, T.R. (2001). *Multiclass cancer diagnosis using tumor gene expression signatures*. *Proceedings of the National Academy of Sciences USA*, 98(26), 15149–15154. PMID: 11742071; PMCID: PMC64998.
227. Lindblad-Toh, K., Lander, E.S., McPherson, J.D., Waterston, R.H., Rodgers, J., & Birney, E. (2001). *Progress in sequencing the mouse genome*. *Genesis*, 31(4), 137–141. PMID: 11783003.
228. Bhattacharjee, A., Richards, W.G., Staunton, J., Li, C., Monti, S., Vasa, P., Ladd, C., Beheshti, J., Bueno, R., Gillette, M., Loda, M., Weber, G., Mark, E.J., Lander, E.S., Wong, W., Johnson, B.E., Golub, T.R., Sugarbaker, D.J., & Meyerson, M. (2001). *Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses*. *Proceedings of the National Academy of Sciences USA*, 98(24), 13790–13795. PMID: 11707567; PMCID: PMC61120.
229. Shipp, M.A., Ross, K.N., Tamayo, P., Weng, A.P., Kutok, J.L., Aguiar, R.C., Gaasenbeek, M., Angelo, M., Reich, M., Pinkus, G.S., Ray, T.S., Koval, M.A., Last, K.W., Norton, A., Lister, T.A., Mesirov, J., Neuberg, D.S., Lander, E.S., Aster, J.C., & Golub, T.R. (2002). *Diffuse large B-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning*. *Nature Medicine*, 8(1), 68–74. PMID: 11786909.
230. Armstrong, S.A., Staunton, J.E., Silverman, L.B., Pieters, R., den Boer, M.L., Minden, M.D., Sallan, S.E., Lander, E.S., Golub, T.R., & Korsmeyer, S.J. (2002).

MLL translocations specify a distinct gene expression profile that distinguishes a unique leukemia. *Nature Genetics*, 30(1), 41–47. PMID: 11731795.

231. Pomeroy, S.L., Tamayo, P., Gaasenbeek, M., Sturla, L.M., Angelo, M., McLaughlin, M.E., Kim, J.Y., Goumnerova, L.C., Black, P.M., Lau, C., Allen, J.C., Zagzag, D., Olson, J.M., Curran, T., Wetmore, C., Biegel, J.A., Poggio, T., Mukherjee, S., Rifkin, R., Califano, A., Stolovitzky, G., Louis, D.N., Mesirov, J.P., Lander, E.S., & Golub, T.R. (2002). *Prediction of central nervous system embryonal tumour outcome based on gene expression*. *Nature*, 415(6870), 436–442. PMID: 11807556.

232. Lindgren, C.M., Mahtani, M.M., Widen, E., McCarthy, M.I., Daly, M.J., Kirby, A., Reeve, M.P., Kruglyak, L., Parker, A., Meyer, J., Almgren, P., Lehto, M., Kanninen, T., Tuomi, T., Groop, L.C., & Lander, E.S. (2002). *Genomewide search for type 2 diabetes mellitus susceptibility loci in Finnish families: the Botnia study*. *The American Journal of Human Genetics*, 70(2), 509–516. PMID: 11791216; PMCID: PMC384923.

233. Batzoglou, S., Jaffe, D.B., Stanley, K., Butler, J., Gnerre, S., Mauceli, E., Berger, B., Mesirov, J.P., & Lander, E.S. (2002). *ARACHNE: a whole-genome shotgun assembler*. *Genome Research*, 12(1), 177–189. PMID: 11779843; PMCID: PMC155255.

234. Nau, G.J., Richmond, J.F., Schlesinger, A., Jennings, E.G., Lander, E.S., & Young, R.A. (2002). *Human macrophage activation programs induced by bacterial pathogens*. *Proceedings of the National Academy of Sciences USA*, 99(3), 1503–1508. PMID: 11805289; PMCID: PMC122220.

235. Waterston, R.H., Lander, E.S., & Sulston, J.E. (2002). *On the sequencing of the human genome*. *Proceedings of the National Academy of Sciences USA*, 99(6), 3712–3716. PMID: 11880605; PMCID: PMC122589.

236. Singh, D., Febbo, P.G., Ross, K., Jackson, D.G., Manola, J., Ladd, C., Tamayo, P., Renshaw, A.A., D'Amico, A.V., Richie, J.P., Lander, E.S., Loda, M., Kantoff, P.W., Golub, T.R., & Sellers, W.R. (2002). *Gene expression correlates of clinical prostate cancer behavior*. *Cancer Cell*, 1(2), 203–209. PMID: 12086878.

237. Galagan, J.E., Nusbaum, C., Roy, A., Endrizzi, M.G., Macdonald, P., FitzHugh, W., Calvo, S., Engels, R., Smirnov, S., Atnoor, D., Brown, A., Allen, N., Naylor, J., Stange-Thomann, N., DeArellano, K., Johnson, R., Linton, L., McEwan, P., McKernan, K., Talamas, J., Tirrell, A., Ye, W., Zimmer, A., Barber, R.D., Cann, I., Graham, D.E., Grahame, D., Guss, A.M., Hedderich, R., Ingram-Smith, C., Kuettner, H.C., Krzycki, J., Leigh, J.A., Li, W., Liu, J., Mukhopadhyay, B., Reeve, J.N., Smith, K., Springer, T., Umayam, L.A., White, O., White, R.H., de Macario, E.C., Ferry, J.G., Jarrell, K.F., Jing, H., Macario, A.J.L., Paulsen, I., Pritchett, M., Sowers, K.R., Swanson, R.V., Zinder, S.H., Lander, E.S., Metcalf, W.W., & Birren, B.W. (2002). *The genome of M. acetivorans reveals extensive metabolic and physiological diversity*. *Genome Research*, 12(4), 532–542. PMID: 11932238; PMCID: PMC187521.

238. Gabriel, S.B., Schaffner, S.F., Nguyen, H., Moore, J.M., Roy, J., Blumenstiel, B., Higgins, J., DeFelice, M., Lochner, A., Faggart, M., Liu-Cordero, S.N., Rotimi, C., Adeyemo, A., Cooper, R., Ward, R., Lander, E.S., Daly, M.J., & Altshuler, D. (2002). *The structure of haplotype blocks in the human genome*. *Science*, 296(5576), 2225–2229. PMID: 12029063.

239. Ferrando, A.A., Neuberg, D.S., Staunton, J., Loh, M.L., Huard, C., Raimondi, S.C., Behm, F.G., Pui, C.H., Downing, J.R., Gilliland, D.G., Lander, E.S., Golub, T.R., & Look, A.T. (2002). *Gene expression signatures define novel oncogenic pathways in T cell acute lymphoblastic leukemia*. *Cancer Cell*, 1(1), 75–87. PMID: 12086890.

240. MacMurray, A.J., Moralejo, D.H., Kwitek, A.E., Rutledge, E.A., Van Yserloo, B., Gohlke, P., Speros, S.J., Snyder, B., Schaefer, J., Bieg, S., Jiang, J., Ettinger, R.A., Fuller, J., Daniels, T.L., Pettersson, A., Orlebeke, K., Birren, B.W., Jacob, H.J., Lander, E.S., & Lernmark, A. (2002). *Lymphopenia in the BB rat model of type 1 diabetes is due to a mutation in a novel immune-associated nucleotide (Ian)-related gene*. *Genome Research*, 12(7), 1029–1039. PMID: 12097339; PMCID: PMC186618.

241. Reich, D.E., Schaffner, S.F., Daly, M.J., McVean, G., Mullikin, J.C., Higgins, J.M., Richter, D.J., Lander, E.S., & Altshuler, D. (2002). *Human genome sequence variation and the influence of gene history, mutation and recombination*. *Nature Genetics*, 32(1), 135–142. PMID: 12161752.

242. Humpherys, D., Eggan, K., Akutsu, H., Friedman, A., Hochedlinger, K., Yanagimachi, R., Lander, E.S., Golub, T.R., & Jaenisch, R. (2002). *Abnormal gene expression in cloned mice derived from embryonic stem cell and cumulus cell nuclei*. *Proceedings of the National Academy of Sciences USA*, 99(20), 12889–12894. PMID: 12235366; PMCID: PMC130555.

243. Sabeti, P.C., Reich, D.E., Higgins, J.M., Levine, H.Z., Richter, D.J., Schaffner, S.F., Gabriel, S.B., Platko, J.V., Patterson, N.J., McDonald, G.J., Ackerman, H.C., Campbell, S.J., Altshuler, D., Cooper, R., Kwiatkowski, D., Ward, R., & Lander, E.S. (2002). *Detecting recent positive selection in the human genome from haplotype structure*. *Nature*, 419(6909), 832–837. PMID: 12397357.
244. Sklar, P., Gabriel, S.B., McInnis, M.G., Bennett, P., Lim, Y., Tsan, G., Schaffner, S., Kirov, G., Jones, I., Owen, M., Craddock, N., DePaulo, J.R., & Lander, E.S. (2002). *Family-based association study of 76 candidate genes in bipolar disorder: BDNF is a potential risk locus. Brain-derived neurotrophic factor*. *Molecular Psychiatry*, 7(6), 579–593. PMID: 12140781.
245. Cowles, C.R., Hirschhorn, J.N., Altshuler, D., & Lander, E.S. (2002). *Detection of regulatory variation in mouse genes*. *Nature Genetics*, 32(3), 432–437. PMID: 12410233.
246. Mouse Genome Sequencing Consortium, Waterston, R.H., Lindblad-Toh, K., Birney, E., Rogers, J., Abril, J.F., Agarwal, P., Agarwala, R., Ainscough, R., Alexandersson, M., An, P., Antonarakis, S.E., Attwood, J., Baertsch, R., Bailey, J., Barlow, K., Beck, S., Berry, E., Birren, B., Bloom, T., Bork, P., Botcherby, M., Bray, N., Brent, M.R., Brown, D.G., Brown, S.D., Bult, C., Burton, J., Butler, J., Campbell, R.D., Carninci, P., Cawley, S., Chiaromonte, F., Chinwalla, A.T., Church, D.M., Clamp, M., Clee, C., Collins, F.S., Cook, L.L., Copley, R.R., Coulson, A., Couronne, O., Cuff, J., Curwen, V., Cutts, T., Daly, M., David, R., Davies, J., Delehaunty, K.D., Deri, J., Dermitzakis, E.T., Dewey, C., Dickens, N.J., Diekhans, M., Dodge, S., Dubchak, I., Dunn, D.M., Eddy, S.R., Elnitski, L., Emes, R.D., Eswara, P., Eyraes, E., Felsenfeld, A., Fewell, G.A., Flicek, P., Foley, K., Frankel, W.N., Fulton, L.A., Fulton, R.S., Furey, T.S., Gage, D., Gibbs, R.A., Glusman, G., Gnerre, S., Goldman, N., Goodstadt, L., Grafham, D., Graves, T.A., Green, E.D., Gregory, S., Guigó, R., Guyer, M., Hardison, R.C., Haussler, D., Hayashizaki, Y., Hillier, L.W., Hinrichs, A., Hlavina, W., Holzer, T., Hsu, F., Hua, A., Hubbard, T., Hunt, A., Jackson, I., Jaffe, D.B., Johnson, L.S., Jones, M., Jones, T.A., Joy, A., Kamal, M., Karlsson, E.K., Karolchik, D., Kasprzyk, A., Kawai, J., Keibler, E., Kells, C., Kent, W.J., Kirby, A., Kolbe, D.L., Korf, I., Kucherlapati, R.S., Kulbokas, E.J., Kulp, D., Landers, T., Leger, J.P., Leonard, S., Letunic, I., Levine, R., Li, J., Li, M., Lloyd, C., Lucas, S., Ma, B., Maglott, D.R., Mardis, E.R., Matthews, L., Mauceli, E., Mayer, J.H., McCarthy, M., McCombie, W.R., McLaren, S., McLay, K., McPherson, J.D., Meldrum, J., Meredith, B., Mesirov, J.P., Miller, W., Miner, T.L., Mongin, E., Montgomery, K.T., Morgan, M., Mott, R., Mullikin, J.C., Muzny, D.M., Nash, W.E., Nelson, J.O., Nhan, M.N., Nicol, R., Ning, Z., Nusbaum, C., O'Connor, M.J., Okazaki, Y., Oliver, K., Overton-Larty, E., Pachter, L., Parra, G., Pepin, K.H., Peterson, J., Pevzner, P., Plumb, R., Pohl, C.S., Poliakov, A., Ponce, T.C., Ponting, C.P., Potter, S., Quail, M., Reymond, A., Roe, B.A., Roskin, K.M., Rubin, E.M., Rust, A.G., Santos, R., Sapojnikov, V., Schultz, B., Schultz, J., Schwartz, M.S., Schwartz, S., Scott, C., Seaman, S., Searle, S., Sharpe, T., Sheridan, A., Shownkeen, R., Sims, S., Singer, J.B., Slater, G., Smit, A., Smith, D.R., Spencer, B., Stabenau, A., Stange-Thomann, N., Sugnet, C., Suyama, M., Tesler, G., Thompson, J., Torrents, D., Trevaskis, E., Tromp, J., Ucla, C., Ureta-Vidal, A., Vinson, J.P., Von Niederhausern, A.C., Wade, C.M., Wall, M., Weber, R.J., Weiss, R.B., Wendl, M.C., West, A.P., Wetterstrand, K., Wheeler, R., Whelan, S., Wierzbowski, J., Willey, D., Williams, S., Wilson, R.K., Winter, E., Worley, K.C., Wyman, D., Yang, S., Yang, S.P., Zdobnov, E.M., Zody, M.C., & Lander, E.S. (2002). *Initial sequencing and comparative analysis of the mouse genome*. *Nature*, 420(6915), 520–562. PMID: 12466850.
247. Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusica, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N.,

- Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., Hayashizaki, Y., FANTOM Consortium, & RIKEN Genome Exploration Research Group Phase I & II Team. (2002). *Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs*. *Nature*, 420(6915), 563–573. PMID: 12466851.
248. Wade, C.M., Kulbokas, E.J., Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K., & Daly, M.J. (2002). *The mosaic structure of variation in the laboratory mouse genome*. *Nature*, 420(6915), 563–573. PMID: 12466852.
249. Williams, C.N., Kocher, K., Lander, E.S., Daly, M.J., & Rioux, J.D. (2002). *Using a genome-wide scan and meta-analysis to identify a novel IBD locus and confirm previously identified IBD loci*. *Inflammatory Bowel Diseases*, 8(6), 375–381. PMID: 12454612.
250. Chen, C.Z., Li, M., de Graaf, D., Monti, S., Götting, B., Sanchez, M.J., Lander, E.S., Golub, T.R., Green, A.R., & Lodish, H.F. (2002). *Identification of endoglin as a functional marker that defines long-term repopulating hematopoietic stem cells*. *Proceedings of the National Academy of Sciences USA*, 99(24), 15468–15473. PMID: 12438646; PMCID: PMC137740.
251. Ramaswamy, S., Ross, K.N., Lander, E.S., & Golub, T.R. (2003). *A molecular signature of metastasis in primary solid tumors*. *Nature Genetics*, 33(1), 49–54. PMID: 12469122.
252. Lohmueller, K.E., Pearce, C.L., Pike, M., Lander, E.S., & Hirschhorn, J.N. (2003). *Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease*. *Nature Genetics*, 33(2), 177–182. PMID: 12524541.
253. Jaffe, D.B., Butler, J., Gnerre, S., Mauceli, E., Lindblad-Toh, K., Mesirov, J.P., Zody, M.C., & Lander, E.S. (2003). *Whole-genome sequence assembly for mammalian genomes: Arachne 2*. *Genome Research*, 13(1), 91–96. PMID: 12529310; PMCID: PMC430950.
254. Mootha, V.K., Lepage, P., Miller, K., Bunkenborg, J., Reich, M., Hjerrild, M., Delmonte, T., Villeneuve, A., Sladek, R., Xu, F., Mitchell, G.A., Morin, C., Mann, M., Hudson, T.J., Robinson, B., Rioux, J.D., & Lander, E.S. (2003). *Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics*. *Proceedings of the National Academy of Sciences USA*, 100(2), 605–610. PMID: 12529507; PMCID: PMC141043.
255. Waterston, R.H., Lander, E.S., & Sulston, J.E. (2003). *More on the sequencing of the human genome*. *Proceedings of the National Academy of Sciences USA*, 100(6), 3022–3024. PMID: 12631699; PMCID: PMC152236.
256. Xu, Y., Stange-Thomann, N., Weber, G., Bo, R., Dodge, S., David, R.G., Foley, K., Beheshti, J., Harris, N.L., Birren, B.W., Lander, E.S., & Meyerson, M. (2003). *Pathogen discovery from human tissue by sequence-based computational subtraction*. *Genomics*, 81(3), 329–335. PMID: 12659816.
257. Kamvysselis, M., Patterson, N., Birren, B., Berger, B., & Lander, E.S. (2003). *Whole-genome comparative annotation and regulatory motif discovery in multiple yeast species*. In *Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology* (pp. 157–166).
258. Chiang, D.Y., Moses, A.M., Kellis, M., Lander, E.S., & Eisen, M.B. (2003). *Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts*. *Genome Biology*, 4(7), R43. PMID: 12844359; PMCID: PMC193630.
259. Galagan, J.E., Calvo, S.E., Borkovich, K.A., Selker, E.U., Read, N.D., Jaffe, D., FitzHugh, W., Ma, L.J., Smirnov, S., Purcell, S., Rehman, B., Elkins, T., Engels, R., Wang, S., Nielsen, C.B., Butler, J., Endrizzi, M., Qui, D., Ianakiev, P., Bell-Pedersen, D., Nelson, M.A., Werner-Washburne, M., Selitrennikoff, C.P., Kinsey, J.A., Braun, E.L., Zelter, A., Schulte, U., Kothe, G.O., Jedd, G., Mewes, W., Staben, C., Marcotte, E., Greenberg, D., Roy, A., Foley, K., Naylor, J., Stange-Thomann, N., Barrett, R., Gnerre, S., Kamal, M., Kamvysselis, M., Mauceli, E., Bielke, C., Rudd, S., Frishman, D., Krystofova, S., Rasmussen, C., Metzenberg, R.L., Perkins, D.D., Kroken, S., Cogoni, C., Macino, G., Catcheside, D., Li, W., Pratt, R.J., Osmani, S.A., DeSouza, C.P., Glass, L., Orbach, M.J., Berglund, J.A., Voelker, R., Yarden, O., Plamann, M., Seiler, S., Dunlap, J., Radford, A., Aramayo, R., Natvig, D.O., Alex, L.A., Mannhaupt, G., Ebbole, D.J., Freitag, M., Paulsen, I., Sachs, M.S., Lander, E.S., Nusbaum, C., & Birren, B.W. (2003). *The genome sequence of the filamentous fungus Neurospora crassa*. *Nature*, 422(6934), 859–868. PMID: 12712197.
260. Kellis, M., Patterson, N., Endrizzi, M., Birren, B.W., & Lander, E.S. (2003). *Sequencing and comparison of yeast species to identify genes and regulatory elements*. *Nature*, 423(6937), 241–254. PMID: 12748633.

261. Giallourakis, C., Stoll, M., Miller, K., Hampe, J., Lander, E.S., Daly, M.J., Schreiber, S., & Rioux, J.D. (2003). *IBD5 is a general risk factor for inflammatory bowel disease: replication of association with Crohn disease and identification of a novel association with ulcerative colitis. The American Journal of Human Genetics*, 73(1), 205–211. PMID: 12776251; PMCID: PMC1180582.
262. Giallourakis, C., Stoll, M., Miller, K., Hampe, J., Lander, E.S., Daly, M.J., Schreiber, S., & Rioux, J.D. (2003). *PGC-1 α -responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. Nature Genetics*, 34(3), 267–273. PMID: 12808457.
263. Lowe, C.J., Wu, M., Salic, A., Evans, L., Lander, E.S., Stange-Thomann, N., Gruber, C.E., Gerhart, J., & Kirschner, M. (2003). *Anteroposterior patterning in hemichordates and the origins of the chordate nervous system. Cell*, 113(7), 853–865. PMID: 12837244.
264. Rifkin, R., Mukherjee, S., Tamayo, P., Ramaswamy, S., Yeang, C.H., Angelo, M., Reich, M., Poggio, T., Lander, E.S., Golub, T.R., & Mesirov, J.P. (2003). *An analytical method for multiclass molecular cancer classification. Siam Review*, 45(4), 706–723.
265. Walsh, E.C., Mather, K.A., Schaffner, S.F., Farwell, L., Daly, M.J., Patterson, N., Cullen, M., Carrington, M., Bugawan, T.L., Erlich, H., Campbell, J., Barrett, J., Miller, K., Thomson, G., Lander, E.S., & Rioux, J.D. (2003). *An integrated haplotype map of the human major histocompatibility complex. The American Journal of Human Genetics*, 73(3), 580–590. PMID: 12920676; PMCID: PMC1180682.
266. Moses, A.M., Chiang, D.Y., Kellis, M., Lander, E.S., & Eisen, M.B. (2003). *Position specific variation in the rate of evolution in transcription factor binding sites. BMC Evolutionary Biology*, 3, 19. PMID: 12946282; PMCID: PMC212491.
267. Moralejo, D.H., Park, H.A., Speros, S.J., MacMurray, A.J., Kwitek, A.E., Jacob, H.J., Lander, E.S., & Lernmark, A. (2003). *Genetic dissection of lymphopenia from autoimmunity by introgression of mutated *Ian5* gene onto the F344 rat. Journal of Autoimmunity*, 21(4), 315–324. PMID: 14624755.
268. Mootha, V.K., Bunkenborg, J., Olsen, J.V., Hjerrild, M., Wisniewski, J.R., Stahl, E., Bolouri, M.S., Ray, H.N., Sihag, S., Kamal, M., Patterson, N., Lander, E.S., & Mann, M. (2003). *Integrated analysis of protein composition, tissue diversity, and gene regulation in mouse mitochondria. Cell*, 115(5), 629–640. PMID: 14651853.
269. International HapMap Consortium. (2003). *The International HapMap Project. Nature* 426, 789–796.
270. Sklar, P., Pato, M.T., Kirby, A., Petryshen, T.L., Medeiros, H., Carvalho, C., Macedo, A., Dourado, A., Coelho, I., Valente, J., Soares, M.J., Ferreira, C.P., Lei, M., Verner, A., Hudson, T.J., Morley, C.P., Kennedy, J.L., Azevedo, M.H., Lander, E.S., Daly, M.J., & Pato, C.N. (2004). *Genome-wide scan in Portuguese Island families identifies 5q31–5q35 as a susceptibility locus for schizophrenia and psychosis. Molecular Psychiatry*, 9(2), 213–218. PMID: 14699422.
271. Kellis, M., Birren, B.W., & Lander, E.S. (2004). *Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae*. Nature*, 428(6983), 617–624. PMID: 15004568.
272. Singer, J.B., Hill, A.E., Burrage, L.C., Olszens, K.R., Song, J., Justice, M., O'Brien, W.E., Conti, D.V., Witte, J.S., Lander, E.S., & Nadeau, J.H. (2004). *Genetic dissection of complex traits with chromosome substitution strains of mice. Science*, 304(5669), 445–448. PMID: 15031436.
273. Freedman, M.L., Reich, D., Penney, K.L., McDonald, G.J., Mignault, A.A., Patterson, N., Gabriel, S.B., Topol, E.J., Smoller, J.W., Pato, C.N., Pato, M.T., Petryshen, T.L., Kolonel, L.N., Lander, E.S., Sklar, P., Henderson, B., Hirschhorn, J.N., & Altshuler, D. (2004). *Assessing the impact of population stratification on genetic association studies. Nature Genetics*, 36(4), 388–393. PMID: 15052270.
274. Mootha, V.K., Handschin, C., Arlow, D., Xie, X., St. Pierre, J., Sihag, S., Yang, W., Altshuler, D., Puigserver, P., Patterson, N., Willy, P.J., Schulman, I.G., Heyman, R.A., Lander, E.S., & Spiegelman, B.M. (2004). *Erralpha and Gabpa/b specify PGC-1 α -dependent oxidative phosphorylation gene expression that is altered in diabetic muscle. Proceedings of the National Academy of Sciences USA*, 101(17), 6570–6575. PMID: 15100410; PMCID: PMC404086.
275. Tantisira, K.G., Lake, S., Silverman, E.S., Palmer, L.J., Lazarus, R., Silverman, E.K., Liggett, S.B., Gelfand, E.W., Rosenwasser, L.J., Richter, B., Israel, E., Wechsler, M., Gabriel, S., Altshuler, D., Lander, E.S., Drazen, J., & Weiss, S.T. (2004). *Corticosteroid pharmacogenetics: association of sequence variants in *CRHR1* with improved lung function in asthmatics treated with inhaled corticosteroids. Human Molecular Genetics*, 13(13), 1353–1359. PMID: 15128701.
276. Sawcer, S.J., Maranian, M., Singlehurst, S., Yeo, T., Compston, A., Daly, M.J., De Jager, P.L., Gabriel, S., Hafler, D.A., Ivinson, A.J., Lander, E.S., Rioux, J.D., Walsh, E., Gregory, S.G., Schmidt, S., Pericak-Vance, M.A., Barcellos, L.,

- Hauser, S.L., Oksenberg, J.R., Kenealy, S.J., & Haines, J.L. (2004). *Enhancing linkage analysis of complex disorders: an evaluation of high-density genotyping*. *Human Molecular Genetics*, 13(17), 1943–1949. PMID: 15238506.
277. Kellis, M., Patterson, N., Birren, B.W., Berger, B., & Lander, E.S. (2004). *Methods in comparative genomics: genome correspondence, gene identification and regulatory motif discovery*. *Journal of Computational Biology*, 11(2–3), 319–355. PMID: 15285895.
278. Krewson, T.D., Supelak, P.J., Hill, A.E., Singer, J.B., Lander, E.S., Nadeau, J.H., & Palmert, M.R. (2004). *Chromosomes 6 and 13 harbor genes that regulate pubertal timing in mouse chromosome substitution strains*. *Endocrinology*, 145(10), 4447–4451. PMID: 15284200.
279. Michalkiewicz, M., Michalkiewicz, T., Ettinger, R.A., Rutledge, E.A., Fuller, J.M., Moralejo, D.H., Van Yserloo, B., MacMurray, A.J., Kwitek, A.E., Jacob, H.J., Lander, E.S., & Lernmark, A. (2004). *Transgenic rescue demonstrates involvement of the *Ian5* gene in T cell development in the rat*. *Physiological Genomics*, 19(2), 232–232. PMID: 15328390.
280. Harbison, C.T., Gordon, D.B., Lee, T.I., Rinaldi, N.J., Macisaac, K.D., Danford, T.W., Hannett, N.M., Tagne, J.B., Reynolds, D.B., Yoo, J., Jennings, E.G., Zeitlinger, J., Pokholok, D.K., Kellis, M., Rolfe, P.A., Takusagawa, K.T., Lander, E.S., Gifford, D.K., Fraenkel, E., & Young, R.A. (2004). *Transcriptional regulatory code of a eukaryotic genome*. *Nature*, 431(7004), 99–104. PMID: 15343339; PMCID: PMC3006441.
281. Rioux, J.D., Karinen, H., Kocher, K., McMahon, S.G., Kärkkäinen, P., Janatuinen, E., Heikkinen, M., Julkunen, R., Pihlajamäki, J., Naukkarinen, A., Kosma, V.M., Daly, M.J., Lander, E.S., & Laakso, M. (2004). *Genomewide search and association studies in a Finnish celiac disease population: Identification of a novel locus and replication of the HLA and CTLA4 loci*. *American Journal of Medical Genetics Part A*, 130(4), 345–350. PMID: 15386476.
282. International Human Genome Sequencing Consortium. (2004). *Finishing the euchromatic sequence of the human genome*. *Nature*, 431(7011), 931–945. PMID: 15496913.
283. Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biémont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigó, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B.W., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quétier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J., & Roest Crollius, H. (2004). *Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals the early vertebrate proto-karyotype*. *Nature*, 431(7011), 946–957. PMID: 15496914.
284. Poirier, C., Qin, Y., Adams, C.P., Anaya, Y., Singer, J.B., Hill, A.E., Lander, E.S., Nadeau, J.H., & Bishop, C.E. (2004). *A complex interaction of imprinted and maternal-effect genes modifies sex determination in Odd Sex (Ods) mice*. *Genetics*, 168(3), 855–862. PMID: 15579706; PMCID: PMC1448764.
285. Singer, J.B., Hill, A.E., Nadeau, J.H., & Lander, E.S. (2005). *Mapping quantitative trait loci for anxiety in chromosome substitution strains of mice*. *Genetics*, 169(2), 855–862. PMID: 15371360; PMCID: PMC1449086.
286. Bernstein, B.E., Kamal, M., Lindblad-Toh, K., Bekiranov, S., Bailey, D.K., Huebert, D.J., McMahon, S., Karlsson, E.K., Kulbokas, E.J., Gingeras, T.R., Schreiber, S.L., & Lander, E.S. (2005). *Genomic maps and comparative analysis of histone modifications in human and mouse*. *Cell*, 120(2), 169–181. PMID: 15680324.
287. International HapMap Consortium. (2005). *A haplotype map of the human genome*. *Nature*, 437(7063), 1299–320. PMCID: PMC1880871.
288. Coordinating Committee of the Global HIV/AIDS Vaccine Enterprise. (2005). *The Global HIV/AIDS Vaccine Enterprise: Scientific Strategic Plan*. *PLoS Medicine*, 2(2), e25. PMID: 15740411; PMCID: PMC544553.
289. Ackerman, K.G., Huang, H., Grasemann, H., Puma, C., Singer, J.B., Hill, A.E., Lander, E.S., Nadeau, J.H., Churchill, G.A., Drazen, J.M., & Beier, D.R. (2005). *Interacting genetic loci cause airway hyperresponsiveness*. *Physiological Genomics*, 21(1), 105–111. PMID: 15657107.
290. Xie, X., Lu, J., Kulbokas, E.J., Golub, T.R., Mootha, V., Lindblad-Toh, K., Lander, E.S., & Kellis, M. (2005). *Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammals*. *Nature*, 434(7031), 338–345. PMID: 15735639; PMCID: PMC2923337.

291. Miretti, M.M., Walsh, E.C., Ke, X., Delgado, M., Griffiths, M., Hunt, S., Morrison, J., Whittaker, P., Lander, E.S., Cardon, L.R., Bentley, D.R., Rioux, J.D., Beck, S., & Deloukas, P. (2005). A high-resolution linkage-disequilibrium map of the human major histocompatibility complex and first generation of tag single-nucleotide polymorphisms. *The American Journal of Human Genetics*, 76(4), 634–646. PMID: 15747258; PMCID: PMC1199300.
292. Margulies, E.H., Vinson, J.P., NISC Comparative Sequencing Program, Miller, W., Jaffe, D.B., Lindblad-Toh, K., Chang, J.L., Green, E.D., Lander, E.S., Mullikin, J.C., & Clamp, M. (2005). An initial strategy for the systematic identification of functional elements in the human genome by low-redundancy comparative sequencing. *Proceedings of the National Academy of Sciences USA*, 102(13), 4795–4800. PMID: 15778292; PMCID: PMC555705.
293. Vinson, J.P., Jaffe, D.B., O'Neill, K., Karlsson, E.K., Stange-Thomann, N., Anderson, S., Mesirov, J.P., Satoh, N., Satou, Y., Nusbaum, C., Birren, B.W., Galagan, J.E., & Lander, E.S. (2005). Assembly of polymorphic genomes: algorithms and application to *Ciona savignyi*. *Genome Research*, 15(8), 1127–1135. PMID: 16077012; PMCID: PMC1182225.
294. Sawcer, S., Ban, M., Maranian, M., Yeo, T.W., Compston, A., Kirby, A., Daly, M.J., De Jager, P.L., Walsh, E., Lander, E.S., Rioux, J.D., Hafler, D.A., Ivinson, A., Rimmler, J., Gregory, S.G., Schmidt, S., Pericak-Vance, M.A., Akesson, E., Hillert, J., Datta, P., Oturai, A., Ryder, L.P., Harbo, H.F., Spurkland, A., Myhr, K.M., Laaksonen, M., Booth, D., Heard, R., Stewart, G., Lincoln, R., Barcellos, L.F., Hauser, S.L., Oksenberg, J.R., Kenealy, S.J., Haines, J.L., International Multiple Sclerosis Genetics Consortium. (2005). A high-density screen for linkage in multiple sclerosis. *The American Journal of Human Genetics*, 77(3), 454–467. PMID: 16080120; PMCID: PMC1226210.
295. Chimpanzee Sequencing and Analysis Consortium. (2005). Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, 437(7055), 69–87. PMID: 16136131.
296. Nusbaum, C., Zody, M.C., Borowsky, M.L., Kamal, M., Kodira, C.D., Taylor, T.D., Whittaker, C.A., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Yang, X., Abouelleil, A., Allen, N.R., Anderson, S., Bloom, T., Bugalter, B., Butler, J., Cook, A., DeCaprio, D., Engels, R., Garber, M., Gnirke, A., Hafez, N., Hall, J.L., Norman, C.H., Itoh, T., Jaffe, D.B., Kuroki, Y., Lehoczy, J., Lui, A., Macdonald, P., Mauceli, E., Mikkelsen, T.S., Naylor, J.W., Nicol, R., Nguyen, C., Noguchi, H., O'Leary, S.B., O'Neill, K., Pigani, B., Smith, C.L., Talamas, J.A., Topham, K., Totoki, Y., Toyoda, A., Wain, H.M., Young, S.K., Zeng, Q., Zimmer, A.R., Fujiyama, A., Hattori, M., Birren, B.W., Sakaki, Y., & Lander, E.S. (2005). DNA sequence and analysis of human chromosome 18. *Nature*, 437(7058), 551–555. PMID: 16177791.
297. Subramanian, A., Tamayo, P., Mootha, V.K., Mukherjee, S., Ebert, B.L., Gillette, M.A., Paulovich, A., Pomeroy, S.L., Golub, T.R., Lander, E.S., & Mesirov, J.P. (2005). Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proceedings of the National Academy of Sciences USA*, 102(43), 15545–15550. PMID: 16199517; PMCID: PMC1239896.
298. Meissner, A., Gnirke, A., Bell, G.W., Ramsahoye, B., Lander, E.S., & Jaenisch, R. (2005). Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis. *Nucleic Acids Research*, 33(18), 5868–5877. PMID: 16224102; PMCID: PMC1258174.
299. Sabeti, P.C., Walsh, E., Schaffner, S.F., Varilly, P., Fry, B., Cullen, M., Mikkelsen, T.S., Roy, J., Patterson, N., Cooper, R., Altshuler, D., & Lander, E.S. (2005). The case for selection of CCR5-delta32. *PloS Biology*, 3(11): e378. PMID: 16248677; PMCID: PMC1275522.
300. Lindblad-Toh, K., Wade, C.M., Mikkelsen, T.S., Karlsson, E.K., Jaffe, D.B., Kamal, M., Clamp, M., Chang, J.L., Kulbokas, E.J., Zody, M.C., Mauceli, E., Xie, X., Breen, M., Wayne, R.K., Ostrander, E.A., Ponting, C.P., Galibert, F., Smith, D.R., DeJong, P.J., Kirkness, E., Alvarez, P., Biagi, T., Brockman, W., Butler, J., Chin, C.W., Cook, A., Cuff, J., Daly, M.J., DeCaprio, D., Gnerre, S., Grabherr, M., Kellis, M., Kleber, M., Bardeleben, C., Goodstadt, L., Heger, A., Hitte, C., Kim, L., Koepfli, K.P., Parker, H.G., Pollinger, J.P., Searle, S.M., Sutter, N.B., Thomas, R., Webber, C., Baldwin, J., Abebe, A., Abouelleil, A., Aftuck, L., Ait-Zahra, M., Aldredge, T., Allen, N., An, P., Anderson, S., Antoine, C., Arachchi, H., Aslam, A., Ayotte, L., Bachantsang, P., Barry, A., Bayul, T., Benamara, M., Berlin, A., Bessette, D., Blitshteyn, B., Bloom, T., Blye, J., Boguslavskiy, L., Bonnet, C., Boukhgalter, B., Brown, A., Cahill, P., Calixte, N., Camarata, J., Cheshatsang, Y., Chu, J., Citroen, M., Collymore, A., Cooke, P., Dawoe, T., Daza, R., Decktor, K., DeGray, S., Dhargay, N., Dooley, K., Dooley, K., Dorje, P., Dorjee, K., Dorris, L., Duffey, N., Dupes, A., Egbiremolun, O., Elong, R., Falk, J., Farina, A., Faro, S., Ferguson, D., Ferreira, P., Fisher, S., FitzGerald, M., Foley, K., Foley, C., Franke, A.,

- Friedrich, D., Gage, D., Garber, M., Gearin, G., Giannoukos, G., Goode, T., Goyette, A., Graham, J., Grandbois, E., Gyaltsen, K., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Healy, C., Hegarty, R., Honan, T., Horn, A., Houde, N., Hughes, L., Hunnicutt, L., Husby, M., Jester, B., Jones, C., Kamat, A., Kanga, B., Kells, C., Khazanovich, D., Kieu, A.C., Kisner, P., Kumar, M., Lance, K., Landers, T., Lara, M., Lee, W., Leger, J.P., Lennon, N., Leuper, L., LeVine, S., Liu, J., Liu, X., Lokyitsang, Y., Lokyitsang, T., Lui, A., Macdonald, J., Major, J., Marabella, R., Maru, K., Matthews, C., McDonough, S., Mehta, T., Meldrim, J., Melnikov, A., Meneus, L., Mihalev, A., Mihova, T., Miller, K., Mittelman, R., Mlenga, V., Mulrain, L., Munson, G., Navidi, A., Naylor, J., Nguyen, T., Nguyen, N., Nguyen, C., Nguyen, T., Nicol, R., Norbu, N., Norbu, C., Novod, N., Nyima, T., Olandt, P., O'Neill, B., O'Neill, K., Osman, S., Oyono, L., Patti, C., Perrin, D., Phunkhang, P., Pierre, F., Priest, M., Rachupka, A., Raghuraman, S., Rameau, R., Ray, V., Raymond, C., Rege, F., Rise, C., Rogers, J., Rogov, P., Sahalie, J., Settipalli, S., Sharpe, T., Shea, T., Sheehan, M., Sherpa, N., Shi, J., Shih, D., Sloan, J., Smith, C., Sparrow, T., Stalker, J., Stange-Thomann, N., Stavropoulos, S., Stone, C., Stone, S., Sykes, S., Tchuinga, P., Tenzing, P., Tesfaye, S., Thoulutsang, D., Thoulutsang, Y., Topham, K., Topping, I., Tsamla, T., Vassiliev, H., Venkataraman, V., Vo, A., Wangchuk, T., Wangdi, T., Weiland, M., Wilkinson, J., Wilson, A., Yadav, S., Yang, S., Yang, X., Young, G., Yu, Q., Zainoun, J., Zembek, L., Zimmer, A., & Lander, E.S. (2005). *Genome sequence, comparative analysis and haplotype structure of the domestic dog*. *Nature*, 438(7069), 803–819. PMID: 16341006.
301. Nusbaum, C., Mikkelsen, T.S., Zody, M.C., Asakawa, S., Taudien, S., Garber, M., Kodira, C.D., Schueler, M.G., Shimizu, A., Whittaker, C.A., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Yang, X., Allen, N.R., Anderson, S., Asakawa, T., Blechschmidt, K., Bloom, T., Borowsky, M.L., Butler, J., Cook, A., Corum, B., DeArellano, K., DeCaprio, D., Dooley, K.T., Dorris, L., Engels, R., Glöckner, G., Hafez, N., Hagopian, D.S., Hall, J.L., Ishikawa, S.K., Jaffe, D.B., Kamat, A., Kudoh, J., Lehmann, R., Lokitsang, J., Macdonald, P., Major, J.E., Matthews, C.D., Mauceli, E., Menzel, U., Mihalev, A.H., Minoshima, S., Murayama, Y., Naylor, J.W., Nicol, R., Nguyen, C., O'Leary, S.B., O'Neill, K., Parker, S.C., Polley, A., Raymond, C.K., Reichwald, K., Rodriguez, J., Sasaki, T., Schilhabel, M., Siddiqui, R., Smith, C.L., Sneddon, T.P., Talamas, J.A., Tenzin, P., Topham, K., Venkataraman, V., Wen, G., Yamazaki, S., Young, S.K., Zeng, Q., Zimmer, A.R., Rosenthal, A., Birren, B.W., Platzer, M., Shimizu, N., & Lander, E.S. (2006). *DNA sequence and analysis of human chromosome 8*. *Nature*, 439(7074), 331–335. PMID: 16421571.
302. Walsh, E.C., Sabeti, P., Hutcheson, H.B., Fry, B., Schaffner, S.F., de Bakker, P.I., Varilly, P., Palma, A.A., Roy, J., Cooper, R., Winkler, C., Zeng, Y., de The, G., Lander, E.S., O'Brien, S., & Altshuler, D. (2006). *Searching for signals of evolutionary selection in 168 genes related to immune function*. *Human Genetics*, 119(1–2), 92–102. PMID: 16362345.
303. Hill, A.E., Lander, E.S., & Nadeau, J.H. (2006). *Chromosome substitution strains: a new way to study genetically complex traits*. *Methods in Molecular Medicine*, 128, 153–172. PMID: 17071995.
304. Taylor, T.D., Noguchi, H., Totoki, Y., Toyoda, A., Kuroki, Y., Dewar, K., Lloyd, C., Itoh, T., Takeda, T., Kim, D.W., She, X., Barlow, K.F., Bloom, T., Bruford, E., Chang, J.L., Cuomo, C.A., Eichler, E., FitzGerald, M.G., Jaffe, D.B., LaButti, K., Nicol, R., Park, H.S., Seaman, C., Sougnez, C., Yang, X., Zimmer, A.R., Zody, M.C., Birren, B.W., Nusbaum, C., Fujiyama, A., Hattori, M., Rogers, J., Lander, E.S., & Sakaki, Y. (2006). *Human chromosome 11 DNA sequence and analysis including novel gene identification*. *Nature*, 440(7083), 497–500. PMID: 16477033; PMCID: PMC1413850.
305. Kamal, M., Xie, X., & Lander, E.S. (2006). *A large family of ancient repeat elements in the human genome is under strong selection*. *Proceedings of the National Academy of Sciences USA*, 103(8), 2740–2745.
306. Moffat, J., Grueneberg, D.A., Yang, X., Kim, S.Y., Kloepper, A.M., Hinkle, G., Piqani, B., Eisenhaure, T.M., Luo, B., Grenier, J.K., Carpenter, A.E., Foo, S.Y., Stewart, S.A., Stockwell, B.R., Hacohen, N., Hahn, W.C., Lander, E.S., Sabatini, D.M., & Root, D.E. (2006). *A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen*. *Cell*, 124(6), 1283–1298. PMID: 16564017.
307. Zody, M.C., Garber, M., Sharpe, T., Young, S.K., Rowen, L., O'Neill, K., Whittaker, C.A., Kamal, M., Chang, J.L., Cuomo, C.A., Dewar, K., FitzGerald, M.G., Kodira, C.D., Madan, A., Qin, S., Yang, X., Abbasi, N., Abouelleil, A., Arachchi, H.M., Baradarani, L., Birditt, B., Bloom, S., Bloom, T., Borowsky, M.L., Burke, J., Butler, J., Cook, A., DeArellano, K., DeCaprio, D., Dorris, L., Dors, M., Eichler, E.E., Engels, R., Fahey, J., Fleetwood, P., Friedman, C., Gearin, G., Hall, J.L., Hensley, G., Johnson, E., Jones, C., Kamat, A., Kaur, A., Locke, D.P., Madan, A., Munson,

- G., Jaffe, D.B., Lui, A., Macdonald, P., Mauceli, E., Naylor, J.W., Nesbitt, R., Nicol, R., O'Leary, S.B., Ratcliffe, A., Rounsley, S., She, X., Sneddon, K.M., Stewart, S., Sougnez, C., Stone, S.M., Topham, K., Vincent, D., Wang, S., Zimmer, A.R., Birren, B.W., Hood, L., Lander, E.S., & Nusbaum, C. (2006). *Analysis of the DNA sequence and duplication history of human chromosome 15*. *Nature*, 440(7084), 671–675. PMID: 16572171.
308. Tello-Ruiz, M.K., Curley, C., DelMonte, T., Giallourakis, C., Kirby, A., Miller, K., Wild, G., Cohen, A., Langelier, D., Latiano, A., Wedemeyer, N., Lander, E.S., Schreiber, S., Annese, V., Daly, M.J., & Rioux, J.D. (2006). *Haplotype-based association analysis of 56 functional candidate genes in the IBD6 locus on chromosome 19*. *European Journal of Human Genetics*, 14(6), 780–790. PMID: 16570073.
309. Kamal, M., Xie, X., & Lander, E.S. (2006). *A large family of ancient repeat elements in the human genome is under strong selection*. *Proceedings of the National Academy of Sciences USA*, 103(8), 2740–2745. PMID: 16477033; PMCID: PMC1413850.
310. Root, D.E., Hacohen, N., Hahn, W.C., Lander, E.S., & Sabatini, D.M. (2006). *Genome-scale loss-of-function screening with a lentiviral RNAi library*. *Nature Methods*, 3(9), 715–719. PMID: 16929317.
311. Houstis, N., Rosen, E.D., & Lander, E.S. (2006). *Reactive oxygen species have a causal role in multiple forms of insulin resistance*. *Nature*, 440(7086), 944–948. PMID: 16612386.
312. Zody, M.C., Garber, M., Adams, D.J., Sharpe, T., Harrow, J., Lupski, J.R., Nicholson, C., Searle, S.M., Wilming, L., Young, S.K., Abouelleil, A., Allen, N.R., Bi, W., Bloom, T., Borowsky, M.L., Bugalter, B.E., Butler, J., Chang, J.L., Chen, C.K., Cook, A., Corum, B., Cuomo, C.A., de Jong, P.J., DeCaprio, D., Dewar, K., Fitzgerald, M., Gilbert, J., Gibson, R., Gnerre, S., Goldstein, S., Grafham, D.V., Grocock, R., Hafez, N., Hagopian, D.S., Hart, E., Norman, C.H., Humphray, S., Jaffe, D.B., Jones, M., Kamal, M., Khodiyar, V.K., LaButti, K., Laird, G., Lehoczky, J., Liu, X., Lokysang, T., Loveland, J., Lui, A., Macdonald, P., Major, J.E., Mathews, L., Mauceli, E., McCarroll, S.A., Mihalev, A.H., Mudge, J., Nguyen, C., Nicol, R., O'Leary, S.B., Osoegawa, K., Schwartz, D.C., Shaw-Smith, C., Stankiewicz, P., Steward, C., Swarbreck, D., Venkataraman, V., Whittaker, C.A., Yang, X., Zimmer, A.R., Bradley, A., Hubbard, T., Birren, B.W., Rogers, J., Lander, E.S., & Nusbaum, C. (2006). *DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage*. *Nature*, 440(7087), 1045–1049. PMID: 16625196; PMCID: PMC2610434.
313. Bernstein, B.E., Mikkelsen, T.S., Xie, X., Kamal, M., Huebert, D.J., Cuff, J., Fry, B., Meissner, A., Wernig, M., Plath, K., Jaenisch, R., Wagschal, A., Feil, R., Schreiber, S.L., & Lander, E.S. (2006). *A bivalent chromatin structure marks key developmental genes in embryonic stem cells*. *Cell*, 125(2), 315–326. PMID: 16630819.
314. Pedersen, J.S., Bejerano, G., Siepel, A., Rosenbloom, K., Lindblad-Toh, K., Lander, E.S., Kent, J., Miller, W., & Haussler, D. (2006). *Identification and classification of conserved RNA secondary structures in the human genome*. *PLoS Computational Biology*, 2(4), e33. PMID: 16628248; PMCID: PMC1440920.
315. Patterson, N., Richter, D.J., Gnerre, S., Lander, E.S., & Reich, D. (2006). *Genetic evidence for complex speciation of humans and chimpanzees*. *Nature*, 441(7097), 1103–1108. PMID: 16710306.
316. Sabeti, P.C., Schaffner, S.F., Fry, B., Lohmueller, J., Varilly, P., Shamovsky, O., Palma, A., Mikkelsen, T.S., Altshuler, D., & Lander, E.S. (2006). *Positive natural selection in the human lineage*. *Science*, 312(5780), 1614–1620. PMID: 16778047.
317. Xie, X., Kamal, M., & Lander, E.S. (2006). *A family of conserved noncoding elements derived from an ancient transposable element*. *Proceedings of the National Academy of Sciences USA*, 103(31), 11659–11664. PMID: 16864796; PMCID: PMC1518811.
318. Lowe, C.J., Terasaki, M., Wu, M., Freeman, R.M., Runft, L., Kwan, K., Haigo, S., Aronowicz, J., Lander, E.S., Gruber, C., Smith, M., Kirschner, M., & Gerhart, J. (2006). *Dorsoventral patterning in hemichordates: insights into early chordate evolution*. *PLoS Biology*, 4(9), e291. PMID: 16933975; PMCID: PMC1551926.
319. Lamb, J., Crawford, E.D., Peck, D., Modell, J.W., Blat, I.C., Wrobel, M.J., Lerner, J., Brunet, J.P., Subramanian, A., Ross, K.N., Reich, M., Hieronymus, H., Wei, G., Armstrong, S.A., Haggarty, S.J., Clemons, P.A., Wei, R., Carr, S.A., Lander, E.S., & Golub, T.R. (2006). *The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease*. *Science*, 313(5795), 1929–1935. PMID: 17008526.
320. Wei, B.Q., Mikkelsen, T.S., McKinney, M.K., Lander, E.S., & Cravatt, B.F. (2006). *A second fatty acid amide hydrolase with variable distribution among pla-*

- central mammals. *Journal of Biological Chemistry*, 281(48), 36569-36578. PMID: 17015445.
321. Bourlat, S.J., Juliusdottir, T., Lowe, C.J., Freeman, R., Aronowicz, J., Kirschner, M., Lander, E.S., Thorndyke, M., Nakano, H., Kohn, A.B., Heyland, A., Moroz, L.L., Copley, R.R., & Telford, M.J. (2006). *Deuterostome phylogeny reveals monophyletic chordates and the new phylum Xenoturbellida*. *Nature*, 444(7115), 85–88. PMID: 17051155.
322. Hill, A.E., Lander, E.S., & Nadeau, J.H. (2006). *Chromosome substitution strains: A new way to study genetically complex traits*. *Methods in Molecular Medicine*, 128, 153–172. PMID: 17071995.
323. Volkman, S.K., Sabeti, P.C., DeCaprio, D., Neafsey, D.E., Schaffner, S.F., Milner, D.A., Daily, J.P., Sarr, O., Ndiaye, D., Ndir, O., Mboup, S., Duraisingh, M.T., Lukens, A., Derr, A., Stange-Thomann, N., Waggoner, S., Onofrio, R., Ziaugra, L., Mauceli, E., Gnerre, S., Jaffe, D.B., Zainoun, J., Wiegand, R.C., Birren, B.W., Hartl, D.L., Galagan, J.E., Lander, E.S., & Wirth, D.F. (2007). *A genome-wide map of diversity in Plasmodium falciparum*. *Nature Genetics*, 39(1), 113–119. PMID: 17159979.
324. Yeo, T.W., De Jager, P.L., Gregory, S.G., Barcellos, L.F., Walton, A., Goris, A., Fenoglio, C., Ban, M., Taylor, C.J., Goodman, R.S., Walsh, E., Wolfish, C.S., Horton, R., Traherne, J., Beck, S., Trowsdale, J., Caillier, S.J., Ivinson, A.J., Green, T., Pobywajlo, S., Lander, E.S., Pericak-Vance, M.A., Haines, J.L., Daly, M.J., Oksenberg, J.R., Hauser, S.L., Compston, A., Hafler, D.A., Rioux, J.D., & Sawcer, S. (2007). *A second major histocompatibility complex susceptibility locus for multiple sclerosis*. *Annals of Neurology*, 61(3), 228–236. PMID: 17252545; PMCID: PMC2737610.
325. Bernstein, B.E., Meissner, A., & Lander, E.S. (2007). *The mammalian epigenome*. *Cell*, 128(4), 669–681. PMID: 17320505.
326. Strohl, K.P., Gallagher, L., Lynn, A., Friedman, L., Hill, A., Singer, J.B., Lander, E.S., & Nadeau, J. (2007). *Sleep-related epilepsy in the A/J mouse*. *Sleep*, 30(2), 169–176. PMID: 17326542.
327. Xie, X., Mikkelsen, T.S., Gnirke, A., Lindblad-Toh, K., Kellis, M., & Lander, E.S. (2007). *Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites*. *Proceedings of the National Academy of Sciences USA*, 104(17), 7145–7150. PMID: 17442748; PMCID: PMC1852749.
328. Mikkelsen, T.S., Wakefield, M.J., Aken, B., Amemiya, C.T., Chang, J.L., Duke, S., Garber, M., Gentles, A.J., Goodstadt, L., Heger, A., Jurka, J., Kamal, M., Mauceli, E., Searle, S.M., Sharpe, T., Baker, M.L., Batzer, M.A., Benos, P.V., Belov, K., Clamp, M., Cook, A., Cuff, J., Das, R., Davidow, L., Deakin, J.E., Fazzari, M.J., Glass, J.L., Grabherr, M., Greally, J.M., Gu, W., Hore, T.A., Huttley, G.A., Kleber, M., Jirtle, R.L., Koina, E., Lee, J.T., Mahony, S., Marra, M.A., Miller, R.D., Nicholls, R.D., Oda, M., Papenfuss, A.T., Parra, Z.E., Pollock, D.D., Ray, D.A., Schein, J.E., Speed, T.P., Thompson, K., VandeBerg, J.L., Wade, C.M., Walker, J.A., Waters, P.D., Webber, C., Weidman, J.R., Xie, X., Zody, M.C., Broad Institute Genome Sequencing Platform, Broad Institute Whole Genome Assembly Team, Graves, J.A., Ponting, C.P., Breen, M., Samollow, P.B., Lander, E.S., & Lindblad-Toh, K. (2007). *Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences*. *Nature*, 447(7141), 167–177. PMID: 17495919.
329. Margulies, E.H., Cooper, G.M., Asimenos, G., Thomas, D.J., Dewey, C.N., Siepel, A., Birney, E., Keefe, D., Schwartz, A.S., Hou, M., Taylor, J., Nikolaev, S., Montoya-Burgos, J.I., Löytynoja, A., Whelan, S., Pardi, F., Massingham, T., Brown, J.B., Bickel, P., Holmes, I., Mullikin, J.C., Ureta-Vidal, A., Paten, B., Stone, E.A., Rosenbloom, K.R., Kent, W.J., Bouffard, G.G., Guan, X., Hansen, N.F., Idol, J.R., Maduro, V.V., Maskeri, B., McDowell, J.C., Park, M., Thomas, P.J., Young, A.C., Blakesley, R.W., Muzny, D.M., Sodergren, E., Wheeler, D.A., Worley, K.C., Jiang, H., Weinstock, G.M., Gibbs, R.A., Graves, T., Fulton, R., Mardis, E.R., Wilson, R.K., Clamp, M., Cuff, J., Gnerre, S., Jaffe, D.B., Chang, J.L., Lindblad-Toh, K., Lander, E.S., Hinrichs, A., Trumbower, H., Clawson, H., Zweig, A., Kuhn, R.M., Barber, G., Harte, R., Karolchik, D., Field, M.A., Moore, R.A., Matthewson, C.A., Schein, J.E., Marra, M.A., Antonarakis, S.E., Batzoglu, S., Goldman, N., Hardison, R., Haussler, D., Miller, W., Pachter, L., Green, E.D., & Sidow, A. (2007). *Analyses of deep mammalian sequence alignments and constraint predictions for 1 percent of the human genome*. *Genome Research*, 17(6), 760–774. PMID: 17567995; PMCID: PMC1891336.
330. ENCODE Project Consortium. (2007). *Identification and analysis of functional elements in 1 percent of the human genome by the ENCODE pilot project*. *Nature*, 447(7146), 799–816. PMID: 17571346; PMCID: PMC2212820.
331. Boehm, J.S., Zhao, J.J., Yao, J., Kim, S.Y., Firestein, R., Dunn, I.F., Sjostrom, S.K., Garraway, L.A., Weremowicz, S., Richardson, A.L., Greulich, H.,

- Stewart, C.J., Mulvey, L.A., Shen, R.R., Ambrogio, L., Hirozane-Kishikawa, T., Hill, D.E., Vidal, M., Meyerson, M., Grenier, J.K., Hinkle, G., Root, D.E., Roberts, T.M., Lander, E.S., Polyak, K., & Hahn, W.C. (2007). *Integrative genomic approaches identify IKBKE as a breast cancer oncogene*. *Cell*, 129(6), 1065–1079. PMID: 17574021.
332. Mikkelsen, T.S., Ku, M., Jaffe, D.B., Issac, B., Lieberman, E., Giannoukos, G., Alvarez, P., Brockman, W., Kim, T.K., Koche, R.P., Lee, W., Mendenhall, E., O'Donovan, A., Presser, A., Russ, C., Xie, X., Meissner, A., Wernig, M., Jaenisch, R., Nusbaum, C., Lander, E.S., & Bernstein, B.E. (2007). *Genome-wide maps of chromatin state in pluripotent and lineage-committed cells*. *Nature*, 448(7153), 553–560. PMID: 17603471; PMCID: PMC2921165.
333. International Multiple Sclerosis Genetics Consortium, Hafler, D.A., Compston, A., Sawcer, S., Lander, E.S., Daly, M.J., De Jager, P.L., de Bakker, P.I., Gabriel, S.B., Mirel, D.B., Ivinson, A.J., Pericak-Vance, M.A., Gregory, S.G., Rioux, J.D., McCauley, J.L., Haines, J.L., Barcellos, L.F., Cree, B., Oksenberg, J.R., & Hauser, S.L. (2007). *Risk alleles for multiple sclerosis identified by a genomewide study*. *New England Journal of Medicine*, 357(9), 851–862. PMID: 17660530.
334. Sabeti, P.C., Varilly, P., Fry, B., Lohmueller, J., Hostetter, E., Cotsapas, C., Xie, X., Byrne, E.H., McCarroll, S.A., Gaudet, R., Schaffner, S.F., Lander, E.S., International HapMap Consortium, Frazer, K.A., Ballinger, D.G., Cox, D.R., Hinds, D.A., Stuve, L.L., Gibbs, R.A., Belmont, J.W., Boudreau, A., Hardenbol, P., Leal, S.M., Pasternak, S., Wheeler, D.A., Willis, T.D., Yu, F., Yang, H., Zeng, C., Gao, Y., Hu, H., Hu, W., Li, C., Lin, W., Liu, S., Pan, H., Tang, X., Wang, J., Wang, W., Yu, J., Zhang, B., Zhang, Q., Zhao, H., Zhou, J., Gabriel, S.B., Barry, R., Blumenstiel, B., Camargo, A., Defelice, M., Faggart, M., Goyette, M., Gupta, S., Moore, J., Nguyen, H., Onofrio, R.C., Parkin, M., Roy, J., Stahl, E., Winchester, E., Ziaugra, L., Altshuler, D., Shen, Y., Yao, Z., Huang, W., Chu, X., He, Y., Jin, L., Liu, Y., Shen, Y., Sun, W., Wang, H., Wang, Y., Wang, Y., Xiong, X., Xu, L., Wayne, M.M., Tsui, S.K., Xue, H., Wong, J.T., Galver, L.M., Fan, J.B., Gunderson, K., Murray, S.S., Oliphant, A.R., Chee, M.S., Montpetit, A., Chagnon, F., Ferretti, V., Leboeuf, M., Olivier, J.F., Phillips, M.S., Roumy, S., Sallée, C., Verner, A., Hudson, T.J., Kwok, P.Y., Cai, D., Koboldt, D.C., Miller, R.D., Pawlikowska, L., Taillon-Miller, P., Xiao, M., Tsui, L.C., Mak, W., Song, Y.Q., Tam, P.K., Nakamura, Y., Kawaguchi, T., Kitamoto, T., Morizono, T., Nagashima, A., Ohnishi, Y., Sekine, A., Tanaka, T., Tsunoda, T., Deloukas, P., Bird, C.P., Delgado, M., Dermitzakis, E.T., Gwilliam, R., Hunt, S., Morrison, J., Powell, D., Stranger, B.E., Whittaker, P., Bentley, D.R., Daly, M.J., de Bakker, P.I., Barrett, J., Chretien, Y.R., Maller, J., McCarroll, S., Patterson, N., Pe'er, I., Price, A., Purcell, S., Richter, D.J., Sabeti, P., Saxena, R., Schaffner, S.F., Sham, P.C., Varilly, P., Altshuler, D., Stein, L.D., Krishnan, L., Smith, A.V., Tello-Ruiz, M.K., Thorisson, G.A., Chakravarti, A., Chen, P.E., Cutler, D.J., Kashuk, C.S., Lin, S., Abecasis, G.R., Guan, W., Li, Y., Munro, H.M., Qin, Z.S., Thomas, D.J., McVean, G., Auton, A., Bottolo, L., Cardin, N., Eyheramendy, S., Freeman, C., Marchini, J., Myers, S., Spencer, C., Stephens, M., Donnelly, P., Cardon, L.R., Clarke, G., Evans, D.M., Morris, A.P., Weir, B.S., Tsunoda, T., Johnson, T.A., Mullikin, J.C., Sherry, S.T., Feolo, M., Skol, A., Zhang, H., Zeng, C., Zhao, H., Matsuda, I., Fukushima, Y., Macer, D.R., Suda, E., Rotimi, C.N., Adebamowo, C.A., Ajayi, I., Aniagwu, T., Marshall, P.A., Nkwodimmah, C., Royal, C.D., Leppert, M.F., Dixon, M., Peiffer, A., Qiu, R., Kent, A., Kato, K., Niikawa, N., Adewole, I.F., Knoppers, B.M., Foster, M.W., Clayton, E.W., Watkin, J., Gibbs, R.A., Belmont, J.W., Muzny, D., Nazareth, L., Sodergren, E., Weinstock, G.M., Wheeler, D.A., Yakub, I., Gabriel, S.B., Onofrio, R.C., Richter, D.J., Ziaugra, L., Birren, B.W., Daly, M.J., Altshuler, D., Wilson, R.K., Fulton, L.L., Rogers, J., Burton, J., Carter, N.P., Clee, C.M., Griffiths, M., Jones, M.C., McLay, K., Plumb, R.W., Ross, M.T., Sims, S.K., Willey, D.L., Chen, Z., Han, H., Kang, L., Godbout, M., Wallenburg, J.C., L'Archevêque, P., Bellemare, G., Saeki, K., Wang, H., An, D., Fu, H., Li, Q., Wang, Z., Wang, R., Holden, A.L., Brooks, L.D., McEwen, J.E., Guyer, M.S., Wang, V.O., Peterson, J.L., Shi, M., Spiegel, J., Sung, L.M., Zacharia, L.F., Collins, F.S., Kennedy, K., Jamieson, R., & Stewart, J. (2007). *Genome-wide detection and characterization of positive selection in human populations*. *Nature*, 449(7164), 913–918. PMID: 17943131; PMCID: PMC2687721.
335. GAIN Collaborative Research Group, Manolio, T.A., Rodriguez, L.L., Brooks, L., Abecasis, G., Collaborative Association Study of Psoriasis, Ballinger, D., Daly, M., Donnelly, P., Faraone, S.V., International Multi-Center ADHD Genetics Project, Frazer, K., Gabriel, S., Gejman, P., Molecular Genetics of Schizophrenia Collaboration, Guttmacher, A., Harris, E.L., Insel, T., Kelsoe, J.R., Bipolar Genome Study, Lander, E.S., McCowin, N., Mailman, M.D., Nabel, E., Ostell, J., Pugh, E., Sherry, S., Sullivan, P.F., Major Depression Stage 1 Genomewide Association in Population-Based Samples Study, Thompson, J.F., Warram, J., Genetics of Kidneys in Diabetes (GoKinD) Study, Wholley, D., Milos, P.M., & Collins, F.S. (2007). *New models of col-*

laboration in genome-wide association studies: the Genetic Association Information Network. *Nature Genetics*, 39(9), 1045–1051. PMID: 17728769.

336. Getz, G., Hofling, H., Mesirov, J.P., Golub, T.R., Meyerson, M., Tibshirani, R., & Lander E.S. (2007). *The consensus coding sequences of human breast and colorectal cancers [Comment]*. *Science* 317(5844), 1500. PMID: 17872428.

337. Karlsson, E.K., Baranowska, I., Wade, C.M., Salmon Hillbertz, N.H., Zody, M.C., Anderson, N., Biagi, T.M., Patterson, N., Pielberg, G.R., Kulbokas, E.J., Comstock, K.E., Keller, E.T., Mesirov, J.P., von Euler, H., Kämpe, O., Hedhammar, A., Lander, E.S., Andersson, G., Andersson, L., & Lindblad-Toh, K. (2007). *Efficient mapping of mendelian traits in dogs through genome-wide association*. *Nature Genetics*, 39(11), 1321–1328. PMID: 17906626.

338. Weir, B.A., Woo, M.S., Getz, G., Perner, S., Ding, L., Beroukhi, R., Lin, W.M., Province, M.A., Kraja, A., Johnson, L.A., Shah, K., Sato, M., Thomas, R.K., Barletta, J.A., Borecki, I.B., Broderick, S., Chang, A.C., Chiang, D.Y., Chirieac, L.R., Cho, J., Fujii, Y., Gazdar, A.F., Giordano, T., Greulich, H., Hanna, M., Johnson, B.E., Kris, M.G., Lash, A., Lin, L., Lindeman, N., Mardis, E.R., McPherson, J.D., Minna, J.D., Morgan, M.B., Nadel, M., Orringer, M.B., Osborne, J.R., Ozenberger, B., Ramos, A.H., Robinson, J., Roth, J.A., Rusch, V., Sasaki, H., Shepherd, F., Sougnez, C., Spitz, M.R., Tsao, M.S., Twomey, D., Verhaak, R.G., Weinstock, G.M., Wheeler, D.A., Winckler, W., Yoshizawa, A., Yu, S., Zakowski, M.F., Zhang, Q., Beer, D.G., Wistuba, I.I., Watson, M.A., Garraway, L.A., Ladanyi, M., Travis, W.D., Pao, W., Rubin, M.A., Gabriel, S.B., Gibbs, R.A., Varmus, H.E., Wilson, R.K., Lander, E.S., & Meyerson, M. (2007). *Characterizing the cancer genome in lung adenocarcinoma*. *Nature*, 450(7171), 893–898. PMID: 17982442; PMCID: PMC2538683.

339. Miller, W., Rosenbloom, K., Hardison, R.C., Hou, M., Taylor, J., Raney, B., Burhans, R., King, D.C., Baertsch, R., Blankenberg, D., Kosakovsky Pond, S.L., Nekrutenko, A., Giardine, B., Harris, R.S., Tyekucheva, S., Diekhans, M., Pringle, T.H., Murphy, W.J., Lesk, A., Weinstock, G.M., Lindblad-Toh, K., Gibbs, R.A., Lander, E.S., Siepel, A., Haussler, D., & Kent, W.J. (2007). *28-way vertebrate alignment and conservation track in the UCSC Genome Browser*. *Genome Research*, 17(12), 1797–1808. PMID: 17984227; PMCID: PMC2099589.

340. Drosophila 12 Genomes Consortium, Clark, A.G., Eisen, M.B., Smith, D.R., Bergman, C.M., Oliver, B., Markow, T.A., Kaufman, T.C., Kellis, M., Gelbart, W., Iyer, V.N., Pollard, D.A., Sackton, T.B., Larracuenta, A.M., Singh, N.D., Abad, J.P., Abt, D.N., Adryan, B., Aguade, M., Akashi, H., Anderson, W.W., Aquadro, C.F., Ardell, D.H., Arguello, R., Artieri, C.G., Barbash, D.A., Barker, D., Barsanti, P., Batterham, P., Batzoglou, S., Begun, D., Bhutkar, A., Blanco, E., Bosak, S.A., Bradley, R.K., Brand, A.D., Brent, M.R., Brooks, A.N., Brown, R.H., Butlin, R.K., Caggese, C., Calvi, B.R., Bernardo de Carvalho, A., Caspi, A., Castrezana, S., Celniker, S.E., Chang, J.L., Chapple, C., Chatterji, S., Chinwalla, A., Civetta, A., Clifton, S.W., Comeron, J.M., Costello, J.C., Coyne, J.A., Daub, J., David, R.G., Delcher, A.L., Delehaunty, K., Do, C.B., Ebling, H., Edwards, K., Eickbush, T., Evans, J.D., Filipinski, A., Findeiss, S., Freyhult, E., Fulton, L., Fulton, R., Garcia, A.C., Gardiner, A., Garfield, D.A., Garvin, B.E., Gibson, G., Gilbert, D., Gnerre, S., Godfrey, J., Good, R., Gotea, V., Gravely, B., Greenberg, A.J., Griffiths-Jones, S., Gross, S., Guigo, R., Gustafson, E.A., Haerty, W., Hahn, M.W., Halligan, D.L., Halpern, A.L., Halter, G.M., Han, M.V., Heger, A., Hillier, L., Hinrichs, A.S., Holmes, I., Hoskins, R.A., Hubisz, M.J., Hultmark, D., Huntley, M.A., Jaffe, D.B., Jagadeeshan, S., Jeck, W.R., Johnson, J., Jones, C.D., Jordan, W.C., Karpen, G.H., Kataoka, E., Keightley, P.D., Kheradpour, P., Kirkness, E.F., Koerich, L.B., Kristiansen, K., Kudrna, D., Kulathinal, R.J., Kumar, S., Kwok, R., Lander, E.S., Langley, C.H., Lapoint, R., Lazzaro, B.P., Lee, S.J., Levesque, L., Li, R., Lin, C.F., Lin, M.F., Lindblad-Toh, K., Llopart, A., Long, M., Low, L., Lozovsky, E., Lu, J., Luo, M., Machado, C.A., Makalowski, W., Marzo, M., Matsuda, M., Matzkin, L., McAllister, B., McBride, C.S., McKernan, B., McKernan, K., Mendez-Lago, M., Minx, P., Mollenhauer, M.U., Montooth, K., Mount, S.M., Mu, X., Myers, E., Negre, B., Newfield, S., Nielsen, R., Noor, M.A., O'Grady, P., Pachter, L., Papaceit, M., Parisi, M.J., Parisi, M., Parts, L., Pedersen, J.S., Pesole, G., Phillippy, A.M., Ponting, C.P., Pop, M., Porcelli, D., Powell, J.R., Prohaska, S., Pruitt, K., Puig, M., Quesneville, H., Ram, K.R., Rand, D., Rasmussen, M.D., Reed, L.K., Reenan, R., Reilly, A., Remington, K.A., Rieger, T.T., Ritchie, M.G., Robin, C., Rogers, Y.H., Rohde, C., Rozas, J., Rubenfield, M.J., Ruiz, A., Russo, S., Salzberg, S.L., Sanchez-Gracia, A., Saranga, D.J., Sato, H., Schaeffer, S.W., Schatz, M.C., Schlenke, T., Schwartz, R., Segarra, C., Singh, R.S., Sirot, L., Sirota, M., Sisneros, N.B., Smith, C.D., Smith, T.F., Spieth, J., Stage, D.E., Stark, A., Stephan, W., Strausberg, R.L., Strempel, S., Sturgill, D., Sutton, G., Sutton, G.G., Tao, W., Teichmann, S., Tobar, Y.N., Tomimura, Y., Tsolaj, J.M., Valente, V.L., Venter, E., Venter, J.C., Vicario, S., Vieira, F.G., Vilella, A.J., Villasante, A., Walenz, B., Wang, J., Wasserman, M., Watts, T., Wilson, D.,

- Wilson, R.K., Wing, R.A., Wolfner, M.F., Wong, A., Wong, G.K., Wu, C.I., Wu, G., Yamamoto, D., Yang, H.P., Yang, S.P., Yorke, J.A., Yoshida, K., Zdobnov, E., Zhang, P., Zhang, Y., Zimin, A.V., Baldwin, J., Abdouelleil, A., Abdulkadir, J., Abebe, A., Abera, B., Abreu, J., Acer, S.C., Aftuck, L., Alexander, A., An, P., Anderson, E., Anderson, S., Arachi, H., Azer, M., Bachantsang, P., Barry, A., Bayul, T., Berlin, A., Bessette, D., Bloom, T., Blye, J., Boguslavskiy, L., Bonnet, C., Boukhgalter, B., Bourzgui, I., Brown, A., Cahill, P., Channer, S., Cheshatsang, Y., Chuda, L., Citroen, M., Collymore, A., Cooke, P., Costello, M., D'Aco, K., Daza, R., De Haan, G., DeGray, S., DeMaso, C., Dhargay, N., Dooley, K., Dooley, E., Doricent, M., Dorje, P., Dorjee, K., Dupes, A., Elong, R., Falk, J., Farina, A., Faro, S., Ferguson, D., Fisher, S., Foley, C.D., Franke, A., Friedrich, D., Gadbois, L., Gearin, G., Gearin, C.R., Giannoukos, G., Goode, T., Graham, J., Grandbois, E., Grewal, S., Gyaltsen, K., Hafez, N., Hagos, B., Hall, J., Henson, C., Hollinger, A., Honan, T., Huard, M.D., Hughes, L., Hurhula, B., Husby, M.E., Kamat, A., Kanga, B., Kashin, S., Khazanovich, D., Kisner, P., Lance, K., Lara, M., Lee, W., Lennon, N., Letendre, F., LeVine, R., Lipovsky, A., Liu, X., Liu, J., Liu, S., Lokyitsang, T., Lokyitsang, Y., Lubonja, R., Lui, A., MacDonald, P., Magnisalis, V., Maru, K., Matthews, C., McCusker, W., McDonough, S., Mehta, T., Meldrim, J., Meneus, L., Mihai, O., Mihalev, A., Mihova, T., Mittelman, R., Mlenga, V., Montmayeur, A., Mulrain, L., Navidi, A., Naylor, J., Negash, T., Nguyen, T., Nguyen, N., Nicol, R., Norbu, C., Norbu, N., Novod, N., O'Neill, B., Osman, S., Markiewicz, E., Oyono, O.L., Patti, C., Phunkhang, P., Pierre, F., Priest, M., Raghuraman, S., Rege, F., Reyes, R., Rise, C., Rogov, P., Ross, K., Ryan, E., Settipalli, S., Shea, T., Sherpa, N., Shi, L., Shih, D., Sparrow, T., Spaulding, J., Stalker, J., Stange-Thomann, N., Stavropoulos, S., Stone, C., Strader, C., Tesfaye, S., Thomson, T., Thoulutsang, Y., Thoulutsang, D., Topham, K., Topping, I., Tsamla, T., Vassiliev, H., Vo, A., Wangchuk, T., Wangdi, T., Weiland, M., Wilkinson, J., Wilson, A., Yadav, S., Young, G., Yu, Q., Zembek, L., Zhong, D., Zimmer, A., Zwirko, Z., Jaffe, D.B., Alvarez, P., Brockman, W., Butler, J., Chin, C., Gnerre, S., Grabherr, M., Kleber, M., Mauceli, E., & MacCallum, I. (2007). *Evolution of genes and genomes on the Drosophila phylogeny*. *Nature*, 450(7167), 203–218. PMID: 17994087.
341. Clamp, M., Fry, B., Kamal, M., Xie, X., Cuff, J., Lin, M.F., Kellis, M., Lindblad-Toh, K., & Lander, E.S. (2007). *Distinguishing protein-coding and non-coding genes in the human genome*. *Proceedings of the National Academy of Sciences USA*, 104(49), 19428–19433. PMID: 18040051; PMCID: PMC2148306.
342. Beroukhi, R., Getz, G., Nghiemphu, L., Barretina, J., Hsueh, T., Linhart, D., Vivanco, I., Lee, J.C., Huang, J.H., Alexander, S., Du, J., Kau, T., Thomas, R.K., Shah, K., Soto, H., Perner, S., Prensner, J., Debiasi, R.M., Demichelis, F., Hatton, C., Rubin, M.A., Garraway, L.A., Nelson, S.F., Liao, L., Mischel, P.S., Cloughesy, T.F., Meyerson, M., Golub, T.A., Lander, E.S., Mellinghoff, I.K., & Sellers, W.R. (2007). *Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma*. *Proceedings of the National Academy of Sciences USA*, 104(50), 20007–20012. PMID: 18077431; PMCID: PMC2148413.
343. Daily, J.P., Scandell, D., Pochet, N., Le Roch, K., Plouffe, D., Kamal, M., Sarr, O., Mboup, S., Ndir, O., Wypij, D., Levasseur, K., Thomas, E., Tamayo, P., Dong, C., Zhou, Y., Lander, E.S., Ndiaye, D., Wirth, D., Winzeler, E.A., Mesirov, J.P., & Regev, A. (2007). *Distinct physiological states of Plasmodium falciparum in malaria-infected patients*. *Nature*, 450(7172), 1091–1095. PMID: 18046333.
344. Brockman, W., Alvarez, P., Young, S., Garber, M., Giannoukos, G., Lee, W.L., Russ, C., Lander, E.S., Nusbaum, C., & Jaffe, D.B. (2008). *Quality scores and SNP detection in sequencing-by-synthesis systems*. *Genome Research*, 18(5), 763–770. PMID: 18212088; PMCID: PMC2336812.
345. Butler, J., MacCallum, I., Kleber, M., Shlyakhter, I.A., Belmonte, M.K., Lander, E.S., Nusbaum, C., & Jaffe, D.B. (2008). *ALLPATHS: de novo assembly of whole-genome shotgun microreads*. *Genome Research*, 18(5), 810–820. PMID: 18340039; PMCID: PMC2336810.
346. Onder, T.T., Gupta, P.B., Mani, S.A., Yang, J., Lander, E.S., & Weinberg, R.A. (2008). *Loss of E-cadherin promotes metastasis via multiple downstream transcriptional pathways*. *Cancer Research*, 68(10), 3645–3654. PMID: 18483246.
347. Freeman, R.M., Wu, M., Cordonnier-Pratt, M.M., Pratt, L.H., Gruber, C.E., Smith, M., Lander, E.S., Stange-Thomann, N., Lowe, C.J., Gerhart, J., & Kirschner, M. (2008). *cDNA sequences for transcription factors and signaling proteins of the hemichordate Saccoglossus kowalevskii: efficacy of the expressed sequence tag (EST) approach for evolutionary and developmental studies of a new organism*. *The Biological Bulletin*, 214(3), 284–302. PMID: 18574105.
348. Mikkelsen, T.S., Hanna, J., Zhang, X., Ku, M., Wernig, M., Schorderet, P., Bernstein, B.E., Jaenisch, R., Lander, E.S., & Meissner, A. (2008). *Dissecting direct*

reprogramming through integrative genomic analysis. *Nature*, 454(7200), 49–55. PMID: 18509334; PMCID: PMC2754827.

349. Meissner, A., Mikkelsen, T.S., Gu, H., Wernig, M., Hanna, J., Sivachenko, A., Zhang, X., Bernstein, B.E., Nusbaum, C., Jaffe, D.B., Gnirke, A., Jaenisch, R., & Lander, E.S. (2008). *Genome-scale DNA methylation maps of pluripotent and differentiated cells*. *Nature*, 454(7205), 766–770. PMID: 18600261; PMCID: PMC2896277.

350. Cancer Genome Atlas Research Network. (2008). *Comprehensive genomic characterization defines human glioblastoma genes and core pathways*. *Nature*, 455(7216), 1061–1068. PMID: 18772890; PMCID: PMC2671642.

351. Ku, M., Koche, R.P., Rheinbay, E., Mendenhall, E.M., Endoh, M., Mikkelsen, T.S., Presser, A., Nusbaum, C., Xie, X., Chi, A.S., Adli, M., Kasif, S., Ptaszek, L.M., Cowan, C.A., Lander, E.S., Koseki, H., & Bernstein, B.E. (2008). *Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains*. *PLoS Genetics*, 4(10), e1000242. PMID: 18974828; PMCID: PMC2567431.

352. Ding, L., Getz, G., Wheeler, D.A., Mardis, E.R., McLellan, M.D., Cibulskis, K., Sougnez, C., Greulich, H., Muzny, D.M., Morgan, M.B., Fulton, L., Fulton, R.S., Zhang, Q., Wendl, M.C., Lawrence, M.S., Larson, D.E., Chen, K., Dooling, D.J., Sabo, A., Hawes, A.C., Shen, H., Jhangiani, S.N., Lewis, L.R., Hall, O., Zhu, Y., Mathew, T., Ren, Y., Yao, J., Scherer, S.E., Clerc, K., Metcalf, G.A., Ng, B., Milosavljevic, A., Gonzalez-Garay, M.L., Osborne, J.R., Meyer, R., Shi, X., Tang, Y., Koboldt, D.C., Lin, L., Abbott, R., Miner, T.L., Pohl, C., Fewell, G., Haipke, C., Schmidt, H., Dunford-Shore, B.H., Kraja, A., Crosby, S.D., Sawyer, C.S., Vickery, T., Sander, S., Robinson, J., Winckler, W., Baldwin, J., Chirieac, L.R., Dutt, A., Fennell, T., Hanna, M., Johnson, B.E., Onofrio, R.C., Thomas, R.K., Tonon, G., Weir, B.A., Zhao, X., Ziaugra, L., Zody, M.C., Giordano, T., Orringer, M.B., Roth, J.A., Spitz, M.R., Wistuba, I.I., Ozenberger, B., Good, P.J., Chang, A.C., Beer, D.G., Watson, M.A., Ladanyi, M., Broderick, S., Yoshizawa, A., Travis, W.D., Pao, W., Province, M.A., Weinstock, G.M., Varmus, H.E., Gabriel, S.B., Lander, E.S., Gibbs, R.A., Meyerson, M., & Wilson, R.K. (2008). *Somatic mutations affect key pathways in lung adenocarcinoma*. *Nature*, 455(7216), 1069–1075. PMID: 18948947; PMCID: PMC2694412.

353. Altshuler, D., Daly, M.J., & Lander, E.S. (2008). *Genetic mapping in human disease*. *Science*, 322(5903), 881–888. PMID: 18988837; PMCID: PMC2694957.

354. Miller, W., Drautz, D.I., Ratan, A., Pusey, B., Qi, J., Lesk, A.M., Tomsho, L.P., Packard, M.D., Zhao, F., Sher, A., Tikhonov, A., Raney, B., Patterson, N., Lindblad-Toh, K., Lander, E.S., Knight, J.R., Irzyk, G.P., Fredrikson, K.M., Harkins, T.T., Sheridan, S., Pringle, T., & Schuster, S.C. (2008). *Sequencing the nuclear genome of the extinct woolly mammoth*. *Nature*, 456(7220), 387–390. PMID: 19020620.

355. Shao, H., Burrage, L.C., Sinasac, D.S., Hill, A.E., Ernest, S.R., O'Brien, W., Courtland, H.W., Jepsen, K.J., Kirby, A., Kulbokas, E.J., Daly, M.J., Broman, K.W., Lander, E.S., & Nadeau, J.H. (2008). *Genetic architecture of complex traits: large phenotypic effects and pervasive epistasis*. *Proceedings of the National Academy of Sciences USA*, 105(50), 19910–19914. PMID: 19066216; PMCID: PMC2604967.

356. Luo, B., Cheung, H.W., Subramanian, A., Sharifnia, T., Okamoto, M., Yang, X., Hinkle, G., Boehm, J.S., Beroukhim, R., Weir, B.A., Mermel, C., Barbie, D.A., Awad, T., Zhou, X., Nguyen, T., Piquani, B., Li, C., Golub, T.R., Meyerson, M., Hacohen, N., Hahn, W.C., Lander, E.S., Sabatini, D.M., & Root, D.E. (2008). *Highly parallel identification of essential genes in cancer cells*. *Proceedings of the National Academy of Sciences USA*, 105(51), 20380–20385. PMID: 19091943; PMCID: PMC2629277.

357. Chiang, D.Y., Getz, G., Jaffe, D.B., O'Kelly, M.J., Zhao, X., Carter, S.L., Russ, C., Nusbaum, C., Meyerson, M., & Lander, E.S. (2009). *High-resolution mapping of copy-number alterations with massively parallel sequencing*. *Nature Methods*, 6(1), 99–103. PMID: 19043412; PMCID: PMC2630795.

358. Nusbaum, C., Ohsumi, T.K., Gomez, J., Aquadro, J., Victor, T.C., Warren, R.M., Hung, D.T., Birren, B.W., Lander, E.S., & Jaffe, D.B. (2009). *Sensitive, specific polymorphism discovery in bacteria using massively parallel sequencing*. *Nature Methods*, 6(1), 67–69. PMID: 19079253; PMCID: PMC2613166.

359. Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E.M., Brockman, W., Fennell, T., Giannoukos, G., Fisher, S., Russ, C., Gabriel, S., Jaffe, D.B., Lander, E.S., & Nusbaum, C. (2009). *Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing*. *Nature Biotechnology*, 27(2), 182–189. PMID: 19182786; PMCID: PMC2663421.

360. Guttman, M., Amit, I., Garber, M., French, C., Lin, M.F., Feldser, D., Huarte, M., Zuk, O., Carey, B.W., Cassady, J.P., Cabili, M.N., Jaenisch, R., Mikkelsen, T.S., Jacks, T., Hacohen, N., Bernstein, B.E., Kellis, M., Regev, A., Rinn, J.L., & Lander, E.S. (2009). *Chromatin signature reveals over a thousand highly conserved large*

non-coding RNAs in mammals. Nature, 458(7235), 223–227. PMID: 19182780; PMCID: PMC2754849.

361. Vasudevan, K.M., Barbie, D.A., Davies, M.A., Rabinovsky, R., McNear, C.J., Kim, J.J., Hennessy, B.T., Tseng, H., Pochanard, P., Kim, S.Y., Dunn, I.F., Schinzel, A.C., Sandy, P., Hoersch, S., Sheng, Q., Gupta, P.B., Boehm, J.S., Reiling, J.H., Silver, S., Lu, Y., Stemke-Hale, K., Dutta, B., Joy, C., Sahin, A.A., Gonzalez-Angulo, A.M., Lluch, A., Rameh, L.E., Jacks, T., Root, D.E., Lander, E.S., Mills, G.B., Hahn, W.C., Sellers, W.R., & Garraway, L.A. (2009). *AKT-independent signaling downstream of oncogenic PIK3CA mutations in human cancer. Cancer Cell*, 16(1), 21–32. PMID: 19573809; PMCID: PMC2752826.

362. Khalil, A.M., Guttman, M., Huarte, M., Garber, M., Raj, A., Rivea Morales, D., Thomas, K., Presser, A., Bernstein, B.E., van Oudenaarden, A., Regev, A., Lander, E.S., & Rinn, J.L. (2009). *Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences USA*, 106(28), 11667–11672. PMID: 19571010; PMCID: PMC2704857.

363. Gupta, P.B., Onder, T.T., Jiang, G., Tao, K., Kuperwasser, C., Weinberg, R.A., & Lander, E.S. (2009). *Identification of selective inhibitors of cancer stem cells by high-throughput screening. Cell*, 138(4), 645–659. PMID: 19682730; PMCID: PMC4892125.

364. Gnerre, S., Lander, E.S., Lindblad-Toh, K., & Jaffe, D.B. (2009). *Assisted assembly: how to improve a de novo genome assembly by using related species. Genome Biology*, 10(8), R88. PMID: 19712469; PMCID: PMC2745769.

365. Lieberman-Aiden, E., van Berkum, N.L., Williams, L., Imakaev, M., Ragoczy, T., Telling, A., Amit, I., Lajoie, B.R., Sabo, P.J., Dorschner, M.O., Sandstrom, R., Bernstein, B., Bender, M.A., Groudine, M., Gnirke, A., Stamatoyannopoulos, J., Mirny, L.A., Lander, E.S., & Dekker, J. (2009). *Comprehensive mapping of long-range interactions reveals folding principles of the human genome. Science*, 326(5950), 289–293. PMID: 19815776; PMCID: PMC2858594.

366. Barbie, D.A., Tamayo, P., Boehm, J.S., Kim, S.Y., Moody, S.E., Dunn, I.F., Schinzel, A.C., Sandy, P., Meylan, E., Scholl, C., Fröhling, S., Chan, E.M., Sos, M.L., Michel, K., Mermel, C., Silver, S.J., Weir, B.A., Reiling, J.H., Sheng, Q., Gupta, P.B., Wadlow, R.C., Le, H., Hoersch, S., Wittner, B.S., Ramaswamy, S., Livingston, D.M., Sabatini, D.M., Meyerson, M., Thomas, R.K., Lander, E.S., Mesirov, J.P., Root, D.E., Gilliland, D.G., Jacks, T., & Hahn, W.C. (2009). *Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. Nature*, 462(7269), 108–112. PMID: 19847166; PMCID: PMC2783335.

367. Wade, C.M., Giulotto, E., Sigurdsson, S., Zoli, M., Gnerre, S., Imsland, F., Lear, T.L., Adelson, D.L., Bailey, E., Bellone, R.R., Blöcker, H., Distl, O., Edgar, R.C., Garber, M., Leeb, T., Mauceli, E., MacLeod, J.N., Penedo, M.C., Raison, J.M., Sharpe, T., Vogel, J., Andersson, L., Antczak, D.F., Biagi, T., Binns, M.M., Chowdhary, B.P., Coleman, S.J., Della Valle, G., Fryc, S., Guérin, G., Hasegawa, T., Hill, E.W., Jurka, J., Kiialainen, A., Lindgren, G., Liu, J., Magnani, E., Mickelson, J.R., Murray, J., Nergadze, S.G., Onofrio, R., Pedroni, S., Piras, M.F., Raudsepp, T., Rocchi, M., Rønsbo, K.H., Ryder, O.A., Searle, S., Skow, L., Swinburne, J.E., Syvänen, A.C., Tozaki, T., Valberg, S.J., Vaudin, M., White, J.R., Zody, M.C., Broad Institute Genome Sequencing Platform, Broad Institute Whole Genome Assembly Team, Lander, E.S., & Lindblad-Toh, K. (2009). *Genome sequence, comparative analysis, and population genetics of the domestic horse. Science*, 326(5954), 865–867. PMID: 19892987; PMCID: PMC3785132.

368. Markljung, E., Jiang, L., Jaffe, J.D., Mikkelsen, T.S., Wallerman, O., Larhammar, M., Zhang, X., Wang, L., Saenz-Vash, V., Gnirke, A., Lindroth, A.M., Barrés, R., Yan, J., Strömberg, S., De, S., Pontén, F., Lander, E.S., Carr, S.A., Zierath, J.R., Kullander, K., Wadelius, C., Lindblad-Toh, K., Andersson, G., Hjälm, G., & Andersson, L. (2009). *ZBED6, a novel transcription factor derived from a domesticated DNA transposon regulates IGF2 expression and muscle growth. PLoS Biology*, 7(12), e1000256. PMID: 20016685; PMCID: PMC2780926.

369. Lander, E.S., Jiang, G., & Tao, K. (2009). *Taking aim at aggressive cancer cells. Cancer Biology & Therapy*, 8(16), ii. PMID: 19830887.

370. Grossman, S.R., Shlyakhter, I., Karlsson, E.K., Byrne, E.H., Morales, S., Frieden, G., Hostetter, E., Angelino, E., Garber, M., Zuk, O., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2010). *A composite of multiple signals distinguishes causal variants in regions of positive selection. Science*, 327(5967), 883–886. PMID: 20056855.

371. Gu, H., Bock, C., Mikkelsen, T.S., Jäger, N., Smith, Z.D., Tomazou, E., Gnirke, A., Lander, E.S., & Meissner, A. (2010). *Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. Nature Methods*, 7(2), 133–136. PMID: 20062050; PMCID: PMC2860480.

372. Kim, S.Y., Dunn, I.F., Firestein, R., Gupta, P., Wardwell, L., Repich, K., Schinzel, A.C., Wittner, B., Silver, S.J., Root, D.E., Boehm, J.S., Ramaswamy, S., Lander, E.S., & Hahn, W.C. (2010). *CK1 ϵ is required for breast cancers dependent on β -catenin activity*. *PLoS One*, 5(2), e8979. PMID: 20126544; PMCID: PMC2813871.
373. Grossman, S.R., Shlyakhter, I., Karlsson, E.K., Byrne, E.H., Morales, S., Frieden, G., Hostetter, E., Angelino, E., Garber, M., Zuk, O., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2010). *A composite of multiple signals distinguishes causal variants in regions of positive selection*. *Science*, 327(5967), 883–886. PMID: 20056855.
374. Burrage, L.C., Baskin-Hill, A.E., Sinasac, D.S., Singer, J.B., Croniger, C.M., Kirby, A., Kulbokas, E.J., Daly, M.J., Lander, E.S., Broman, K.W., & Nadeau, J.H. (2010). *Genetic resistance to diet-induced obesity in chromosome substitution strains of mice*. *Mammalian Genome*, 21(3–4), 115–129. PMID: 20127486; PMCID: PMC3831885.
375. Beroukhi, R., Mermel, C.H., Porter, D., Wei, G., Raychaudhuri, S., Donovan, J., Barretina, J., Boehm, J.S., Dobson, J., Urashima, M., Mc Henry, K.T., Pinchback, R.M., Ligon, A.H., Cho, Y.J., Haery, L., Greulich, H., Reich, M., Winckler, W., Lawrence, M.S., Weir, B.A., Tanaka, K.E., Chiang, D.Y., Bass, A.J., Loo, A., Hoffman, C., Prensner, J., Liefeld, T., Gao, Q., Yecies, D., Signoretti, S., Maher, E., Kaye, F.J., Sasaki, H., Tepper, J.E., Fletcher, J.A., Tabernero, J., Baselga, J., Tsao, M.S., Demicheli, F., Rubin, M.A., Janne, P.A., Daly, M.J., Nucera, C., Levine, R.L., Ebert, B.L., Gabriel, S., Rustgi, A.K., Antonescu, C.R., Ladanyi, M., Letai, A., Garraway, L.A., Loda, M., Beer, D.G., True, L.D., Okamoto, A., Pomeroy, S.L., Singer, S., Golub, T.R., Lander, E.S., Getz, G., Sellers, W.R., & Meyerson, M. (2010). *The landscape of somatic copy-number alteration across human cancers*. *Nature*, 463(7283), 899–905. PMID: 20164920; PMCID: PMC2826709.
376. Berger, M.F., Levin, J.Z., Vijayendran, K., Sivachenko, A., Adiconis, X., Maguire, J., Johnson, L.A., Robinson, J., Verhaak, R.G., Sougnez, C., Onofrio, R.C., Ziaugra, L., Cibulskis, K., Laine, E., Barretina, J., Winckler, W., Fisher, D.E., Getz, G., Meyerson, M., Jaffe, D.B., Gabriel, S.B., Lander, E.S., Dummer, R., Gnirke, A., Nusbaum, C., & Garraway, L.A. (2010). *Integrative analysis of the melanoma transcriptome*. *Genome Research*, 20(4), 413–427. PMID: 20179022; PMCID: PMC2847744.
377. Guttman, M., Garber, M., Levin, J.Z., Donaghey, J., Robinson, J., Adiconis, X., Fan, L., Koziol, M.J., Gnirke, A., Nusbaum, C., Rinn, J.L., Lander, E.S., & Regev, A. (2010). *Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs*. *Nature Biotechnology*, 28(5), 503–510. PMID: 20436462; PMCID: PMC2868100.
378. International Cancer Genome Consortium, Hudson, T.J., Anderson, W., Artez, A., Barker, A.D., Bell, C., Bernabé, R.R., Bhan, M.K., Calvo, F., Eerola, I., Gerhard, D.S., Gutmacher, A., Guyer, M., Hemsley, F.M., Jennings, J.L., Kerr, D., Klatt, P., Kolar, P., Kusada, J., Lane, D.P., Laplace, F., Youyong, L., Nettekoven, G., Ozenberger, B., Peterson, J., Rao, T.S., Remacle, J., Schafer, A.J., Shibata, T., Stratton, M.R., Vockley, J.G., Watanabe, K., Yang, H., Yuen, M.M., Knoppers, B.M., Bobrow, M., Cambon-Thomsen, A., Dressler, L.G., Dyke, S.O., Joly, Y., Kato, K., Kennedy, K.L., Nicolás, P., Parker, M.J., Rial-Sebbag, E., Romeo-Casabona, C.M., Shaw, K.M., Wallace, S., Wiesner, G.L., Zeps, N., Lichter, P., Biankin, A.V., Chabannon, C., Chin, L., Clément, B., de Alava, E., Degos, F., Ferguson, M.L., Geary, P., Hayes, D.N., Hudson, T.J., Johns, A.L., Kasprzyk, A., Nakagawa, H., Penny, R., Piris, M.A., Sarin, R., Scarpa, A., Shibata, T., van de Vijver, M., Futreal, P.A., Aburatani, H., Bayés, M., Botwell, D.D., Campbell, P.J., Estivill, X., Gerhard, D.S., Grimmond, S.M., Gut, I., Hirst, M., López-Otin, C., Majumder, P., Marra, M., McPherson, J.D., Nakagawa, H., Ning, Z., Puente, X.S., Ruan, Y., Shibata, T., Stratton, M.R., Stunnenberg, H.G., Swerdlow, H., Velculescu, V.E., Wilson, R.K., Xue, H.H., Yang, L., Spellman, P.T., Bader, G.D., Boutros, P.C., Campbell, P.J., Flicek, P., Getz, G., Guigó, R., Guo, G., Haussler, D., Heath, S., Hubbard, T.J., Jiang, T., Jones, S.M., Li, Q., López-Bigas, N., Luo, R., Muthuswamy, L., Ouellette, B.F., Pearson, J.V., Puente, X.S., Quesada, V., Raphael, B.J., Sander, C., Shibata, T., Speed, T.P., Stein, L.D., Stuart, J.M., Teague, J.W., Totoki, Y., Tsunoda, T., Valencia, A., Wheeler, D.A., Wu, H., Zhao, S., Zhou, G., Stein, L.D., Guigó, R., Hubbard, T.J., Joly, Y., Jones, S.M., Kasprzyk, A., Lathrop, M., López-Bigas, N., Ouellette, B.F., Spellman, P.T., Teague, J.W., Thomas, G., Valencia, A., Yoshida, T., Kennedy, K.L., Axton, M., Dyke, S.O., Futreal, P.A., Gerhard, D.S., Gunter, C., Guyer, M., Hudson, T.J., McPherson, J.D., Miller, L.J., Ozenberger, B., Shaw, K.M., Kasprzyk, A., Stein, L.D., Zhang, J., Haider, S.A., Wang, J., Yung, C.K., Cros, A., Liang, Y., Gnaneshan, S., Guberman, J., Hsu, J., Bobrow, M., Chalmers, D.R., Hasel, K.W., Joly, Y., Kaan, T.S., Kennedy, K.L., Knoppers, B.M., Lowrance, W.W., Masui, T., Nicolas, P., Rial-

- Sebbag, E., Rodriguez, L.L., Vergely, C., Yoshida, T., Grimmond, S.M., Biankin, A.V., Bowtell, D.D., Cloonan, N., deFazio, A., Eshleman, J.R., Etemadmoghadam, D., Gardiner, B.B., Kench, J.G., Scarpa, A., Sutherland, R.L., Tempero, M.A., Waddell, N.J., Wilson, P.J., McPherson, J.D., Gallinger, S., Tsao, M.S., Shaw, P.A., Petersen, G.M., Mukhopadhyay, D., Chin, L., DePinho, R.A., Thayer, S., Muthuswamy, L., Shazand, K., Beck, T., Sam, M., Timms, L., Ballin, V., Lu, Y., Ji, J., Zhang, X., Chen, F., Hu, X., Zhou, G., Yang, Q., Tian, G., Zhang, L., Xing, X., Li, X., Zhu, Z., Yu, Y., Yu, J., Yang, H., Lathrop, M., Tost, J., Brennan, P., Holcatova, I., Zaridze, D., Brazma, A., Egevard, L., Prokhortchouk, E., Banks, R.E., Uhlen, M., Cambon-Thomsen, A., Viksna, J., Ponten, F., Skryabin, K., Stratton, M.R., Futreal, P.A., Birney, E., Borg, A., Børesen-Dale, A.L., Caldas, C., Foekens, J.A., Martin, S., Reis-Filho, J.S., Richardson, A.L., Sotiriou, C., Stunnenberg, H.G., Thoms, G., van de Vijver, M., van't Veer, L., Calvo, F., Birnbaum, D., Blanche, H., Boucher, P., Boyault, S., Chabannon, C., Gut, I., Masson-Jacquemier, J.D., Lathrop, M., Pauporté, I., Pivot, X., Vincent-Salomon, A., Tabone, E., Theillet, C., Thomas, G., Tost, J., Treilleux, I., Calvo, F., Bioulac-Sage, P., Clément, B., Decaens, T., Degos, F., Franco, D., Gut, I., Gut, M., Heath, S., Lathrop, M., Samuel, D., Thomas, G., Zucman-Rossi, J., Lichter, P., Eils, R., Brors, B., Korbel, J.O., Korshunov, A., Landgraf, P., Lehrach, H., Pfister, S., Radlwimmer, B., Reifemberger, G., Taylor, M.D., von Kalle, C., Majumder, P.P., Sarin, R., Rao, T.S., Bhan, M.K., Scarpa, A., Pederzoli, P., Lawlor, R.A., Delledonne, M., Bardelli, A., Biankin, A.V., Grimmond, S.M., Gress, T., Klimstra, D., Zamboni, G., Shibata, T., Nakamura, Y., Nakagawa, H., Kusada, J., Tsunoda, T., Miyano, S., Aburatani, H., Kato, K., Fujimoto, A., Yoshida, T., Campo, E., López-Otín, C., Estivill, X., Guigó, R., de Sanjosé, S., Piris, M.A., Montserrat, E., González-Díaz, M., Puente, X.S., Jares, P., Valencia, A., Himmelbauer, H., Quesada, V., Bea, S., Stratton, M.R., Futreal, P.A., Campbell, P.J., Vincent-Salomon, A., Richardson, A.L., Reis-Filho, J.S., van de Vijver, M., Thomas, G., Masson-Jacquemier, J.D., Aparicio, S., Borg, A., Børesen-Dale, A.L., Caldas, C., Foekens, J.A., Stunnenberg, H.G., van't Veer, L., Easton, D.F., Spellman, P.T., Martin, S., Barker, A.D., Chin, L., Collins, F.S., Compton, C.C., Ferguson, M.L., Gerhard, D.S., Getz, G., Gunter, C., Guttmacher, A., Guyer, M., Hayes, D.N., Lander, E.S., Ozenberger, B., Penny, R., Peterson, J., Sander, C., Shaw, K.M., Speed, T.P., Spellman, P.T., Vockley, J.G., Wheeler, D.A., Wilson, R.K., Hudson, T.J., Chin, L., Knoppers, B.M., Lander, E.S., Lichter, P., Stein, L.D., Stratton, M.R., Anderson, W., Barker, A.D., Bell, C., Bobrow, M., Burke, W., Collins, F.S., Compton, C.C., DePinho, R.A., Easton, D.F., Futreal, P.A., Gerhard, D.S., Green, A.R., Guyer, M., Hamilton, S.R., Hubbard, T.J., Kallioniemi, O.P., Kennedy, K.L., Ley, T.J., Liu, E.T., Lu, Y., Majumder, P., Marra, M., Ozenberger, B., Peterson, J., Schafer, A.J., Spellman, P.T., Stunnenberg, H.G., Wainwright, B.J., Wilson, R.K., & Yang, H. (2010). *International network of cancer genome projects*. *Nature*, 464(7291), 993–998. PMID: 20393554; PMCID: PMC2902243.
379. Green, R.E., Krause, J., Briggs, A.W., Maricic, T., Stenzel, U., Kircher, M., Patterson, N., Li, H., Zhai, W., Fritz, M.H., Hansen, N.F., Durand, E.Y., Malaspinas, A.S., Jensen, J.D., Marques-Bonet, T., Alkan, C., Prüfer, K., Meyer, M., Burbano, H.A., Good, J.M., Schultz, R., Aximu-Petri, A., Butthof, A., Höber, B., Höffner, B., Siegemund, M., Weihmann, A., Nusbaum, C., Lander, E.S., Russ, C., Novod, N., Affourtit, J., Egholm, M., Verna, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Doronichev, V.B., Golovanova, L.V., Lalueva-Fox, C., de la Rasilla, M., Fordea, J., Rosas, A., Schmitz, R.W., Johnson, P.L., Eichler, E.E., Falush, D., Birney, E., Mullikin, J.C., Slatkin, M., Nielsen, R., Kelso, J., Lachmann, M., Reich, D., & Pääbo, S. (2010). *A draft sequence of the Neandertal genome*. *Science*, 328(5979), 710–722. PMID: 20448178.
380. van Berkum, N.L., Lieberman-Aiden, E., Williams, L., Imakaev, M., Gnirke, A., Mirny, L.A., Dekker, J., & Lander, E.S. (2010). *Hi-C: a method to study the three-dimensional architecture of genomes*. *Journal of Visualized Experiments*, (39), e1869-e1869. PMID: 20461051; PMCID: PMC3149993.
381. Aiden, A.P., Rivera, M.N., Rheinbay, E., Ku, M., Coffman, E.J., Truong, T.T., Vargas, S.O., Lander, E.S., Haber, D.A., & Bernstein, B.E. (2010). *Wilms tumor chromatin profiles highlight stem cell properties and a renal developmental network*. *Cell Stem Cell*, 6(6), 591–602. PMID: 20569696; PMCID: PMC2897075.
382. Barretina, J., Taylor, B.S., Banerji, S., Ramos, A.H., Lagos-Quintana, M., Decarolis, P.L., Shah, K., Socci, N.D., Weir, B.A., Ho, A., Chiang, D.Y., Reva, B., Mermel, C.H., Getz, G., Antipin, Y., Beroukhi, R., Major, J.E., Hatton, C., Nicoletti, R., Hanna, M., Sharpe, T., Fennell, T.J., Cibulskis, K., Onofrio, R.C., Saito, T., Shukla, N., Lau, C., Nelander, S., Silver, S.J., Sougnez, C., Viale, A., Winckler, W., Maki, R.G., Garraway, L.A., Lash, A., Greulich, H., Root, D.E., Sellers, W.R., Schwartz, G.K., Antonescu, C.R., Lander, E.S., Varmus, H.E., Ladanyi,

- M., Sander, C., Meyerson, M., & Singer, S. (2010). *Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy*. *Nature Genetics*, 42(8), 715–721. PMID: 20601955; PMCID: PMC2911503.
383. Huarte, M., Guttman, M., Feldser, D., Garber, M., Koziol, M.J., Kenzelmann-Broz, D., Khalil, A.M., Zuk, O., Amit, I., Rabani, M., Attardi, L.D., Regev, A., Lander, E.S., Jacks, T., & Rinn, J.L. (2010). *A large intergenic noncoding RNA induced by p53 mediates global gene repression in the p53 response*. *Cell*, 142(3), 409–419. PMID: 20673990; PMCID: PMC2956184.
384. Taube, J.H., Herschkowitz, J.I., Komurov, K., Zhou, A.Y., Gupta, S., Yang, J., Hartwell, K., Onder, T.T., Gupta, P.B., Evans, K.W., Hollier, B.G., Ram, P.T., Lander, E.S., Rosen, J.M., Weinberg, R.A., & Mani, S.A. (2010). *Core epithelial-to-mesenchymal transition interactome gene-expression signature is associated with claudin-low and metaplastic breast cancer subtypes*. *Proceedings of the National Academy of Sciences USA*, 107(35), 15449–15454. PMID: 20713713; PMCID: PMC2932589.
385. Bernstein, B.E., Stamatoyannopoulos, J.A., Costello, J.F., Ren, B., Milosavljevic, A., Meissner, A., Kellis, M., Marra, M.A., Beaudet, A.L., Ecker, J.R., Farnham, P.J., Hirst, M., Lander, E.S., Mikkelsen, T.S., & Thomson, J.A. (2010). *The NIH roadmap epigenomics mapping consortium*. *Nature Biotechnology*, 28(10), 1045–1048. PMID: 20944595; PMCID: PMC3607281.
386. Mikkelsen, T.S., Xu, Z., Zhang, X., Wang, L., Gimble, J.M., Lander, E.S., & Rosen, E.D. (2010). *Comparative epigenomic analysis of murine and human adipogenesis*. *Cell*, 143(1), 156–169. PMID: 20887899; PMCID: PMC2950833.
387. Lander, E.S., & Gates, S.J. (2010). *Prepare and inspire*. *Science*, 330(6001), 151. PMID: 20929738.
388. Neafsey, D.E., Lawniczak, M.K., Park, D.J., Redmond, S.N., Coulibaly, M.B., Traoré, S.F., Sagnon, N., Costantini, C., Johnson, C., Wiegand, R.C., Collins, F.H., Lander, E.S., Wirth, D.F., Kafatos, F.C., Besansky, N.J., Christophides, G.K., & Muskavitch, M.A. (2010). *SNP genotyping defines complex gene-flow boundaries among African malaria vector mosquitoes*. *Science*, 330(6003), 514–517. PMID: 20966254; PMCID: PMC4811326.
389. Loewer, S., Cabili, M.N., Guttman, M., Loh, Y.H., Thomas, K., Park, I.H., Garber, M., Curran, M., Onder, T., Agarwal, S., Manos, P.D., Datta, S., Lander, E.S., Schlaeger, T.M., Daley, G.Q., & Rinn, J.L. (2010). *Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells*. *Nature Genetics*, 42(12), 1113–1117. PMID: 21057500; PMCID: PMC3040650.
390. Fillmore, C.M., Gupta, P.B., Rudnick, J.A., Caballero, S., Keller, P.J., Lander, E.S., & Kuperwasser, C. (2010). *Estrogen expands breast cancer stem-like cells through paracrine FGF/Tbx3 signaling*. *Proceedings of the National Academy of Sciences USA*, 107(50), 21737–21742. PMID: 21098263; PMCID: PMC3003123.
391. Gnerre, S., Maccallum, I., Przybylski, D., Ribeiro, F.J., Burton, J.N., Walker, B.J., Sharpe, T., Hall, G., Shea, T.P., Sykes, S., Berlin, A.M., Aird, D., Costello, M., Daza, R., Williams, L., Nicol, R., Gnirke, A., Nusbaum, C., Lander, E.S., & Jaffe, D.B. (2011). *High-quality draft assemblies of mammalian genomes from massively parallel sequence data*. *Proceedings of the National Academy of Sciences USA*, 108(4), 1513–1518. PMID: 21187386; PMCID: PMC3029755.
392. Robinson, J.T., Thorvaldsdóttir, H., Winckler, W., Guttman, M., Lander, E.S., Getz, G., & Mesirov, J.P. (2011). *Integrative genomics viewer*. *Nature Biotechnology*, 29(1), 24–26. PMID: 21221095; PMCID: PMC3346182.
393. Sankaran, V.G., Menne, T.F., Scepanovic, D., Vergilio, J.A., Ji, P., Kim, J., Thiru, P., Orkin, S.H., Lander, E.S., & Lodish H.F. (2011). *MicroRNA-15a and -16-1 act via MYB to elevate fetal hemoglobin expression in human trisomy 13*. *Proceedings of the National Academy of Sciences USA*, 108(4), 1519–1524. PMID: 21205891; PMCID: PMC3029749.
394. Mills, R.E., Walter, K., Stewart, C., Handsaker, R.E., Chen, K., Alkan, C., Abyzov, A., Yoon, S.C., Ye, K., Cheetham, R.K., Chinwalla, A., Conrad, D.F., Fu, Y., Grubert, F., Hajirasouliha, I., Hormozdiari, F., Iakoucheva, L.M., Iqbal, Z., Kang, S., Kidd, J.M., Konkel, M.K., Korn, J., Khurana, E., Kural, D., Lam, H.Y., Leng, J., Li, R., Li, Y., Lin, C.Y., Luo, R., Mu, X.J., Nemesh, J., Peckham, H.E., Rausch, T., Scally, A., Shi, X., Stromberg, M.P., Stütz, A.M., Urban, A.E., Walker, J.A., Wu, J., Zhang, Y., Zhang, Z.D., Batzer, M.A., Ding, L., Marth, G.T., McVean, G., Sebat, J., Snyder, M., Wang, J., Ye, K., Eichler, E.E., Gerstein, M.B., Hurles, M.E., Lee, C., McCarroll, S.A., Korb, J.O., & 1000 Genomes Project. (2011). *Mapping copy number variation by population-scale genome sequencing*. *Nature*, 470(7332), 59–65. PMID: 21293372; PMCID: PMC3077050.
395. Proia, T.A., Keller, P.J., Gupta, P.B., Klebba, I., Jones, A.D., Sedic, M., Gilmore, H., Tung, N., Nabar, S.P., Schnitt, S., Lander, E.S., & Kuperwasser, C. (2011).

Genetic predisposition directs breast cancer phenotype by dictating progenitor cell fate. Cell Stem Cell, 8(2), 149–163. PMID: 21295272; PMCID: PMC3050563.

396. Lander, E.S. (2011). *Initial impact of the sequencing of the human genome. Nature*, 470(7333), 187–197. PMID: 21307931.

397. Berger, M.F., Lawrence, M.S., Demichelis, F., Drier, Y., Cibulskis, K., Sivachenko, A.Y., Sboner, A., Esgueva, R., Pflueger, D., Sougnez, C., Onofrio, R., Carter, S.L., Park, K., Habegger, L., Ambrogio, L., Fennell, T., Parkin, M., Saksena, G., Voet, D., Ramos, A.H., Pugh, T.J., Wilkinson, J., Fisher, S., Winckler, W., Mahan, S., Ardlie, K., Baldwin, J., Simons, J.W., Kitabayashi, N., MacDonald, T.Y., Kantoff, P.W., Chin, L., Gabriel, S.B., Gerstein, M.B., Golub, T.R., Meyerson, M., Tewari, A., Lander, E.S., Getz, G., Rubin, M.A., & Garraway, L.A. (2011). *The genomic complexity of primary human prostate cancer. Nature*, 470(7333), 214–220. PMID: 21307934; PMCID: PMC3075885.

398. Reshef, D.N., Reshef, Y.A., Finucane, H.K., Grossman, S.R., McVean, G., Turnbaugh, P.J., Lander, E.S., Mitzenmacher, M., & Sabeti, P.C. (2011). *Detecting novel associations in large data sets. Science*, 334(6062), 1518–1524. PMID: 22174245; PMCID: PMC3325791.

399. Wang, L., Lawrence, M.S., Wan, Y., Stojanov, P., Sougnez, C., Stevenson, K., Werner, L., Sivachenko, A., DeLuca, D.S., Zhang, L., Zhang, W., Vartanov, A.R., Fernandes, S.M., Goldstein, N.R., Folco, E.G., Cibulskis, K., Tesar, B., Sievers, Q.L., Shefler, E., Gabriel, S., Hacohen, N., Reed, R., Meyerson, M., Golub, T.R., Lander, E.S., Neuber, D., Brown, J.R., Getz, G., & Wu, C.J. (2011). *SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. New England Journal of Medicine*, 365(26), 2497–2506. PMID: 22150006; PMCID: PMC3685413.

400. Lander, E.S. (2011). *Genome-sequence. The accelerator. Science* 331:1024.

401. Chapman, M.A., Lawrence, M.S., Keats, J.J., Cibulskis, K., Sougnez, C., Schinzel, A.C., Harview, C.L., Brunet, J.P., Ahmann, G.J., Adli, M., Anderson, K.C., Ardlie, K.G., Auclair, D., Baker, A., Bergsagel, P.L., Bernstein, B.E., Drier, Y., Fonseca, R., Gabriel, S.B., Hofmeister, C.C., Jagannath, S., Jakubowiak, A.J., Krishnan, A., Levy, J., Liefeld, T., Lonial, S., Mahan, S., Mfuko, B., Monti, S., Perkins, L.M., Onofrio, R., Pugh, T.J., Rajkumar, S.V., Ramos, A.H., Siegel, D.S., Sivachenko, A., Stewart, A.K., Trudel, S., Vij, R., Voet, D., Winckler, W., Zimmerman, T., Carpten, J., Trent, J., Hahn, W.C., Garraway, L.A., Meyerson, M., Lander, E.S., Getz, G., & Golub, T.R. (2011). *Initial genome sequencing and analysis of multiple myeloma. Nature*, 471(7339), 467–472. PMID: 21430775; PMCID: PMC3560292.

402. Van Tyne, D., Park, D.J., Schaffner, S.F., Neafsey, D.E., Angelino, E., Cortese, J.F., Barnes, K.G., Rosen, D.M., Lukens, A.K., Daniels, R.F., Milner, D.A., Johnson, C.A., Shlyakhter, I., Grossman, S.R., Becker, J.S., Yamins, D., Karlsson, E.K., Ndiaye, D., Sarr, O., Mboup, S., Hapli, C., Furlotte, N.A., Eskin, E., Kang, H.M., Hartl, D.L., Birren, B.W., Wiegand, R.C., Lander, E.S., Wirth, D.F., Volkman, S.K., & Sabeti, P.C. (2011). *Identification and functional validation of the novel anti-malarial resistance locus PF10_0355 in Plasmodium falciparum. PLoS Genetics*, 7(4), e1001383. PMID: 21533027; PMCID: PMC3080868.

403. Conrad, D.F., Keebler, J.E., DePristo, M.A., Lindsay, S.J., Zhang, Y., Casals, F., Idaghdour, Y., Hartl, C.L., Torroja, C., Garimella, K.V., Zilvermit, M., Cartwright, R., Rouleau, G.A., Daly, M., Stone, E.A., Hurles, M.E., Awadalla, P., & 1000 Genomes Project. (2011). *Variation in genome-wide mutation rates within and between human families. Nature Genetics*, 43(7), 712–714. PMID: 21666693; PMCID: PMC3322360.

404. Cheung, H.W., Cowley, G.S., Weir, B.A., Boehm, J.S., Rusin, S., Scott, J.A., East, A., Ali, L.D., Lizotte, P.H., Wong, T.C., Jiang, G., Hsiao, J., Mermel, C.H., Getz, G., Barretina, J., Gopal, S., Tamayo, P., Gould, J., Tsherniak, A., Stransky, N., Luo, B., Ren, Y., Drapkin, R., Bhatia, S.N., Mesirov, J.P., Garraway, L.A., Meyerson, M., Lander, E.S., Root, D.E., & Hahn, W.C. (2011). *Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. Proceedings of the National Academy of Sciences USA*, 108(30), 12372–12377. PMID: 21746896; PMCID: PMC3145679.

405. Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., McVean, G., Durbin, R., & 1000 Genomes Project Analysis Group. (2011). *The variant call format and VCFtools. Bioinformatics*, 27(15), 2156–2158. PMID: 21653522; PMCID: PMC3137218.

406. Gupta, P.B., Fillmore, C.M., Jiang, G., Shapira, S.D., Tao, K., Kuperwasser, C., & Lander, E.S. (2011). *Stochastic state transitions give rise to phenotypic equilibrium in populations of cancer cells. Cell*, 146(4), 633–644. PMID: 21854987.

407. Stransky, N., Egloff, A.M., Tward, A.D., Kostic, A.D., Cibulskis, K., Sivachenko, A., Kryukov, G.V., Lawrence, M.S., Sougnez, C., McKenna, A., Shefler, E., Ramos, A.H., Stojanov, P., Carter, S.L., Voet, D., Cortés, M.L., Auclair, D.,

- Berger, M.F., Saksena, G., Guiducci, C., Onofrio, R.C., Parkin, M., Romkes, M., Weissfeld, J.L., Seethala, R.R., Wang, L., Rangel-Escareño, C., Fernandez-Lopez, J.C., Hidalgo-Miranda, A., Melendez-Zajgla, J., Winckler, W., Ardlie, K., Gabriel, S.B., Meyerson, M., Lander, E.S., Getz, G., Golub, T.R., Garraway, L.A., & Grandis, J.R. (2011). *The mutational landscape of head and neck squamous cell carcinoma*. *Science*, 333(6046), 1157–1160. PMID: 21798893; PMCID: PMC3415217.
408. Guttman, M., Donaghey, J., Carey, B.W., Garber, M., Grenier, J.K., Munson, G., Young, G., Lucas, A.B., Ach, R., Bruhn, L., Yang, X., Amit, I., Meissner, A., Regev, A., Rinn, J.L., Root, D.E., & Lander, E.S. (2011). *lincRNAs act in the circuitry controlling pluripotency and differentiation*. *Nature*, 477(7364), 295–300. PMID: 21874018; PMCID: PMC3175327.
409. Alföldi, J., Di Palma, F., Grabherr, M., Williams, C., Kong, L., Mauceli, E., Russell, P., Lowe, C.B., Glor, R.E., Jaffe, J.D., Ray, D.A., Boissinot, S., Shedlock, A.M., Botka, C., Castoe, T.A., Colbourne, J.K., Fujita, M.K., Moreno, R.G., ten Hallers, B.F., Haussler, D., Heger, A., Heiman, D., Janes, D.E., Johnson, J., de Jong, P.J., Koriabine, M.Y., Lara, M., Novick, P.A., Organ, C.L., Peach, S.E., Poe, S., Pollock, D.D., de Queiroz, K., Sanger, T., Searle, S., Smith, J.D., Smith, Z., Swofford, R., Turner-Maier, J., Wade, J., Young, S., Zadissa, A., Edwards, S.V., Glenn, T.C., Schneider, C.J., Losos, J.B., Lander, E.S., Breen, M., Ponting, C.P., & Lindblad-Toh, K. (2011). *The genome of the green anole lizard and a comparative analysis with birds and mammals*. *Nature*, 477(7366), 587–591. PMID: 21881562; PMCID: PMC3184186.
410. Bass, A.J., Lawrence, M.S., Brace, L.E., Ramos, A.H., Drier, Y., Cibulskis, K., Sougnez, C., Voet, D., Saksena, G., Sivachenko, A., Jing, R., Parkin, M., Pugh, T., Verhaak, R.G., Stransky, N., Boutin, A.T., Barretina, J., Solit, D.B., Vakiani, E., Shao, W., Mishina, Y., Warmuth, M., Jimenez, J., Chiang, D.Y., Signoretti, S., Kaelin, W.G., Spardy, N., Hahn, W.C., Hoshida, Y., Ogino, S., Depinho, R.A., Chin, L., Garraway, L.A., Fuchs, C.S., Baselga, J., Tabernero, J., Gabriel, S., Lander, E.S., Getz, G., & Meyerson, M. (2011). *Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion*. *Nature Genetics*, 43(10), 964–968. PMID: 21892161; PMCID: PMC3802528.
411. Lindblad-Toh, K., Garber, M., Zuk, O., Lin, M.F., Parker, B.J., Washietl, S., Kheradpour, P., Ernst, J., Jordan, G., Mauceli, E., Ward, L.D., Lowe, C.B., Holloway, A.K., Clamp, M., Gnerre, S., Alföldi, J., Beal, K., Chang, J., Clawson, H., Cuff, J., Di Palma, F., Fitzgerald, S., Flicek, P., Guttman, M., Hubisz, M.J., Jaffe, D.B., Jungreis, I., Kent, W.J., Kostka, D., Lara, M., Martins, A.L., Massingham, T., Molke, I., Raney, B.J., Rasmussen, M.D., Robinson, J., Stark, A., Vilella, A.J., Wen, J., Xie, X., Zody, M.C., Broad Institute Sequencing Platform and Whole Genome Assembly Team, Baldwin, J., Bloom, T., Chin, C.W., Heiman, D., Nicol, R., Nusbaum, C., Young, S., Wilkinson, J., Worley, K.C., Kovar, C.L., Muzny, D.M., Gibbs, R.A., Baylor College of Medicine Human Genome Sequencing Center Sequencing Team, Cree, A., Dihn, H.H., Fowler, G., Jhangiani, S., Joshi, V., Lee, S., Lewis, L.R., Nazareth, L.V., Okwuonu, G., Santibanez, J., Warren, W.C., Mardis, E.R., Weinstock, G.M., Wilson, R.K., Genome Institute at Washington University, Delehaunty, K., Dooling, D., Fronik, C., Fulton, L., Fulton, B., Graves, T., Minx, P., Sodergren, E., Birney, E., Margulies, E.H., Herrero, J., Green, E.D., Haussler, D., Siepel, A., Goldman, N., Pollard, K.S., Pedersen, J.S., Lander, E.S., & Kellis, M. (2011). *A high-resolution map of human evolutionary constraint using 29 mammals*. *Nature*, 478(7370), 476–482. PMID: 21993624; PMCID: PMC3207357.
412. Zuk, O., Hechter, E., Sunyaev, S.R., & Lander, E.S. (2012). *The mystery of missing heritability: Genetic interactions create phantom heritability*. *Proceedings of the National Academy of Sciences USA*, 109(4), 1193–1198. PMID: 22223662; PMCID: PMC3268279.
413. Grad, Y.H., Lipsitch, M., Feldgarden, M., Arachchi, H.M., Cerqueira, G.C., Fitzgerald, M., Godfrey, P., Haas, B.J., Murphy, C.I., Russ, C., Sykes, S., Walker, B.J., Wortman, J.R., Young, S., Zeng, Q., Abouelleil, A., Bochicchio, J., Chauvin, S., Desmet, T., Gujja, S., McCowan, C., Montmayeur, A., Steelman, S., Frimodt-Møller, J., Petersen, A.M., Struve, C., Krogfelt, K.A., Bingen, E., Weill, F.X., Lander, E.S., Nusbaum, C., Birren, B.W., Hung, D.T., & Hanage, W.P. (2012). *Genomic epidemiology of the Escherichia coli O104: H4 outbreaks in Europe, 2011*. *Proceedings of the National Academy of Sciences USA*, 109(8), 3065–3070. PMID: 22315421; PMCID: PMC3286951.
414. Lohr, J.G., Stojanov, P., Lawrence, M.S., Auclair, D., Chapuy, B., Sougnez, C., Cruz-Gordillo, P., Knoechel, B., Asmann, Y.W., Slager, S.L., Novak, A.J., Dogan, A., Ansell, S.M., Link, B.K., Zou, L., Gould, J., Saksena, G., Stransky, N., Rangel-Escareño, C., Fernandez-Lopez, J.C., Hidalgo-Miranda, A., Melendez-Zajgla, J., Hernández-Lemus, E., Schwarz-Cruz y Celis, A., Imaz-Rosshandler, I., Ojesina, A.I., Jung, J., Peadarallu, C.S., Lander, E.S., Habermann, T.M., Cerhan, J.R., Shipp,

- M.A., Getz, G., & Golub, T.R. (2012). *Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. Proceedings of the National Academy of Sciences USA*, 109(10), 3879–3884. PMID: 22343534; PMCID: PMC3309757.
415. Melnikov, A., Murugan, A., Zhang, X., Tesileanu, T., Wang, L., Rogov, P., Feizi, S., Gnirke, A., Callan, C.G., Kinney, J.B., Kellis, M., Lander, E.S., & Mikkelsen, T.S. (2012). *Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. Nature Biotechnology*, 30(3), 271–277. PMID: 22371084; PMCID: PMC3297981.
416. Onder, T.T., Kara, N., Cherry, A., Sinha, A.U., Zhu, N., Bernt, K.M., Cahan, P., Marcarci, B.O., Unternaehrer, J., Gupta, P.B., Lander, E.S., Armstrong, S.A., & Daley, G.Q. (2012). *Chromatin-modifying enzymes as modulators of reprogramming. Nature*, 483(7391), 598–602. PMID: 22388813; PMCID: PMC3501145.
417. Jones, F.C., Grabherr, M.G., Chan, Y.F., Russell, P., Mauceli, E., Johnson, J., Swofford, R., Pirun, M., Zody, M.C., White, S., Birney, E., Searle, S., Schmutz, J., Grimwood, J., Dickson, M.C., Myers, R.M., Miller, C.T., Summers, B.R., Knecht, A.K., Brady, S.D., Zhang, H., Pollen, A.A., Howes, T., Amemiya, C., Broad Institute Genome Sequencing Platform & Whole Genome Assembly Team, Baldwin, J., Bloom, T., Jaffe, D.B., Nicol, R., Wilkinson, J., Lander, E.S., Di Palma, F., Lindblad-Toh, K., & Kingsley, D.M. (2012). *The genomic basis of adaptive evolution in threespine sticklebacks. Nature*, 484(7392), 55–61. PMID: 22481358; PMCID: PMC3322419.
418. Cancer Genome Atlas Research Network. (2012). *Comprehensive genomic characterization of squamous cell lung cancers. Nature*, 489(7417), 519–525. PMID: 22960745; PMCID: PMC3466113.
419. Carter, S.L., Cibulskis, K., Helman, E., McKenna, A., Shen, H., Zack, T., Laird, P.W., Onofrio, R.C., Winckler, W., Weir, B.A., Beroukhi, R., Pellman, D., Levine, D.A., Lander, E.S., Meyerson, M., & Getz, G. (2012). *Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology*, 30(5), 413–421. PMID: 22544022; PMCID: PMC4383288.
420. Berger, M.F., Hodis, E., Heffernan, T.P., Deribe, Y.L., Lawrence, M.S., Protopopov, A., Ivanova, E., Watson, I.R., Nickerson, E., Ghosh, P., Zhang, H., Zeid, R., Ren, X., Cibulskis, K., Sivachenko, A.Y., Wagle, N., Sucker, A., Sougnez, C., Onofrio, R., Ambrogio, L., Auclair, D., Fennell, T., Carter, S.L., Drier, Y., Stojanov, P., Singer, M.A., Voet, D., Jing, R., Saksena, G., Barretina, J., Ramos, A.H., Pugh, T.J., Stransky, N., Parkin, M., Winckler, W., Mahan, S., Ardlie, K., Baldwin, J., Wargo, J., Schadendorf, D., Meyerson, M., Gabriel, S.B., Golub, T.R., Wagner, S.N., Lander, E.S., Getz, G., Chin, L., & Garraway, L.A. (2012). *Melanoma genome sequencing reveals frequent PREX2 mutations. Nature*, 485(7399), 502–506. PMID: 22622578; PMCID: PMC3367798.
421. Germain, A.R., Carmody, L.C., Morgan, B., Fernandez, C., Forbeck, E., Lewis, T.A., Nag, P.P., Ting, A., VerPlank, L., Feng, Y., Perez, J.R., Dandapani, S., Palmer, M., Lander, E.S., Gupta, P.B., Schreiber, S.L., & Munoz, B. (2012). *Identification of a selective small molecule inhibitor of breast cancer stem cells. Bioorganic & Medicinal Chemistry Letters*, 22(10), 3571–3574. PMID: 22503247.
422. Barbieri, C.E., Baca, S.C., Lawrence, M.S., Demichelis, F., Blattner, M., Theurillat, J.P., White, T.A., Stojanov, P., Van Allen, E., Stransky, N., Nickerson, E., Chae, S.S., Boysen, G., Auclair, D., Onofrio, R.C., Park, K., Kitabayashi, N., MacDonald, T.Y., Sheikh, K., Vuong, T., Guiducci, C., Cibulskis, K., Sivachenko, A., Carter, S.L., Saksena, G., Voet, D., Hussain, W.M., Ramos, A.H., Winckler, W., Redman, M.C., Ardlie, K., Tewari, A.K., Mosquera, J.M., Rupp, N., Wild, P.J., Moch, H., Morrissey, C., Nelson, P.S., Kantoff, P.W., Gabriel, S.B., Golub, T.R., Meyerson, M., Lander, E.S., Getz, G., Rubin, M.A., & Garraway, L.A. (2012). *Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics*, 44(6), 685–689. PMID: 22610119; PMCID: PMC3673022.
423. Banerji, S., Cibulskis, K., Rangel-Escareno, C., Brown, K.K., Carter, S.L., Frederick, A.M., Lawrence, M.S., Sivachenko, A.Y., Sougnez, C., Zou, L., Cortes, M.L., Fernandez-Lopez, J.C., Peng, S., Ardlie, K.G., Auclair, D., Bautista-Piña, V., Duke, F., Francis, J., Jung, J., Maffuz-Aziz, A., Onofrio, R.C., Parkin, M., Pho, N.H., Quintanar-Jurado, V., Ramos, A.H., Rebollar-Vega, R., Rodriguez-Cuevas, S., Romero-Cordoba, S.L., Schumacher, S.E., Stransky, N., Thompson, K.M., Uribe-Figueroa, L., Baselga, J., Beroukhi, R., Polyak, K., Sgroi, D.C., Richardson, A.L., Jimenez-Sanchez, G., Lander, E.S., Gabriel, S.B., Garraway, L.A., Golub, T.R., Melendez-Zajgla, J., Toker, A., Getz, G., Hidalgo-Miranda, A., & Meyerson, M. (2012). *Sequence analysis of mutations and translocations across breast cancer subtypes. Nature*, 486(7403), 405–409. PMID: 22722202; PMCID: PMC4148686.
424. Sankaran, V.G., Ghazvinian, R., Do, R., Thiru, P., Vergilio, J.A., Beggs, A.H., Sieff, C.A., Orkin, S.H., Nathan, D.G., Lander, E.S., & Gazda, H.T. (2012). *Exome*

sequencing identifies GATA1 mutations resulting in Diamond-Blackfan anemia. *The Journal of Clinical Investigation*, 122(7), 2439–2443. PMID: 22706301; PMCID: PMC3386831.

425. Hodis, E., Watson, I.R., Kryukov, G.V., Arold, S.T., Imielinski, M., Theurillat, J.P., Nickerson, E., Auclair, D., Li, L., Place, C., Dicara, D., Ramos, A.H., Lawrence, M.S., Cibulskis, K., Sivachenko, A., Voet, D., Saksena, G., Stransky, N., Onofrio, R.C., Winckler, W., Ardlie, K., Wagle, N., Wargo, J., Chong, K., Morton, D.L., Stemke-Hale, K., Chen, G., Noble, M., Meyerson, M., Ladbury, J.E., Davies, M.A., Gershenwald, J.E., Wagner, S.N., Hoon, D.S., Schadendorf, D., Lander, E.S., Gabriel, S.B., Getz, G., Garraway, L.A., & Chin, L. (2012). A landscape of driver mutations in melanoma. *Cell*, 150(2), 251–263. PMID: 22817889; PMCID: PMC3600117.

426. Imielinski, M., Berger, A.H., Hammerman, P.S., Hernandez, B., Pugh, T.J., Hodis, E., Cho, J., Suh, J., Capelletti, M., Sivachenko, A., Sougnez, C., Auclair, D., Lawrence, M.S., Stojanov, P., Cibulskis, K., Choi, K., de Waal, L., Sharifnia, T., Brooks, A., Greulich, H., Banerji, S., Zander, T., Seidel, D., Leenders, F., Ansén, S., Ludwig, C., Engel-Riedel, W., Stoelben, E., Wolf, J., Goparaju, C., Thompson, K., Winckler, W., Kwiatkowski, D., Johnson, B.E., Jänne, P.A., Miller, V.A., Pao, W., Travis, W.D., Pass, H.I., Gabriel, S.B., Lander, E.S., Thomas, R.K., Garraway, L.A., Getz, G., & Meyerson, M. (2012). Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. *Cell*, 150(6), 1107–1120. PMID: 22980975; PMCID: PMC3557932.

427. Sankaran, V.G., Ludwig, L.S., Sicinska, E., Xu, J., Bauer, D.E., Eng, J.C., Patterson, H.C., Metcalf, R.A., Natkunam, Y., Orkin, S.H., Sicinski, P., Lander, E.S., & Lodish, H.F. (2012). Cyclin D3 coordinates the cell cycle during differentiation to regulate erythrocyte size and number. *Genes & Development*, 26(18), 2075–2087. PMID: 22929040; PMCID: PMC3444733.

428. Gire, S.K., Stremlau, M., Andersen, K.G., Schaffner, S.F., Bjornson, Z., Rubins, K., Hensley, L., McCormick, J.B., Lander, E.S., Garry, R.F., Hapoi, C., & Sabeti, P.C. (2012). *Epidemiology. Emerging disease or diagnosis?* *Science*, 338(6108), 750–752. PMID: 23139320.

429. Drier, Y., Lawrence, M.S., Carter, S.L., Stewart, C., Gabriel, S.B., Lander, E.S., Meyerson, M., Beroukheim, R., & Getz, G. (2013). Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. *Genome Research*, 23(2), 228–235. PMID: 23124520; PMCID: PMC3561864.

430. Pugh, T.J., Morozova, O., Attiyeh, E.F., Asgharzadeh, S., Wei, J.S., Auclair, D.D., Carter, S.L., Cibulskis, K., Hanna, M., Kiezun, A., Kim, J., Lawrence, M.S., Lichtenstein, L., McKenna, A., Peadarallu, C.S., Ramos, A.H., Shefler, E., Sivachenko, A., Sougnez, C., Stewart, C., Ally, A., Birol, I., Chiu, R., Corbett, R.D., Hirst, M., Jackman, S.D., Kamoh, B., Khodabakshi, A.H., Krzywinski, M., Lo, A., Moore, R.A., Mungall, K.L., Qian, J., Tam, A., Thiessen, N., Zhao, Y., Cole, K.A., Diamond, M., Diskin, S.J., Mosse, Y.P., Wood, A.C., Ji, L., Spoto, R., Badgett, T., London, W.B., Moyer, Y., Gastier-Foster, J.M., Smith, M.A., Auvil, J.M., Gerhard, D.S., Hogarty, M.D., Jones, S.J., Lander, E.S., Gabriel, S.B., Getz, G., Seeger, R.C., Khan, J., Marra, M.A., Meyerson, M., & Maris, J.M. (2013). The genetic landscape of high-risk neuroblastoma. *Nature Genetics*, 45(3), 279–284. PMID: 23334666; PMCID: PMC3682833.

431. Costello, M., Pugh, T.J., Fennell, T.J., Stewart, C., Lichtenstein, L., Meldrim, J.C., Fostel, J.L., Friedrich, D.C., Perrin, D., Dionne, D., Kim, S., Gabriel, S.B., Lander, E.S., Fisher, S., & Getz, G. (2013). Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. *Nucleic Acids Research*, 41(6), e67. PMID: 23303777; PMCID: PMC3616734.

432. Drier, Y., Lawrence, M.S., Carter, S.L., Stewart, C., Gabriel, S.B., Lander, E.S., Meyerson, M., Beroukheim, R., & Getz, G. (2013). Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. *Genome Research*, 23(2), 228–235. PMID: 23124520; PMCID: PMC3561864.

433. Engreitz, J.M., Pandya-Jones, A., McDonel, P., Shishkin, A., Sirokman, K., Surka, C., Kadri, S., Xing, J., Goren, A., Lander, E.S., Plath, K., & Guttman, M. (2013). The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. *Science*, 341(6147), 1237973. PMID: 23828888; PMCID: PMC3778663.

434. Cibulskis, K., Lawrence, M.S., Carter, S.L., Sivachenko, A., Jaffe, D., Sougnez, C., Gabriel, S., Meyerson, M., Lander, E.S., & Getz, G. (2013). Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nature Biotechnology*, 31(3), 213–219. PMID: 23396013; PMCID: PMC3833702.

435. Grossman, S.R., Andersen, K.G., Shlyakhter, I., Tabrizi, S., Winnicki, S., Yen, A., Park, D.J., Griesemer, D., Karlsson, E.K., Wong, S.H., Cabili, M., Adegbola, R.A., Bamezai, R.N., Hill, A.V., Vannberg, F.O., Rinn, J.L., 1000 Genomes Project, Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2013). *Identifying recent adaptations in large-scale genomic data*. *Cell*, 152(4), 703–713. PMID: 23415221; PMCID: PMC3674781.
436. Cancer Genome Atlas Research Network. (2013). *Comprehensive molecular characterization of clear cell renal cell carcinoma*. *Nature*, 499(7456), 43–49. PMID: 23792563; PMCID: PMC3771322.
437. Gifford, C.A., Ziller, M.J., Gu, H., Trapnell, C., Donaghey, J., Tsankov, A., Shalek, A.K., Kelley, D.R., Shishkin, A.A., Issner, R., Zhang, X., Coyne, M., Fostel, J.L., Holmes, L., Meldrim, J., Guttman, M., Epstein, C., Park, H., Kohlbacher, O., Rinn, J., Gnirke, A., Lander, E.S., Bernstein, B.E., & Meissner, A. (2013). *Transcriptional and epigenetic dynamics during specification of human embryonic stem cells*. *Cell*, 153(5), 1149–1163. PMID: 23664763; PMCID: PMC3709577.
438. Dulak, A.M., Stojanov, P., Peng, S., Lawrence, M.S., Fox, C., Stewart, C., Bandla, S., Imamura, Y., Schumacher, S.E., Shefler, E., McKenna, A., Carter, S.L., Cibulskis, K., Sivachenko, A., Saksena, G., Voet, D., Ramos, A.H., Auclair, D., Thompson, K., Sougnez, C., Onofrio, R.C., Guiducci, C., Beroukhi, R., Zhou, Z., Lin, L., Lin, J., Reddy, R., Chang, A., Landrenau, R., Pennathur, A., Ogino, S., Luketich, J.D., Golub, T.R., Gabriel, S.B., Lander, E.S., Beer, D.G., Godfrey, T.E., Getz, G., & Bass, A.J. (2013). *Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity*. *Nature Genetics*, 45(5), 478–486. PMID: 23525077; PMCID: PMC3678719.
439. Baca, S.C., Prandi, D., Lawrence, M.S., Mosquera, J.M., Romanel, A., Drier, Y., Park, K., Kitabayashi, N., MacDonald, T.Y., Ghandi, M., Van Allen, E., Kryukov, G.V., Sboner, A., Theurillat, J.P., Soong, T.D., Nickerson, E., Auclair, D., Tewari, A., Beltran, H., Onofrio, R.C., Boysen, G., Guiducci, C., Barbieri, C.E., Cibulskis, K., Sivachenko, A., Carter, S.L., Saksena, G., Voet, D., Ramos, A.H., Winckler, W., Cipicchio, M., Ardlie, K., Kantoff, P.W., Berger, M.F., Gabriel, S.B., Golub, T.R., Meyerson, M., Lander, E.S., Elemento, O., Getz, G., Demicheli, F., Rubin, M.A., & Garraway, L.A. (2013). *Punctuated evolution of prostate cancer genomes*. *Cell*, 153(3), 666–677. PMID: 23622249; PMCID: PMC3690918.
440. Garraway, L.A., & Lander, E.S. (2013). *Lessons from the cancer genome*. *Cell*, 153(1), 17–37. PMID: 23540688.
441. Germain, A.R., Carmody, L.C., Nag, P.P., Morgan, B., Verplank, L., Fernandez, C., Donckele, E., Feng, Y., Perez, J.R., Dandapani, S., Palmer, M., Lander, E.S., Gupta, P.B., Schreiber, S.L., & Munoz, B. (2013). *Cinnamides as selective small-molecule inhibitors of a cellular model of breast cancer stem cells*. *Bioorganic & Medicinal Chemistry Letters*, 23(6), 1834–1838. PMID: 23403082.
442. Kirby, A., Gnirke, A., Jaffe, D.B., Barešová, V., Pochet, N., Blumenstiel, B., Ye, C., Aird, D., Stevens, C., Robinson, J.T., Cabili, M.N., Gat-Viks, I., Kelliher, E., Daza, R., DeFelice, M., Hůlková, H., Sovová, J., Vylet'al, P., Antignac, C., Guttman, M., Handsaker, R.E., Perrin, D., Steelman, S., Sigurdsson, S., Scheinman, S.J., Sougnez, C., Cibulskis, K., Parkin, M., Green, T., Rossin, E., Zody, M.C., Xavier, R.J., Pollak, M.R., Alper, S.L., Lindblad-Toh, K., Gabriel, S., Hart, P.S., Regev, A., Nusbaum, C., Knoch, S., Bleyer, A.J., Lander, E.S., & Daly, M.J. (2013). *Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing*. *Nature Genetics*, 45(3), 299–303. PMID: 23396133; PMCID: PMC3901305.
443. Landau, D.A., Carter, S.L., Stojanov, P., McKenna, A., Stevenson, K., Lawrence, M.S., Sougnez, C., Stewart, C., Sivachenko, A., Wang, L., Wan, Y., Zhang, W., Shukla, S.A., Vartanov, A., Fernandes, S.M., Saksena, G., Cibulskis, K., Tesar, B., Gabriel, S., Hacohen, N., Meyerson, M., Lander, E.S., Neuberg, D., Brown, J.R., Getz, G., & Wu, C.J. (2013). *Evolution and impact of subclonal mutations in chronic lymphocytic leukemia*. *Cell*, 152(4), 714–726. PMID: 23415222; PMCID: PMC3575604.
444. Guttman, M., Russell, P., Ingolia, N.T., Weissman, J.S., & Lander, E.S. (2013). *Ribosome profiling provides evidence that large noncoding RNAs do not encode proteins*. *Cell*, 154(1), 240–251. PMID: 23810193; PMCID: PMC3756563.
445. Hacohen, N., Fritsch, E.F., Carter, T.A., Lander, E.S., & Wu, C.J. (2013). *Getting personal with neoantigen-based therapeutic cancer vaccines*. *Cancer Immunology Research*, 1(1), 11–15. PMID: 24777245; PMCID: PMC4033902.
446. Lawrence, M.S., Stojanov, P., Polak, P., Kryukov, G.V., Cibulskis, K., Sivachenko, A., Carter, S.L., Stewart, C., Mermel, C.H., Roberts, S.A., Kiezun, A., Hammerman, P.S., McKenna, A., Drier, Y., Zou, L., Ramos, A.H., Pugh, T.J., Stransky, N., Helman, E., Kim, J., Sougnez, C., Ambrogio, L., Nickerson, E., Shefler, E., Cortes, M.L., Auclair, D., Saksena, G., Voet, D., Noble, M., DiCara, D., Lin, P.,

- Lichtenstein, L., Heiman, D.I., Fennell, T., Imielinski, M., Hernandez, B., Hodis, E., Baca, S., Dulak, A.M., Lohr, J., Landau, D.A., Wu, C.J., Melendez-Zajgla, J., Hidalgo-Miranda, A., Koren, A., McCarroll, S.A., Mora, J., Lee, R.S., Crompton, B., Onofrio, R., Parkin, M., Winckler, W., Ardlie, K., Gabriel, S.B., Roberts, C.W., Biegel, J.A., Stegmaier, K., Bass, A.J., Garraway, L.A., Meyerson, M., Golub, T.R., Gordenin, D.A., Sunyaev, S., Lander, E.S., & Getz, G. (2013). *Mutational heterogeneity in cancer and the search for new cancer-associated genes*. *Nature*, 499(7457), 214–218. PMID: 23770567; PMCID: PMC3919509.
447. Farhat, M.R., Shapiro, B.J., Kieser, K.J., Sultana, R., Jacobson, K.R., Victor, T.C., Warren, R.M., Streicher, E.M., Calver, A., Sloutsky, A., Kaur, D., Posey, J.E., Plikaytis, B., Oggioni, M.R., Gardy, J.L., Johnston, J.C., Rodrigues, M., Tang, P.K., Kato-Maeda, M., Borowsky, M.L., Muddukrishna, B., Kreiswirth, B.N., Kurepina, N., Galagan, J., Gagneux, S., Birren, B., Rubin, E.J., Lander, E.S., Sabeti, P.C., & Murray, M. (2013). *Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis*. *Nature Genetics*, 45(10), 1183–1189. PMID: 23995135; PMCID: PMC3887553.
448. Schwartz, S., Agarwala, S.D., Mumbach, M.R., Jovanovic, M., Mertins, P., Shishkin, A., Tabach, Y., Mikkelsen, T.S., Satija, R., Ruvkun, G., Carr, S.A., Lander, E.S., Fink, G.R., & Regev, A. (2013). *High-resolution mapping reveals a conserved, widespread, dynamic mRNA methylation program in yeast meiosis*. *Cell*, 155(6), 1409–1421. PMID: 24269006; PMCID: PMC3956118.
449. Karlsson, E.K., Sigurdsson, S., Ivansson, E., Thomas, R., Elvers, I., Wright, J., Howald, C., Tonomura, N., Perloski, M., Swofford, R., Biagi, T., Fryc, S., Anderson, N., Courtay-Cahen, C., Youell, L., Ricketts, S.L., Mandlebaum, S., Rivera, P., von Euler, H., Kisseberth, W.C., London, C.A., Lander, E.S., Couto, G., Comstock, K., Starkey, M.P., Modiano, J.F., Breen, M., & Lindblad-Toh, K. (2013). *Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B*. *Genome Biology*, 14(12), R132. PMID: 24330828; PMCID: PMC4053774.
450. Wang, T., Wei, J.J., Sabatini, D.M., & Lander, E.S. (2014). *Genetic screens in human cells using the CRISPR-Cas9 system*. *Science*, 343(6166), 80–84. PMID: 24336569; PMCID: PMC3972032.
451. Lawrence, M.S., Stojanov, P., Mermel, C.H., Robinson, J.T., Garraway, L.A., Golub, T.R., Meyerson, M., Gabriel, S.B., Lander, E.S., & Getz, G. (2014). *Discovery and saturation analysis of cancer genes across 21 tumour types*. *Nature*, 505(7484), 495–501. PMID: 24390350; PMCID: PMC4048962.
452. Zuk, O., Schaffner, S.F., Samocha, K., Do, R., Hechter, E., Kathiresan, S., Daly, M.J., Neale, B.M., Sunyaev, S.R., & Lander, E.S. (2014). *Searching for missing heritability: designing rare variant association studies*. *Proceedings of the National Academy of Sciences USA*, 111(4), E455–E464. PMID: 24443550; PMCID: PMC3910587.
453. Hacisuleyman, E., Goff, L.A., Trapnell, C., Williams, A., Henao-Mejia, J., Sun, L., McClanahan, P., Hendrickson, D.G., Sauvageau, M., Kelley, D.R., Morse, M., Engreitz, J., Lander, E.S., Guttman, M., Lodish, H.F., Flavell, R., Raj, A., & Rinn, J.L. (2014). *Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre*. *Nature Structural & Molecular Biology*, 21(2), 198–206. PMID: 24463464; PMCID: PMC3950333.
454. Purcell, S.M., Moran, J.L., Fromer, M., Ruderfer, D., Solovieff, N., Roussos, P., O'Dushlaine, C., Chambert, K., Bergen, S.E., Kähler, A., Duncan, L., Stahl, E., Genovese, G., Fernández, E., Collins, M.O., Komiyama, N.H., Choudhary, J.S., Magnusson, P.K., Banks, E., Shakir, K., Garimella, K., Fennell, T., DePristo, M., Grant, S.G., Haggarty, S.J., Gabriel, S., Scolnick, E.M., Lander, E.S., Hultman, C.M., Sullivan, P.F., McCarroll, S.A., & Sklar, P. (2014). *A polygenic burden of rare disruptive mutations in schizophrenia*. *Nature*, 506(7487), 185–190. PMID: 24463508; PMCID: PMC4136494.
455. Hoepfner, M.P., Lundquist, A., Pirun, M., Meadows, J.R., Zamani, N., Johnson, J., Sundström, G., Cook, A., FitzGerald, M.G., Swofford, R., Mauceli, E., Moghadam, B.T., Greka, A., Alföldi, J., Abouelleil, A., Aftuck, L., Bessette, D., Berlin, A., Brown, A., Gearin, G., Lui, A., Macdonald, J.P., Priest, M., Shea, T., Turner-Maier, J., Zimmer, A., Lander, E.S., di Palma, F., Lindblad-Toh, K., & Grubert, M.G. (2014). *An improved canine genome and a comprehensive catalogue of coding genes and non-coding transcripts*. *PloS One*, 9(3), e91172. PMID: 24625832; PMCID: PMC3953330.
456. Wagle, N., Grabiner, B.C., Van Allen, E.M., Hodis, E., Jacobus, S., Supko, J.G., Stewart, M., Choueiri, T.K., Gandhi, L., Cleary, J.M., Elfiky, A.A., Taplin, M.E., Stack, E.C., Signoretti, S., Loda, M., Shapiro, G.I., Sabatini, D.M., Lander, E.S., Gabriel, S.B., Kantoff, P.W., Garraway, L.A., & Rosenberg, J.E. (2014). *Activating mTOR mutations in a patient with an extraordinary response on a phase I*

- trial of everolimus and pazopanib. *Cancer Discovery*, 4(5), 546–553. PMID: 24625776; PMCID: PMC4122326.
457. Van Allen, E.M., Wagle, N., Stojanov, P., Perrin, D.L., Cibulskis, K., Marlow, S., Jane-Valbuena, J., Friedrich, D.C., Kryukov, G., Carter, S.L., McKenna, A., Sivachenko, A., Rosenberg, M., Kiezun, A., Voet, D., Lawrence, M., Lichtenstein, L.T., Gentry, J.G., Huang, F.W., Fostel, J., Farlow, D., Barbie, D., Gandhi, L., Lander, E.S., Gray, S.W., Joffe, S., Janne, P., Garber, J., MacConaill, L., Lindeman, N., Rollins, B., Kantoff, P., Fisher, S.A., Gabriel, S., Getz, G., & Garraway, L.A. (2014). Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. *Nature Medicine*, 20(6), 682–688. PMID: 24836576; PMCID: PMC4048335.
458. Cho, J., Bass, A.J., Lawrence, M.S., Cibulskis, K., Cho, A., Lee, S.N., Yamauchi, M., Wagle, N., Pochanard, P., Kim, N., Park, A.K., Won, J., Hur, H.S., Greulich, H., Ogino, S., Sougnez, C., Voet, D., Tabernero, J., Jimenez, J., Baselga, J., Gabriel, S.B., Lander, E.S., Getz, G., Eck, M.J., Park, W.Y., & Meyerson, M. (2014). Colon cancer-derived oncogenic *EGFR* G724S mutant identified by whole genome sequence analysis is dependent on asymmetric dimerization and sensitive to cetuximab. *Molecular Cancer*, 13, 141. PMID: 24894453; PMCID: PMC4072491.
459. Hsu, P.D., Lander, E.S., & Zhang, F. (2014). Development and applications of CRISPR-Cas9 for genome engineering. *Cell*, 157(6), 1262–1278. PMID: 24906146; PMCID: PMC4343198.
460. Wang, L., Shalek, A.K., Lawrence, M., Ding, R., Gaublot, J.T., Pochet, N., Stojanov, P., Sougnez, C., Shukla, S.A., Stevenson, K.E., Zhang, W., Wong, J., Sievers, Q.L., MacDonald, B.T., Vartanov, A.R., Goldstein, N.R., Neuberg, D., He, X., Lander, E.S., Hacohen, N., Regev, A., Getz, G., Brown, J.R., Park, H., & Wu, C.J. (2014). Somatic mutation as a mechanism of *Wnt/β-catenin* pathway activation in CLL. *Blood*, 124(7), 1089–1098. PMID: 24778153; PMCID: PMC4133483.
461. Rajasagi, M., Shukla, S.A., Fritsch, E.F., Keskin, D.B., DeLuca, D., Carmona, E., Zhang, W., Sougnez, C., Cibulskis, K., Sidney, J., Stevenson, K., Ritz, J., Neuberg, D., Brusic, V., Gabriel, S., Lander, E.S., Getz, G., Hacohen, N., & Wu, C.J. (2014). Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, 124(3), 453–462. PMID: 24891321; PMCID: PMC4102716.
462. Ludwig, L.S., Gazda, H.T., Eng, J.C., Eichhorn, S.W., Thiru, P., Ghazvinian, R., George, T.I., Gotlib, J.R., Beggs, A.H., Sieff, C.A., Lodish, H.F., Lander, E.S., & Sankaran, V.G. (2014). Altered translation of *GATA1* in Diamond-Blackfan anemia. *Nature Medicine*, 20(7), 748–753. PMID: 24952648; PMCID: PMC4087046.
463. Schwartz, S., Mumbach, M.R., Jovanovic, M., Wang, T., Maciag, K., Bushkin, G.G., Mertins, P., Ter-Ovanesyan, D., Habib, N., Cacchiarelli, D., Sanjana, N.E., Freinkman, E., Pacold, M.E., Satija, R., Mikkelsen, T.S., Hacohen, N., Zhang, F., Carr, S.A., Lander, E.S., & Regev, A. (2014). Perturbation of m6A writers reveals two distinct classes of mRNA methylation at internal and 5' sites. *Cell Reports*, 8(1), 284–296. PMID: 24981863; PMCID: PMC4142486.
464. Rajasagi, M., Shukla, S.A., Fritsch, E.F., Keskin, D.B., DeLuca, D., Carmona, E., Zhang, W., Sougnez, C., Cibulskis, K., Sidney, J., Stevenson, K., Ritz, J., Neuberg, D., Brusic, V., Gabriel, S., Lander, E.S., Getz, G., Hacohen, N., & Wu, C.J. (2014). Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, 124(3), 453–462. PMID: 24891321; PMCID: PMC4102716.
465. Carneiro, M., Rubin, C.J., Di Palma, F., Albert, F.W., Alföldi, J., Barrio, A.M., Pielberg, G., Rafati, N., Sayyab, S., Turner-Maier, J., Younis, S., Afonso, S., Aken, B., Alves, J.M., Barrell, D., Bolet, G., Boucher, S., Burbano, H.A., Campos, R., Chang, J.L., Duranthon, V., Fontanesi, L., Garreau, H., Heiman, D., Johnson, J., Mage, R.G., Peng, Z., Queney, G., Rogel-Gaillard, C., Ruffier, M., Searle, S., Villafuerte, R., Xiong, A., Young, S., Forsberg-Nilsson, K., Good, J.M., Lander, E.S., Ferrand, N., Lindblad-Toh, K., & Andersson, L. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. *Science*, 345(6200), 1074–1079. PMID: 25170157.
466. Gire, S.K., Goba, A., Andersen, K.G., Sealfon, R.S., Park, D.J., Kanneh, L., Jalloh, S., Momoh, M., Fullah, M., Dudas, G., Wohl, S., Moses, L.M., Yozwiak, N.L., Winnicki, S., Matranga, C.B., Malboeuf, C.M., Qu, J., Gladden, A.D., Schaffner, S.F., Yang, X., Jiang, P.P., Nekoui, M., Colubri, A., Coomber, M.R., Fonnie, M., Moigboi, A., Gbokie, M., Kamara, F.K., Tucker, V., Konuwa, E., Saffa, S., Sellu, J., Jalloh, A.A., Kovoma, A., Koninga, J., Mustapha, I., Kargbo, K., Foday, M., Yillah, M., Kanneh, F., Robert, W., Massally, J.L., Chapman, S.B., Bochicchio, J., Murphy, C., Nusbaum, C., Young, S., Birren, B.W., Grant, D.S., Scheffelin, J.S., Lander, E.S., Hapii, C., Geva, S.M., Gnirke, A., Rambaut, A., Garry, R.F., Khan, S.H., & Sabeti, P.C. (2014). Genomic surveillance elucidates Ebola virus origin and transmission

- during the 2014 outbreak. *Science*, 345(6202), 1369–1372. PMID: 25214632; PMCID: PMC4431643.
467. Brawand, D., Wagner, C.E., Li, Y.I., Malinsky, M., Keller, I., Fan, S., Simakov, O., Ng, A.Y., Lim, Z.W., Bezaul, E., Turner-Maier, J., Johnson, J., Alcazar, R., Noh, H.J., Russell, P., Aken, B., Alföldi, J., Amemiya, C., Azzouzi, N., Baroiller, J.F., Barloy-Hubler, F., Berlin, A., Bloomquist, R., Carleton, K.L., Conte, M.A., D'Cotta, H., Eshel, O., Gaffney, L., Galibert, F., Gante, H.F., Gnerre, S., Greuter, L., Guyon, R., Haddad, N.S., Haerty, W., Harris, R.M., Hofmann, H.A., Hourlier, T., Hulata, G., Jaffe, D.B., Lara, M., Lee, A.P., MacCallum, I., Mwaiko, S., Nikaido, M., Nishihara, H., Ozouf-Costaz, C., Penman, D.J., Przybylski, D., Rakotomanga, M., Renn, S.C., Ribeiro, F.J., Ron, M., Salzburger, W., Sanchez-Pulido, L., Santos, M.E., Searle, S., Sharpe, T., Swofford, R., Tan, F.J., Williams, L., Young, S., Yin, S., Okada, N., Kocher, T.D., Miska, E.A., Lander, E.S., Venkatesh, B., Fernald, R.D., Meyer, A., Ponting, C.P., Streelman, J.T., Lindblad-Toh, K., Seehausen, O., & Di Palma, F. (2014). *The genomic substrate for adaptive radiation in African cichlid fish*. *Nature*, 513(7518), 375–381. PMID: 25186727; PMCID: PMC4353498.
468. Schwartz, S., Bernstein, D.A., Mumbach, M.R., Jovanovic, M., Herbst, R.H., León-Ricardo, B.X., Engreitz, J.M., Guttman, M., Satija, R., Lander, E.S., Fink, G., & Regev, A. (2014). *Transcriptome-wide mapping reveals widespread dynamic-regulated pseudouridylation of ncRNA and mRNA*. *Cell*, 159(1), 148–162. PMID: 25219674; PMCID: PMC4180118.
469. Engreitz, J.M., Sirokman, K., McDonel, P., Shishkin, A.A., Surka, C., Russell, P., Grossman, S.R., Chow, A.Y., Guttman, M., & Lander, E.S. (2014). *RNA–RNA interactions enable specific targeting of noncoding RNAs to nascent Pre-mRNAs and chromatin sites*. *Cell*, 159(1), 188–199. PMID: 25259926; PMCID: PMC4177037.
470. Myocardial Infarction Genetics Consortium Investigators. (2014). *Inactivating mutations in NPC1L1 and protection from coronary heart disease*. *New England Journal of Medicine*, 371(22), 2072–2082. PMID: 25390462; PMCID: PMC4335708.
471. Weisenfeld, N.I., Yin, S., Sharpe, T., Lau, B., Hegarty, R., Holmes, L., Sogoloff, B., Tabbaa, D., Williams, L., Russ, C., Nusbaum, C., Lander, E.S., MacCallum, I., & Jaffe, D.B. (2014). *Comprehensive variation discovery in single human genomes*. *Nature Genetics*, 46(12), 1350–1355. PMID: 25326702; PMCID: PMC4244235.
472. Giannakis, M., Hodis, E., Jasmine Mu, X., Yamauchi, M., Rosenbluh, J., Cibulskis, K., Saksena, G., Lawrence, M.S., Qian, Z.R., Nishihara, R., Van Allen, E.M., Hahn, W.C., Gabriel, S.B., Lander, E.S., Getz, G., Ogino, S., Fuchs, C.S., & Garraway, L.A. (2014). *RNF43 is frequently mutated in colorectal and endometrial cancers*. *Nature Genetics*, 46(12), 1264–1266. PMID: 25344691; PMCID: PMC4283570.
473. Landau, D.A., Clement, K., Ziller, M.J., Boyle, P., Fan, J., Gu, H., Stevenson, K., Sougnez, C., Wang, L., Li, S., Kotliar, D., Zhang, W., Ghandi, M., Garraway, L., Fernandes, S.M., Livak, K.J., Gabriel, S., Gnirke, A., Lander, E.S., Brown, J.R., Neuberg, D., Kharchenko, P.V., Hacohen, N., Getz, G., Meissner, A., & Wu, C.J. (2014). *Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia*. *Cancer Cell*, 26(6), 813–825. PMID: 25490447; PMCID: PMC4302418.
474. Golan, D., Lander, E.S., & Rosset, S. (2014). *Measuring missing heritability: inferring the contribution of common variants*. *Proceedings of the National Academy of Sciences USA*, 111(49), E5272–E5281. PMID: 25422463; PMCID: PMC4267399.
475. Rao, S.S., Huntley, M.H., Durand, N.C., Stamenova, E.K., Bochkov, I.D., Robinson, J.T., Sanborn, A.L., Machol, I., Omer, A.D., Lander, E.S., & Aiden, E.L. (2014). *A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping*. *Cell*, 159(7), 1665–1680. PMID: 25497547.
476. Perry, J.A., Kiezun, A., Tonzi, P., Van Allen, E.M., Carter, S.L., Baca, S.C., Cowley, G.S., Bhatt, A.S., Rheinbay, E., Pedamallu, C.S., Helman, E., Taylor-Weiner, A., McKenna, A., DeLuca, D.S., Lawrence, M.S., Ambrogio, L., Sougnez, C., Sivachenko, A., Walensky, L.D., Wagle, N., Mora, J., de Torres, C., Lavarino, C., Dos Santos Aguiar, S., Yunes, J.A., Brandalise, S.R., Mercado-Celis, G.E., Melendez-Zajgla, J., Cárdenas-Cardós, R., Velasco-Hidalgo, L., Roberts, C.W., Garraway, L.A., Rodriguez-Galindo, C., Gabriel, S.B., Lander, E.S., Golub, T.R., Orkin, S.H., Getz, G., & Janeway, K.A. (2014). *Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma*. *Proceedings of the National Academy of Sciences USA*, 111(51), E5564–E5573. PMID: 25512523; PMCID: PMC4280630.
477. Genovese, G., Kähler, A.K., Handsaker, R.E., Lindberg, J., Rose, S.A., Bakhoum, S.F., Chambert, K., Mick, E., Neale, B.M., Fromer, M., Purcell, S.M., Svantesson, O., Landén, M., Höglund, M., Lehmann, S., Gabriel, S.B., Moran, J.L.,

Lander, E.S., Sullivan, P.F., Sklar, P., Grönberg, H., Hultman, C.M., & McCarroll, S.A. (2014). *Clonal hematopoiesis and blood-cancer risk inferred from blood DNA sequence*. *New England Journal of Medicine*, 371(26), 2477–2487. PMID: 25426838; PMCID: PMC4290021.

478. Delaneau, O., Marchini, J., & 1000 Genomes Project Consortium. (2014). *Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel*. *Nature Communications*, 5, 3934. PMID: 25653097; PMCID: PMC4338501.

479. Engreitz, J., Lander, E.S., & Guttman, M. (2015). *RNA antisense purification (RAP) for mapping RNA interactions with chromatin*. *Methods in Molecular Biology*, 1262, 183–197. PMID: 25555582.

480. Cancer Genome Atlas Research Network, Brat, D.J., Verhaak, R.G., Aldape, K.D., Yung, W.K., Salama, S.R., Cooper, L.A., Rheinbay, E., Miller, C.R., Vitucci, M., Morozova, O., Robertson, A.G., Nushmeh, H., Laird, P.W., Cherniack, A.D., Akbani, R., Huse, J.T., Ciriello, G., Poisson, L.M., Barnholtz-Sloan, J.S., Berger, M.S., Brennan, C., Colen, R.R., Colman, H., Flanders, A.E., Giannini, C., Grifford, M., Iavarone, A., Jain, R., Joseph, I., Kim, J., Kasaian, K., Mikkelsen, T., Murray, B.A., O'Neill, B.P., Pachter, L., Parsons, D.W., Sougnez, C., Sulman, E.P., Vandenberg, S.R., Van Meir, E.G., von Deimling, A., Zhang, H., Crain, D., Lau, K., Mallory, D., Morris, S., Paulauskis, J., Penny, R., Shelton, T., Sherman, M., Yena, P., Black, A., Bowen, J., Dicostanzo, K., Gastier-Foster, J., Leraas, K.M., Lichtenberg, T.M., Pierson, C.R., Ramirez, N.C., Taylor, C., Weaver, S., Wise, L., Zmuda, E., Davidson, T., Demchok, J.A., Eley, G., Ferguson, M.L., Hutter, C.M., Mills Shaw, K.R., Ozenberger, B.A., Sheth, M., Sofia, H.J., Tarnuzzer, R., Wang, Z., Yang, L., Zenklusen, J.C., Ayala, B., Baboud, J., Chudamani, S., Jensen, M.A., Liu, J., Pihl, T., Raman, R., Wan, Y., Wu, Y., Ally, A., Auman, J.T., Balasundaram, M., Balu, S., Baylin, S.B., Beroukhi, R., Bootwalla, M.S., Bowlby, R., Bristow, C.A., Brooks, D., Butterfield, Y., Carlsen, R., Carter, S., Chin, L., Chu, A., Chuah, E., Cibulskis, K., Clarke, A., Coetzee, S.G., Dhalla, N., Fennell, T., Fisher, S., Gabriel, S., Getz, G., Gibbs, R., Guin, R., Hadjipanayis, A., Hayes, D.N., Hinoue, T., Hoadley, K., Holt, R.A., Hoyle, A.P., Jefferys, S.R., Jones, S., Jones, C.D., Kucherlapati, R., Lai, P.H., Lander, E.S., Lee, S., Lichtenstein, L., Ma, Y., Maglinte, D.T., Mahadeshwar, H.S., Marra, M.A., Mayo, M., Meng, S., Meyerson, M.L., Mieczkowski, P.A., Moore, R.A., Mose, L.E., Mungall, A.J., Pantazi, A., Parfenov, M., Park, P.J., Parker, J.S., Perou, C.M., Protopopov, A., Ren, X., Roach, J., Sabedot, T.S., Schein, J., Schumacher, S.E., Seidman, J.G., Seth, S., Shen, H., Simons, J.V., Sipahimalani, P., Soloway, M.G., Song, X., Sun, H., Tabak, B., Tam, A., Tan, D., Tang, J., Thiessen, N., Triche, T., Van Den Berg, D.J., Veluvolu, U., Waring, S., Weisenberger, D.J., Wilkerson, M.D., Wong, T., Wu, J., Xi, L., Xu, A.W., Yang, L., Zack, T.I., Zhang, J., Aksoy, B.A., Arachchi, H., Benz, C., Bernard, B., Carlin, D., Cho, J., DiCara, D., Frazer, S., Fuller, G.N., Gao, J., Gehlenborg, N., Haussler, D., Heiman, D.I., Iype, L., Jacobsen, A., Ju, Z., Katzman, S., Kim, H., Knijnenburg, T., Kreisberg, R.B., Lawrence, M.S., Lee, W., Leinonen, K., Lin, P., Ling, S., Liu, W., Liu, Y., Liu, Y., Lu, Y., Mills, G., Ng, S., Noble, M.S., Paull, E., Rao, A., Reynolds, S., Saksena, G., Sanborn, Z., Sander, C., Schultz, N., Senbabaoglu, Y., Shen, R., Shmulevich, I., Sinha, R., Stuart, J., Sumer, S.O., Sun, Y., Tasman, N., Taylor, B.S., Voet, D., Weinhold, N., Weinstein, J.N., Yang, D., Yoshihara, K., Zheng, S., Zhang, W., Zou, L., Abel, T., Sadeghi, S., Cohen, M.L., Eschbacher, J., Hattab, E.M., Raghunathan, A., Schniederjan, M.J., Aziz, D., Barnett, G., Barrett, W., Bigner, D.D., Boice, L., Brewer, C., Calatrazzolo, C., Campos, B., Carlotti, C.G., Chan, T.A., Cuppini, L., Curley, E., Cuzzubbo, S., Devine, K., DiMeo, F., Duell, R., Elder, J.B., Fehrenbach, A., Finocchiaro, G., Friedman, W., Fulop, J., Gardner, J., Hermes, B., Herold-Mende, C., Jungk, C., Kendler, A., Lehman, N.L., Lipp, E., Liu, O., Mandt, R., McGraw, M., McLendon, R., McPherson, C., Neder, L., Nguyen, P., Noss, A., Nunziata, R., Ostrom, Q.T., Palmer, C., Perin, A., Pollo, B., Potapov, A., Potapova, O., Rathmell, W.K., Rotin, D., Scarpone, L., Schilero, C., Senecal, K., Shimmel, K., Shurkay, V., Sifri, S., Singh, R., Sloan, A.E., Smolenski, K., Staugaitis, S.M., Steele, R., Thorne, L., Tirapelli, D.P., Unterberg, A., Vallurupalli, M., Wang, Y., Warnick, R., Williams, F., Wolinsky, Y., Bell, S., Rosenberg, M., Stewart, C., Huang, F., Grimsby, J.L., Radenbaugh, A.J., & Zhang, J. (2015). *Comprehensive, integrative genomic analysis of diffuse lower-grade gliomas*. *New England Journal of Medicine*, 372(26), 2481–2498. PMID: 26061751; PMCID: PMC4530011.

481. Do, R., Stitzel, N.O., Won, H.H., Jørgensen, A.B., Duga, S., Angelica Merlini, P., Kiezun, A., Farrall, M., Goel, A., Zuk, O., Guella, I., Asselta, R., Lange, L.A., Peloso, G.M., Auer, P.L., NHLBI Exome Sequencing Project, Girelli, D., Martinelli, N., Farlow, D.N., DePristo, M.A., Roberts, R., Stewart, A.F., Saleheen, D., Danesh, J., Epstein, S.E., Sivapalaratnam, S., Hovingh, G.K., Kastelein, J.J., Samani, N.J., Schunkert, H., Erdmann, J., Shah, S.H., Kraus, W.E., Davies, R.,

- Nikpay, M., Johansen, C.T., Wang, J., Hegele, R.A., Hechter, E., Marz, W., Kleber, M.E., Huang, J., Johnson, A.D., Li, M., Burke, G.L., Gross, M., Liu, Y., Assimes, T.L., Heiss, G., Lange, E.M., Folsom, A.R., Taylor, H.A., Olivieri, O., Hamsten, A., Clarke, R., Reilly, D.F., Yin, W., Rivas, M.A., Donnelly, P., Rossouw, J.E., Psaty, B.M., Herrington, D.M., Wilson, J.G., Rich, S.S., Bamshad, M.J., Tracy, R.P., Cupples, L.A., Rader, D.J., Reilly, M.P., Spertus, J.A., Cresci, S., Hartiala, J., Tang, W.H., Hazen, S.L., Allayee, H., Reiner, A.P., Carlson, C.S., Kooperberg, C., Jackson, R.D., Boerwinkle, E., Lander, E.S., Schwartz, S.M., Siscovick, D.S., McPherson, R., Tybjaerg-Hansen, A., Abecasis, G.R., Watkins, H., Nickerson, D.A., Ardissono, D., Sunyaev, S.R., O'Donnell, C.J., Altshuler, D., Gabriel, S., & Kathiresan, S. (2015). *Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction*. *Nature*, 518(7537), 102–106. PMID: 25487149; PMCID: PMC4319990.
482. Tonomura, N., Elvers, I., Thomas, R., Megquier, K., Turner-Maier, J., Howald, C., Sarver, A.L., Swofford, R., Frantz, A.M., Ito, D., Mauceli, E., Arendt, M., Noh, H.J., Koltoorian, M., Biagi, T., Fryc, S., Williams, C., Avery, A.C., Kim, J.H., Barber, L., Burgess, K., Lander, E.S., Karlsson, E.K., Azuma, C., Modiano, J.F., Breen, M., & Lindblad-Toh, K. (2015). *Genome-wide association study identifies shared risk loci common to two malignancies in golden retrievers*. *PLoS Genetics*, 11(2), e1004922. PMID: 25642983; PMCID: PMC4333733.
483. Thormaehlen, A.S., Schubert, C., Won, H.H., Blattmann, P., Joggerst-Thomalla, B., Theiss, S., Asselta, R., Duga, S., Merlini, P.A., Ardissono, D., Lander, E.S., Gabriel, S., Rader, D.J., Peloso, G.M., Pepperkok, R., Kathiresan, S., & Runz, H. (2015). *Systematic cell-based phenotyping of missense alleles empowers rare variant association studies: a case for LDLR and myocardial infarction*. *PLoS Genetics*, 11(2), e1004855. PMID: 25647241; PMCID: PMC4409815.
484. Kim, H., Zheng, S., Amini, S.S., Virk, S.M., Mikkelsen, T., Brat, D.J., Grimsby, J., Sougnez, C., Muller, F., Hu, J., Sloan, A.E., Cohen, M.L., Van Meir, E.G., Scarpace, L., Laird, P.W., Weinstein, J.N., Lander, E.S., Gabriel, S., Getz, G., Meyerson, M., Chin, L., Barnholtz-Sloan, J.S., & Verhaak, R.G. (2015). *Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution*. *Genome Research*, 25(3), 316–327. PMID: 25650244; PMCID: PMC4352879.
485. Lander, E.S. (2015). *Cutting the Gordian helix—regulating genomic testing in the era of precision medicine*. *New England Journal of Medicine*, 372(13), 1185–1186. PMID: 25689017.
486. McHugh, C.A., Chen, C.K., Chow, A., Surka, C.F., Tran, C., McDonel, P., Pandya-Jones, A., Blanco, M., Burghard, C., Moradian, A., Sweredoski, M.J., Shishkin, A.A., Su, J., Lander, E.S., Hess, S., Plath, K., & Guttman, M. (2015). *The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3*. *Nature*, 521(7551), 232–236. PMID: 25915022; PMCID: PMC4516396.
487. Lander ES. (2015). *Brave New Genome*. *New England Journal of Medicine*, 373(1), 5–8. PMID: 26039524.
488. Cacchiarelli, D., Trapnell, C., Ziller, M.J., Soumillon, M., Cesana, M., Karnik, R., Donaghey, J., Smith, Z.D., Ratanasirintrao, S., Zhang, X., Ho Sui, S.J., Wu, Z., Akopian, V., Gifford, C.A., Doench, J., Rinn, J.L., Daley, G.Q., Meissner, A., Lander, E.S., & Mikkelsen, T.S. (2015). *Integrative analyses of human reprogramming reveal dynamic nature of induced pluripotency*. *Cell*, 162(2), 412–424. PMID: 26186193; PMCID: PMC4511597.
489. Stachler, M.D., Taylor-Weiner, A., Peng, S., McKenna, A., Agoston, A.T., Odze, R.D., Davison, J.M., Nason, K.S., Loda, M., Leshchiner, I., Stewart, C., Stojanov, P., Seepo, S., Lawrence, M.S., Ferrer-Torres, D., Lin, J., Chang, A.C., Gabriel, S.B., Lander, E.S., Beer, D.G., Getz, G., Carter, S.L., & Bass, A.J. (2015). *Paired exome analysis of Barrett's esophagus and adenocarcinoma*. *Nature Genetics*, 47(9), 1047–1055. PMID: 26192918; PMCID: PMC4552571.
490. Andersen, K.G., Shapiro, B.J., Matranga, C.B., Sealfon, R., Lin, A.E., Moses, L.M., Folarin, O.A., Goba, A., Odi, I., Ehiane, P.E., Momoh, M., England, E.M., Winnicki, S., Branco, L.M., Gire, S.K., Phelan, E., Tariyal, R., Tewhey, R., Omoniyi, O., Fullah, M., Fonnies, R., Fonnies, M., Kanneh, L., Jalloh, S., Gbokie, M., Saffa, S., Karbo, K., Gladden, A.D., Qu, J., Stremlau, M., Nekoui, M., Finucane, H.K., Tabrizi, S., Vitti, J.J., Birren, B., Fitzgerald, M., McCowan, C., Ireland, A., Berlin, A.M., Bochicchio, J., Tazon-Vega, B., Lennon, N.J., Ryan, E.M., Bjornson, Z., Milner, D.A., Lukens, A.K., Brodie, N., Rowland, M., Heinrich, M., Akdag, M., Schieffelin, J.S., Levy, D., Akpan, H., Bausch, D.G., Rubins, K., McCormick, J.B., Lander, E.S., Günther, S., Hensley, L., Okogbenin, S., Viral Hemorrhagic Fever Consortium, Schaffner, S.F., Okokhere, P.O., Khan, S.H., Grant, D.S., Akpede, G.O., Asogun, D.A., Gnirke, A., Levin, J.Z., Happi, C.T., Garry, R.F., & Sabeti, P.C.

- (2015). *Clinical sequencing uncovers origins and evolution of Lassa virus*. *Cell*, 162(4), 738–750. PMID: 26276630; PMCID: PMC4537774.
491. Kamburov, A., Lawrence, M.S., Polak, P., Leshchiner, I., Lage, K., Golub, T.R., Lander, E.S., & Getz, G. (2015). *Comprehensive assessment of cancer missense mutation clustering in protein structures*. *Proceedings of the National Academy of Sciences USA*, 112(40), E5486–E5495. PMID: 26392535; PMCID: PMC4603469.
492. Brastianos, P.K., Carter, S.L., Santagata, S., Cahill, D.P., Taylor-Weiner, A., Jones, R.T., Van Allen, E.M., Lawrence, M.S., Horowitz, P.M., Cibulskis, K., Ligon, K.L., Taberner, J., Seoane, J., Martinez-Saez, E., Curry, W.T., Dunn, I.F., Paek, S.H., Park, S.H., McKenna, A., Chevalier, A., Rosenberg, M., Barker, F.G., Gill, C.M., Van Hummelen, P., Thorner, A.R., Johnson, B.E., Hoang, M.P., Choueiri, T.K., Signoretti, S., Sougnez, C., Rabin, M.S., Lin, N.U., Winer, E.P., Stemmer-Rachamimov, A., Meyerson, M., Garraway, L., Gabriel, S., Lander, E.S., Beroukhi, R., Batchelor, T.T., Baselga, J., Louis, D.N., Getz, G., & Hahn, W.C. (2015). *Genomic characterization of brain metastases reveals branched evolution and potential therapeutic targets*. *Cancer Discovery*, 5(11), 1164–1177. PMID: 26410082; PMCID: PMC4916970.
493. Wang, T., Birsoy, K., Hughes, N.W., Krupczak, K.M., Post, Y., Wei, J.J., Lander, E.S., & Sabatini, D.M. (2015). *Identification and characterization of essential genes in the human genome*. *Science*, 350(6264), 1096–1101. PMID: 26472758; PMCID: PMC4662922.
494. Landau, D.A., Tausch, E., Taylor-Weiner, A.N., Stewart, C., Reiter, J.G., Bahlo, J., Kluth, S., Bozic, I., Lawrence, M., Böttcher, S., Carter, S.L., Cibulskis, K., Mertens, D., Sougnez, C.L., Rosenberg, M., Hess, J.M., Edelman, J., Kless, S., Kneba, M., Ritgen, M., Fink, A., Fischer, K., Gabriel, S., Lander, E.S., Nowak, M.A., Döhner, H., Hallek, M., Neuber, D., Getz, G., Stilgenbauer, S., & Wu, C.J. (2015). *Mutations driving CLL and their evolution in progression and relapse*. *Nature*, 526(7574), 525–530. PMID: 26466571; PMCID: PMC4815041.
495. Golan, D., Rosset, S., & Lander, E.S. (2015). *Downward bias in heritability estimation is not due to simplified linkage equilibrium SNP simulation [Reply]*. *Proceedings of the National Academy of Sciences USA*, 112(40), E5452–E5453. PMID: 26417112; PMCID: PMC4603505.
496. Sanborn, A.L., Rao, S.S., Huang, S.C., Durand, N.C., Huntley, M.H., Jewett, A.I., Bochkov, I.D., Chinnappan, D., Cutkosky, A., Li, J., Geeting, K.P., Gnirke, A., Melnikov, A., McKenna, D., Stamenova, E.K., Lander, E.S., & Aiden, E.L. (2015). *Chromatin extrusion explains key features of loop and domain formation in wild-type and engineered genomes*. *Proceedings of the National Academy of Sciences USA*, 112(47), E6456–E6465. PMID: 26499245; PMCID: PMC4664323.
497. Kasar, S., Kim, J., Improgo, R., Tiao, G., Polak, P., Haradhvala, N., Lawrence, M.S., Kiezun, A., Fernandes, S.M., Bahl, S., Sougnez, C., Gabriel, S., Lander, E.S., Kim, H.T., Getz, G., & Brown, J.R. (2015). *Whole-genome sequencing reveals activation-induced cytidine deaminase signatures during indolent chronic lymphocytic leukaemia evolution*. *Nature Communications*, 6, 8866. PMID: 26638776; PMCID: PMC4686820.
498. Lander, E.S. (2016). *The Heroes of CRISPR*. *Cell*, 164(1–2), 18–28. PMID: 26771483.
499. Yassour, M., Lim, M.Y., Yun, H.S., Tickle, T.L., Sung, J., Song, Y.M., Lee, K., Franzosa, E.A., Morgan, X.C., Gevers, D., Lander, E.S., Xavier, R.J., Birren, B.W., Ko, G., & Huttenhower, C. (2016). *Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes*. *Genome Medicine*, 8(1), 17. PMID: 26884067; PMCID: PMC4756455.
500. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Single guide RNA library design and construction*. *Cold Spring Harbor Protocols*, 3, pdb.prot090803. PMID: 26933249; PMCID: PMC4804709.
501. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Viral packaging and cell culture for CRISPR-based screens*. *Cold Spring Harbor Protocols*, 3, pdb.prot090811. PMID: 26933250; PMCID: PMC4804706.
502. Wang, T., Lander, E.S., & Sabatini, D.M. (2016). *Large-scale single guide RNA library construction and use for CRISPR-Cas9-based genetic screens*. *Cold Spring Harbor Protocols*, 3, pdb.top086892. PMID: 26933254; PMCID: PMC4804892.
503. Giannakis, M., Mu, X.J., Shukla, S.A., Qian, Z.R., Cohen, O., Nishihara, R., Bahl, S., Cao, Y., Amin-Mansour, A., Yamauchi, M., Sukawa, Y., Stewart, C., Rosenberg, M., Mima, K., Inamura, K., Nosh, K., Nowak, J.A., Lawrence, M.S., Giovannucci, E.L., Chan, A.T., Ng, K., Meyerhardt, J.A., Van Allen, E.M., Getz, G., Gabriel, S.B., Lander, E.S., Wu, C.J., Fuchs, C.S., Ogino, S., & Garraway, L.A. (2016). *Genomic correlates of immune-cell infiltrates in colorectal carcinoma*. *Cell Reports*, 15(4), 857–865. PMID: 27149842; PMCID: PMC4850357.

504. Blumenstiel, B., DeFelice, M., Birsoy, O., Bleyer, A.J., Kmoch, S., Carter, T.A., Gnirke, A., Kidd, K., Rehm, H.L., Ronco, L., Lander, E.S., Gabriel, S., & Lennon, N.J. (2016). *Development and validation of a mass spectrometry-based assay for the molecular diagnosis of Mucin-1 kidney disease. The Journal of Molecular Diagnostics*, 18(4), 566–571. PMID: 27157321.
505. Abudayyeh, O.O., Gootenberg, J.S., Konermann, S., Joung, J., Slaymaker, I.M., Cox, D.B., Shmakov, S., Makarova, K.S., Semenova, E., Minakhin, L., Severinov, K., Regev, A., Lander, E.S., Koonin, E.V., & Zhang, F. (2016). *C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science*, 353(6299), aaf5573. PMID: 27256883.
506. Tewhey, R., Kotliar, D., Park, D.S., Liu, B., Winnicki, S., Reilly, S.K., Andersen, K.G., Mikkelsen, T.S., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2016). *Direct identification of hundreds of expression-modulating variants using a multiplexed reporter assay. Cell*, 165(6), 1519–1529. PMID: 27259153; PMCID: PMC4957403.
507. Yassour, M., Vatanen, T., Siljander, H., Hämäläinen, A.M., Härkönen, T., Ryhänen, S.J., Franzosa, E.A., Vlamakis, H., Huttenhower, C., Gevers, D., Lander, E.S., Knip, M., DIABIMMUNE Study Group, & Xavier, R.J. (2016). *Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. Science Translational Medicine*, 8(343), 343ra81. PMID: 27306663; PMCID: PMC5032909.
508. Darrow, E.M., Huntley, M.H., Dudchenko, O., Stamenova, E.K., Durand, N.C., Sun, Z., Huang, S.C., Sanborn, A.L., Machol, I., Shamim, M., Seberg, A.P., Lander, E.S., Chadwick, B.P., & Aiden, E.L. (2016). *Deletion of DXZ4 on the human inactive X chromosome alters higher-order genome architecture. Proceedings of the National Academy of Sciences USA*, 113(31), E4504–E4512. PMID: 27432957; PMCID: PMC4978254.
509. Durand, N.C., Robinson, J.T., Shamim, M.S., Machol, I., Mesirov, J.P., Lander, E.S., & Aiden, E.L. (2016). *Juicebox provides a visualization system for Hi-C contact maps with unlimited zoom. Cell Systems*, 3(1), 99–101. PMID: 27467250.
510. Durand, N.C., Shamim, M.S., Machol, I., Rao, S.S., Huntley, M.H., Lander, E.S., & Aiden, E.L. (2016). *Juicer provides a one-click system for analyzing loop-resolution Hi-C experiments. Cell Systems*, 3(1), 95–98. PMID: 27467249.
511. Burger, J.A., Landau, D.A., Taylor-Weiner, A., Bozic, I., Zhang, H., Sarosiek, K., Wang, L., Stewart, C., Fan, J., Hoellenriegel, J., Sivina, M., Dubuc, A.M., Fraser, C., Han, Y., Li, S., Livak, K.J., Zou, L., Wan, Y., Konoplev, S., Sougnez, C., Brown, J.R., Abruzzo, L.V., Carter, S.L., Keating, M.J., Davids, M.S., Wierda, W.G., Cibulskis, K., Zenz, T., Werner, L., Dal Cin, P., Kharchenko, P., Neuberg, D., Kantarjian, H., Lander, E.S., Gabriel, S., O'Brien, S., Letai, A., Weitz, D.A., Nowak, M.A., Getz, G., & Wu, C.J. (2016). *Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications*, 20(7), 11589. PMID: 27199251; PMCID: PMC4876453.
512. Khera, A.V., Won, H.H., Peloso, G.M., Lawson, K.S., Bartz, T.M., Deng, X., van Leeuwen, E.M., Natarajan, P., Emdin, C.A., Bick, A.G., Morrison, A.C., Brody, J.A., Gupta, N., Nomura, A., Kessler, T., Duga, S., Bis, J.C., van Duijn, C.M., Cupples, L.A., Psaty, B., Rader, D.J., Danesh, J., Schunkert, H., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Wilson, J.G., Correa, A., Boerwinkle, E., Merlini, P.A., Ardisino, D., Saleheen, D., Gabriel, S., & Kathiresan, S. (2016). *Diagnostic yield and clinical utility of sequencing familial hypercholesterolemia genes in patients with severe hypercholesterolemia. Journal of the American College of Cardiology*, 67(22), 2578–2589. PMID: 27050191.
513. Engreitz, J.M., Haines, J.E., Perez, E.M., Munson, G., Chen, J., Kane, M., McDonel, P.E., Guttman, M., & Lander, E.S. (2016). *Local regulation of gene expression by lncRNA promoters, transcription and splicing. Nature* 539(7629), 452–455. PMID: 27783602
514. Dixit, A., Parnas, O., Li, B., Chen, J., Fulco, C.P., Jerby-Arnon, L., Marjanovic, N.D., Dionne, D., Burks, T., Raychowdhury, R., Adamson, B., Norman, T.M., Lander, E.S., Weissman, J.S., Friedman, N., & Regev, A. (2016). *Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. Cell*, 167(7), 1853–1866.e1817.
515. Emdin, C.A., Khera, A.V., Natarajan, P., Klarin, D., Won, H.H., Peloso, G.M., Stitzel, N.O., Nomura, A., Zekavat, S.M., Bick, A.G., Gupta, N., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Willer, C., Abecasis, G.R., Felix, J.F., Vasan, R.S., Lander, E., Rader, D.J., Danesh, J., Ardisino, D., Gabriel, S., Saleheen, D., & Kathiresan, S. (2016). *Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology*, 68(25), 2761–2772.

516. Fuchsberger, C., Flannick, J., Teslovich, T.M., Mahajan, A., Agarwala, V., Gaulton, K.J., Ma, C., Fontanillas, P., Moutsianas, L., McCarthy, D.J., Rivas, M.A., Perry, J.R., Sim, X., Blackwell, T.W., Robertson, N.R., Rayner, N.W., Cingolani, P., Locke, A.E., Fernandez Tajes, J., Highland, H.M., Dupuis, J., Chines, P.S., Lindgren, C.M., Hartl, C., Jackson, A.U., Chen, H., Huyghe, J.R., van de Bunt, M., Pearson, R.D., Kumar, A., Muller-Nurasyid, M., Grarup, N., Stringham, H.M., Gamazon, E.R., Lee, J., Chen, Y., Scott, R.A., Below, J.E., Chen, P., Huang, J., Go, M.J., Stitzel, M.L., Pasko, D., Parker, S.C., Varga, T.V., Green, T., Beer, N.L., Day-Williams, A.G., Ferreira, T., Fingerlin, T., Horikoshi, M., Hu, C., Huh, I., Ikram, M.K., Kim, B.J., Kim, Y., Kim, Y.J., Kwon, M.S., Lee, J., Lee, S., Lin, K.H., Maxwell, T.J., Nagai, Y., Wang, X., Welch, R.P., Yoon, J., Zhang, W., Barzilai, N., Voight, B.F., Han, B.G., Jenkinson, C.P., Kuulasmaa, T., Kuusisto, J., Manning, A., Ng, M.C., Palmer, N.D., Balkau, B., Stancakova, A., Abboud, H.E., Boeing, H., Giedraitis, V., Prabhakaran, D., Gottesman, O., Scott, J., Carey, J., Kwan, P., Grant, G., Smith, J.D., Neale, B.M., Purcell, S., Butterworth, A.S., Howson, J.M., Lee, H.M., Lu, Y., Kwak, S.H., Zhao, W., Danesh, J., Lam, V.K., Park, K.S., Saleheen, D., So, W.Y., Tam, C.H., Afzal, U., Aguilar, D., Arya, R., Aung, T., Chan, E., Navarro, C., Cheng, C.Y., Palli, D., Correa, A., Curran, J.E., Rybin, D., Farook, V.S., Fowler, S.P., Freedman, B.I., Griswold, M., Hale, D.E., Hicks, P.J., Khor, C.C., Kumar, S., Lehne, B., Thuillier, D., Lim, W.Y., Liu, J., van der Schouw, Y.T., Loh, M., Musani, S.K., Puppala, S., Scott, W.R., Yengo, L., Tan, S.T., Taylor, H.A., Jr., Thameem, F., Wilson, G., Sr., Wong, T.Y., Njolstad, P.R., Levy, J.C., Mangino, M., Bonnycastle, L.L., Schwarzmayr, T., Fadista, J., Surdulescu, G.L., Herder, C., Groves, C.J., Wieland, T., Bork-Jensen, J., Brandslund, I., Christensen, C., Koistinen, H.A., Doney, A.S., Kinnunen, L., Esko, T., Farmer, A.J., Hakaste, L., Hodgkiss, D., Kravic, J., Lyssenko, V., Hollensted, M., Jorgensen, M.E., Jorgensen, T., Ladenvall, C., Justesen, J.M., Karajamaki, A., Kriebel, J., Rathmann, W., Lannfelt, L., Lauritzen, T., Narisu, N., Linneberg, A., Melander, O., Milani, L., Neville, M., Orho-Melander, M., Qi, L., Qi, Q., Roden, M., Rolandsson, O., Swift, A., Rosengren, A.H., Stirrups, K., Wood, A.R., Mihailov, E., Blancher, C., Carneiro, M.O., Maguire, J., Poplin, R., Shakir, K., Fennell, T., DePristo, M., Hrabe de Angelis, M., Deloukas, P., Gjesing, A.P., Jun, G., Nilsson, P., Murphy, J., Onofrio, R., Thorand, B., Hansen, T., Meisinger, C., Hu, F.B., Isomaa, B., Karpe, F., Liang, L., Peters, A., Huth, C., O'Rahilly, S.P., Palmer, C.N., Pedersen, O., Rauramaa, R., Tuomilehto, J., Salomaa, V., Watanabe, R.M., Syvanen, A.C., Bergman, R.N., Bharadwaj, D., Bottinger, E.P., Cho, Y.S., Chandak, G.R., Chan, J.C., Chia, K.S., Daly, M.J., Ebrahim, S.B., Langenberg, C., Elliott, P., Jablonski, K.A., Lehman, D.M., Jia, W., Ma, R.C., Pollin, T.I., Sandhu, M., Tandon, N., Froguel, P., Barroso, I., Teo, Y.Y., Zeggini, E., Loos, R.J., Small, K.S., Ried, J.S., DeFronzo, R.A., Grallert, H., Glaser, B., Metspalu, A., Wareham, N.J., Walker, M., Banks, E., Gieger, C., Ingelsson, E., Im, H.K., Illig, T., Franks, P.W., Buck, G., Trakalo, J., Buck, D., Prokopenko, I., Magi, R., Lind, L., Farjoun, Y., Owen, K.R., Gloyn, A.L., Strauch, K., Tuomi, T., Kooner, J.S., Lee, J.Y., Park, T., Donnelly, P., Morris, A.D., Hattersley, A.T., Bowden, D.W., Collins, F.S., Atzmon, G., Chambers, J.C., Spector, T.D., Laakso, M., Strom, T.M., Bell, G.I., Blangero, J., Duggirala, R., Tai, E.S., McVean, G., Hanis, C.L., Wilson, J.G., Seielstad, M., Frayling, T.M., Meigs, J.B., Cox, N.J., Sladek, R., Lander, E.S., Gabriel, S., Burt, N.P., Mohlke, K.L., Meitinger, T., Groop, L., Abecasis, G., Florez, J.C., Scott, L.J., Morris, A.P., Kang, H.M., Boehnke, M., Altshuler, D., & McCarthy, M.I. (2016). *The genetic architecture of type 2 diabetes*. *Nature*, 536(7614), 41–47.
517. Fulco, C.P., Munschauer, M., Anyoha, R., Munson, G., Grossman, S.R., Perez, E.M., Kane, M., Cleary, B., Lander, E.S., & Engreitz, J.M. (2016). *Systematic mapping of functional enhancer-promoter connections with CRISPR interference*. *Science*, 354(6313), 769–773.
518. Park, R.J., Wang, T., Koundakjian, D., Hultquist, J.F., Lamothe-Molina, P., Monel, B., Schumann, K., Yu, H., Krupczak, K.M., Garcia-Beltran, W., Piechocka-Trocha, A., Krogan, N.J., Marson, A., Sabatini, D.M., Lander, E.S., Hacohen, N., & Walker, B.D. (2017). *A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors*. *Nature Genetics*, 49(2), 193–203. doi: 10.1038/ng.3741.
519. Guo, M.H., Nandakumar, S.K., Ulirsch, J.C., Zekavat, S.M., Buenrostro, J.D., Natarajan, P., Salem, R.M., Chiarle, R., Mitt, M., Kals, M., Parn, K., Fischer, K., Milani, L., Magi, R., Palta, P., Gabriel, S.B., Metspalu, A., Lander, E.S., Kathiresan, S., Hirschhorn, J.N., Esko, T., & Sankaran, V.G. (2017). *Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms*. *Proceedings of the National Academy of Sciences U S A*, 114(3), E327–e336.
520. The Cancer Genome Atlas Research Network (2017). *Integrated genomic characterization of oesophageal carcinoma*. *Nature*, 541(7636), 169–175.

521. Grossman, S.R., Zhang, X., Wang, L., Engreitz, J., Melnikov, A., Rogov, P., Tewhey, R., Isakova, A., Deplancke, B., Bernstein, B.E., Mikkelsen, T.S., & Lander, E.S. (2017). *Systematic dissection of genomic features determining transcription factor binding and enhancer function. Proceedings of the National Academy of Sciences U S A*, 114(7), E1291–e1300.
522. Khera, A.V., Won, H.H., Peloso, G.M., O'Dushlaine, C., Liu, D., Stitzel, N.O., Natarajan, P., Nomura, A., Emdin, C.A., Gupta, N., Borecki, I.B., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartzel, D.N., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Rader, D.J., Danesh, J., Ardissino, D., Gabriel, S., Willer, C., Abecasis, G.R., Saleheen, D., Dewey, F.E., & Kathiresan, S. (2017). *Association of rare and common variation in the lipoprotein lipase gene with coronary artery disease. Journal of the American Medical Association*, 317(9), 937–946.
523. Kim, A.R., Ulirsch, J.C., Wilmes, S., Unal, E., Moraga, I., Karakukcu, M., Yuan, D., Kazerounian, S., Abdulhay, N.J., King, D.S., Gupta, N., Gabriel, S.B., Lander, E.S., Patiroglu, T., Ozcan, A., Ozdemir, M.A., Garcia, K.C., Piehler, J., Gazda, H.T., Klein, D.E., & Sankaran, V.G. (2017). *Functional selectivity in cytokine signaling revealed through a pathogenic EPO mutation. Cell*, 168(6), 1053–1064.e1015.
524. Wang, T., Yu, H., Hughes, N.W., Liu, B., Kendirli, A., Klein, K., Chen, W.W., Lander, E.S., & Sabatini, D.M. (2017). *Gene essentiality profiling reveals gene networks and synthetic lethal interactions with oncogenic Ras. Cell*, 168(5), 890–903.e815.
525. Dudchenko, O., Batra, S.S., Omer, A.D., Nyquist, S.K., Hoeger, M., Durand, N.C., Shamim, M.S., Machol, I., Lander, E.S., Aiden, A.P., & Aiden, E.L. (2017). *De novo assembly of the aedes aegypti genome using hi-c yields chromosome-length scaffolds. Science*, 356(6333), 92–95.
526. Khera, A.V., Won, H.H., Peloso, G.M., O'Dushlaine, C., Liu, D., Stitzel, N.O., Natarajan, P., Nomura, A., Emdin, C.A., Gupta, N., Borecki, I.B., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartzel, D.N., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Lander, E.S., Rader, D.J., Danesh, J., Ardissino, D., Gabriel, S., Willer, C., Abecasis, G.R., Saleheen, D., Dewey, F.E., & Kathiresan, S. (2017). *Association of rare and common variation in the lipoprotein lipase gene with coronary artery disease. Journal of the American Medical Association*, 317(9), 937–946.
527. Kim, A.R., Ulirsch, J.C., Wilmes, S., Unal, E., Moraga, I., Karakukcu, M., Yuan, D., Kazerounian, S., Abdulhay, N.J., King, D.S., Gupta, N., Gabriel, S.B., Lander, E.S., Patiroglu, T., Ozcan, A., Ozdemir, M.A., Garcia, K.C., Piehler, J., Gazda, H.T., Klein, D.E., & Sankaran, V.G. (2017). *Functional selectivity in cytokine signaling revealed through a pathogenic epo mutation. Cell*, 168(6), 1053–1064.e1015.
528. Mitt, M., Kals, M., Parn, K., Gabriel, S.B., Lander, E.S., Palotie, A., Ripatti, S., Morris, A.P., Metspalu, A., Esko, T., Magi, R., & Palta, P. (2017). *Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage wgs-based imputation reference panel. European Journal of Human Genetics*, 25(7), 869–876.
529. Nomura, A., Won, H.H., Khera, A.V., Takeuchi, F., Ito, K., McCarthy, S., Emdin, C.A., Klarin, D., Natarajan, P., Zekavat, S.M., Gupta, N., Peloso, G.M., Borecki, I.B., Teslovich, T.M., Asselta, R., Duga, S., Merlini, P.A., Correa, A., Kessler, T., Wilson, J.G., Bown, M.J., Hall, A.S., Braund, P.S., Carey, D.J., Murray, M.F., Kirchner, H.L., Leader, J.B., Lavage, D.R., Manus, J.N., Hartzel, D.N., Samani, N.J., Schunkert, H., Marrugat, J., Elosua, R., McPherson, R., Farrall, M., Watkins, H., Juang, J.J., Hsiung, C.A., Lin, S.Y., Wang, J.S., Tada, H., Kawashiri, M.A., Inazu, A., Yamagishi, M., Katsuya, T., Nakashima, E., Nakatochi, M., Yamamoto, K., Yokota, M., Momozawa, Y., Rotter, J.I., Lander, E.S., Rader, D.J., Danesh, J., Ardissino, D., Gabriel, S., Willer, C.J., Abecasis, G.R., Saleheen, D., Kubo, M., Kato, N., Ida Chen, Y.D., Dewey, F.E., & Kathiresan, S. (2017). *Protein-truncating variants at the cholesteryl ester transfer protein gene and risk for coronary heart disease. Circulation Research*, 121(1), 81–88.
530. Ott, P.A., Hu, Z., Keskin, D.B., Shukla, S.A., Sun, J., Bozym, D.J., Zhang, W., Luoma, A., Giobbie-Hurder, A., Peter, L., Chen, C., Olive, O., Carter, T.A., Li, S., Lieb, D.J., Eisenhaure, T., Gjini, E., Stevens, J., Lane, W.J., Javeri, I., Nelliappan, K., Salazar, A.M., Daley, H., Seaman, M., Buchbinder, E.I., Yoon, C.H., Harden, M., Lennon, N., Gabriel, S., Rodig, S.J., Barouch, D.H., Aster, J.C., Getz,

G., Wucherpennig, K., Neuberg, D., Ritz, J., Lander, E.S., Fritsch, E.F., Hacohen, N., & Wu, C.J. (2017). *An immunogenic personal neoantigen vaccine for patients with melanoma. Nature*, 547(7662), 217–221.

531. Rheinbay, E., Parasuraman, P., Grimsby, J., Tiao, G., Engreitz, J.M., Kim, J., Lawrence, M.S., Taylor-Weiner, A., Rodriguez-Cuevas, S., Rosenberg, M., Hess, J., Stewart, C., Maruvka, Y.E., Stojanov, P., Cortes, M.L., Seepo, S., Cibulskis, C., Tracy, A., Pugh, T.J., Lee, J., Zheng, Z., Ellisen, L.W., Iafrate, A.J., Boehm, J.S., Gabriel, S.B., Meyerson, M., Golub, T.R., Baselga, J., Hidalgo-Miranda, A., Shioda, T., Bernards, A., Lander, E.S., & Getz, G. (2017). *Recurrent and functional regulatory mutations in breast cancer. Nature*, 547(7661), 55–60.

532. Rusu, V., Hoch, E., Mercader, J.M., Tenen, D.E., Gymrek, M., Hartigan, C.R., DeRan, M., von Grotthuss, M., Fontanillas, P., Spooner, A., Guzman, G., Deik, A.A., Pierce, K.A., Dennis, C., Clish, C.B., Carr, S.A., Wagner, B.K., Schenone, M., Ng, M.C.Y., Chen, B.H., Centeno-Cruz, F., Zerrweck, C., Orozco, L., Altshuler, D.M., Schreiber, S.L., Florez, J.C., Jacobs, S.B.R., & Lander, E.S. (2017). *Type 2 diabetes variants disrupt function of slc16a11 through two distinct mechanisms. Cell*, 170(1), 199–212.e120.

533. Saleheen, D., Natarajan, P., Armean, I.M., Zhao, W., Rasheed, A., Khetarpal, S.A., Won, H.H., Karczewski, K.J., O'Donnell-Luria, A.H., Samocha, K.E., Weisburd, B., Gupta, N., Zaidi, M., Samuel, M., Imran, A., Abbas, S., Majeed, F., Ishaq, M., Akhtar, S., Trindade, K., Mucksavage, M., Qamar, N., Zaman, K.S., Yaqoob, Z., Saghir, T., Rizvi, S.N.H., Memon, A., Hayyat Mallick, N., Ishaq, M., Rasheed, S.Z., Memon, F.U., Mahmood, K., Ahmed, N., Do, R., Krauss, R.M., MacArthur, D.G., Gabriel, S., Lander, E.S., Daly, M.J., Frossard, P., Danesh, J., Rader, D.J., & Kathiresan, S. (2017). *Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature*, 544(7649), 235–239.

534. Stitzel, N.O., Khera, A.V., Wang, X., Bierhals, A.J., Vourakis, A.C., Sperry, A.E., Natarajan, P., Klarin, D., Emdin, C.A., Zekavat, S.M., Nomura, A., Erdmann, J., Schunkert, H., Samani, N.J., Kraus, W.E., Shah, S.H., Yu, B., Boerwinkle, E., Rader, D.J., Gupta, N., Frossard, P.M., Rasheed, A., Danesh, J., Lander, E.S., Gabriel, S., Saleheen, D., Musunuru, K., & Kathiresan, S. (2017). *Angptl3 deficiency and protection against coronary artery disease. J Am Coll Cardiol*, 69(16), 2054–2063.

535. Tiao, G., Improgo, M.R., Kasar, S., Poh, W., Kamburov, A., Landau, D.A., Tausch, E., Taylor-Weiner, A., Cibulskis, C., Bahl, S., Fernandes, S.M., Hoang, K., Rheinbay, E., Kim, H.T., Bahlo, J., Robrecht, S., Fischer, K., Hallek, M., Gabriel, S., Lander, E.S., Stilgenbauer, S., Wu, C.J., Kiezun, A., Getz, G., & Brown, J.R. (2017). *Rare germline variants in atm are associated with chronic lymphocytic leukemia. Leukemia* 31(10), 2244–2247.

536. Joung, J., Engreitz, J.M., Konermann, S., Abudayyeh, O.O., Verdine, V.K., Aguet, F., Gootenberg, J.S., Sanjana, N.E., Wright, J.B., Fulco, C.P., Tseng, Y.Y., Yoon, C.H., Boehm, J.S., Lander, E.S., & Zhang, F. (2017). *Genome-scale activation screen identifies a lncrna locus regulating a gene neighbourhood. Nature*, 548(7667), 343–346.

537. Polak, P., Kim, J., Braunstein, L.Z., Karlic, R., Haradhavala, N.J., Tiao, G., Rosebrock, D., Livitz, D., Kubler, K., Mouw, K.W., Kamburov, A., Maruvka, Y.E., Leshchiner, I., Lander, E.S., Golub, T.R., Zick, A., Orthwein, A., Lawrence, M.S., Batra, R.N., Caldas, C., Haber, D.A., Laird, P.W., Shen, H., Ellisen, L.W., D'Andrea, A.D., Chanock, S.J., Foulkes, W.D., & Getz, G. (2017). *A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics* 49(10), 1476–1486.

538. Abudayyeh, O.O., Gootenberg, J.S., Essletzbichler, P., Han, S., Joung, J., Belanto, J.J., Verdine, V., Cox, D.B.T., Kellner, M.J., Regev, A., Lander, E.S., Voytas, D.F., Ting, A.Y., & Zhang, F. (2017). *Rna targeting with crispr-cas13. Nature*, 550(7675), 280–284.

539. Rao, S.S.P., Huang, S.C., Glenn St Hilaire, B., Engreitz, J.M., Perez, E.M., Kieffer-Kwon, K.R., Sanborn, A.L., Johnstone, S.E., Bascom, G.D., Bochkov, I.D., Huang, X., Shamim, M.S., Shin, J., Turner, D., Ye, Z., Omer, A.D., Robinson, J.T., Schlick, T., Bernstein, B.E., Casellas, R., Lander, E.S., & Aiden, E.L. (2017). *Cohesin loss eliminates all loop domains. Cell*, 171(2), 305–320.e324.

540. Cleary, B., Cong, L., Cheung, A., Lander, E.S., & Regev, A. (2017). *Efficient generation of transcriptomic profiles by random composite measurements. Cell*, 171(6), 1424–1436.e1418.

541. Hall, A.B., Yassour, M., Sauk, J., Garner, A., Jiang, X., Arthur, T., Lagoudas, G.K., Vatanen, T., Fornelos, N., Wilson, R., Bertha, M., Cohen, M., Garber, J., Khalili, H., Gevers, D., Ananthakrishnan, A.N., Kugathasan, S., Lander, E.S., Blainey, P., Vlamakis, H., Xavier, R.J., & Huttenhower, C. (2017). *A novel*

ruminococcus gnavus clade enriched in inflammatory bowel disease patients. *Genome Med*, 9(1), 103.

542. Flannick, J., Fuchsberger, C., Mahajan, A., Teslovich, T.M., Agarwala, V., Gaulton, K.J., Caulkins, L., Koesterer, R., Ma, C., Moutsianas, L., McCarthy, D.J., Rivas, M.A., Perry, J.R.B., Sim, X., Blackwell, T.W., Robertson, N.R., Rayner, N.W., Cingolani, P., Locke, A.E., Tajes, J.F., Highland, H.M., Dupuis, J., Chines, P.S., Lindgren, C.M., Hartl, C., Jackson, A.U., Chen, H., Huyghe, J.R., van de Bunt, M., Pearson, R.D., Kumar, A., Muller-Nurasyid, M., Grarup, N., Stringham, H.M., Gamazon, E.R., Lee, J., Chen, Y., Scott, R.A., Below, J.E., Chen, P., Huang, J., Go, M.J., Stitzel, M.L., Pasko, D., Parker, S.C.J., Varga, T.V., Green, T., Beer, N.L., Day-Williams, A.G., Ferreira, T., Fingerlin, T., Horikoshi, M., Hu, C., Huh, I., Ikram, M.K., Kim, B.J., Kim, Y., Kim, Y.J., Kwon, M.S., Lee, J., Lee, S., Lin, K.H., Maxwell, T.J., Nagai, Y., Wang, X., Welch, R.P., Yoon, J., Zhang, W., Barzilai, N., Voight, B.F., Han, B.G., Jenkinson, C.P., Kuulasmaa, T., Kuusisto, J., Manning, A., Ng, M.C.Y., Palmer, N.D., Balkau, B., Stancakova, A., Abboud, H.E., Boeing, H., Giedraitis, V., Prabhakaran, D., Gottesman, O., Scott, J., Carey, J., Kwan, P., Grant, G., Smith, J.D., Neale, B.M., Purcell, S., Butterworth, A.S., Howson, J.M.M., Lee, H.M., Lu, Y., Kwak, S.H., Zhao, W., Danesh, J., Lam, V.K.L., Park, K.S., Saleheen, D., So, W.Y., Tam, C.H.T., Afzal, U., Aguilar, D., Arya, R., Aung, T., Chan, E., Navarro, C., Cheng, C.Y., Palli, D., Correa, A., Curran, J.E., Rybin, D., Farook, V.S., Fowler, S.P., Freedman, B.I., Griswold, M., Hale, D.E., Hicks, P.J., Khor, C.C., Kumar, S., Lehne, B., Thuillier, D., Lim, W.Y., Liu, J., Loh, M., Musani, S.K., Puppala, S., Scott, W.R., Yengo, L., Tan, S.T., Taylor, H.A., Thameem, F., Wilson, G., Wong, T.Y., Njolstad, P.R., Levy, J.C., Mangino, M., Bonnycastle, L.L., Schwarzmayr, T., Fadista, J., Surdulescu, G.L., Herder, C., Groves, C.J., Wieland, T., Bork-Jensen, J., Brandslund, I., Christensen, C., Koistinen, H.A., Doney, A.S.F., Kinnunen, L., Esko, T., Farmer, A.J., Hakaste, L., Hodgkiss, D., Kravic, J., Lyssenko, V., Hollensted, M., Jorgensen, M.E., Jorgensen, T., Ladenvall, C., Justesen, J.M., Karajamaki, A., Kriebel, J., Rathmann, W., Lannfelt, L., Lauritzen, T., Narisu, N., Linneberg, A., Melander, O., Milani, L., Neville, M., Orho-Melander, M., Qi, L., Qi, Q., Roden, M., Rolandsson, O., Swift, A., Rosengren, A.H., Stirrups, K., Wood, A.R., Mihailov, E., Blancher, C., Carneiro, M.O., Maguire, J., Poplin, R., Shaker, K., Fennell, T., DePristo, M., de Angelis, M.H., Deloukas, P., Gjesing, A.P., Jun, G., Nilsson, P., Murphy, J., Onofrio, R., Thorand, B., Hansen, T., Meisinger, C., Hu, F.B., Isomaa, B., Karpe, F., Liang, L., Peters, A., Huth, C., O'Rahilly, S.P., Palmer, C.N.A., Pedersen, O., Rauramaa, R., Tuomilehto, J., Salomaa, V., Watanabe, R.M., Syvanen, A.C., Bergman, R.N., Bharadwaj, D., Bottinger, E.P., Cho, Y.S., Chandak, G.R., Chan, J.C., Chia, K.S., Daly, M.J., Ebrahim, S.B., Langenberg, C., Elliott, P., Jablonski, K.A., Lehman, D.M., Jia, W., Ma, R.C.W., Pollin, T.I., Sandhu, M., Tandon, N., Froguel, P., Barroso, I., Teo, Y.Y., Zeggini, E., Loos, R.J.F., Small, K.S., Ried, J.S., DeFronzo, R.A., Grallert, H., Glaser, B., Metspalu, A., Wareham, N.J., Walker, M., Banks, E., Gieger, C., Ingelsson, E., Im, H.K., Illig, T., Franks, P.W., Buck, G., Trakalo, J., Buck, D., Prokopenko, I., Magi, R., Lind, L., Farjoun, Y., Owen, K.R., Gloyn, A.L., Strauch, K., Tuomi, T., Koener, J.S., Lee, J.Y., Park, T., Donnelly, P., Morris, A.D., Hattersley, A.T., Bowden, D.W., Collins, F.S., Atzmon, G., Chambers, J.C., Spector, T.D., Laakso, M., Strom, T.M., Bell, G.I., Blangero, J., Duggirala, R., Tai, E.S., McVean, G., Hani, C.L., Wilson, J.G., Seielstad, M., Frayling, T.M., Meigs, J.B., Cox, N.J., Sladek, R., Lander, E.S., Gabriel, S., Mohlke, K.L., Meitinger, T., Groop, L., Abecasis, G., Scott, L.J., Morris, A.P., Kang, H.M., Altshuler, D., Burtt, N.P., Florez, J.C., Boehnke, M., & McCarthy, M.I. (2017). *Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Sci Data*, 4, 170–179.

543. Regev, A., Teichmann, S.A., Lander, E.S., Amit, I., Benoist, C., Birney, E., Bodenmiller, B., Campbell, P., Carninci, P., Clatworthy, M., Clevers, H., Deplancke, B., Dunham, I., Eberwine, J., Eils, R., Enard, W., Farmer, A., Fugger, L., Gottgens, B., Hacohen, N., Haniffa, M., Hemberg, M., Kim, S., Klenerman, P., Kriegstein, A., Lein, E., Linnarsson, S., Lundberg, E., Lundberg, J., Majumder, P., Marioni, J.C., Merad, M., Mhlanga, M., Nawijn, M., Netea, M., Nolan, G., Pe'er, D., Phillipakis, A., Ponting, C.P., Quake, S., Reik, W., Rozenblatt-Rosen, O., Sanes, J., Satija, R., Schumacher, T.N., Shalek, A., Shapiro, E., Sharma, P., Shin, J.W., Stegle, O., Stratton, M., Stubbington, M.J.T., Theis, F.J., Uhlen, M., van Oudenaarden, A., Wagner, A., Watt, F., Weissman, J., Wold, B., Xavier, R., & Yosef, N. (2017). *The human cell atlas. Elife*, 6.

544. Zhou, Y., Castonguay, P., Sidhom, E.H., Clark, A.R., Dvula-Levitt, M., Kim, S., Sieber, J., Wieder, N., Jung, J.Y., Andreeva, S., Reichardt, J., Dubois, F., Hoffmann, S.C., Basgen, J.M., Montesinos, M.S., Weins, A., Johnson, A.C., Lander, E.S., Garrett, M.R., Hopkins, C.R., & Greka, A. (2017). *A small-molecule inhibitor of trpc5*

- ion channels suppresses progressive kidney disease in animal models. Science*, 358(6368), 1332–1336.
545. Grasso, C.S., Giannakis, M., Wells, D.K., Hamada, T., Mu, X.J., Quist, M., Nowak, J.A., Nishihara, R., Qian, Z.R., Inamura, K., Morikawa, T., Noshio, K., Abril-Rodriguez, G., Connolly, C., Escuin-Ordinas, H., Geybels, M.S., Grady, W.M., Hsu, L., Hu-Lieskovan, S., Huyghe, J.R., Kim, Y.J., Krystofinski, P.E., Leiserson, M.D., Montoya, D.J., Nadel, B.B., Pellegrini, M., Pritchard, C.C., Puig-Saus, C., Quist, E.H., Raphael, B.J., Salipante, S.J., Shin, D.S., Shinbrot, E., Shirts, B., Shukla, S., Stanford, J.L., Sun, W., Tsoi, J., Upfill-Brown, A., Wheeler, D.A., Wu, C.J., Yu, M., Zaidi, S.H., Zaretsky, J.M., Gabriel, S.B., Lander, E.S., Garraway, L.A., Hudson, T.J., Fuchs, C.S., Ribas, A., Ogino, S., & Peters, Ü. (2018). *Genetic mechanisms of immune evasion in colorectal cancer. Cancer Discovery*, 8(6):730–749.
546. Ott, P. A., Hu, Z., Keskin, D. B., Shukla, S. A., Sun, J., Bozym, D. J., Zhang, W., Luoma, A., Giobbie-Hurder, A., Peter, L., Chen, C., Olive, O., Carter, T. A., Li, S., Lieb, D. J., Eisenhaure, T., Gjini, E., Stevens, J., Lane, W. J., Javeri, I., Nellaiappan, K., Salazar, A. M., Daley, H., Seaman, M., Buchbinder, E. I., Yoon, C. H., Harden, M., Lennon, N., Gabriel, S., Rodig, S. J., Barouch, D. H., Aster, J. C., Getz, G., Wucherpfennig, K., Neuberg, D., Ritz, J., Lander, E. S., Fritsch, E. F., Hacohen, N. & Wu, C. J. (2018). *Corrigendum: An immunogenic personal neoantigen vaccine for patients with melanoma. Nature*, 555(7696): 402.
547. Khajuria, R.K., Munschauer, M., Ulirsch, J.C., Fiorini, C., Ludwig, L.S., McFarland, S.K., Abdulhay, N.J., Specht, H., Keshishian, H., Mani, D.R., Jovanovic, M., Ellis, S.R., Fulco, C.P., Engreitz, J.M., Schutz, S., Lian, J., Gripp, K.W., Weinberg, O.K., Pinkus, G.S., Gehrke, L., Regev, A., Lander, E.S., Gazda, H.T., Lee, W.Y., Panse, V.G., Carr, S.A., & Sankaran, V.G. (2018). *Ribosome levels selectively regulate translation and lineage commitment in human hematopoiesis. Cell*, 173(1):90–103.
548. Tewhey, R., Kotliar, D., Park, D.S., Liu, B., Winnicki, S., Reilly, S.K., Andersen, K.G., Mikkelsen, T.S., Lander, E.S., Schaffner, S.F., & Sabeti, P.C. (2018). *Direct identification of hundreds of expression-modulating variants using a multiplexed reporter assay. Cell*, 172(5), 1132–1134.
549. Grossman, S.R., Engreitz, J., Ray, J.P., Nguyen, T.H., Hacohen, N., & Lander, E.S. (2018). *Positional specificity of different transcription factor classes within enhancers. Proceedings of the National Academy of Sciences U S A*, 115(30), E7222–E7230.
550. Yassour, M., Jason, E., Hogstrom, L.J., Arthur, T.D., Tripathi, S., Siljander, H., Selvenius, J., Oikarinen, S., Hyoty, H., Virtanen, S.M., Ilonen, J., Ferretti, P., Pasolli, E., Tett, A., Asnicar, F., Segata, N., Vlamakis, H., Lander, E.S., Huttenhower, C., Knip, M., & Xavier, R.J. (2018). *Strain-level analysis of mother-to-child bacterial transmission during the first few months of life. Cell Host Microbe*, 24(1), 146–154.e144.
551. Khera, A. V., Chaffin, M., Aragam, K. G., Haas, M. E., Roselli, C., Choi, S. H., Natarajan, P., Lander, E. S., Lubitz, S. A., Ellinor, P. T. & Kathiresan, S. (2018). *Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. Nature Genetics*, 50(9): 1219–1224.
552. Bis, J. C., Jian, X., Kunkle, B. W., Chen, Y., Hamilton-Nelson, K. L., Bush, W. S., Salerno, W. J., Lancour, D., Ma, Y., Renton, A. E., Marcora, E., Farrell, J. J., Zhao, Y., Qu, L., Ahmad, S., Amin, N., Amouyel, P., Beecham, G. W., Below, J. E., Campion, D., Charbonnier, C., Chung, J., Crane, P. K., Cruchaga, C., Cupples, L. A., Dartigues, J. F., Debette, S., Deleuze, J. F., Fulton, L., Gabriel, S. B., Genin, E., Gibbs, R. A., Goate, A., Grenier-Boley, B., Gupta, N., Haines, J. L., Havulinna, A. S., Helisalmi, S., Hiltunen, M., Howrigan, D. P., Ikram, M. A., Kaprio, J., Konrad, J., Kuzma, A., Lander, E. S., Lathrop, M., Lehtimäki, T., Lin, H., Mattila, K., Mayeux, R., Muzny, D. M., Nasser, W., Neale, B., Nho, K., Nicolas, G., Patel, D., Pericak-Vance, M. A., Perola, M., Psaty, B. M., Quenez, O., Rajabli, F., Redon, R., Reitz, C., Remes, A. M., Salomaa, V., Sarnowski, C., Schmidt, H., Schmidt, M., Schmidt, R., Soininen, H., Thornton, T. A., Tosto, G., Tzourio, C., van der Lee, S. J., van Duijn, C. M., Vardarajan, B., Wang, W., Wijsman, E., Wilson, R. K., Witten, D., Worley, K. C., Zhang, X., Bellenguez, C., Lambert, J. C., Kurki, M. I., Palotie, A., Daly, M., Boerwinkle, E., Lunetta, K. L., Destefano, A. L., Dupuis, J., Martin, E. R., Schellenberg, G. D., Seshadri, S., Naj, A. C., Fornage, M. & Farrer, L. A. (2018). *Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry*. [Epub ahead of print]
553. Natarajan, P., Peloso, G. M., Zekavat, S. M., Montasser, M., Ganna, A., Chaffin, M., Khera, A. V., Zhou, W., Bloom, J. M., Engreitz, J. M., Ernst, J., O'Connell, J. R., Ruotsalainen, S. E., Alver, M., Manichaikul, A., Johnson, W. C., Perry, J. A., Poterba, T., Seed, C., Surakka, I. L., Esko, T., Ripatti, S., Salomaa, V.,

- Correa, A., Vasani, R. S., Kellis, M., Neale, B. M., Lander, E. S., Abecasis, G., Mitchell, B., Rich, S. S., Wilson, J. G., Cupples, L. A., Rotter, J. I., Willer, C. J. & Kathiresan, S. (2018). *Deep-coverage whole genome sequences and blood lipids among 16,324 individuals*. *Nature Communications*, 9(1): 3391.
554. Munschauer, M., Nguyen, C. T., Sirokman, K., Hartigan, C. R., Hogstrom, L., Engreitz, J. M., Ulirsch, J. C., Fulco, C. P., Subramanian, V., Chen, J., Schenone, M., Guttman, M., Carr, S. A. & Lander, E. S. (2018). *The NORAD lncRNA assembles a topoisomerase complex critical for genome stability*. *Nature*, 561(7721): 132–136.
555. Alver, M., Palover, M., Saar, A., Lall, K., Zekavat, S. M., Tonisson, N., Leitsalu, L., Reigo, A., Nikopensius, T., Ainla, T., Kals, M., Magi, R., Gabriel, S. B., Eha, J., Lander, E. S., Irs, A., Philippakis, A., Marandi, T., Natarajan, P., Metspalu, A., Kathiresan, S. & Esko, T. (2018). *Recall by genotype and cascade screening for familial hypercholesterolemia in a population-based biobank from Estonia*. *Genetics in Medicine*. [Epub ahead of print]
556. Ulirsch, J. C., Verboon, J. M., Kazerounian, S., Guo, M. H., Yuan, D., Ludwig, L. S., Handsaker, R. E., Abdulhay, N. J., Fiorini, C., Genovese, G., Lim, E. T., Cheng, A., Cummings, B. B., Chao, K. R., Beggs, A. H., Genetti, C. A., Sieff, C. A., Newburger, P. E., Niewiadomska, E., Matysiak, M., Vlachos, A., Lipton, J. M., Atsidaftos, E., Glader, B., Narla, A., Gleizes, P. E., O'Donohue, M. F., Montel-Lehry, N., Amor, D. J., McCarroll, S. A., O'Donnell-Luria, A. H., Gupta, N., Gabriel, S. B., MacArthur, D. G., Lander, E. S., Lek, M., Da Costa, L., Nathan, D. G., Korostelev, A. A., Do, R., Sankaran, V. G. & Gazda, H. T. (2018). *The Genetic Landscape of Diamond-Blackfan Anemia*. *American Journal of Human Genetics*, 103(6): 930–947.
557. Hsu, J. Y., Fulco, C. P., Cole, M. A., Canver, M. C., Pellin, D., Sher, F., Farouni, R., Clement, K., Guo, J. A., Biasco, L., Orkin, S. H., Engreitz, J. M., Lander, E. S., Joung, J. K., Bauer, D. E. & Pinello, L. (2018). *CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data*. *Nature Methods*, 15(12): 992–993.
558. Khera, A. V., Chaffin, M., Zekavat, S. M., Collins, R. L., Roselli, C., Natarajan, P., Lichtman, J. H., D'Onofrio, G., Mattera, J. A., Dreyer, R. P., Spertus, J. A., Taylor, K. D., Psaty, B. M., Rich, S. S., Post, W. S., Gupta, N., Gabriel, S., Lander, E., Chen, Y. I., Talkowski, M. E., Rotter, J. I., Krumholz, H. M., & Kathiresan, S. (2018). *Whole Genome Sequencing to Characterize Monogenic and Polygenic Contributions in Patients Hospitalized with Early-Onset Myocardial Infarction*. *Circulation*.
559. Adelman, C. H., Wang, T., Sabatini, D. M. & Lander, E. S. (2019). *Genome-Wide CRISPR/Cas9 Screening for Identification of Cancer Genes in Cell Lines*. *Methods in Molecular Biology*, 1907: 125–136.
560. Keskin, D. B., Anandappa, A. J., Sun, J., Tirosh, I., Mathewson, N. D., Li, S., Oliveira, G., Giobbie-Hurder, A., Felt, K., Gjini, E., Shukla, S. A., Hu, Z., Li, L., Le, P. M., Allesoe, R. L., Richman, A. R., Kowalczyk, M. S., Abdelrahman, S., Geduldig, J. E., Charbonneau, S., Pelton, K., Iorgulescu, J. B., Elagina, L., Zhang, W., Olive, O., McCluskey, C., Olsen, L. R., Stevens, J., Lane, W. J., Salazar, A. M., Daley, H., Wen, P. Y., Chiocca, E. A., Harden, M., Lennon, N. J., Gabriel, S., Getz, G., Lander, E. S., Regev, A., Ritz, J., Neuberg, D., Rodig, S. J., Ligon, K. L., Suva, M. L., Wucherpennig, K. W., Hacohen, N., Fritsch, E. F., Livak, K. J., Ott, P. A., Wu, C. J. & Reardon, D. A. (2019). *Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial*. *Nature*, 565(7738): 234–239.
561. Schiebinger, G., Shu, J., Tabaka, M., Cleary, B., Subramanian, V., Solomon, A., Gould, J., Liu, S., Lin, S., Berube, P., Lee, L., Chen, J., Brumbaugh, J., Rigollet, P., Hochedlinger, K., Jaenisch, R., Regev, A., & Lander, E. S. (2019). *Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming*. *Cell*, 176(4): 928–943.e22.
562. Lander, E. S. (2019). *2018 William Allan Award: Discovering the Genes for Common Disease: From Families to Populations*. *Am J Hum Genet*, 104(3): 375–383.
563. Khera, A. V., Chaffin, M., Wade, K. H., Zahid, S., Brancale, J., Xia, R., Distefano, M., Senol-Cosar, O., Haas, M. E., Bick, A., Aragam, K. G., Lander, E. S., Smith, G. D., Mason-Suarez, H., Fornage, M., Lebo, M., Timpson, N. J., Kaplan, L. M. & Kathiresan, S. (2019). *Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood*. *Cell*, 177: 587–596 e589.
564. Lander, E. S., Baylis, F., Zhang, F., Charpentier, E., Berg, P., Bourgain, C., Friedrich, B., Joung, J. K., Li, J., Liu, D., Naldini, L., Nie, J. B., Qiu, R., Schoene-Seifert, B., Shao, F., Terry, S., Wei, W. & Winnacker, E. L. (2019). *Adopt a moratorium on heritable genome editing*. *Nature*, 567: 165–168.
565. Poulsen, B. E., Yang, R., Clatworthy, A. E., White, T., Osmulski, S. J., Li, L., Penaranda, C., Lander, E. S., Shores, N. & Hung, D. T. (2019). *Defining the core essential genome of Pseudomonas aeruginosa*. *Proc Natl Acad Sci U S A*.

566. Ulirsch, J. C., Verboon, J. M., Kazerounian, S., Guo, M. H., Yuan, D., Ludwig, L. S., Handsaker, R. E., Abdulhay, N. J., Fiorini, C., Genovese, G., Lim, E. T., Cheng, A., Cummings, B. B., Chao, K. R., Beggs, A. H., Genetti, C. A., Sieff, C. A., Newburger, P. E., Niewiadomska, E., Matysiak, M., Vlachos, A., Lipton, J. M., Atsidaftos, E., Glader, B., Narla, A., Gleizes, P. E., O'Donohue, M. F., Montel-Lehry, N., Amor, D. J., McCarroll, S. A., O'Donnell-Luria, A. H., Gupta, N., Gabriel, S. B., MacArthur, D. G., Lander, E. S., Lek, M., Da Costa, L., Nathan, D. G., Korostelev, A. A., Do, R., Sankaran, V. G. & Gazda, H. T. (2019). *The Genetic Landscape of Diamond-Blackfan Anemia. Am J Hum Genet.* 104: 356.
567. Johnson, E. O., LaVerriere, E., Office, E., Stanley, M., Meyer, E., Kawate, T., Gomez, J. E., Audette, R.E., Bandyopadhyay, N., Betancourt, N., Delano, K., Da Silva, I., Davis, J., Gallo, C., Gardner, M., Golas, A. J., Guinn, K. M., Kennedy, S., Korn, R., McConnell, J. A., Moss, C. E., Murphy, K. C., Nietupski, R. M., Papavinasundaram, K. G., Pinkham, J. T., Pino, P. A., Proulx, M. K., Ruecker, N., Song, N., Thompson, M., Trujillo, C., Wakabayashi, S., Wallach, J. B., Watson, C., Ioerger, T. R., Lander, E. S., Hubbard, B. K., Serrano-Wu, M. H., Ehrt, S., Fitzgerald, M., Rubin, E. J., Sasseti C. M., Schnappinger, D., & Hung, D. T. (2019). *Large-scale chemical-genetics yields new M. tuberculosis inhibitor classes. Nature.* 571(7763): 72–78.
568. Feng, Y. A., Howrigan, D. P., Abbott, L. E., Tashman, K., Cerrato, F., Singh, T., Heyne, H., Byrnes, A., Churchhouse, C., Watts, N., Solomonson, M., Lal, D., Heinzen, E. L., Dhindsa, R. S., Stanley, K. E., Cavalleri, G. L., Hakonarson, H., Helbig, I., Krause, R., May, P., Weckhuysen, S., Petrovski, S., Kamalakaran, S., Sisodiya, S. M., Cossette, P., Cotsapas, C., De Jonghe, P., Dixon-Salazar, T., Guerrini, R., Kwan, P., Marson, A. G., Stewart, R., Depondt, C., Dlugos, D. J., Scheffer, I. E., Striano, P., Freyer, C., McKenna, K., Regan, B. M., Bellows, S. T., Leu, C., Bennett, C. A., Johns, E. M. C., Macdonald, A., Shilling, H., Burgess, R., Weckhuysen, D., Bahlo, M., O'Brien, T. J., Todaro, M., Stamberger, H., Andrade, D. M., Sadoway, T. R., Mo, K., Krestel, H., Gallati, S., Papacostas, S. S., Kousiappa, I., Tanteles, G. A., Štěrbová, K., Vlčková, M., Sedláčková, L., Laššuthová, P., Klein, K. M., Rosenow, F., Reif, P. S., Knake, S., Kunz, W. S., Zsurka, G., Elger, C. E., Bauer, J., Rademacher, M., Pendziwiat, M., Muhle, H., Rademacher, A., van Baalen, A., von Spiczak, S., Stephani, U., Afawi, Z., Korczyn, A. D., Kanaan, M., Canavati, C., Kurlmann, G., Müller-Schlüter, K., Kluger, G., Häusler, M., Blatt, I., Lemke, J. R., Krey, I., Weber, Y. G., Wolking, S., Becker, F., Hengsbach, C., Rau, S., Maisch, A. F., Steinhoff, B. J., Schulze-Bonhage, A., Schubert-Bast, S., Schreiber, H., Borggräfe, I., Schankin, C. J., Mayer, T., Korinthenberg, R., Brockmann, K., Kurlmann, G., Dennig, D., Madeleyn, R., Kälviäinen, R., Auvinen, P., Saarela, A., Linnankivi, T., Lehesjoki, A. E., Rees, M. I., Chung, S. K., Pickrell, W. O., Powell, R., Schneider, N., Balestrini, S., Zagaglia, S., Braatz, V., Johnson, M. R., Auce, P., Sills, G. J., Baum, L. W., Sham, P. C., Cherny, S. S., Lui, C. H. T., Barišić, N., Delanty, N., Doherty, C. P., Shukralla, A., McCormack, M., El-Naggar, H., Canafoglia, L., Franceschetti, S., Castellotti, B., Granata, T., Zara, F., Iacomino, M., Madio, F., Vari, M. S., Mancardi, M. M., Salpietro, V., Bisulli, F., Tinuper, P., Licchetta, L., Pippucci, T., Stipa, C., Minardi, R., Gambardella, A., Labate, A., Annesi, G., Manna, L., Gagliardi, M., Parrini, E., Mei, D., Vetro, A., Bianchini, C., Montomoli, M., Doccini, V., Marini, C., Suzuki, T., Inoue, Y., Yamakawa, K., Tumiene, B., Sadleir, L. G., King, C., Mountier, E., Caglayan, S. H., Arslan, M., Yapıcı, Z., Yis, U., Topaloglu, P., Kara, B., Turkdogan, D., Gundogdu-Eken, A., Bebek, N., Ugurıseri, S., Baykan, B., Salman, B., Haryanyan, G., Yücesan, E., Kesim, Y., Ozkara, Ç., Poduri, A., Shiedley, B. R., Shain, C., Buono, R. J., Ferraro, T. N., Sperling, M. R., Lo, W., Privitera, M., French, J. A., Schachter, S., Kuzniecky, R. I., Devinsky, O., Hegde, M., Khankhanian, P., Helbig, K. L., Ellis, C. A., Spalletta, G., Piras, F., Piras, F., Gili, T., Ciullo, V., Reif, A., McQuillin, A., Bass, N., McIntosh, A., Blackwood, D., Johnstone, M., Palotie, A., Pato, M. T., Pato, C. N., Bromet, E. J., Carvalho, C. B., Achtyes, E. D., Azevedo, M. H., Kotov, R., Lehrer, D. S., Malaspina, D., Marder, S. R., Medeiros, H., Morley, C. P., Perkins, D. O., Sobell, J. L., Buckley, P. F., Macciardi, F., Rapaport, M. H., Knowles, J. A., Fanous, A. H., McCarroll, S. A., Gupta, N., Gabriel, S. B., Daly, M. J., Lander, E. S., Lowenstein, D. H., Goldstein, D. B., Lerche, H., Berkovic, S. F., & Neale, B. M. (2019). *Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. Am J Hum Genet.* 105(2): 267–282.
569. Dvela-Levitt, M., Kost-Alimova, M., Emani, M., Kohnert, E., Thompson, R., Sidhom, E. H., Rivadeneira, A., Sahakian, N., Roignot, J., Papagregoriou, G., Montesinos, M. S., Clark, A. R., McKinney, D., Gutierrez, J., Roth, M., Ronco, L., Elonga, E., Carter, T. A., Gnirke, A., Melanson, M., Hartland, K., Wiedner, N., Hsu, J. C., Deltas, C., Hughey, R., Bleyer, A. J., Kmoch, S., Zivná, M., Barešova, V., Kota,

- S., Schlondorff, J., Heiman, M., Alper, S. L., Wagner, F., Weins, A., Golub, T. R., Lander, E. S., & Greka, A. (2019). *Small Molecule Targets TMED9 and Promotes Lysosomal Degradation to Reverse Proteinopathy*. *Cell*. 178(3): 521–535 e23.
570. Albers, J., Aoun, J. E., Audia, J. E., Bailey, M. P., Barrett, P., Bartel, D., Bienamie, J. J., Blum, R. I., Boger, J., Bollenbacher, J., Bonney, M. W., Booth, B., Bradbury, D. M., Brandicourt, O., Braunwald, E., Carpenter, A. E., Chang, H. E., Cheruvu, P., Christensen, G., Church, G., Clayman, M. D., Cooney, C. L., Cox, G. F., Curley, S. J., Dahiyat, B., DePinho, R. A., Diekman, J., Doerfler, D., Dornbusch, D., Douglas, R. H., Dunsire, D., Ebright, R. H., Eskridge, W., Flesher, G. J., Fong, K., Formela, J. F., Foster-Cheek, K., Francois, C., Franken, M. P., Franklin, H., Fu, Y. X., Gage, L. P., Gardner, P., Gardner, J., Genead, M., Geraghty, J. A., Gerweck, L., Gill, S., Gillis, S., Goeddel, D. V., Goldsmith, M., Graves, K., Gray, M. A., Grayzel, D., Greene, B., Gregory, R. J., Greve-Philips, C. A., Gros, D. A., Hamburg, M. A., Hammerschmidt, M., Hao, Y., Hartounian, H., Hasnain, F., Hastings, P. J., Hawkins, E. S., He, W. W., He, W., Hirzel, A., Hong, Z., Hoppenot, H., Jia, W., Kaplan, J., Keiper, J., King, V., Kolchinsky, P., Koller, D., Laikind, P., Lander, E. S., Langer, R. S., LaVoie, D. L., Lawton, A., Lee, J. J., Leff, J. S., Lepore, J., Leschly, N., Li, Q., Liang, M. H., Lieberman, J., Lim, J., Lindenberg, M., Lippard, S. J., Liu, D. R., Liu, Y., Liu, S. L., Lodish, H., Loncar, B., Lopatin, U., Love, T. W., Lowe, D., Lowy, I., Lu, H., Luo, L., Mahanthappa, N. K., Martin, P. W. Jr., Martini, A., Martucci, W. E., McArthur, J., McCann, C. M., McCarthy, S., McLachlan, D., Mello, C., Mento, S. J., Meyers, J., Meyers, R., Mills, K., Moch, K. I., Moos, W. H., Narachi, M., Nashat, A., Newell, W. J., Nodelman, O., Olle, B., Osborn, J. E., Oyler, J. V., Pao, W., Patel, N., Perez, R., Peterkin, D., Pompino, A., Pruzanski, M., Dan Quinn, Qutub, A. A., Raab, M. G., Radaelli, M., Rakhit, A., Ramamoorthi, K., Rastetter, W., Reed, J. C., Reinhart, H., Rhodes, J. P., Rieflin, W. J., Rong, L., Rosan, D. E., Rosenblatt, M., Rutter, W. J., Samudio, I., Samuels, C., Sato, V. L., Saunders, B., Scadden, D., Scangos, G., Scarlett, J. A., Schegerin, M., Schimmel, P., Schreiber, S. L., Schubert, C. R., Schulman, A., Shaff, E., Shaffer, R., Sharp, P. A., Sheng, M., Sheng, G., Shenk, T., Shi, F., Silos-Santiago, A., Simonian, N., Slaterry, W., Smith, J. A., Stocks, C., Stoffel, M., Su, M., Su, L., Tandon, N., Tang, C. M., Taunton-Rigby, A., Tezapsidis, N., Theuer, C., Thornberry, N. A., Tolar, M., Topol, E., Tormos, W., Trask, A., Truex, S., Tuschl, T., Varmus, H. E., Vasconcelles, M. J., Vounatsos, M., Walbert, T. P., Walsh, C. T., Wang, J., Wang, J., Wang, N., Westphal, C., Wierenga, W., Williams, D. E., Williams, L. T., Wingham, R. E., Wirth, P., Witt, R., Wood, C., Woodhouse, D. J., Wright, R., Wu, Y., Xanthopoulos, K. G., Xiao, C., Xiao, T. S., Xie, J., Xu, Y., Xu, Z. C., Yakatan, G. J., Yuan, L., Yung, W. K. A., Zamore, P. D., Zaydman, M., Zeng, X. M., Zerhouni, E., Zhang, F., Zhang, Q., & Zhang, S. (2019). *Chinese scientists and U.S. leadership in the life sciences*. *Nat Biotechnol*. 37(11): 1261–1263.
571. Hoch, E., Florez, J. C., Lander, E. S., & Jacobs, S. B. R. (2019). *Gain-of-Function Claims for Type-2-Diabetes-Associated Coding Variants in SLC16A11 Are Not Supported by the Experimental Data*. *Cell Rep*. 29(3): 778–780.
572. Khera, A. V., Mason-Suares, H., Brockman, D., Wang, M., VanDenburgh, M. J., Senol-Cosar, O., Patterson, C., Newton-Cheh, C., Zekavat, S. M., Pester, J., Chasman, D. I., Kabrhel, C., Jensen, M. K., Manson, J. E., Gaziano, J. M., Taylor, K. D., Sotoodehnia, N., Post, W. S., Rich, S. S., Rotter, J. I., Lander, E. S., Rehm, H. L., Ng K., Philippakis, A., Lebo, M., Albert, CM, & Kathiresan, S. (2019). *Rare Genetic Variants Associated With Sudden Cardiac Death in Adults*. *J Am Coll Cardiol*. 74(21): 2623–2634.
573. Fulco, C. P., Nasser, J., Jones, T. R., Munson, G., Bergman, D. T., Subramanian, V., Grossman, S. R., Anyoha, R., Doughty, B. R., Patwardhan, T. A., Nguyen, T. H., Kane, M., Perez, E. M., Durand, N. C., Lareau, C. A., Stamenova, E. K., Aiden, E. L., Lander, E. S., & Engreitz, J. M. (2019). *Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations*. *Nat Genet*. 51(12): 1664–1669.
574. Basak, A., Munschauer, M., Lareau, C. A., Montbleau, K. E., Ulirsch, J. C., Hartigan, C. R., Schenone, M., Lian, J., Wang, Y., Huang, Y., Wu, X., Gehrke, L., Rice, C. M., An, X., Christou, H. A., Mohandas, N., Carr, S. A., Chen, J. J., Orkin, S. H., Lander, E. S. & Sankaran, V. G. (2020). *Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation*. *Nature genetics*. 52(2): 138–145.
575. Dietlein, F., Weghorn, D., Taylor-Weiner, A., Richters, A., Reardon, B., Liu, D., Lander, E. S., Van Allen, E. M. & Sunyaev, S. R. (2020). *Identification of cancer driver genes based on nucleotide context*. *Nature genetics*. 52(2): 208–218.
576. Painter, C. A., Jain, E., Tomson, B. N., Dunphy, M., Stoddard, R. E., Thomas, B. S., Damon, A. L., Shah, S., Kim, D., Gomez Tejeda Zano, J., Hornick, J. L., Chen, Y. L., Merriam, P., Raut, C. P., Demetri, G. D., Van Tine, B. A., Lander, E.

S., Golub, T. R. & Wagle, N. (2020). *The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. Nature medicine.* 26(2): 181–187.

577. Ray, J. P., de Boer, C. G., Fulco, C. P., Lareau, C. A., Kanai, M., Ulirsch, J. C., Tewhey, R., Ludwig, L. S., Reilly, S. K., Bergman, D. T., Engreitz, J. M., Issner, R., Finucane, H. K., Lander, E. S., Regev, A. & Hacohen, N. (2020). *Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature communications.* 11(1): 1237.

578. Vallabh, S. M., Minikel, E. V., Schreiber, S. L. & Lander, E. S. (2020). *Towards a treatment for genetic prion disease: trials and biomarkers. The Lancet. Neurology.* 19(4): 361–368.

579. Abel, H. J., Larson, D. E., Regier, A. A., Chiang, C., Das, I., Kanchi, K. L., Laver, R. M., Neale, B. M., Salerno, W. J., Reeves, C., Buyske, S., NHGRI Centers for Common Disease Genomics, Matise, T. C., Muzny, D. M., Zody, M. C., Lander, E. S., Dutcher, S. K., Stitzel, N. O., & Hall, I. M. (2020). *Mapping and characterization of structural variation in 17,795 human genomes. Nature.* 583(7814): 83–89.

580. Fahed, A. C., Wang, M., Homburger, J. R., Patel, A. P., Bick, A. G., Nebel, C. L., Lai, C., Brockman, D., Philippakis, A., Ellinor, P. T., Cassa, C. A., Lebo, M., Ng, K., Lander, E. S., Zhou, A. Y., Kathiresan, S., & Khera, A. V. (2020). *Polygenic background modifies penetrance of monogenic variants for tier 1 genomic conditions. Nature communications.* 11(1): 3635.

581. Zoonomia Consortium. (2020). *A comparative genomics multitool for scientific discovery and conservation. Nature* 587(7833): 240–245.

582. Bick A.G., Weinstock J.S., Nandakumar S.K., Fulco C.P., Bao E.L., Zekavat S.M., Szeto M.D., Liao X., Leventhal M.J., Nasser J., Chang K., Laurie C., Burugula B.B., Gibson C.J., Lin A.E., Taub M.A., Aguet F., Ardlie K., Mitchell B.D., Barnes K.C., Moscati A., Fornage M., Redline S., Psaty B.M., Silverman E.K., Weiss S.T., Palmer N.D., Vasan R.S., Burchard E.G., Kardia S.L.R., He J., Kaplan R.C., Smith N.L., Arnett D.K., Schwartz D.A., Correa A., de Andrade M., Guo X., Konkole B.A., Custer B., Peralta J.M., Gui H., Meyers D.A., McGarvey S.T., Chen I.Y., Shoemaker M.B., Peyser P.A., Broome J.G., Gogarten S.M., Wang F.F., Wong Q., Montasser M.E., Daya M., Kenny E.E., North K.E., Launer L.J., Cade B.E., Bis J.C., Cho M.H., Lasky-Su J., Bowden D.W., Cupples L.A., Mak A.C.Y., Becker L.C., Smith J.A., Kelly T.N., Aslibekyan S., Heckbert S.R., Tiwari H.K., Yang I.V., Heit J.A., Lubitz S.A., Johnson J.M., Curran J.E., Wenzel S.E., Weeks D.E., Rao D.C., Darbar D., Moon J.Y., Tracy R.P., Buth E.J., Rafaels N., Loos R.J.F., Durda P., Liu Y., Hou L., Lee J., Kachroo P., Freedman B.I., Levy D., Bielak L.F., Hixson J.E., Floyd J.S., Whitsel E.A., Ellinor P.T., Irvin M.R., Fingerlin T.E., Raffield L.M., Armasu S.M., Wheeler M.M., Sabino E.C., Blangero J., Williams L.K., Levy B.D., Sheu W.H., Roden D.M., Boerwinkle E., Manson J.E., Mathias R.A., Desai P., Taylor K.D., Johnson A.D.; NHLBI Trans-Omics for Precision Medicine Consortium, Auer P.L., Kooperberg C., Laurie C.C., Blackwell T.W., Smith A.V., Zhao H., Lange E., Lange L., Rich S.S., Rotter J.I., Wilson J.G., Scheet P., Kitzman J.O., Lander E.S., Engreitz J.M., Ebert B.L., Reiner A.P., Jaiswal S., Abecasis G., Sankaran V.G., Kathiresan S., & Natarajan P. (2020). *Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature.* 586(7831): 763–768.

583. Schmidt N., Lareau C.A., Keshishian H., Ganskih S., Schneider C., Hennig T., Melanson R., Werner S., Wei Y., Zimmer M., Ade J., Kirschner L., Zielinski S., Dölken L., Lander E.S., Caliskan N., Fischer U., Vogel J., Carr S.A., Bodem J., & Munschauer M. (2020). *The SARS-CoV-2 RNA-protein interactome in infected human cells. Nature Microbiology.* Epub ahead of print.

584. Marshall J.L., Doughty B.R., Subramanian V., Guckelberger P., Wang Q., Chen L.M., Rodrigues S.G., Zhang K., Fulco C.P., Nasser J., Grinkevich E.J., Noel T., Mangiameli S., Bergman D.T., Greka A., Lander E.S., Chen F., & Engreitz J.M. *HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequencing of DNA probes.* (2020). *Proceedings of the National Academy of Sciences.* 117(52): 33404–33413.

585. Mitchell C.M., Mazzoni C., Hogstrom L., Bryant A., Bergerat A., Cher A., Pochan S., Herman P., Carrigan M., Sharp K., Huttenhower C., Lander E.S., Vlamakis H., Xavier R.J., & Yassour M. *Delivery Mode Affects Stability of Early Infant Gut Microbiota.* (2020). *Cell Reports Medicine.* 1(9): 100156.

586. Collins F.S., Doudna J.A., Lander E.S., Rotimi C.N. *Human Molecular Genetics and Genomics—Important Advances and Exciting Possibilities.* (2021). *New England Journal of Medicine.* Epub ahead of print.

587. Sinnott-Armstrong N., Sousa I.S., Laber S., Rendina-Ruedy E., Nitter Dankel S.E., Ferreira T., Mellgren G., Karasik D., Rivas M., Pritchard J., Guntur A.R., Cox R.D., Lindgren C.M., Hauner H., Sallari R., Rosen C.J., Hsu Y.H., Lander E.S., Kiel D.P., Claussnitzer M. *A regulatory variant at 3q21.1 confers an increased pleiotropic*

risk for hyperglycemia and altered bone mineral density. (2021) *Cell Metab.* Epub ahead of print.

Senator DUCKWORTH. Thank you, Dr. Lander. I will start with the first round of questions.

As a member of the Senate, I have a strong commitment to ensuring that our country is a leader in innovation and technology. This simply cannot be done without women and without diversity in our STEM work force. Dr. Lander, you have been the leader of the Broad Institute for 17 years and just explained to this committee that you have sought to support women in science. However, statistics compiled by the Broad Institute, suggest that it struggles to ensure robust representation by women in STEM roles. For example, at Broad in 2018, women made up only about 25 percent of employees in computational science and software engineering roles. While this may track with national figures, maintaining the status quo is not what we need to be competitive. We must do better.

Dr. Lander, my question to you is this. Did you do enough at the Broad Institute to address gender gaps in STEM roles? And if confirmed as Director, what concrete steps will you take to rectify gender and diversity gaps in the STEM fields?

Dr. LANDER. Well, Senator, I really appreciate the question because it is a topic I care tremendously about. When we did the survey, to look at representation across the Broad, we found that we had equal representation in all areas other than the computational field. And as you know, representation in the computational fields is terrible, with regard to gender and tech. It is 15 percent.

We were very concerned that the one area in the Broad where we were not at parity, was at the computational field and that led us to an institute-wide process involving our group, Women at Broad, to look at ways to increase that representation, to go out to the conferences for women in computational sciences, and invite more people to come and apply, to go out and present at more of these conferences. And we have already made a significant difference, particularly increasing women the more senior roles in computational science.

It is not at the 50 percent that it is across the whole rest of the Broad, but it is tracking up and we are very committed to getting it up there.

Senator DUCKWORTH. If confirmed as Director, what concrete steps will you take to rectify gender and diversity gaps in the STEM fields, for our Nation?

Dr. LANDER. Well, thank you for that question, because I am really excited about that and, as I say, have worked on it.

The first thing I would do—I have a lot of ideas, myself, but the first thing—the place I know to start is to invite to the table all of the people who are most effected and, therefore, know the most. So, if confirmed, the first thing I would do is, OSTP would convene the amazing organizations that advocate for women and people of color in STEM fields, to gather the best ideas and recruit—to recruit, support, and retain women and underrepresented peoples.

I think OSTP also has this ability to look at diversity across Federal agencies and look at what has worked there. And from all of

this, I think OSTP can develop best practices and work with companies and institutions to adopt them.

I would bring my own ideas to it, but I do not want to privilege my ideas over others. But some of the things I think matter a lot, ensuring mentorship and opportunities early, starting in middle school where we lose most girls—many girls and people of color. I am a huge supporter and fan of groups like, Girls Who Code and Resilient Coders.

I think science is not about knowing the answer in the back of the book. Science is about asking questions that are not in the book at all. And experiences like this, well, if a young person builds something, creates something, invents something, discovers something, they are hooked. That is what we have got to do, and we have got to do it early and often and consistently.

We also have to lift up role models. Life them up high so that people can see themselves as scientist. We have to work with academia and industry to address power dynamics in academic labs and in corporate labs. And we have to commit and get people to commit to diverse slates in every search.

Then, finally, like we tried to do at the Broad, we have to set goals, we have to measure, and we have to hold ourselves accountable. And when we fall short, we have to shine a spotlight on it.

Those are some of the things I would offer of—based on my experience. But as I say, I would very much want to first bring everyone to the table, because there are people who will know more and there are people who will know different. And we have got to start with that. But, if confirmed, this would be one of the first things I would do, in the role at OSTP.

Senator DUCKWORTH. Thank you. I now recognize Ranking Member Wicker for his questions.

Senator WICKER. Thank you very much. And very fascinating testimony so far.

You know, Dr. Lander, I wish I could spend my first round asking you to elaborate on the Human Genome project and prospects for Alzheimer's and, also, a few more examples of why it is important for scientists to have a dose of humility. Unfortunately, I have got to ask questions about—

Dr. LANDER. Sure.

Senator WICKER.—some requests that we have made. And of course, Senator Duckworth eluded to these, also.

We have asked for 10 years of donors to the Broad Institute. We do not have a complete list yet. Are you going to be able to get those to us?

Dr. LANDER. I—Senator, I believe we sent you eight years, which is what was available. I can ask to see if they can go back two more.

Senator WICKER. OK, well, I wish would. It is important to us that we—we asked for 10 for a reason. So, you are going to try to do that?

Dr. LANDER. I will try to do that, sir.
[The information referred to follows:]

Donors, 2011–2012

The Broad Institute became a 501(c)(3) in FY 2010. Beginning in FY 2013, it began regularly preparing an annual donor report, based on gifts received of \$1,000

or more. Lists were provided to the Committee covering the past eight Fiscal Years (2013–2020).

To address the Committee's request for two additional years of donors (2011–2012), the Broad Institute agreed to review its files and was able to provide a donor list for these years (below).

Academia-Sinica
 Agilent Technologies Foundation
 Agilent Technologies, Inc.
 Airedale Health Foundation
 Jill and David Altshuler
 American Kennel Club, Canine Health Foundation
 Amgen, Inc.
 Valerie C. Anastasio
 AstraZeneca UK Limited
 Dennis Ausiello, M.D.
 Autism Consortium
 Drs. David Baltimore and Alice S. Huang
 Blavatnik Family Foundation
 Katherine and David Bradley
 Brain and Behavior Research Foundation
 Bristol-Myers Squibb Company
 Eli and Edythe L. Broad
 Leslie Burke Sampson
 Burroughs Wellcome Fund
 Sadiya Carr
 Centocor
 Christopher and Diana Chapman Walsh
 CHDI Foundation, Inc.
 Crohn's and Colitis Foundation of America
 Cubist Pharmaceuticals
 Damon Runyon Cancer Research Foundation
 Kent and Liz Dauten
 Doris Duke Charitable Foundation
 Jamie Walters El-Erian and Dr. Mohamed El-Erian
 Eli Lilly and Company
 The European Bioinformatics Institute
 Joan Faubion, Ph.D.
 Alan Fein and Ellen Kolton
 Fondation Leducq
 John B. Forrest, Jr.
 Foundation for Neurologic Diseases
 Galenea Corporation
 Patty and Paul Gannon
 Bill & Melinda Gates Foundation
 Stephen and Wendy Gellman Gerstner Family Foundation
 Todd and Martha Golub
 Bill Helman
 The Leona M. and Harry B. Helmsley Charitable Trust
 Sylvan C. Herman Foundation
 Human Frontier Science Program
 International SAE Consortium, LTD.
 Irish Wolfhound Foundation
 Irish Wolfhound Club of America
 Jewish Communal Fund
 Johnson & Johnson Pharmaceutical Research & Development LLC
 Juvenile Diabetes Foundation International
 Juvenile Diabetes Research Foundation
 Klarman Family Foundation
 Seth and Beth Klarman
 Johanna L. Klein
 The Esther A. & Joseph Klingenstein Fund, Inc.
 Eric and Lori Lander
 William and Leslie Lee Leonberger Health Foundation
 Arthur D. Levinson
 Lilly USA, LLC
 The John F. MacDonald Fund for Pseudomonas Research in memory of John F. MacDonald

Barbara V. McInnes
 The McKnight Endowment Fund for Neuroscience
 Medicines for Malaria Venture
 Merck Genome Research Institute
 The Merkin Family Foundation
 Montreal Heart Institute
 Gordon & Betty Moore Foundation
 Multiple Myeloma Research Consortium
 Nestlé Research Center
 The New York Community Trust
 Novartis Institutes for BioMedical Research
 Ontario Cancer Research Institute
 Peter and Minou Palandjian
 Sarah Pearson and Don Balcom
 Pfizer, Inc.
 Prostate Cancer Foundation
 Julian H. Robertson, Jr.
 Paul Rotiroti
 SAIC-Frederick, Inc.
 Sanofi-Aventis U.S., LLC
 Stuart Schreiber and Mimi Packman
 Phillip and Ann Sharp
 Sigma-Aldrich
 Instituto Carlos Slim de la Salud
 Ted and Vada Stanley
 Stanley Medical Research Institute
 Starr Foundation
 Patty Stonesifer and Michael Kinsley
 Kathan and Don Tracy
 Peg Van Doren
 Nancy Vollmer & Chris McDonough
 Christopher and Diana Chapman Walsh
 Helen Hay Whitney Foundation
 The Wodecroft Foundation

Senator WICKER. OK, thank you very much. And then—and then, Senator Duckworth mentioned Jeffrey Epstein. We asked for information regarding the second time you met with him in 2012. Can you commit to fulfilling this outstanding request for information? [The information referred to follows:]

As previously reported to the Committee: Neither the Broad Institute nor Dr. Lander had any relationship with Epstein, and neither ever requested or received any funding from him or his foundations. The only interaction consisted of meeting him briefly at two events, a few weeks apart in the spring of 2012, with multiple Harvard donors, faculty and others.

The Committee has asked for a description of the two events. This is provided below:

The two Harvard events were organized by the university and donors, to give donors and prospective donors an opportunity to meet a range of Harvard-affiliated faculty.

Event #1: April 15, 2012

- Lunch, involving about fifteen people, including three or four donors or prospective donors.
- Each of the faculty, including Dr. Lander, made presentations about the state of research in their respective fields, and answered questions from the group, including Epstein.
- Event lasted for approximately sixty minutes. Dr. Lander attended the entire event.

Event #2: May 12, 2012

- Dinner involving about forty people, including about ten Harvard donors or prospective donors.

- Dr. Lander was invited to dinner but did not attend. He stopped by the pre-dinner reception and spoke with several donors or prospective donors, including Epstein.
- Dr. Lander stayed for about thirty minutes.

After these two events, Dr. Lander never saw or spoke to Epstein again.

Dr. LANDER. Yes, sir, I can. May I say something about Epstein?
Senator WICKER. Certainly.

Dr. LANDER. Jeffrey Epstein was an abhorrent individual and my heart goes out to his victims. I chose to have no association whatsoever with him. We never requested funds. We never received funds—from him, from his foundation. The sum total of my interactions was that I met him briefly at two events within the span of three weeks, in the Spring of 2012.

Senator WICKER. OK, well, I think it is important that you be given a chance to say that.

Dr. LANDER. I will. And I am going to say, I did not know about his sordid history before that point.

Senator WICKER. Right.

Dr. LANDER. As soon as I learned about it, I had nothing to do with him, thereafter.

Senator WICKER. If you could simply answer——

Dr. LANDER. Yes, sir, I will.

Senator WICKER.—our specific question, it would—I think it would help your case.

Dr. LANDER. Absolutely.

Senator WICKER. And I think people on both sides of the dais would be well served.

Dr. LANDER. Absolutely.

Senator WICKER. And then, with regard to your future plans with the Broad Institute, those of us that are in public service have a date in which our public service will end. It is expected that you would go back to the Broad Institute. And there are questions that need to be answered about whether you are going to be able to avoid prioritizing your work with the Broad Institute that might favor people back there at the Institute, at the expense of others.

So, I want to give you an opportunity to address that concern which, undoubtedly, does not come as a surprise to you, at this point.

Dr. LANDER. Senator, if confirmed, I will do that job in a completely even-handed way. I have said I particularly care about the fact that we concentrate far too much funding in a few place in this country. One of my priorities is to make sure that, in fact, we bring in all of America into science. And so, I can assure you, I will not favor, in any way, institutions I have been associated with. And to the contrary, really think it is important that we broaden that scope.

Senator WICKER. OK. Well, do you—do you think you will go back to the Broad Institute when you leave this position?

Dr. LANDER. I have said, and I think I probably will.

Senator WICKER. Well, just be aware that is a concern. But you did segue to a matter that I will ask you to drill down on in the last 45 seconds that I have. How—what steps can we take to make sure the research is not just concentrated in two favored states,

that—states like, perhaps, Illinois and Mississippi, that might be able contribute to this great quest we have for knowledge?

Dr. LANDER. Well, Senator, I—as I say, I care a lot about this. And I think creating programs that support and expand the national labs, which are distributed across the country, creating regional technology hubs, supporting focuses of particular excellence in different states. I think there are a large number of programs that can help create critical masses that become magnets.

We have seen it happen with the manufacturing institutes that were created. A PCAST report, when I was the Co-chair of PCAST, called for these Manufacturing USA institutes and there are these institutes in a number of states. There is one in Illinois, for example. But we need to—we need to be thinking about mechanisms to create critical mass, all over the country, because we cannot succeed without it.

So, I of course—I am very sensitive to the fact that I come from a State and a city, and institutions that have received lots of funding. That cannot be the way we run funding in the country is that things are just concentrated. It will not succeed.

Senator WICKER. Thank you, sir and thank you, Madam Chair.

Senator DUCKWORTH. Thank you.

Remotely, Senator Hickenlooper.

**STATEMENT OF HON. JOHN HICKENLOOPER,
U.S. SENATOR FROM COLORADO**

Senator HICKENLOOPER. Thank you very much, Madam Chair. And Dr. Lander, thank you so much for being willing to step into public service and what a remarkable career and what a remarkable life you have had.

Let me ask my first question. As a former geologist, I have seen firsthand how intricate Earth Science can be. Climate action is, and should remain, a priority in this Administration. One of OSTP's duties is to oversee the U.S. Global Change Research Program, to try and coalesce climate research across all 13 Federal agencies that are working on it, to produce the quadrennial, The National Climate Assessment. Can you describe how OSTP will preserve scientific integrity, when producing the next National Climate Assessment?

Dr. LANDER. Well, thank you, Senator. The—all of—all of the work at OSTP has to be rooted in scientific integrity. With regard to the Climate Assessment, the first thing is good process. It is—that National Climate Assessment involves a process that brings together lots of voices to wrestle in a structured way, so that lots of evidence is presented, and transparently.

And then, the other really fundamental part is to embrace dissent and disagreements. I think science is strong, because science debates, because science embraces dissent. And so, if at the end of a process we do not all agree on the answers, we have to represent that range of dissent. That is what scientific integrity is about is to speak the truth. And we have to keep that separate from any external interference from any direction that is not about the evidence itself. And if committed, I will promise to support and enforce that kind of integrity, not just for the National Climate Assessment, but for everything that OSTP does.

Senator HICKENLOOPER. That is great. I appreciate that. Second question, COVID-19, the pandemic, has highlighted so many things, including the importance of science to provide solutions to these modern problems. And the U.S. research enterprises span numerous Federal agencies, national labs, as we have already been discussing. We also have to recognize the contributions from many of the leading universities and graduate researchers, including of course, the University of Colorado and Colorado State University, Colorado School of Mines. I have to list them.

Two things, can you comment on how you believe COVID-19—the COVID-19 pandemic impacted Federal researchers and how you would lead OSTP to reinvigorate the research workforce? And then, if you can tag onto that, and how do we work to prevent future pandemics?

Dr. LANDER. Well, what great questions. Thank you very much, Senator. The COVID-19 pandemic has had a devastating effect in many parts—you know, in all parts of the country. It has certainly had a huge impact in the research enterprise. The biggest impact has been on women scientists. As the economy shutdown, the burdens of childcare fell disproportionately on women scientists. It is part of an overall pattern of more than two million women leaving the workforce since the pandemic.

It had impacts on labs whose funding may have run out in the middle of this period and will not have been able to reach the goals they had promised to reach. And has impacts on graduate students and post-docs, who have a limited time and they have lost critical time in their projects. So, it is going to require from the Federal Government that we have a flexibility with regard to supporting the research enterprise through an enormous disruption, to support people in laboratories.

What we really have to do is make sure we never have this again. There will always be emerging infectious diseases. We have to make sure that they never turn into pandemics like this. And I think we have to set very bold goals.

It was great that we could produce a vaccine in a year and then, get it distributed. We have to do much better. I think the sort of goals we need—and I think what is possible with science today, is to say within 100 days from the detection of a potential pandemic, we should be able to have enough doses of an approved vaccine, clinically tested, for the whole country. Within 100 days. And when you say something like that, you gulp. But then, you take it apart and you say, yes, we can do those pieces. It will require thinking differently about every one of them.

What interests me, what excites me about this potential role, if confirmed, is to try to help us come together and set really bold goals and respond to them. Because I have seen America do it again and again and I think we can do it with regard to pandemics. This should be the last time—the last time that we have a pandemic like this. Not the last time we are going to need to respond, but the last time something devastates our country and the whole world, in this way, if we play—if we play our role. We owe that to future generations. It is a generational responsibility.

Senator HICKENLOOPER. I appreciate very much your willingness to take on those big challenges and to make real bold commit-

ments. A hundred days, that is—that is amazing if that can be done, and I believe that you could do it.

Anyway, I will yield—I am out of time. I have many more questions, but I will yield my time back to the Chair—or my lack of time back to the Chair. Again, Dr. Lander, thank you for being willing to do this. I look forward to working with you.

Dr. LANDER. Thank you.

Senator DUCKWORTH. Senator Thune.

**STATEMENT OF HON. JOHN THUNE,
U.S. SENATOR FROM SOUTH DAKOTA**

Senator THUNE. Thank you, Madam Chair and thank you, Dr. Lander for being here today. The Office of Science and Technology Policy always plays a significant role in coordinating Federal R&D initiatives and the rise in scientific prowess of China and other nations has made that role only more crucial today. It is imperative that the United States maintain its global leadership in the development, commercialization, and standardization of innovative technologies.

During my time as Chairman of this Committee, we successfully enacted the American Innovation and Competitiveness Act to better coordinate R&D efforts at the Department of Commerce and the NSF, as well as the National Quantum Initiative Act to strengthen and unify the focus of the Federal Government on developing quantum technologies. Both of these bills were bipartisan and drew broad support from industry and the scientific community.

The U.S. continues to lead the world in the development and commercialization of innovative technologies, and we cannot cede that competitive advantage to China. And it is crucial that the U.S. act boldly to solidify American leadership in science and in technology.

Dr. Lander, at a hearing two weeks ago, Dr. Kelvin Droegemeier made an insightful comment on the need for private sector to be involved in strategic decisionmaking when it comes to research partnerships, rather than simply being brought in after the program has been established. How do you believe the Federal Government can better incorporate the private sector as a partner in R&D initiatives?

Dr. LANDER. Thank you, Senator. The biggest challenges facing the country today, many of them involve these technologies of the future. And I think a gap has become apparent between what we can do amazingly well in foundational research, and what we can do amazingly well with vibrant industry. And there is a gap of things that fall between, where government needs to work both with basic research and with industry to help fill that gap for things that are not yet a business plan but could launch 100 businesses or 1,000 businesses.

So, I think partnerships in many of these technologies, quantum computing, artificial intelligence, synthetic biology, different kind of telecommunications, are going to be really crucial. We have to do this in an American way. We watch China doing this, in the way of a civil-military fusion and that is just not our way of doing it.

But we need an American solution to it that brings together these great sectors we have to fill that middle. And sometimes, that

is going to be creating the infrastructure that many startup businesses need but cannot afford to produce themselves. We see that with manufacturing, for example. Sometimes, it is going to be derisking technologies because no sensible investor would invest in those technologies because of the risk. But as a country, we can say we are going to need this technology. Let us derisk it together.

I think that is, perhaps, the most interesting question about our scientific—science and technology strategy going forward is, 75 years ago that really was not the case. Today we face international competition, and we face big technologies that will require us to act together as a country, and yet, still do it in a way that is based on free enterprise.

So, I—if confirmed, I am very eager to help and to work with you and your colleagues to figure how we do this best. And I see many ideas already being floated for this.

Senator THUNE. Last year, several Federal agencies were breached in a supply chain attack by malicious hackers. An attack at this scale has an enormous effect on our economy and national security. If confirmed, how would OSTP respond to this economic espionage and work with industry to combat ongoing cyber-attacks?

Dr. LANDER. Well, Senator, the nature of cyber-attacks that steal intellectual property from the United States, for example, are very concerning. We have to approach these things in multiple ways—security, of course, and then, also, technology. Sometimes we are patching holes in cyber and I think it is important to be able to step back and ask, how can we make fundamental changes to the integrity of our cyber defense, that would ensure fewer holes?

I think there is a lot of active discussion right now, about ways to rethink aspects of our cyber defense. And if confirmed, OSTP has important roles in this, and I would be a very active participant in trying to see how we defend ourselves technologically. And then, of course, we have to defend ourselves with regard to research security.

Senator THUNE. I see my time has expired, Madam Chair. Thank you. Thank you, Dr. Lander.

Senator DUCKWORTH. Thank you. Senator Blumenthal.

**STATEMENT OF HON. RICHARD BLUMENTHAL,
U.S. SENATOR FROM CONNECTICUT**

Senator BLUMENTHAL. Thanks, Madam Chair. Welcome to the Committee, Dr. Lander. You have an extraordinary and very impressive background in both academia and elsewhere. And I want to ask you, at the outset, a question that will not determine my vote on your nomination. Since I am in the middle of reading Walter Isaacson's book, "The Codebreakers", I would like your opinion of the book—what you think of it. And I do have a reason for asking about it, though.

Dr. LANDER. OK. I am—Senator, it is an excellent question, and I am going to have to say, I have not read the book yet. Having been in—

Senator BLUMENTHAL. That is fair enough.

Dr. LANDER. Yes.

Senator BLUMENTHAL. Let me just say, one of the—there are a couple of themes of the book. One is a recurrent theme in Walter

Isaacson's works, which is that great inventions and innovation are the result of cooperation and collaboration among teams of scientists and also, academia, private industry, and government. And I think your appointment would further that kind for collaboration and partnership.

But another kind of subplot of the book, since it is about a woman scientist, is that women are sometimes discriminated against or harassed in the world of science, as they are in many other professions, as well. I have introduced a measure called Combatting Sexual Harassment in Science Act. I have done it with Senator Smith of Minnesota. It was originally championed by then Senator Kamala Harris. I would like your commitment to support, at least, the goals of the legislation to end harassment and perhaps, for the legislation itself, which I hope will be incorporated in the Endless Frontier Act.

Dr. LANDER. You have my enthusiastic support and commitment toward those goals. They are extremely important, and I think there are many, many approaches we have to take to end that.

Senator BLUMENTHAL. I have also introduced a measure called Supporting Early Career Researchers Act, to give American STEM researchers, who are just beginning in their fields—especially women and traditionally underrepresented minorities more opportunities in the world of science, particularly important, as you have noted, because of the impact of COVID. It would direct NSF to establish a new post-doctoral fellowship program to support the next generation of STEM talent. One of my colleagues, Senator Klobuchar has been particularly instrumental in joining this effort. I think we lose valuable talent because of the potential obstacles for, and inequalities for, certain minorities. So, again, I would ask for your support, as Director of OSTP for this kind of effort, and in particular, that legislation.

Dr. LANDER. Senator, I commit to that.

Senator BLUMENTHAL. I have been very interested—I am a former prosecutor. I still think of myself as a litigator. Particularly interested in your work on forensic science, the Innocence Project. Do you think that the legal profession, and our justice system, has made sufficient use of science in the kind of forensic evidence that is submitted and particularly, in the more serious cases that were involved in the Innocence Project?

Dr. LANDER. Senator, the—science is a force for truth, for getting the right answer and our justice system needs that as a foundation. For anything else, is to know the right answers. I think we have not always availed ourselves of the best science to get those answers, or more troublingly, not always done it in the rigorous ways to be able to trust those answers. That all of these scientific methods, when they come to court, need empirical evidence.

So, this is an extremely important topic, to make sure that science can be a really strong supporter of the search for justice. It has mattered to me for 30 years and, if confirmed, I will devote attention to making sure we fully realize the promise of this for justice.

Senator BLUMENTHAL. Thank you. My time has expired, but there is a wealth of conversation that I would like to have with

you, and I would hope that we could spend some time talking about that last topic, as well as some of the others.

Dr. LANDER. If confirmed, I would love to do that.

Senator BLUMENTHAL. Great, thank you very much.

Senator DUCKWORTH. A very patient Senator Blunt.

**STATEMENT OF HON. ROY BLUNT,
U.S. SENATOR FROM MISSOURI**

Senator BLUNT. Thank you, Chairman. Dr. Lander, it is good to see you here. The President is seeking a lot of new authorities for research entities in the government, from the National Science Foundation to the Department of Energy. The one he mentioned last night was a new concept in health, ARPA-H. Talk about how that would be different than what NIH has been doing. And also, talk about your view of whether the best place for that is at the National Institute of Health.

Dr. LANDER. Well, Senator, first let me say thank you to you for your tremendous and consistent support of biomedical research. Biomedical research is an extraordinary gem of the United States and it is because the Congress has supported it for so long and so strongly. So, thank you.

The idea of an ARPA-H has arisen, again, because of one of these gaps that I was referring to before, in the discussion with Senator Thune. We have unbelievable foundational research in this country that, through NIH grants, can discover all sorts of things. We have a vibrant biotech industry that is able to take a business plan and run with it. There are a lot of things that have big gaps in between. They are, you might call them, platforms.

I will give one example, if I may. Very often drugs have side effects because they do not just act in the place you want them to act, but they act in other places in the body. What if you could build a post office, a zip code, that would deliver this drug to the right cell type? Well, you could dramatically reduce many side effects and probably be able to increase the dose if you know it is going to the right place. No, NIH basic research grant could do such a thing, not your traditional R01s. And no sensible startup biotech would take that on.

These are the kinds of DARPA-like projects that led to the Internet and the GPS and we now see they could lead to things that would launch 1,000 opportunities. To me, this idea of DARPA, within biomedicine, is exactly that. It is to build those platforms to be able to overcome market failures, to take on bold challenges. And where should it sit? My answer is within the NIH. If you were to try to set up a separate thing, I think there would be duplication and competition.

Senator BLUNT. Let me see if I can get another question in here.

Dr. LANDER. Please.

Senator BLUNT. With what NIH did during the pandemic with, particularly, what we call the shark tank on developing tests and becoming an active partner with 34 different businesses, would that make them more prepared to do this than they would have been, say, 2 years ago?

Dr. LANDER. Absolutely. I think this program, the RADx program, the Rapid Acceleration of Diagnostics initiative, is a perfect

example that says, NIH can pivot and take on bold things like this that lift up, as you said, 34 or maybe many more, such opportunities. There is not a natural way to do it. It has been ad hoc, and it was amazing that it was spun up so quickly, as an ad hoc approach.

Imagine the possibility if we had a structured way to be able to seize those opportunities each year. I think that it very much supports the idea.

Senator BLUNT. Let me see if I can get in one more question. This whole, what is happening in synthetic biology and agriculture, developing advanced materials, if you are confirmed, what would do to ensure that the United States continues to advance our innovation and maintain a global advantage in that quickly growing area?

Dr. LANDER. Well, Senator, synthetic biology has enormous potential to do things like reprogram cells to fight cancer or reprogram crops to be able to have a higher yield. And it requires a kind of toolkit. The same way the early days of semiconductors, people had the bits and pieces that they would assemble into integrated circuits. Biology is at that early stage where it needs to build those toolkits and get them in the hands of thousands of innovators. And I think that the Federal Government has a really important role in being able to support the creation and dissemination and the sharing of best practices, about how to use those.

Senator BLUNT. Thank you. Thank you, Chairman.

Senator DUCKWORTH. Thank you. Senator Markey.

Senator MARKEY. Thank you, Madam Chair. I would like to follow up on the direction that Senator Blunt was going, looking over at NIH and looking at what the President said last night about Alzheimer's and diabetes and cancer. And perhaps, you know, give you an opportunity to integrate that in what you have done in your career, thus far, and what your hopes would be, you know, the promise for families. Because research is medicine's field of dreams, from which we harvest the findings to give hope that there will be a cure.

So, can you speak a little bit about what your goals would be? Just take those three disease, you know, and synchronize it, perhaps, with what the Biden Administration's dreams might be, over the next 4 years.

Dr. LANDER. Well, cancer, diabetes, Alzheimer's, the problem in all three diseases had been we did not know what was wrong under the hood. We could give you an account of symptoms, but we could not give you an account of what was actually wrong.

I think the Federal Government's investments, starting with the Human Genome project and many other investments, are now telling us how these diseases actually work. Which cells are going wrong and which ones to target. I think that has been a tremendous success. And now, the question is, can we target those cells? Alzheimer's, we used to think it was the problem in a nerve cells, but it is actually some other kind of cell entirely, that is likely the place to look.

How do we manage to, now build the next generation of tools, to target things to the right places, do it safely, do clinical evaluations more quickly than five or eight years, for Alzheimer's, so that we

can test many ideas? These are the sort of things that only Federal research can support and then, unleash innovators.

Senator MARKEY. And do you think there is enough funding? Or are we going to have to increase funding, if we take this new model for having a doppler for healthcare research focusing upon those three diseases? Will it require a reallocation of funding? Or do you think an increase in funding would be called for?

Dr. LANDER. Well, Senator, I think the opportunities are so extraordinary that we are not fulfilling all the opportunities, in part, for lack of funding. I think we also always have to be thinking about using funding most wisely. But if you are asking are there remarkable opportunities ahead that we are not seizing today, the answer is yes.

Senator MARKEY. When you look at the COVID crisis, where we are today, from your experience, what do you think is going to be needed, from an American perspective as a leader, in helping the rest of the world to deal with that issue, as well, so, that we anticipate, perhaps, a recurring phenomenon in the years ahead? What recommendation would you be giving to our country?

Dr. LANDER. We never want to see something like this happen again, hence, we have to take apart all the pieces of it. And we will need to have capacities in place—hot capacities that can be turned on a dime, because these things—well, we have learned what it means to have an exponential increase in something.

Those are capacities for diagnostics. The ability, in a week, to reprogram existing diagnostics being used in public health, to take on a new pathogen and to do it so cheaply that we do not agonize about how to pay for it. The ability to produce vaccines against any of the classes of viruses that infect humans. There are 5 of them. The ability to make therapeutics very rapidly. We did not succeed in making therapeutics—new therapeutics, in this pandemic, rapidly enough to respond. Yet, there are approaches to do it. I think we need a top to bottom look at the components.

The good news is, there are scientific approaches for all of those things. And we need to pull together, and we need to pull tighter across agencies, and we need to pull together, even across some countries. I think the United Kingdom is an obvious partner in something like this. Because we all have to prevent this from happening again.

Senator MARKEY. Beautiful, thank you. Again, thank you for your service. Thank you, Madam Chair.

Senator DUCKWORTH. We have, via WebEx, my good friend from Tennessee, Senator Blackburn.

**STATEMENT OF HON. MARSHA BLACKBURN,
U.S. SENATOR FROM TENNESSEE**

Senator BLACKBURN. I thank you, Madam Chairman. And, Dr. Lander, I wanted to thank you for your phone call and the time that we had to visit. I so enjoyed that. I want to join Ranking Member Wicker in his request that the Broad Institute please provide to us that 10 year of donor records. The Epstein connection is of tremendous concern to us, and we would like to have that information.

A question that I have for you. In your opening statement, you had said, you know, the OSTP's work will be rooted in equity, tackling issues from STEM inclusion to algorithmic bias. You also state, this administration poses big questions like, how can science create market driven solutions for climate change. So, first question to you is, I want you to provide some clarification around your utilization of algorithmic bias. And then, second, we will talk about market driven solutions.

Dr. LANDER. So, thank you, Senator. Those are—those are really important questions, and I am very glad to respond to them.

When—a computer scientist uses the word algorithmic bias, they mean that an algorithm is not producing the correct answer because of, typically, the data that was used to train it not applying to the circumstance in which it is being used. There are many ways that that can occur, but it means the results are not reliable. They do not reflect whether the person you are looking at really should get a loan. What they reflect is a data set that does not actually describe the person that has come before, requesting a loan, for example.

I think it is a very important question right now, in artificial intelligence. How to be able to verify that programs produce the correct result, in circumstances other than the ways in which they were first constructed.

Senator BLACKBURN. I agree with you on the concern with algorithmic bias. I think that your application to artificial intelligence is so appropriately placed.

It is of concern, when you look at building these algorithms out. If you are pointing one direction, that algorithm, instead of opening up new potential options to you, it narrows those options that are presented to you. And I will look forward to continuing a conversation about how we change that and how we work with tech—Big Tech companies to change that. It is not helpful, whether it is in research, or whether it is in public discourse.

I would love for you to talk just a minute—President Biden has been very aggressive in executive orders. And I sometimes wonder how this aligns with market driven solutions when you talk about climate, when you talk about energy, because what he is putting forward in executive orders does not seem to line up with market driven solutions. You can look at a variety of different things and look at how the Chinese have so adversely impacted the market, when it comes to solar panels, or to polysilicon being made in the United States.

So—and then, you look at President Biden's executive orders, and what he did around the Keystone pipeline—which, by the way, natural gas. A good way to move oil and gas is through a pipeline. I look at some of these executive orders and I wonder what the desired outcome is because it does not seem to be a market driven solution.

So, I would like for you to bridge that gap, between what has been happening by executive order, when it comes to fuels, when it comes to energy, and what is going to become market driven solutions that are affordable for the vast majority of the American people?

Dr. LANDER. Well, thank you, Senator. I think all of us are very concerned about addressing the issues around climate change and technological innovation is a critical part of that. That technological innovation, ultimately, has to include innovations that just make clean, net zero carbon energy cheaper than any alternative. In the long run, that will lead to market driven solutions. And I think science, uniquely, can contribute in those ways.

Senator BLACKBURN. Thank you so much. Thank you, Mr. Chairman.

Senator DUCKWORTH. Thank you. Senator Luján, remotely.

**STATEMENT OF HON. BEN RAY LUJÁN,
U.S. SENATOR FROM NEW MEXICO**

Senator LUJÁN. Thank you so much, Chair Duckworth. Dr. Lander, New Mexico is home to world class science and research facilities, including Los Alamos National Labs, Sandia National Lab, the Air Force Research Lab, Spaceport America, small businesses, universities, and community colleges, and more. From the Manhattan Project to the Human Genome project to the fuel that propelled the Mars 2020 Perseverance rover, New Mexican scientists are playing a leading role in solving our toughest problems.

I am excited that the Biden-Harris Administration has elevated your position to the Cabinet level. This demonstrates a strong commitment to science and innovation. From climate to emerging health issues, I want to offer my support in making sure that OSTP has the resources and capacity necessary to carry out its mission and offer necessary scientific counsel to the President.

My question, if nominated, how do you plan to use your role to ensure that science and research and development are not just in the room, but are central to solving our most challenging problems?

Dr. LANDER. Scientific research—well, Senator, I very much enjoyed our conversation, particularly about the national labs. And I—I have to say, as I told you, my first experience with the national labs was in your home state with Los Alamos National Laboratory.

So, I am deeply excited about what science can do to solve so many problems. And seeing so many different laboratories and approaches to science flourishing right now, and so many new technologies and opportunities, gives me such hope, if we can draw people into it. So, I think lifting up the possibilities—I mean, this is a—I grew up in the 1960s, which I thought then, was a time of amazing inspiration and opportunity about what the world could accomplish. I think this is a moment like that again. We see possibilities that, I think, should lift the excitement of any young person, to say that being in science will be the most exciting thing that one can do in the coming decades. And we just have to make sure everyone understands all of those opportunities, and that there is a place for everyone in those opportunities.

Senator LUJÁN. Thank you, Dr. Lander. As you know, Congress is currently considering proposals to strengthen America's leadership in science and technological innovation. As a Nation, we are not keeping pace with other countries' increases in their R&D spending. We must invest more in science, including at the Department of Energy, NSF, NIST, and NASA.

The lab directors of the 17 Department of Energy National Labs recently wrote a joint letter offering technical assistance to the Endless Frontiers Act, which proposes an expansion of the NSF to address 10 technology focus areas. This letter recommends that Congress embrace a broad approach to our technology and leadership, economic competitiveness, by strengthening the entire U.S. innovation ecosystem. This means increasing investments at NSF, as well as other agencies that play a key role in important technology areas, such as the Department of Energy.

Yes or no, do you believe that we have an innovation ecosystem and that the Department of Energy is a vital part of it?

Dr. LANDER. Senator, the Department of Energy and its amazing networks of laboratories is a vital part of America's ecosystem of innovation. I very much agree.

Senator LUJÁN. Dr. Lander, do you believe that—do you believe that the Department of Energy and NSF do complimentary work?

Dr. LANDER. I do believe they do complimentary work.

Senator LUJÁN. Do you agree with the lab directors that we must make substantial investments in and strengthen the entire U.S. innovation ecosystem, including at the Department of Energy?

Dr. LANDER. I—I think, if we are going to compete in the years ahead, we need to strengthen all aspects of our innovation ecosystem. This is a very consequential moment for the United States to make sure that we have strong innovation throughout the country, throughout the government support for it, throughout industry. So, it is critical that we strengthen all of it because it is the only way America will remain the leader in science and technology.

Senator LUJÁN. Chair Duckworth, this letter from our Nation's lab directors recommends that Congress embrace a broad approach to our technology leadership and economic competitiveness by strengthening the entire U.S. innovation ecosystem. And I ask unanimous consent that it be entered into the record.

Senator DUCKWORTH. Without objection.

[The information referred to follow:]

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April 13, 2021

The Honorable Joe Manchin
Chairman
Energy and Natural Resources Committee
United States Senate
304 Dirksen Senate Office Building
Washington, DC 20510

The Honorable John Barrasso
Ranking Member
Energy and Natural Resources Committee
United States Senate
304 Dirksen Senate Office Building
Washington, DC 20510

Dear Chairman Manchin and Ranking Member Barrasso:

On behalf of the National Laboratory Directors' Council (NLDC) – comprised of the directors of the seventeen Department of Energy (DOE) national laboratories – we write in response to your recent request for technical assistance on the draft of the Endless Frontier Act.

We commend Majority Leader Chuck Schumer and Senator Todd Young for recognizing the critical role that innovation driven by federal investment in research and technology development plays in competing with China and ensuring U.S. leadership in key technology areas. Their efforts reflect the type of bold and inventive thinking needed to address U.S. international competitiveness and to deliver novel solutions to the challenges facing the nation.

Since their founding in the Manhattan Project, the DOE national laboratories have delivered scientific advances and technology solutions for the nation, while balancing the need for open, collaborative science with the imperative of national security, economic security, and technological superiority. The DOE national laboratories are mission-driven research and development organizations that reside in an important space, with a long-term perspective and operating across the full spectrum from fundamental to applied research to the demonstration and deployment of technologies. This makes them complementary to both academia, which focuses on fundamental research and the advancement of knowledge, and industry, which is primarily concerned with the development and application of research outcomes in the near-term. As such, we believe the DOE and its national laboratories can make significant contributions to out-competing China.

We recommend that the Endless Frontier Act or other related legislation embrace a broader approach to advancing the nation's international technology leadership and economic competitiveness by investing in and strengthening the entire U.S. innovation ecosystem, including the ongoing work and additional initiatives of DOE and the national laboratories across the Act's key technology focus areas. Specifically, we recommend a separate, substantial, targeted investment in research for DOE and the national laboratories to advance key technology areas in coordination and collaboration with the National Science Foundation (NSF), and to fund increased support for and access to world-leading user facilities stewarded by DOE and utilized by NSF-supported scientists to advance scientific discovery and technology development. We share the view that providing much greater resources across the innovation ecosystem is the best way to achieve the Senate's goal of bolstering our competitiveness with China, and indeed with the rest of the world. Our distributed, multi-agency, multi-stakeholder approach to science and technology has served the nation well throughout its history. This approach brings diverse viewpoints, wide ranging capabilities, creativity, and ingenuity to science and technology in a way no other country can match.

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NSF, like DOE, is an essential component of the nation's innovation ecosystem and an important partner to the DOE and its national laboratories. NSF is the only federal agency charged with the promotion of scientific progress across all science and engineering disciplines. The research funded through its rigorous peer review process is vital to the public interest and has led to transformative discoveries that have reshaped our world. Through its sponsorship of cutting-edge, university-based research, NSF supports the education and training of the nation's scientists, engineers, and teachers and the next generation of new ideas.

Complementing these efforts, DOE assembles and nurtures multi-disciplinary teams of scientific experts to meet federal needs and address national priorities by attacking R&D challenges at scale. DOE does this by supporting university research, industrial partnerships, and a network of 17 national laboratories that are responsible for cutting-edge science and technology research and development. The national laboratories are also responsible for constructing and maintaining one-of-a-kind, world-class research capabilities that are leveraged broadly by over 36,000 university and industrial researchers every year.

For example, the DOE Office of Science maintains and operates 28 user facilities at its national laboratories across the country. These major pieces of scientific infrastructure range from advanced supercomputers and particle accelerators to large neutron and x-ray light sources and specialized facilities for nanoscience and genomics. These user facilities are vital tools of scientific discovery and provide unique and often world-leading capabilities. The National Synchrotron Light Source II at Brookhaven National Laboratory, for instance, is currently one of the brightest X-Ray Light sources in the world and enables discoveries in a broad range of fields, including biomedicine, energy storage and conversion, quantum technology, and molecular electronics.

DOE and the national laboratories provide access not only to these major scientific tools but to dedicated experts who help tens of thousands of researchers funded by NSF and other agencies, as well as industry users, conduct scientific experiments with these powerful tools. Access to these facilities is awarded based on merit review of proposals. Technical upgrades are underway at many of these facilities to ensure that they will remain at the international forefront. However, operations of these facilities are highly budget-constrained at the same time that they are in such high demand that they are already oversubscribed in most cases by a factor of two to five. The additional funding proposed for NSF as part of the Endless Frontier Act would place further demand on these valuable tools. DOE would require a complementary and commensurate investment in the tools, capabilities, and staff support for these user facilities to enable the greater volume of high-impact research and development envisioned by the Endless Frontier Act.

DOE and the national laboratories are also at the forefront of advancing emerging technologies, including both fundamental and use-inspired research and development of applied energy technologies. The national laboratories also maintain a complex of energy technology demonstration facilities, such as the Manufacturing Demonstration Facility at Oak Ridge National Laboratory and the Wind Dynamometer Test Facilities at the National Renewable Energy Laboratory, that are critical to the advancement and derisking of U.S. technology innovations.

Coordination between DOE and NSF is essential to leverage each agency's respective strengths to maintain U.S. leadership. In reviewing the key technology focus areas enumerated in the Endless Frontier Act, the National Laboratory Directors' Council identified significant DOE investments at national laboratories and universities in nine of the eleven focus areas. We would welcome an opportunity to discuss with you the full

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portfolio of these efforts and ways that the capabilities and expertise of the national laboratories should be leveraged to support increased investment in these areas. We include four illustrative examples here:

- In quantum computing and information systems, the national laboratories are leading five National Quantum Information Science Research Hubs – each with diverse members that include American industry, universities, and national laboratories – funded by DOE, thanks to bipartisan congressional support for the National Quantum Initiative and subsequent appropriations. These centers are part of a coordinated, multi-agency effort with the NSF and National Institute for Standards and Technology, and serve as an excellent example of a complementary, multi-agency approach.
- On high performance computing, semiconductors, and advanced computing hardware, the national laboratories operate two out of the top three of the world's fastest supercomputers with more coming online later this year and early next through the Exascale Computing Initiative. And by nature of their design, these exascale systems will also represent the most powerful artificial intelligence machines in the world. In addition to the supercomputers, the national laboratories have some of the world's leading experts in computer science and advanced mathematics, which is crucial to leveraging each new generation of bigger and better computing capabilities through advanced software development. This is a key area where DOE, through Office of Science and the National Nuclear Security Administration (NNSA), and the national laboratories have long maintained the delicate balance between the need for open science and imperative for national security as stewards of the nation's nuclear deterrent.
- In advanced energy, batteries, industrial efficiency, and materials science, DOE – across nearly its entire portfolio – is the lead agency for the nation in driving innovation through research and development efforts at national laboratories and universities in partnership with industry; capability development and stewardship, especially at the national laboratories; and supporting robust public-private partnerships.
- In biotechnology, genomics, and synthetic biology, DOE's national laboratories possess one of the world's greatest collections of research facilities, international scientific leadership, and other assets focused on non-human biology for energy, environmental sustainability, and biomanufacturing. The Joint Genome Institute at Lawrence Berkeley National Laboratory and the Environmental Molecular Sciences Laboratory at Pacific Northwest National Laboratory are among the world's most sophisticated research facilities focused on biology by design to address climate change, clean energy, and environmental sustainability. These facilities are utilized annually by thousands of users and tens of thousands of data users. Over the past year the National Virtual Biotechnology Laboratory was rapidly organized to bring DOE and NNSA scientific user facilities, additive manufacturing capabilities, and high-performance computing to bear addressing the threat posed by COVID-19.

In regard to all the key technology areas, the DOE and its national laboratories have the talent and the mechanisms to analyze the dual use implications of new technologies, and the charge to alert government authorities and policymakers to over-the-horizon technical threats that may impact American lives and underpin future U.S. economic competitiveness. The NNSA has been analyzing and identifying threats for decades with respect to U.S.-developed nuclear materials and technologies. All national laboratories have been doing the same with respect to artificial intelligence, biotechnology, and high-performance computing. These at-the-ready capabilities can be expanded and re-tasked as necessary to address ongoing and

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emerging threats, and are vital to advance research frontiers in such a way as to assure our national security and economic competitiveness.

Finally, we recognize that the draft bill makes national laboratories eligible for grants from the new NSF directorate created by the bill. However, historically and currently, the national laboratories as Federally Funded Research and Development Centers are not considered eligible to apply for funding from the NSF, nor do we believe it is appropriate for national laboratories and universities to compete head-to-head for awards except through diverse, multi-institution consortia.

Thank you for requesting our input, and for your part in authorizing and overseeing the important work of the Department and our laboratories. Congress has made significant investments in DOE and the national laboratory complex that address most of the key technology areas outlined in the legislation. We look forward to working with you to ensure that DOE's national laboratories receive the resources necessary to execute additional work in support of the goals of the Endless Frontier Act while also maintaining its stewardship and mission obligations to DOE.

Respectfully,



Adam Schwartz
Director, Ames Laboratory
Executive Committee, NLDC



Paul K. Kearns
Director, Argonne National Laboratory
Executive Committee, NLDC (Ex Officio)



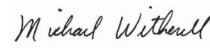
Doon Gibbs
Director, Brookhaven National Laboratory
Chair, NLDC



Nigel Lockyer
Director, Fermilab



John Wagner
Director, Idaho National Laboratory



Michael Witherell
Director, Lawrence Berkeley National
Laboratory

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Kimberly S. Budil
Director, Lawrence Livermore National Laboratory



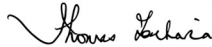
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Thomas Zacharia
Director, Oak Ridge National Laboratory



Steven Ashby
Director, Pacific Northwest National Laboratory



Steve Cowley
Director, Princeton Plasma Physics Laboratory



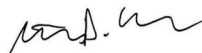
James Peery
Director, Sandia National Laboratories



Vahid Majidi
Director, Savannah River National Laboratory



Chi-Chang Kao
Director, SLAC National Accelerator Laboratory



Stuart Henderson
Director, Thomas Jefferson National Accelerator Facility

Senator LUJÁN. I want to thank Dr. Lander for his time today, for my conversation with him, and with that, Chair Duckworth, I yield back.

Senator DUCKWORTH. Thank you and I recognize the Senator from Minnesota, Senator Klobuchar, who will take over as the Chair.

**STATEMENT OF HON. AMY KLOBUCHAR,
U.S. SENATOR FROM MINNESOTA**

Senator KLOBUCHAR. Thank you very much, Madam Chair and thank you, Dr. Lander, for being here. And we talked on the phone about some of your interests in science and technology. And I want to start with, really, what I consider the biggest scientific challenge in front of us, which is climate change. And I know you have been asked a few things about this and the President certainly focused on it last night in the State of the Union.

As you know, earlier this year, the President asked you how science and technology can create solutions to address climate change, and soon after he issued the executive order establishing the National Climate Task Force. Can you speak to the importance of interagency coordination in addressing climate change and what steps you can take to address the issue?

Dr. LANDER. Well, thank you—thank you so much, Senator. Climate change is—is an incredibly important challenge for our time and we have to move quickly on it. I am impressed, looking back the last decade, that we have seen real progress. That green technologies, zero carbon technologies, used to be hugely more expensive than fossil fuel technologies. That gap is closing. Look at market driven solutions when the gap closes all the way.

But the gap is no longer so huge. We see it with solar; we see it with smart grids; we see it with wind. And I think, what we need to do now is, focus hard from the point of view of science and technology on what we can do to promote the innovation to make each of these things more and more efficient. So that, we reach a point where there is not really a question because—because it is just cheaper to do it that way. I think that is the ultimate goal for science and technology. And I think, amongst the agencies, we have to be coming together and looking on a continuing basis, what those differences in costs are and how we can close them.

Senator KLOBUCHAR. Very good. The—I know Senator Thune talked to you about cybersecurity work force, something that is a major priority and he and I have worked together on a public-private exchange. Do you believe we need to train our cybersecurity workforce better to deal with the hacks and what we have seen out there?

Dr. LANDER. Oh, the cybersecurity problem is a very serious and very worrying problem for the whole country. I believe we do not have enough people trained in it to be able to both defend and then, think about how to construct systems that are just less hackable.

Senator KLOBUCHAR. Mm-hmm.

Dr. LANDER. So, I think this is an area of tremendous opportunity. There are some manufacturing institutes that we actually started that focus on cybersecurity manufacturing. There are pro-

grams I know of at Annapolis. But we really have to do a tremendous amount because the risk of cybersecurity threats is just too big.

Senator KLOBUCHAR. Mm-hmm. And along the lines of cyber, there are still issues, of course, with broadband, really come into magnification during the pandemic. And we have got, you know, in my state, about 16 percent of households—even our state is above the national average—that do not have access. Representative Clyburn and I lead the two major bills together, the same bill, on broadband. And of course, the President included these provisions in his infrastructure package.

In your testimony, you highlight the importance of access to broadband. Can you talk about that, in terms of—I know you do such high-level science, but if you are going to get stuff out to people, so they can actually use it, you do not want a whole bunch of people, like 20 percent of the population not having access.

Dr. LANDER. Well, Senator, this is such an important issue. I mean, it—how can you be a part of 21st century American economy, education, work, healthcare, commerce without access to broadband? And yet, tens of millions of Americans lack access to broadband. And it is disproportionately rural Americans and people on tribal reservations, and people of color, and older, and lower income Americans, and Americans with disabilities.

And for me, it is actually a personal issue because my daughter teaches high school in Lowell, Massachusetts and three-quarters of her kids are on free or reduced lunch. And during this pandemic, when she has been teaching online, we are acutely aware—she is acutely aware every day for how hard it is, for many of her students, to be able to even participate in class.

Senator KLOBUCHAR. Mm-hmm.

Dr. LANDER. We have to solve this.

Senator KLOBUCHAR. Yep, very good. And I think it is just important to put the connection with the high-level science and broadband.

Dr. LANDER. My daughter's class matters even more than the high-level science of this.

Senator KLOBUCHAR. My last question is, you and I talked about Minnesota and we are really proud of the work that we have done in research in our state, at places from the University of Minnesota to Mayo Clinic. And Mayo Clinic, I visited their Personal Medicine area, where they have personalized medicine, using the science we have now to help people. And could you talk a little bit about that, the work, of course, that Francis Collins has done, and where you see the future headed? Because I, as one of the co-chairs of the Rare Disease Caucus, along with Senator—with Senator Hatch and now, Senator Wicker, you know, we have done a lot of work in that area. And there is still so many things we need to know to give people the best treatment. Where do you see this going?

Dr. LANDER. Well, the amazing progress in being able to find the genes that underlie diseases is not just giving us diagnostics, it is now pointing to therapeutics. So, more and more rare genetic diseases, that we never imagined would be treatable, now through different kinds of gene therapies, we are seeing can be treatable.

Senator KLOBUCHAR. Mm-hmm.

Dr. LANDER. And it is just amazing. The hardest problem may be just delivering the therapy to the right cells. But the idea that this is becoming—well, gone from an utter mystery to a problem of careful engineering, and that, we can provide, in some cases, real therapies and cures, and in many other cases, you can at least see paths to them, to me it is—it is just a mind-blowing thing, over the past 10 or 20 years. And if you try to project forward 10 or 20 years, you just think, wow, what is going to happen?

Senator KLOBUCHAR. Exactly. All right, well, we hope in your new job, you will visit Mayo, if you are confirmed, and come to our State. So, with that, I can only chair this for a short period of time. I just happened to—I was at another hearing on patents in Judiciary, but I will toss it over to Senator Rosen, and then, maybe be able to come back in to call on Senator Sullivan. I have a number of calls. I did not know I was going to chair it, so—but do not worry. I guess you will not be abandoned, Dr. Lander. With that, I will turn it over to Senator Rosen, who is with us remotely.

**STATEMENT OF HON. JACKY ROSEN,
U.S. SENATOR FROM NEVADA**

Senator ROSEN. Thank you, Senator Klobuchar. And thank you, Dr. Ladner, for your research, your service, and your willingness to serve in the future.

You know, so many of my colleagues—I have been listening—have asked great questions. We were able to have a great conversation. So, I want to build a little bit on my colleagues' questions to talk about STEM education, because it is really important. That is one of my top priorities in Congress is STEM education and really building our STEM work force. You know, my Building Blocks of STEM Act with Senator Capito, was signed into law last year. It expanded the National Science Foundation programs to help increase participation for girls in computer science. I am glad it was really funded in the last omnibus.

But there is just so much more work that we have to do, particularly in breaking down barriers that stand in the way of students of all ages, of all genders, from all backgrounds, whether they are urban or rural, just across the board. And so, what role do you really see that you have in helping to promote STEM education, workforce training? And really, what I want to ask you is that, how can you partner with all of us? The 21st century economy needs a 21st century workforce to find these wonderful breakthroughs, like we have been doing. And how can you use your platform to help us promote these kinds of exciting things and the work that you can do when you pursue any career in the STEM field?

Dr. LANDER. Well, Senator Rosen, thank you and it was—it was really great to talk to you the other day.

I am, as was mentioned, a veteran teacher. For 25 years I have taught the Introductory Biology course at MIT and I have seen what happens when you can light the fire of imagination in someone's eyes.

I think we need to lift up the possibilities and invite people in to STEM in a way that we have not done before. We need to create curricula that work for teachers in many different settings, so that

everyone, wherever they are, can get as excited about these possibilities.

There are many different approaches. I do not think there is any single answer to STEM. But I do think that one thing, again and again, that works is not book learning, but learning directly by doing. This kind of active learning, discovering something yourself, building something yourself, inventing something yourself, is—people get hooked on it and they do not even know that they are doing STEM. What they are doing is, we are tapping into the natural creativity.

And I am very excited, if confirmed, to work to help pull together and convene to create more of the resources that will let teachers around the country be able to do this, in ways that suit their individual states and their cities and their classes and the diversity of Americans. Because there many ways in but we have make sure all of those paths in are smoothed paths.

Senator ROSEN. No, I could not agree more. We have so many robotics programs. I have been to third grade classrooms where they showed me how they built robots and they created the websites. We have seen cooking classes where they tell the kids, “This is chemistry”. And I see, especially in elementary school, that spark of imagination. If we can just do that, I think you are exactly right.

And so, that leads me to my next question. Because we know that there were concerns about the issues of politics influencing science. And so, we want to be sure that—that, at the new administration, that we let data and evidence direct our policy, in areas of science. Especially now, we have the pandemic and so many other things—rare diseases, cancer, all of the things we talk about.

So, if confirmed, kind of building on this, how can you help restore trust and scientific integrity with the public?

Dr. LANDER. I think, Senator, restoring that trust is one of the most important things that we all have to do, and I think the most important thing is to listen. I think, sometimes, scientists talk first. I think we need to listen. People have valid concerns and I think, listening to people about their concerns—letting them express them, inviting them in—is so important to rebuilding trust. I do not think it is a question of just “educating people”. I think it is sometimes about educating scientists about what concerns people.

So, trust building requires listening and listening very deeply. And, if confirmed, I would want to make sure that OSTP took that approach and tried to promulgate that approach throughout Federal science programs.

Senator ROSEN. Thank you. I appreciate your time and I yield back.

Senator KLOBUCHAR. Thank you very much, Senator Rosen. Next up, Senator Sullivan.

**STATEMENT OF HON. DAN SULLIVAN,
U.S. SENATOR FROM ALASKA**

Senator SULLIVAN. Thank you, Madam Chair, and, Dr. Lander, good to see you. I really enjoyed our Zoom meeting. You know, I take the advice and consent role here in the Senate really importantly. I try to meet with everybody—assistant secretaries, under-secretaries, deputy secretaries, you name it. And some of these are

very informative; some are not. But I really enjoyed our discussion. I learned a lot. I thank you for your time. I am going to be a strong supporter of yours in the confirmation process.

Let me—let me kind of touch on a topic that you and I talked about. You know, we are getting through this pandemic. You know, there has been a lot of finger pointing and blame and everything like that. And—but there are some silver linings, as we talked about. And you know, you never want to highlight the misery of what is going on in other places, but it looks like, right now, if you look at overall—of course, we have had way too many deaths, which is horrible—but with regard to the vaccine and the ability for American states to get it out, my state has been leading the charge remarkably. Vaccine rates in Alaska, for the whole country, but how quickly we are able to do that, the vaccine, knock on wood and we hope this stays the case, appears to be working, relative to, like, the Chinese vaccine that does not seem to be working that well. And other countries are having a real hard time and now, we are—we are kind of leading the world, I would say. And I think there is so much to learn, in a positive way, from Operation Warp Speed and how that came together for—

So, I am going to be working on legislation, and I know you and I talked about it. I would say, you know, I wish President Biden would be a little more magnanimous. You know, his discussion of vaccines always seem to start with his inauguration. Of course, that was not the case. He kind of did it again last night. He never recognizes the Trump Administration's work. I think we need to come together and recognize that.

But could you just tell me, quickly, because I have got a couple other questions, what are some of the lessons that we learned? I mean, it has been a year really, since the pandemic hit us hard, and we already have a vaccine that is getting to most of the country. And most scientists would not have agreed that that could happen at all, and yet we did it. American ingenuity, we did it. It is a great lesson that we should all try to be celebrating and learning from.

Dr. LANDER. Well, Senator, first, let me say, I also tremendously enjoyed our conversation. And I will say, for the record, I did commit to you to come to the great State of Alaska.

Senator SULLIVAN. Yes. Oh, I was going to get to that.

Dr. LANDER. Oh, OK, well—

Senator SULLIVAN. YOU even said you would come in the winter, which a lot of nominees do not. So, we are going to get you out there, at least—

Dr. LANDER. I am proactively recording—

Senator SULLIVAN. I am going to take you to Fairbanks, where it is 40 below zero, and you are going to see.

Dr. LANDER. Well, you have got that great research center up there that we talked about it.

Senator SULLIVAN. You know, I am—that is actually my next question.

Dr. LANDER. Oh, I am sorry. I am just, you know—I will stick to the question in front of us here.

With regard to vaccines, it is amazing how fast it worked, and it is also amazing that it was 10 years in the making.

Senator SULLIVAN. Yes, that is a good point.

Dr. LANDER. It was investments by this American Government, in things like MRNA vaccines, understanding coronaviruses. And so, as we look, going forward, I think we have to look that we have made investments over a long period of time, and then, when it came time, we had things on the shelf—

Senator SULLIVAN. Yes.

Dr. LANDER. We could bring down. We have got to keep doing that.

Senator SULLIVAN. Well, look, I want to—I am going to be proposing legislation. I think it will be very bipartisan. It will be not—it will be non-finger pointing, right? It is going to be, hey, we pulled this off, Democrats, Republicans, Trump Administration, Biden Administration. What have we learned and how can we apply that to other places?

Dr. LANDER. Yes.

Senator SULLIVAN. So, I want to work with you on that legislation. You and I had a good chat about that.

Let us—let us talk about Alaska, here, real quick. Here is my big issue. We are a great state. Everybody loves their own State. I think my State is the most unique, certainly, and you will see it when you are up there. But whether it is climate, arctic, oceans, fisheries, there are so many huge scientific things that we can learn from what is happening in Alaska.

Here is a bit of a frustration. Federal agencies often want to study these, but they do it in places that are not in Alaska. So, I need your commitment to come up, see the State, but also, help me get the scientists who are studying these Alaska issues, to actually be in Alaska.

This has been a problem—I will just give you one example. NOAA, I live NOAA. There was, like, this giant migration of scientists who were studying Alaska issues, who left Alaska. You would not have scientists studying the Grand Canyon do it from Illinois, right? So, I am just saying, we need to fix that. Can you comment on that, at all? I mean, it is best to be a scientist studying something in the place where it is taking place, right?

Dr. LANDER. Senator, I—there are some things you can learn from a distance and some things you can learn from a computer simulation. But you cannot learn about natural places without being there. And so, I think that is a broad statement that I strongly support. We need people there to observe and be part of the ecosystem and all for the exciting opportunities and challenges.

Senator SULLIVAN. Let me—and I—and I know I am a little bit over my time, and I know, I think, Senator Lummis up next, but just one final question.

I agree with what Senator Rosen just said. We have got to take politics out of science. But this works kind of all ways. Right now, I would say there is a definitive area where energy, traditional energy—oil and gas, in particular, mining—seems to be out of favor, right? This current administration is restricting the production of American energy. Crazy in my view, killing jobs, for sure. And even during the Obama Administration you had scientists come out and say the National Petroleum Reserve of Alaska does not really have any oil in it. That was the scientists. Well, it was totally political

because they were wrong. It is a huge area. Some of the biggest finds recently, in the world, have been in what we call the NPRA.

So, that was politicized science to try to get people not to explore for energy in America, based on faulty science. Fake science, in my view. So, can you just talk to me briefly about making sure you stay—keep it straight down the middle? A lot of focus on climate change. OK, we need to focus on that. But also, on energy. I have not—being the world's natural gas largest supplier has benefited our country and the environment and the reduction of greenhouse gas emissions enormously. That is science. Some people do not want to say that, but that is science.

Can you just talk about being even keeled and keeping politics, on both sides, out of science?

Dr. LANDER. Senator, you say it well. We have to be even keeled. Politics does not have a place in science. When we have a problem, we need to look to all the solutions we might have for that problem. And, if confirmed, I can commit that I will bring that approach and I will encourage that approach.

Senator SULLIVAN. Good. I look forward to strongly supporting your confirmation and I believe—I—Senator Lummis, I think is up next. So, I think I am the de facto chair right now.

**STATEMENT OF HON. CYNTHIA LUMMIS,
U.S. SENATOR FROM WYOMING**

Senator LUMMIS. Let me see if I can get it to—can you hear me?

Senator SULLIVAN. Yes, we can hear you.

Senator LUMMIS. Thank you so much. Appreciate it, Mr. Chairman. And I want to follow up on one of the things that you were addressing just now and expand it to rare earth and critical minerals. You know, our supply chain is one of the most important to be secured from Chinese influence. And fortunately, there are places in the United States with large critical mineral deposits. My state is one of them. I suspect Senator Sullivan's state is, as well.

I believe the National Science Foundation should be working with the Department of Energy and other agencies to advance mining research and the development of related technology, to make sure the best use of American rare earth resources are occurring and is advanced now. So, could you talk about your perspective on this? How will you use your position at OSTP to make this a reality?

Dr. LANDER. Well, Senator, thank you. The rare earth minerals is such an important issue because they are used in so many critical technologies today from, you know, lithium-ion batteries, to semiconductors. And because they are a real supply chain problem because, in many cases, perhaps half of cases, the major supply is China. And if we were ever to lose that supply, we would be in a bad way.

So, there is an urgent question facing the United States of, how do we guarantee our supply chain for scores of rare earth minerals. You know, gallium, 100 percent of the supply comes from China. And it is not that we do not have supplies of some of these minerals here, it is that we do not have the mining and refining capacity for those.

So, I would like to see systematic plans. And, if confirmed, I would like to push for systematic plans, to make sure that we know how to secure supply chains in ways that are economically robust and safe for the environment. And I think American manufacturers have been working out ways to do this with new kinds of mining and new kinds of secondary extraction.

So, you have my commitment, Senator, that this is a very important topic, from the point of the economy and national security. And I would be very glad to work with you to make sure that we have the supply chain we need for these rare earth minerals.

Senator LUMMIS. Well, thank you. We will push you to push others to prepare those plans, so they are available to all of us, and we can have the things we need—critically need, in case China pulls the rug out from under us, which they could at any time they chose to.

I also have a question about the disparity in NSF funding allocations. Small universities are at a disadvantage when competing for NSF grants against major institutions like yours. The proof is the fact that just seven states received half of the available NSF funding and the bottom 10 states shared just 3 percent. And this continues to be an issue that I have been following for decades because I used to be involved in these issues at my University of Wyoming.

So, will you commit to using your position as Director of OSTP to work toward more equitable distribution of NSF funding?

Dr. LANDER. Well, Senator, I strongly believe that this country will only fulfill its potential if we involve everyone and that means research going on vibrantly in all the states of this country. And there are many ways to help promote that and I am extremely interested in this topic. And I would commit, if confirmed, to work closely with you to make sure that we engage your state and many, many other states who are not as heavily engaged in this as they need to be and should be and must be. So, I will, indeed, work with you on this topic.

Senator LUMMIS. Well, thank you very much. Now, one last comment. You and I had a good discussion about some of the controversies that were brought up during your nomination earlier and when we spoke, and I looked into the allegations of sexism. And it is not clear to me what your motives were, but it is clear that you wanted to make sure that your labs got the patents and the credit for CRISPR technology, and that, in the process, you may have marginalized, or trivialized, the contribution of two scientists whose work was essential in making CRISPR breakthrough possible. So, that does remain a concern for me, however, I appreciate your candor during our conversations. And thank you for taking my questions today.

Mr. Chairman, I yield back.

Dr. LANDER. And if I may respond—

Senator SULLIVAN. Yes.

Dr. LANDER.—because it is a very important question, Senator. Senator SULLIVAN. It is an important question.

Dr. LANDER. It is a very important question. So, a very important value to me, throughout my whole career, has been championing scientists to make sure they get credit for their work.

So, in 2016, I wrote a long review article championing the work of about a dozen scientists, mostly unsung heroes who had contributed to CRISPR over the course of 20 years. They included young scientists, immigrant scientists, young Asian American scientists, and two remarkable women scientists, Drs. Doudna and Charpentier. And I was excited to tell the whole story, especially because there is a long history of people not receiving proper recognition. And my goal was to show how all of these contributions, from 12 different people, built on each other and fit together. And I am afraid that, in writing it up, I understated the importance of those key advances that you referred to by Drs. Charpentier and Doudna. That was not my intention. I felt terrible about it. I made a mistake and when I make a mistake I own it and try to do better.

I should have written those paragraphs differently to make my intention crystal clear. I have enormous respect for Drs. Doudna and Charpentier and the important work they have done throughout their careers. And over my career, I have tried to lift up others, again and again. And when I fail, as I failed, I try to learn and do better. And I appreciate the question and I take it extremely seriously.

Senator SULLIVAN. Well, thank you for—

Senator LUMMIS. Well, thank you very much for responding. I appreciate your candor now, as well. I—that was very, very helpful. Mr. Chairman, thank you. I yield back.

Senator SULLIVAN. Thank you, Senator Lummis. And I just want to add to her point about the smaller universities that still have great scientists. We have that in Alaska, as well. I believe Senator Lee is on.

**STATEMENT OF HON. MIKE LEE,
U.S. SENATOR FROM UTAH**

Senator LEE. Yes, yes, I am.

Senator SULLIVAN. Great.

Senator LEE. Thank you, Mr. Chairman.

Senator SULLIVAN. Yep.

Senator LEE. Dr. Lander, during our phone call a few weeks ago, we had a brief discussion, as you may recall, about—about your stance on Federal research relating to ethics in certain scientific research areas, like those involving the use of aborted fetal tissue, or embryonic stem cells. As I recall, you indicated, during our conversation, that as Director of OSTP you would have little input in any of these areas. But to be clear, Title 42 states that the Director of OSTP is required to “develop, review, revise, and recommend criteria for determining scientific and technological activities warranting Federal support”.

So, understanding this particular part of the job description, I would like to ask you a series of questions and I would like you, if possible, to keep these to a yes or no, just given the limited time-frame that we have. A series of yes or no questions regarding the ethics of certain scientific research. Do you support Hyde Amendment protections?

Dr. LANDER. I recognize the President’s position and support the President’s position on the Hyde Amendment.

Senator LEE. So, is that a no?

Dr. LANDER. Sorry, I have not got quite which way yes and no went but I think my answer is, I support the President's position.

Senator LEE. Understood. Do you support the use of aborted fetal tissue for research purposes?

Dr. LANDER. I think the role of OSTP is to be able to provide advice on what might be learned. I defer to our elected officials to determine how to balance the ethical questions in the use of it and the possible benefits that could emerge. I think science can provide, to our elected officials, the potential benefits. And I very much respect the importance of these ethical issues and how much they matter to so many people, myself included, and yourself included. And I respect that these are questions for our—

Senator LEE. What about the use of live embryos? What about the use of live embryos in federally funded research, do you support that?

Dr. LANDER. Live embryos?

Senator LEE. Yes.

Dr. LANDER. I am not aware of that.

Senator LEE. OK, how about the creation of three parent embryos?

Dr. LANDER. I believe the creation of embryos for the purpose of human research is unethical. We should never be creating embryos for the purpose of human research.

Senator LEE. OK. So, does that mean—do you support or oppose the use of germline genetic engineering to create genetically modified embryos?

Dr. LANDER. I have—I have been on record supporting a moratorium on the use of germline genome editing to create designer babies. I think there are deep technical questions, but deep ethical questions of creating children with genetic editing.

Senator LEE. Do you support the creation of human animal hybrid embryos?

Dr. LANDER. I have deep ethical concerns about the creation of such hybrids. And certainly, there are strong regulations already and I think it is very much worth looking closely at that.

Senator LEE. Do you support allowing an embryo to gestate in an artificial womb environment, for research purposes, for less than 14 days?

Dr. LANDER. I think the 14 days are the current Federal guidelines and again, I defer to our elected officials and the Federal Government's policies here. But I am very strongly opposed to letting—

Senator LEE. What about longer than 14 days?

Dr. LANDER. Sorry?

Senator LEE. How about longer than 14 days?

Dr. LANDER. I believe that those lines are drawn for very good reasons.

Senator LEE. OK. Switching gears for a minute, the Committee—this committee is likely to take up the Endless Frontiers Act sometime soon. The Commerce Committee's portion of that bill places a great deal of responsibility on the OSTP Director and the National Science Foundation for implementation of \$100+ billion government R&D effort, intended to counter China's expansion. I am concerned that this conversation is one in which we are only trying to

respond to the Chinese Communist Party with more government spending. Should our biggest response to increase China's investment in R&D be to just spend more like China? And will outspending China, through the Federal Government, actually counter the CCP economically?

Dr. LANDER. Senator, I think our competition with China is incredibly important—incredibly important to the future of the country. I do not think we can respond by acting like China. We have to act like America.

Senator LEE. OK.

Dr. LANDER. And so, I think we have to have American solutions to these problems.

Senator LEE. I am glad to hear that we agree on that. And I have often wondered, you know, how much—how much money should the Federal Government spend on research and development in order to counteract that—that threat? The Endless Frontiers Act would propose, you know, something over \$100 billion. But if \$100 billion, why not \$250 billion? Why not \$1 trillion? Is there a point, and can you help me identify at what point Federal Government spending becomes counterproductive?

Dr. LANDER. Well, I think, Senator, that the importance of making sure that we win in these different technologies means that it is appropriate to be developing ways to move things from fundamental research into industry, by filling gaps between those two. Taking on those things that are not yet a business plan could not be something supported by investors but are crucially needed by the country. And I think there is—

Senator LEE. And finally, there are other changes we could meet to—

Senator DUCKWORTH. The gentleman's time has ended. You are a minute over.

Senator LEE. Thank you, Madam Chair.

Senator DUCKWORTH. Thank you. I see no one is waiting in the WebEx. So, before we close today's hearing, Dr. Lander, we have one more question for you, which we ask of all nominees. Dr. Lander, if confirmed, will you pledge to work collaboratively with this committee, provide thorough and timely responses to our request for information, as we put together and address important policy issues, and appear before the Committee when requested?

Dr. LANDER. If confirmed, I will do all of those things and I look forward to it.

Senator DUCKWORTH. The hearing record will remain open for two weeks, until May 13, 2021. Any Senators that would like submit questions for the record for Dr. Lander, should do so by May 13. We ask that your responses be returned to the committee, as quickly as possible, and in no case, later than two weeks after the receipt.

Thank you and that concludes today's hearing.

[Whereupon, at 11:50 a.m., the hearing was adjourned.]

A P P E N D I X



Thomas J. Lynch Jr., MD
President and Director
Raisbeck Endowed Chair
Tel: 206-667-6534 Fax: 206-667-5268
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March 18, 2021

The Honorable Maria Cantwell
Chairwoman

The Honorable Roger Wicker
Ranking Member

Committee on Commerce, Science and Transportation
United States Senate
Washington, DC 20510

Dear Chairwoman Cantwell and Ranking Member Wicker,

I write today to support the nomination of Dr. Eric Lander as Director of White House Office of Science and Technology Policy (OSTP). I have had the pleasure of knowing Dr. Lander for the past 15 years as part of the cancer research community. He is a respected scientist in mathematics, molecular biology, and genetics. His leadership of the Human Genome Project was critical to the program's success and our current knowledge in the field.

Dr. Lander's leadership and pioneering research at the Broad Institute, where he is also a founding director, led to monumental advancements in our genetic understanding of many of the country's most costly diseases, including Alzheimer's, heart disease, diabetes, and cancer. During the COVID-19 pandemic, he used the Broad Institute's resources to sequence samples and increase the country's diagnostic capabilities and capacity to detect variants.

Dr. Lander has received multiple awards from national and international peer organizations. To cite a few, Dr. Lander received the MacArthur Fellowship, AAAS's Abelson Prize and the Award for Public Understanding of Science and Technology, the Mendel Medal of the Genetics Society in the UK, and the Woodrow Wilson Prize for Public Service from Princeton University. He previously advised Secretaries of Defense on technological and organizational innovation issues as a member of the Defense Innovation Board from 2016 to 2020, and for eight years, he served on President Barack Obama's Council of Advisors on Science and Technology.

OSTP deserves a leader who embodies scientific expertise, peer recognition and respect, and experience advising our nation's highest offices. His broad expertise—particularly in biologic sciences and medicine—are of great importance given the challenges we face as a nation. I respectfully urge the Committee to consider his nomination in short order.

Sincerely,

Thomas J. Lynch Jr., M.D.
President & Director
Raisbeck Endowed Chair



Dudley R. Herschbach
Baird Professor of Science, Emeritus
Department of Chemistry and Chemical Biology
Harvard University

Tel: 617-694-9850

Email: dherschbach@gmail.com

11 March 2021

Reference for Dr. Eric Lander

Nomination for the Director of the Office of Science and Technology Policy

Dr. Eric Lander is a sparkling, distinguished scientist, a leader of the Human Genome Project and many other international collaborations. He created a new research institute, the Broad Institute, arguably the best of the 21st century. It has a culture that is highly inclusive to women and underrepresented minorities and highly collaborative.

Lander is a superb choice.

Sincerely yours,

Dudley Herschbach
Nobel Laureate



American Society of Human Genetics

discover. educate. advocate.

March 11, 2021

The Honorable Maria Cantwell
Chairwoman, Committee on Commerce, Science
& Transportation
United States Senate
511 Hart Senate Office Building
Washington, DC 20510

The Honorable Roger Wicker
Ranking Member, Committee on Commerce, Science,
& Transportation
United States Senate
555 Dirksen Senate Office Building
Washington, DC 20510

6120 Executive Boulevard, Suite 500
Rockville, MD 20852

tel: 301.634.7300
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Dear Chairwoman Cantwell and Ranking Member Wicker,

On behalf of the nearly 8000 members of the American Society of Human Genetics (ASHG), we are pleased to endorse the nomination of Dr. Eric Lander as the Director of the Office of Science and Technology Policy (OSTP).

ASHG is the primary professional membership organization for human genetics specialists worldwide. The Society's membership encompasses researchers, clinicians, genetic counselors, nurses, and others who have an interest in human genetics. ASHG is committed to advancing human genetics in science, health, and society in service to the public. We, therefore, recognize the critical role of the OSTP has in leading federal science and technology strategies to drive innovation to serve the nation, and improve public health.

Dr. Lander is a demonstrated leader who brings a wealth of scientific expertise and foresight. He was a major leader in the Human Genome Project and The Cancer Genome Atlas—projects that have been fundamental in the field and research. In 2004, Dr. Lander launched the Broad Institute, a research institution in which scientists collaboratively tackle challenges in genomic medicine. He served as co-chair of the President's Council of Advisors on Science and Technology for President Barack Obama.

Dr. Lander is the 2018 recipient of ASHG's William Allan Award, the Society's top honor which recognizes a scientist for substantial and far-reaching scientific contributions to human genetics. Among his awards and honors are: the Rhodes Scholarship, the MacArthur Fellowship, the Gairdner Foundation International Award in Canada, the Albany Prize in Medicine and Biological Research, the Mendel Medal of the Genetics Society of the UK, and the Breakthrough Prize in Life Sciences.

As we work to emerge from the unprecedented challenges of the past year, it is crucial that the Senate confirm a proven leader in Dr. Lander to help set science and technology policies that benefit all Americans. We urge the Committee to swiftly advance Dr. Lander's nomination. Please do not hesitate to reach out to Derek Scholes (dscholes@ashg.org), Senior Director of Policy and Advocacy, if we can be of assistance.

Sincerely,

Gail P. Jarvik, M.D., Ph.D.
2021 President, ASHG

Mona V. Miller
Chief Executive Officer, ASHG



March 5, 2021

Sudip S. Parikh, PhD
Chief Executive Officer and
Executive Publisher, Science Journals

Senator Maria Cantwell, Chairwoman
Senator Roger Wicker, Ranking Member
United States Senate
Senate Committee on Commerce, Science, and Transportation
Washington, DC 20510

Dear Senators Cantwell and Wicker,

I write on behalf of the American Association for the Advancement of Science (AAAS) to urge the Senate Commerce, Science, and Transportation Committee to move rapidly to hold a hearing and vote on the nomination of Dr. Eric Lander to serve as director of the Office of Science and Technology Policy (OSTP). The early nomination of an accomplished and diverse scientific team, including a pioneering scientist like Dr. Eric Lander to serve as OSTP director signals the vital role that science must serve in our government as a critical component of the decision-making process. This is further amplified by the elevation of the OSTP director to a Cabinet level position.

The United States faces a wide range of domestic and international challenges, such as fighting the COVID-19 pandemic, addressing systemic racism in society, and protecting national and energy security. These challenges share one thing in common: science and technology are essential to addressing them successfully. It is for this reason that we applauded the nomination of Lander, and the appointments of Drs. Alondra Nelson, Maria Zuber, and Frances Arnold to serve as deputy director at OSTP and as co-chairs of the President's Council of Advisors on Science and Technology (PCAST), respectively. Together with Dr. Lander, this team of outstanding scientists bring the necessary diversity of talent, expertise, and experience to serve the President and our nation. We hope the committee will not delay his nomination hearing that can serve as an opportunity to discuss the role of OSTP in addressing the key priorities that President Biden has challenged Lander and his colleagues in undertaking.

Thank you for your consideration and for your leadership of vital efforts to ensure that we have a strong scientific leader at OSTP who will work across government and the research community to respond to the many challenges we face as a nation.

Sincerely,

Sudip S. Parikh
Copy: Mary Guenther, Fern Gibbons



THOMAS COSTABILE, P.E.
Executive Director/CEO
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The American Society
of Mechanical Engineers
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April 28, 2021

The Honorable Maria Cantwell
Chairman
Senate Committee on Commerce,
Science, and Transportation
Washington, D.C. 20515

The Honorable Roger Wicker
Ranking Member
Senate Committee on Commerce,
Science, and Transportation
Washington, D.C. 20515

Dear Chairman Cantwell and Ranking Member Wicker:

The American Society of Mechanical Engineers (ASME) is pleased to support the nomination of Dr. Eric Lander as Director of the White House Office of Science and Technology Policy (OSTP) and Presidential Science Advisor. We applaud President Biden's decision to elevate the position of Presidential Science Advisor to a Cabinet level position and the nomination of a candidate with deep interdisciplinary science and engineering experience to lead the White House science team.

Founded in 1880, ASME is a nonprofit professional organization that enables collaboration, knowledge sharing and skill development across all engineering disciplines, while promoting the vital role of the engineer in society. ASME codes and standards, publications, conferences, continuing education, and professional development programs provide a foundation for advancing technical knowledge and building a safer world.

Science and engineering challenges lie at the heart of each of the most serious problems facing the United States and our allies around the world. As we work to end the global pandemic and continue the difficult work of transforming and modernizing our infrastructure to mitigate the worst effects of climate change, it is essential that we reinvigorate our national science and technology strategy to strengthen U.S. leadership in science and engineering.

On behalf of the ASME community, we look forward to working with the Administration and Congress to help meet the science and engineering societal challenges of today and tomorrow. We encourage a swift confirmation process to ensure that the critical work can move forward.

Sincerely,

Thomas Costabile, P.E.
Executive Director/CEO

Cc: Senate Committee on Commerce, Science, and Transportation



March 16, 2021

Dear Chair Cantwell,

OFFICERS
 Susan Dentzer, Chair
 The Hon. Michael N. Castle, Chair Emeritus
 The Hon. Bart Gordon, Vice Chair
 Mary Woolley, President
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 Keith N. Yamamoto, PhD
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IN MEMORIAM
 Jay A. Gershen, DDS, PhD

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 E info@researchamerica.org

On behalf of the Research!America alliance, thank you for your leadership and demonstrated commitment to science and technology, as exemplified by your role as Chair of the Senate Committee on Commerce, Science, and Transportation. We are writing to respectfully request that you support the nomination of Dr. Eric Lander to be Director of the Office of Science and Technology Policy.

Dr. Lander's breadth of scientific expertise combined with his extraordinary leadership makes him a uniquely qualified candidate for this role. He is a world renowned scientist with expertise in mathematics, molecular biology, and genetics. He is no stranger to spearheading innovative research that yields strategic solutions to some of America's leading health challenges. Over 100,000 discoveries connecting genetic material to disease traits can be credited to Dr. Lander's research methodology.

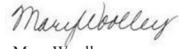
Dr. Lander excels at distilling technical information and is well experienced in communicating and coordinating scientific knowledge across agencies. Having served as Co-Chair of President Obama's President's Council of Advisors on Science and Technology (PCAST) and as a former member of the Department of Defense's Defense Innovation Board, Dr. Lander has greatly contributed to the advancement of America's science and technology enterprise, providing mission-critical thought leadership and guidance.

We agree with the importance of instituting policies and programs that will promote diversity, equity, and inclusion throughout OSTP. As the founding Director of the Broad Institute, Dr. Lander has helmed a highly respected research institute whose leadership and staff models gender and racial/ethnic diversity. The Institute has created partnerships that promote equity in research and empower identity-based affinity groups to succeed in STEMM careers. We are confident that if confirmed, Dr. Lander will continue to cultivate collaborative work environments that include the valuable perspectives of a diverse scientific community. Utilizing the varied expertise of those within the scientific community is critical to overcoming the challenges we face.

Dr. Lander's nomination to be the head of OSTP illustrates the elevated importance of science and technology as our nation endeavors to recover from the devastation COVID-19 has wrought, while also simultaneously pushing new scientific and technological breakthroughs forward. We support President Biden's nomination of Dr. Eric Lander to be Director of the Office of Science and Technology and hope that you will do the same.

Thank you Chair Cantwell, as well as your respective staff members, for your extraordinary commitment and hard work during this unprecedented time.

Sincerely,

A handwritten signature in cursive script, appearing to read "Mary Woolley".

Mary Woolley
President & CEO
Research!America



Christopher F. Chyba
Professor of Astrophysical Sciences and International Affairs

Department of Astrophysical Sciences
 School of Public and International Affairs
 221 Nassau Street, 2nd Floor
 Princeton, NJ 08542-4601
 Phone: 609-258-5633
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 cchyba@princeton.edu

March 11, 2021

Senator Maria Cantwell
 Chair, United States Committee on Commerce Science and Transportation
 Hart Senate Office Building, 420A
 Washington, DC 20510

Senator Roger Wicker
 Ranking Member, United States Committee on Commerce Science and Transportation
 555 Dirksen Senate Office Building,
 Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I write in strong support of Dr. Eric Lander's nomination to become Director of the White House Office of Science and Technology Policy. This has always been an important position, but this appointment may be more important now than it has ever been, even in the depths of the Cold War. In the Biden-Harris Administration, the OSTP Director will for the first time be a standing member of the National Security Council, meaning that the position is essential for the well-being of our Nation.

Many of the most pressing national and international security threats facing the United States have a major scientific or technological component. In most of these cases the pace of scientific or technical advance is so dynamic that it is difficult for the non-expert to keep abreast of the state of the field. Yet an accurate scientific and technical understanding may play a central role, and in some cases even a decisive one, for accurate threat assessment or in deciding the best course of action for the United States.

Even a *short* list of these pressing national security threats with a dynamic scientific or technological component is a long list.

- Although it had been clear for decades, this list now obviously includes naturally occurring pandemics, including prospects for rapid improvements in surveillance and response capabilities driven by biotechnology. It also includes potential applications of biotechnology, and especially the new CRISPR technology, to bioweapons and bioterrorism.
- It includes climate change and scientists' rapidly evolving understanding of the positive feedbacks and widespread security implications this entails, including opening of the Arctic ice, hurricane frequency and strength, and climate-driven migration.

- It includes quantum computing and its implications for decryption and computational power more generally, as well as communications based on quantum entanglement, as demonstrated by the Chinese Micius satellite.
- Even without quantum computing, numerical power and machine learning are now so effective that artificial intelligence (AI) increasingly permeates society, not only in warfighting but in intelligence, persistent surveillance, autonomous machines, and consequent short- and long-term risks. And even without AI, the country faces enormous challenges from cyber operations, including social media and elections manipulation.
- The list also includes the rapidly shifting satellite constellation, space weapons, and space debris landscape and the incorporation of hypersonic weapons and nuclear weapons-carrying drones into major and even lesser powers' arsenals.
- And it includes long-standing issues such as proliferating and evolving technologies for the enrichment of uranium; contested claims for the violation of the Comprehensive Test Ban Treaty by U.S. adversaries; assessments of anti-ballistic missile technologies and countermeasures; and nuclear force reliability, vulnerability, and modernization.
- And finally, it includes the myriad ways these technologies may interact to increase the prospects for "normal" accidents or inadvertent escalation, including escalation to nuclear weapons use.

The right choice for Director of the OSTP will ensure that the technical aspects of these issues, and many others, are recognized, critically assessed, and appropriately brought to bear at the highest levels of decision-making in the U.S. government. Eric Lander is that right choice. Obviously he is one of the world's leaders in biotechnology and the applications of biotechnology to combat disease. His doctorate in mathematics and information theory means that he will readily master, or has already mastered, many other topics he will confront, including cyber and AI issues. His former faculty position at Harvard Business School and his directorship of the Harvard-MIT Broad Institute, in addition to his previous position as PCAST co-chair, guarantees that he has the bureaucratic and administrative skills to hire the right people into the right positions to give him the supplemental expertise that he will need to address the broad range of challenges that will confront the NSC at the level of the President.

I served for eight years on President Obama's PCAST under Dr. Lander's leadership, and can attest to his remarkable range of skills and his high competence in bureaucratic and administrative matters. By choosing to move forward with the confirmation of Eric Lander, you will be ensuring that in our country's next crisis, and in the one after that, and in the one after that, the President and his Cabinet will be well informed by the most accurate scientific advice that can be brought to bear.

Sincerely,



Christopher F. Chyba

cc:
David Strickland, Majority Staff Director, United States Committee on Commerce Science and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and Transportation



February 26, 2021

The Honorable Maria Cantwell
Chair, Committee on Commerce,
Science and Transportation
United States Senate
Washington, D.C. 20510

The Honorable Roger Wicker
Ranking Member, Committee on Commerce,
Science and Transportation
United States Senate
Washington, D.C. 20510

Re: Nomination of Eric Lander as Director of the Office of Science & Technology Policy

Dear Chair Cantwell and Ranking Member Wicker:

On behalf of Elsevier, I write to express our strong support for the nomination of Eric Lander to serve as the Director of the Office of Science & Technology Policy in the White House. We are also excited to learn that this important position is being elevated to Cabinet-level status and we look forward to working with this Committee and the new Administration to further support research for the benefit of society.

As an information analytics company and a leading publisher of scientific, technical, and medical peer-reviewed journals, including *Cell* and *The Lancet*, we have proudly supported Dr. Lander's research over the years and urge the Senate to move forward promptly with his confirmation. Dr. Lander's breadth of experience, ongoing leadership in the scientific community and deep knowledge of the life sciences will be an asset to the Administration and the American people as we continue to face the daunting challenges caused by Covid-19, the impact of climate change and the need for more equitable access to healthcare and technology.

We have worked closely with successive administrations, across both parties, to ensure that science policy is advanced ambitiously, based on scientifically rigorous data and trustworthy information. Under strong leadership, the Office of Science & Technology Policy can effectively align government efforts and marshal robust public-private collaborations to tackle the big questions of our time. Dr. Lander is well-suited to work with and bring together, as President Biden notes, "our brightest minds across academia, medicine, industry, and government—breaking down the barriers that too often limit our vision and our progress, and prioritizing the needs, interests, fears, and aspirations of the American people."

We appreciate and thank you for your commitment to science and for moving quickly on this confirmation hearing. We know our nation will be well served with Dr. Lander leading the Office of Science & Technology Policy.

Sincerely,

Youngsuk "Y.S." Chi
Chairman

Cc: U.S. Senate Committee on Commerce, Science & Transportation

HARVARD
UNIVERSITY

March 11, 2021

To: The Honorable Marcia Cantwell, Chair, Senate Commerce Committee
The Honorable Roger Wicker, Ranking Member, Senate Commerce Committee

I am pleased to write in support of the nomination of Eric Lander to the post of National Science Advisor. I came to know Eric well during my eleven years as president of Harvard because of his leadership of the Broad Institute of Harvard and MIT. As an *ex officio* member of the Broad board, I saw Eric regularly and observed firsthand the combination of scientific and organizational genius that enabled him to build the Broad into a pathbreaking scientific enterprise continually creating new knowledge about human biology and human health. He created a remarkable community of young scientists, "Broadies" as they called themselves, at the cutting edge of discovery, constantly learning from one another in an environment of innovation and exploration. It was this community -- open, diverse in every dimension of gender and race and ethnicity -- that attracted and nurtured the scientific talent that propelled the Broad's many achievements, and it was Eric who established the conditions that made that community possible.

Eric Lander is a visionary, imagining goals that seem impossible -- sequencing the genome was just a start -- and then making them realities. The Broad's response to the coronavirus under Eric's leadership is just a recent example. Eric mobilized the organization to establish systems and protocols that would enable it to offer testing capabilities to a range of organizations -- including Harvard. This provided a foundation for continuing operations for these institutions, as well as safety for thousands of individuals who were able to continue to perform their jobs. The effort represented a unique combination of scientific expertise and practical engagement with a wider population dependent on science for their continuing health and well-being.

During much of my time on the Broad board, Eric was serving on PCAST, and so I had the opportunity to hear him discuss with us the contours of his thinking about science policy and the effects it can have on national health and prosperity. His understanding of these issues extends well beyond his scientific expertise, encompassing astute insights into the nature of the society and culture which both produces science and benefits from it. I cannot imagine a better candidate for the position for which he has been nominated. All Americans will benefit from his leadership and service.

Sincerely,

A handwritten signature in dark ink, reading "Drew Gilpin Faust".

Drew Gilpin Faust
Arthur Kingsley Porter University Professor
President Emerita
Harvard University

Wadsworth House Cambridge, MA 02138

March 17, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

As women who have been mentored and supported by Dr. Eric Lander throughout his decades of groundbreaking scientific work, we write to proudly endorse him as the nominee to be the next Director of the Office of Science and Technology Policy and White House Chief Science Advisor. At a time when our society is more dependent than ever on scientific innovation and the deployment of new technologies to save lives, reopen our economy and build back better, Dr. Lander's record of inclusive leadership and outstanding mentorship that delivers real results will be a tremendous asset to our nation.

Dr. Lander's credentials and experience are exactly what America needs at this crucial moment.

- As one of the principal leaders of the Human Genome Project, Dr. Lander's work has led to more than 100,000 discoveries that utilize DNA, advancing our understanding of and approach to a multitude of medical conditions such as heart disease, Alzheimer's disease, schizophrenia, diabetes, tuberculosis and malaria.
- As the President and Founding Director of the Broad Institute, he's managed, mentored and steered an organization comprised of hundreds of scientific leaders who have worked collaboratively with the international scientific community to make major advances in biology, chemistry, computer science, engineering, mathematics and medicine in ways that have benefited people across the globe.
- At the Broad, Eric has created a culture of open sharing, collaboration, and the breaking down of barriers to our shared understanding of biology. Along the way, he has focused on equity and access, to help ensure the advantages that scientific advances can unlock are available to all and not just some.
- As the Co-Chair of the President's Council of Advisors on Science and Technology for eight years in the Obama-Biden Administration, Dr. Lander will step into this new role with a complete understanding of how to navigate our government and bring diverse, essential voices into the discussion in order to bring science back to the decision-making table.

While Dr. Lander's accomplishments make him more than qualified for this crucial role in the Biden-Harris Administration, his approach to inclusive leadership is equally important.

Throughout his career, Dr. Lander has taught, mentored, and coached all of us and elevated countless women to positions of leadership, helping change the face of science in the 21st century. Many of us in fact, hold leadership roles in science today, because of his support, encouragement, mentorship, and advocacy. He's demonstrated this dedication by ensuring that both the Broad Institute at large, and its senior leadership team, are majority female. Because of Dr. Lander's commitment to implementing policies that advance women in the workplace, the Broad Institute has been recognized by Working Mother Magazine as one of the top 100 places to work for four years in a row.

His vision has benefited the larger community, as well: In early March 2020, before the COVID-19 pandemic had yet gripped the nation, Eric and key leaders at Broad saw the lack of a national testing infrastructure and filled the gap by building their own test processing center nearly from scratch. The team has partnered with the Commonwealth of Massachusetts, the City of Cambridge, hospitals, nursing homes, homeless shelters, public K-12 schools, and more than 100 colleges and universities and to date have processed nearly 14 million tests -- with first priority given to residents of the communities most impacted by COVID-19. When giving credit to the scientific leaders who inspired and directed these efforts, Eric said publicly that it is "**because** the efforts were all led by women" that the Broad was able to succeed in responding to the pandemic.

At a time when the COVID-19 pandemic continues ravaging our people, we need a visionary leader who will rethink, repair and reimagine the role of science and technology in our nation in a way that unites our country, empowers all Americans to reach greatness and brings science back to government.

Without a doubt, Dr. Eric Lander is the right leader to get the job done. We are proud to endorse his nomination.

Sincerely,

Deborah T. Hung, MD, PhD
Core Faculty Member and Co-Director of the Infectious Disease and Microbiome Program,
Broad Institute of MIT & Harvard
Professor of Genetics, Harvard Medical School and Massachusetts General Hospital

Gwen Acton, PhD
CEO, Vivo Group

Aviva Presser Aiden, MD PhD
Clinical Fellow, Stanford University School of Medicine

Kristin Ardlie, PhD
Director, GTEx LDACC, Broad Institute of MIT & Harvard

Paola Arlotta, PhD
Golub Family Professor and Chair, Harvard University

Sangeeta Bhatia, MD, PhD
Wilson Professor of Engineering, Massachusetts Institute of Technology

Anne Carpenter, PhD
Institute Scientist, Broad Institute of MIT & Harvard

Melina Claussnitzer, PhD
Assistant Professor in Medicine, Harvard Medical School and Beth Israel Deaconess Medical Center
Institute Member, Broad Institute of MIT & Harvard

Lisa Cosimi, MD
Associate Physician, Brigham and Women's Hospital
Assistant Professor, Harvard Medical School

Sheila Dodge, MLA, MBA
General Manager, Genomics Platform, Broad Institute of MIT & Harvard

Hilary Finucane, PhD
Member of the Faculty, Harvard Medical School

Stacey Gabriel, PhD
Senior Director, Genomics Platform, Broad Institute of MIT & Harvard

Anna Greka, MD, PhD
Associate Professor of Medicine, Harvard Medical School and Brigham and Women's Hospital
Institute Member, Broad Institute of MIT & Harvard

Sharon Grossman, MD, PhD
Physician, Harvard Medical School

Johanna Hastbacka, MD, PhD
Physician, New Children's Hospital, Helsinki University Hospital, Helsinki, Finland

Karen H. Hong, PhD
Partner, Novo Ventures

Cigall Kadoch, PhD
Associate Professor, Pediatric Oncology, Dana-Farber Cancer Institute, Harvard Medical School, and Broad Institute of MIT & Harvard

Elinor Karlsson, PhD
Associate Professor, University of Massachusetts Medical School

Justine Levin-Allerhand, PhD
Chief Development Officer and Chief External Relations Officer, Broad Institute of MIT & Harvard

Kerstin Lindblad-Toh, PhD
Professor, Uppsala University, Sweden
Scientific Director of Vertebrate Genomics, Broad Institute of MIT & Harvard

Cecilia Lindgren, PhD
Director of Oxford Big Data Institute and Professor, University of Oxford, UK.

Heidi Rehm, PhD
Professor of Pathology, Massachusetts General Hospital and Broad Institute of MIT & Harvard

Pardis Sabeti, MD, PhD
Professor, Harvard University and T.H. Chan School of Public Health

Samantha Singer, MS, MBA
Chief Executive Officer, Abata Therapeutics

Jesse Souweine
Chief Operating Officer, Broad Institute of MIT & Harvard

Beth Stevens, PhD
HHMI Investigator, Broad Institute of MIT & Harvard and Boston Children's Hospital

Vidya Subramanian, PhD
Research Scientist and Group Leader, Broad Institute of MIT & Harvard

Eileen Sun, PhD, JD
Partner, Seed Intellectual Property Law Group LLP

Sarah Teichmann, PhD
Head of Cellular Genetics, Wellcome Sanger Institute, Cambridge, UK

Sonia Vallabh, PhD
Associated Scientist, Broad Institute of MIT & Harvard

Catherine Wu, MD
Chief, Division of Transplant and Cell Therapies and Professor, Harvard Medical School and
Dana-Farber Cancer Institute

Moran Yassour, PhD
Assistant Professor, The Hebrew University of Jerusalem

Cc: David Strickland, Majority Staff Director, United States Committee on Commerce Science
and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and
Transportation



Henry Louis Gates, Jr., Director
Alphonse Fletcher University Professor
P 617.495.5168
F 617.495.9490
gates@harvard.edu

March 15, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce, Science, and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce, Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

It is my pleasure and honor to submit this letter of support for the nomination of Professor Eric Lander to the position of Director of the Office of Science and Technology Policy (OSTP) as well as Presidential Science Advisor.

As a member of Harvard's Medical School, Professor Lander is a colleague of mine, but my acquaintance with him predates my own tenure at Harvard University. In 1981, I became an inaugural member of the MacArthur Fellowship program; in 1987, Professor Lander was awarded the MacArthur Fellowship. We quickly established a relationship based on our shared fascination with genetics. Professor Lander has taught me an enormous amount about the uses of DNA to trace ancestry, long before the commercial DNA tests existed. In 2012, I began my PBS documentary series, "Finding Your Roots." As part of my exploration of my guests' ancestry, I utilize DNA results; the Broad Institute, which Professor Lander founded, has been remarkably generous in assisting my interpretation of DNA results. In all of my conversations with Professor Lander, I have been encouraged and inspired by his knowledge. He is, quite simply, a genius.

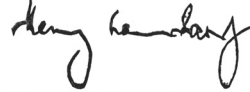


hutchinscenter.fas.harvard.edu
104 Mount Auburn Street, 3R

During his astounding career, Professor Lander, a faculty member at both the Massachusetts Institute of Technology and Harvard Medical School, has achieved ground-breaking innovations in the fields of mathematics, biology, and genetics. In 1990, he founded the Whitehead Institute/MIT Center for Genome Research which quickly became one of the world's leading centers for the analysis of mammalian genomes. In 2001, he was the lead author of *Nature's* first publication of the human genome. Professor Lander broadened his reach as an institution builder in 2004 as the founding director of the Eli and Edythe L. Broad Institute, a biomedical and genomic research institute which brings together the combined resources of the M.I.T., Harvard University, and five Harvard teaching hospitals. The Broad Institute has been instrumental in the COVID-19 pandemic response.

Professor Lander has also had previous governmental experience as a member of President Barack Obama's Council of Advisors on Science and Technology. Despite his many scholarly and administrative duties, Professor Lander has continued his dedication to teaching and has, for years, co-taught MIT's required introductory biology courses. In addition, he has taught online courses through MIT's EdX platform, which provides a larger audience for its world-class scholarship. To his great credit, Professor Lander has an extraordinary ability and desire to communicate his vast array of knowledge to non-scientists. It is my belief that he will serve our country admirably.

Sincerely,



Henry Louis Gates, Jr.

CC:

David Strickland, Majority Staff Director, United States Committee on Commerce, Science, and Transportation

John Keast, Minority Staff Director, United States Committee on Commerce, Science, and Transportation



BIOCHEMISTRY & BIOPHYSICS

Mission Bay Campus
600 16th Street
San Francisco, CA
94158-2517

April 8, 2021

RE: Nomination of Eric Lander as Head of OSTP and Science Advisor to the President of the United States

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to convey to you my strongest support for the appointment of **Dr. Eric Lander** as Head of OSTP and Science Advisor to the President of the United States.

The great fortune of the Nation will be to have such a wonderful scientist and leader as Dr. Lander in this position. To appoint him in this critical role will bring to it his deep expertise and visionary experience and insight. I believe that no time could be so critical as now for our need to rebuild trust in science, so as to create a roadmap for solving our challenging problems.

I have seen and admired Dr. Lander in action in a professional capacity during the last few decades. Every instance (from his discussing scientific vision to his mentoring younger scientists) convinces me that Dr. Lander is a most brilliant scientist, and importantly, also a person who cares deeply for humans and humanity's wellbeing. Dr. Lander's scientific talent is without doubt. But why he is also so well suited for this position of Head of OSTP and Science Advisor to the President is because he thinks clearly and is a true leader and a visionary. And, he communicates well and explains difficult science so well that everyone understands it. He gets things done. His creating and leading the remarkable Broad Institute (a shared Harvard and MIT research institute) attest to that. He will be an effective, constructive public servant in the White House.

Dr. Eric Lander will bring to this position both substantial relevant experience (e.g. 8 years on PCAST, including co-chair, and 4 years on the DoD Innovation Board) and his high ideals. It is important that he is also a marvelously clear and engaging communicator of science. The whole scientific community will be justly proud to have Dr. Lander in this role.

I earnestly hope that Dr. Lander's confirmation will be swift, so that our Nation can have the benefit of Dr. Lander in this important position as soon and as effectively as possible. Truly, we all need him in this job.

Sincerely yours,

A handwritten signature in cursive script, appearing to read "Elizabeth H. Blackburn".

Elizabeth H. Blackburn, Ph.D.
Morris Herzstein Professor of Biology and Physiology
Professor Emerita, Department of Biochemistry and Biophysics
University of California San Francisco
California, USA
2009 Nobel Laureate in Physiology or Medicine

WELLESLEY COLLEGE
OFFICE OF THE PRESIDENT

Paula A. Johnson

March 15, 2021

Senator Maria Cantwell
 Chair, United States Committee on Commerce Science and Transportation
 Hart Senate Office Building, 420A
 Washington, DC 20510

Senator Roger Wicker
 Ranking Member, United States Committee on Commerce Science and Transportation
 555 Dirksen Senate Office Building,
 Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

As the COVID-19 pandemic took hold across the world last spring, U.S. colleges and universities mobilized to send students home and rapidly shift to remote learning. In a matter of days, the traditional model of higher education delivery at the institution I lead, Wellesley College, and at institutions across the country changed. We faced great uncertainty regarding when and how we would be able to return to in-person learning. As a physician who has significant public health experience, I was aware that we would need to overcome many hurdles, and I knew we couldn't do it alone.

To address the unprecedented challenges our institutions were facing during the pandemic and to bring students back to campuses that fall, we needed to take fast, collaborative, innovative action. Massachusetts Gov. Charlie Baker created the state's Higher Education Working Group, which began planning for repopulating campuses in April 2020. As the leader of the working group's testing subcommittee, tasked with developing COVID-19 testing strategies and protocols for higher education, I knew there was one person we needed to collaborate with to set these plans in motion: Dr. Eric Lander, president and founding director of the [Broad Institute of MIT and Harvard](#).

Dr. Lander is a distinguished leader, researcher, and community builder. He has a long track record of public service with the [President's Council of Advisors on Science and Technology](#) and the Department of Defense's [Defense Innovation Board](#), and a breadth of scientific experience—he is one of the most accomplished and senior leaders of the Human Genome Project. He has built and fostered highly inclusive cultures that support women and underrepresented minorities, and he has fought for justice and access in health care.

Dr. Lander and his team at the Broad understood immediately the public health need for accurate, rapid, and widely accessible COVID-19 testing. The Broad pivoted from a focus on genomics research to creating one of the largest-scale, lowest-cost PCR testing labs in the United



106 Central Street, Wellesley, MA 02481 Tel 781.283.2237 pjohnson@wellesley.edu

Senator Maria Cantwell
 Senator Roger Wicker
 March 15, 2021
 Page 2

States, working to ensure affordable access to COVID-19 testing for the public, nursing homes, public schools, and residential schools for children with disabilities, as well as free testing for vulnerable populations.

When I called Dr. Lander in May 2020 to ask about setting up a program that would allow colleges and universities to test at the scale we needed to keep students and our communities safe, he didn't hesitate to take on this challenge. The resulting testing program has been wildly successful and now spans almost 140 public and private institutions. Without Dr. Lander's leadership and the Broad's testing program, which is truly a public service, we would not have been able to bring students back to Wellesley—or for that matter to any residential campus—for in-person instruction and the residential college experience this past fall. Hundreds of thousands of students across New England have been able to resume in-person learning thanks to Dr. Lander and the Broad.

I have no doubt that Dr. Lander will bring his extraordinary dedication to science, public service, ability to develop and execute innovative solutions, and collaborative spirit to the Office of Science and Technology Policy.

Sincerely,



Paula A. Johnson, MD, MPH
 President
 Wellesley College

cc: David Strickland, Majority Staff Director, United States Committee on Commerce
 Science and Transportation
 John Keast, Minority Staff Director, United States Committee on Commerce Science and
 Transportation

Colleges and universities participating in the Broad Institute's COVID-19 testing program:

Amherst College, Babson College, Bard College, Barnard College, Bates College, Bay Path University, Bentley University, Boston College, Bowdoin College, Brandeis University, Bridgewater State University, Bryant University, Champlain College, Clark University, Clarkson University, Colby College, College of the Atlantic, Columbia University, Connecticut College,

Senator Maria Cantwell
 Senator Roger Wicker
 March 15, 2021
 Page 3

Curry College, Dartmouth College, Emerson College, Emmanuel College, Endicott College, Fairfield University, Fisher College, Fitchburg State University, Fordham University, Framingham State University, Gordon College, Hamilton College, Hampshire College, Harvard University, Hobart and William Smith Colleges, Husson University, Lasell University, Lesley University, Massachusetts Maritime Academy, MassArt, Massachusetts College of Pharmacy and Health Sciences, Middlebury College, MIT, Mitchell College, Montserrat College of Art, Mount Holyoke College, New England Conservatory, Nichols College, Northeastern University, Northern Vermont University, Norwich University, Olin College, Providence College, Quinnipiac University, Regis College, Rhode Island School of Design, Rochester Institute of Technology, Roger Williams University, Saint Michael's College, Salem State University, Salve Regina University, Simmons University, Skidmore College, Smith College, Springfield College, St. Lawrence University, Stonehill College, Suffolk University, Trinity College, Tufts University, UMass Amherst, UMass Dartmouth, UMass Lowell, UMass Medical Center, Union College, University of Connecticut, University of New England, University of Rhode Island, University of Vermont, Wagner College, Wellesley College, Wentworth Institute of Technology, Wesleyan University, Westfield State University, Wheaton College, Williams College, Worcester Polytechnic Institute, Worcester State University, and Yale University.



Eccles Institute of Human Genetics
15 North 2030 East, Room 5100
Salt Lake City, UT 84112
Office 801-581-4422
Fax 801-581-7796

March 12, 2021

Dear Chair Cantwell and Ranking Member Wicker,

I am writing in huge support of Dr. Eric Lander for the directorship of the Office of Science and Technology Policy. Dr. Lander is unquestionably one of the most accomplished scientists in the world. The breadth of his scientific accomplishments is simply amazing. He has a long history of public service to our nation, including co-chair of PCAST during the Obama leadership. I cannot imagine a better candidate. COVID-19 perfectly exemplifies why science needs to be at the center of national decision making when drafting, for example, national policies to curb this devastating pandemic. In addition, Dr. Eric Lander is an extraordinary communicator, which will serve him well to explicate the roles and use of science for the betterment of all of our nation's citizens. He is outstanding. Thank you for your consideration. In my opinion you could not do better.

A handwritten signature in dark ink, appearing to read 'Mario R. Capecchi', with a long, sweeping horizontal line extending to the right.

Mario R. Capecchi
Distinguished Professor

University of Utah School of Medicine

2007 Nobel Laureate in Physiology or Medicine

CaltechDivision of Chemistry
and Chemical Engineering MC 210-41Professor Frances H. Arnold
1200 E. California Blvd.
Pasadena, CA 91125
(626) 395-4162
frances@cheme.caltech.edu
web: <http://fhalab.caltech.edu>

March 11, 2021

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to offer my strongest support for Dr. Eric Lander's appointment as Head of OSTP and Science Advisor to the President of the United States. Our Nation is lucky to have such a great scientist and leader in this position—Dr. Lander will bring great experience and insights to this critical role, and at this critical time when we need to rebuild trust in science and create a roadmap for solving the many challenging problems we face.

Dr. Lander may be the most brilliant scientist ever to have this job. But it is not just his scientific talent that makes him so well suited for it. He is also a leader and a visionary, having created and led the remarkable Broad Institute joint between Harvard and MIT, with strong ideals and a great deal of relevant experience (e.g. 8 years on PCAST, including co-chair, and 4 years on the DoD Innovation Board). He is also a fabulous communicator of science and can explain difficult material in a way that anyone can understand. He is a clear thinker, and he is a doer.

The entire scientific community will be proud to have Dr. Lander in this role in the White House, where he will be a constructive and effective public servant. I can think of no one better than Dr. Lander for the job, and I hope that his confirmation will be smooth and swift.

Sincerely,



Frances Hamilton Arnold, PhD
Linus Pauling Professor of Chemical Engineering, Bioengineering and Biochemistry
2018 Nobel Prize in Chemistry

FHA:cn



Joseph L. Goldstein, M.D.
Regental Professor and Chairman
Department of Molecular Genetics

5323 Harry Hines Boulevard
Dallas, Texas 75390-9046
214-648-2141 Telefax 214-648-8804
joe.goldstein@utsouthwestern.edu

March 11, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I write to provide my strong support for the appointment of **Eric S. Lander** for Secretary of Science. Eric is one of the most accomplished, distinguished, and effective scientists in the world. Building on his graduate training in mathematics and postdoctoral work in human genetics, he conceived a mathematical approach for mapping complex diseases in populations. This was followed by his taking a leading role in the Human Genome Project, which in turn led him to the development of Genome Wide Association studies (GWAS) for revealing mechanistic clues to complex human diseases. Throughout his career, Eric has been a peerless expositor of open data-sharing.

For the past 15 years, Eric has served as the Founding Director of the Broad Institute in Boston, which is arguably the best new scientific institute of the 21st century. At the Broad, Eric and his colleagues pioneered new technologies that have been made widely available to scientists throughout the world. For the last 10 years, I have been a member of the Board of Scientific Counselors at the Broad Institute and have served as Chair for the last 5 years. In this capacity, I have witnessed firsthand Eric's extraordinary ability as an institutional builder and leader who has created a highly collaborative culture that is unique for its inclusion of women and underrepresented minorities.

When the Covid-19 first appeared last year, the Broad Institute under Eric's leadership launched one of the largest-scale, lowest-cost PCR testing labs in the U.S. for Covid testing – a prime example of Eric's devotion to public service.

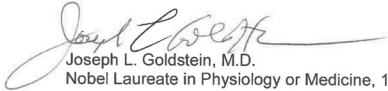
Eric Lander is one of the best, if not the best, communicator of scientific issues – no matter how complex. He is brilliant and visionary, as evidenced by his influential amicus brief to the Supreme Court arguing against patenting of the breast cancer gene.

Page 2
Senator Maria Cantwell
Senator Roger Wicker
March 11, 2021

In my view, Eric Lander is by far the best person to serve as our inaugural Secretary of Science.

Thank you for all your good work in making our country a great place to live and work.

Sincerely,


Joseph L. Goldstein, M.D.
Nobel Laureate in Physiology or Medicine, 1985

JLG/jr
C11/682

cc: David Strickland, Majority Staff Director, United States Committee on Commerce
Science and Transportation

John Keast, Minority Staff Director, United States Committee on Commerce
Science and Transportation

USC Dornsife

Dana and David Dornsife
College of Letters, Arts and Sciences

DEPARTMENT OF CHEMISTRY

*Arieh Warshel
Nobel laureate
Dana and David Dornsife Chair in Chemistry
Distinguished Professor*

March 11, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

Re: Dr. Eric Lander for the Director of the Office of Science and Technology Policy

Dear Chair Cantwell and Ranking Member Wicker:

I would like to give my strongest support for the confirmation of Dr. Eric Lander for the position of Director of the Office of Science and Technology Policy.

I have followed Dr. Lander for a long time and believe that he is the best possible choice in the country for this position. To support my assertion, I point to his contribution in creating what is arguably the best new research institute of the 21st century, the Broad Institute of MIT and Harvard, instilled with a collaborative culture that is highly inclusive of women and minorities. I would also like to mention his effort to ensure affordable access to Covid-19 testing devoted to public uses, by launching one of largest-scale, lowest-cost PCR testing labs in US.

I support his nomination and enthusiastically encourage his appointment!

Sincerely,

Arieh Warshel

Arieh Warshel
Nobel laureate
Member, National Academy of Science, HonFRSC
Foreign Member, Russian Academy of Sciences
Distinguished Professor of Chemistry and Biochemistry
Dana and David Dornsife Chair in Chemistry
Member, USC Norris Comprehensive Cancer Center

AW/mjc

University of Southern California
3620 McClintock Avenue, Los Angeles, California 90089-1062 • Tel: 213 740 4114 • Fax: 213 740 2701



cc:

Email PDF to: David_strickland@commerce.senate.gov
John_keast@commerce.senate.gov

Cc: Melissa_porter@commerce.senate.gov

Cc: Crystal_tully@commerce.senate.gov

Cc: Narda.M.Jones@ostp.eop.gov.



Mark E. Nunnally
79 Newbury Street
Boston, MA 02116

March 11, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

I write in regards to Eric Lander's nomination for the director of the Office of Science and Technology Policy with my HIGHEST recommendation for his confirmation. I have known Eric for some years and have been serving as a member of the Broad Institute's Board of Directors since 2016.

Eric is a remarkable person. He has perhaps the keenest intellect of anyone I have come across during my forty-year career. Even more remarkably is the breadth of topical knowledge he is able to bring to bear on important issues and his extraordinary ability to integrate across disciplines into clear and actionable insights. At the same time, he is a clear and thought-provoking communicator who can take complex subjects and distill them into understandable and accessible language.

As one of the principal leaders of the Human Genome Project, the founder of the Broad Institute, and one of the most cited scientists in the world (to name just several of his many achievements), Eric has truly helped changed the world.

In the midst of this busy and successful career, he has also demonstrated a significant commitment to public service, having served on the Department of Defense's Innovation Board for four years and the President's Council of Advisors on Science and Technology for eight years.

Finally, Eric has repeatedly, consistently, and with determination fought for justice and access to healthcare. He played a central role in the founding of the Innocence Project, wrote an influential amicus brief to Supreme Court against patenting of breast cancer gene, and, most recently and with huge consequences, worked tirelessly to ensure affordable access to Covid-19 testing for the public as well as free testing for vulnerable populations by launching one of largest, lowest-cost, PCR testing labs in U.S.

I hope the U.S. Senate will approve the appointment of this extraordinary American.

With warmest regards,

Mark E. Nunnally
Chairman

CC: David Strickland, Majority Staff Director, United States Committee on Commerce Science and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and Transportation



SHIRLEY M. TILGHMAN
 President Emerita
 Professor of Molecular Biology
 Carl Icahn Laboratory, Room 240
 Princeton, NJ 08544
smt@princeton.edu

Senator Maria Cantwell
 Chair, United States Committee on Commerce Science and Transportation
 Hart Senate Office Building, 420A
 Washington, DC 20510

March 12, 2021

Dear Chair Cantwell,

I am writing to voice my strong and enthusiastic support for the nomination of Dr. Eric S. Lander as Science Advisor to the President and Director of the Office of Science and Technology Policy. Dr. Lander is one of our nation's most accomplished biomedical scientists, and was a key intellectual leader of the very successful Human Genome Project. In 2004 he founded the Broad Institute of MIT and Harvard, on whose board I have served for the past 6 years, building it into an extraordinary research powerhouse that has changed the way in which scientists connect with one another and conduct their science. His commitment to creating a research environment in which everyone could thrive, including women and under-represented minorities, has been clear to me from the outset.

In the last 12 months he has been advising Governor Charlie Baker of Massachusetts on the state's response to the COVID-19 pandemic. At the Broad Institute he rapidly created a automated and scalable testing site that has served hospitals and clinics; nursing homes, long-term care facilities, and homeless shelters; residents in high-impact communities; colleges and universities; and Massachusetts K-12 schools. At one point this small research institute in Cambridge was conducting 20% of the SARS-CoV-2 testing in the state. This reflects Dr. Lander's instinct to think big, and to respond aggressively to a compelling need.

Dr. Lander brings to OSTP three qualities that are essential in a Science Advisor to the President. First he is an amazingly effective communicator of science to *both* scientific and lay audiences. In lectures, op-eds and online courses he ably conveys the excitement of scientific discovery, as well as its very positive impact of the economic wellbeing of the U.S. Second he is intellectually very broad, having trained as a mathematician before turning to biomedical science. Third he has considerable public service experience, having co-chaired the President's Council of Advisors on Science and Technology during the eight years of President Obama's administration, and most recently served on the Department of Defense's Innovation Board. He led the PCAST committee that focused on reforming the practices of forensic science, building on his years of advising the Innocence Project, and prepared one of the key amicus briefs to the Supreme Court on the patenting of genes. Finally I might mention that during the early years of the Human Genome Project, Dr. Lander was a strong advocate for what we now call "open science", ensuring that the DNA sequences rolling off sequencing machines were immediately made free and available to the world on a daily basis.



Office of the President
University of Maryland, Baltimore County
1000 Hilltop Circle
Baltimore, MD 21250
hrabowski@umbc.edu // p: 410.455-2274
president.umbc.edu

March 13, 2021

Senator Maria Cantwell
Chair, United States Senate Committee on Commerce, Science, and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce, Science, and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

President Joseph Biden has nominated Dr. Eric Lander, one of our nation's most distinguished scientists, to serve as Science Advisor to the President and Director of the White House Office of Science and Technology Policy. As you and your Senate colleagues in the Senate Committee on Commerce, Science, and Transportation consider the nomination of Dr. Lander, I would like to convey my support for confirming Dr. Lander in this role.

Dr. Lander will bring many important qualities to the work of science advisor at a time when our nation and the new administration will be reassessing the role of science in policymaking, how our society interacts with science and technology, and our actions to build an inclusive and robust scientific workforce.

Dr. Lander is an accomplished life scientist with great breadth of expertise. He is one of the principal founders of the Human Genome Project and one of the most highly cited scientists in the world. In 2004, he took on the role of president and founding director of the Broad Institute of MIT and Harvard, a research institute focused on using genomics to advance our understanding of the biology and treatment of human disease.

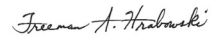
Dr. Lander has also played a critical role in advancing social justice and access to technology. He played a key role in founding the Innocence Project, dedicated to exonerating the wrongfully convicted through DNA testing. He has worked to ensure affordable access to COVID-19 testing by launching one of the lowest-cost PCR testing laboratories in the United States.

For the past four decades, I have dedicated my time and energy to expanding the participation and success of underrepresented minorities in science and engineering. I am greatly encouraged by the positive experiences that African American and other graduates of UMBC have had as doctoral students at the Broad Institute under Dr. Lander's leadership. I believe that Dr. Lander will provide important national leadership as we in the science and engineering community work together in the coming years to advance diversity and inclusion in our fields.

Dr. Lander will be a valuable asset to President Biden and the nation in the role of science advisor. He brings years of experience working for the public, including eight years as co-chair of the President's Council of Advisors on Science and Technology for President Barack Obama. He is also an effective communicator, an invaluable quality in an advocate for our nation's scientific goals at this time.

As a mathematician and an African American educator, I urge your confirmation of Dr. Eric Lander as Science Advisor to the President.

Sincerely,

A handwritten signature in cursive script that reads "Freeman A. Hrabowski, III".

Freeman A. Hrabowski, III
President
University of Maryland, Baltimore County

cc:
David Strickland, Majority Staff Director, United States Committee on Commerce, Science, and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce, Science, and Transportation

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Mar 13, 2021

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I am writing to strongly support the appointment of Dr. Eric Lander to Director of the Office of Science and Technology Policy. I have known Eric for several decades and worked closely with him on certain programs for the National Cancer Institute. Eric was one of the key leaders of the Human Genome Project and has built one of the finest scientific research institutes in the world, the Broad Institute. He is well respected in the scientific community for his openness, leadership and brilliance. I can think of no one more qualified for this position.

Sincerely,
Leland Hartwell
Noble Laureate, 2001

Elias A. Zerhouni, MD
Professor Emeritus Johns Hopkins University
Former Director NIH- 2002-2008

To :

Senator Maria Cantwell. Chair, United States Committee on Commerce, Science and transportation.

And

Senator Roger Wicker. Ranking Member. United States Committee on Commerce, Science and Transportation

Re: Letter of support for the confirmation of Dr. Eric Lander, Nominee for the positions of director of the Office of Science and Technology Policy. (OSTP)

Dear Senators Cantwell and Wicker

Please allow me to share with you my support of the nomination of Dr. Eric Lander as Director of the OSTP as you are considering him for Senate confirmation.

As former director of the NIH from 2002 to 2008 and since then, I have had the privilege of interacting with Dr Eric Lander for nearly two decades in various capacities. I met him first in his role as one of the principal US investigators leading the human Genome sequencing project which was completed in 2003. Dr Lander brought to this role an unusual combination of mathematical, physical and biological Sciences that made him approach problems in a very unique and creative way. He has led the extraordinary development of the Broad Institute at MIT, opening a series of new fields of investigations by bringing computational sciences as well as advanced technologies to bear on the extraordinary possibilities of genomics. He recruited a cadre of investigators who have broken new grounds and are now leaders in their fields, including Cancer, Single cell genomics and more recently CRISPR technologies. The Broad institute is widely recognized as one of the best if not the best new research institute of the 21st century. As an extraordinary institutional leader, he ushered completely novel ways of combining the strength of physical, biological sciences and engineering with a highly inclusive culture of diversity that have become a model for many institutions around the world.

Dr Lander also inspires the current generations of scientists and engineers by his extraordinary communications skills and dedication to public service. He served on the White house Presidential council of Advisers in Science and technology (PCAST) from 2009 to 2016 and the DOD Defensive Innovation Board from 2016 to 2020.

At a time of great geopolitical challenges in Science and Technology, I cannot think of anyone better to serve in this role. He always brings an open attitude of active and creative leadership to his roles leading to impactful change strategies. I believe that more than anything today, we need leadership that can coordinate the actions of our many agencies across the many strategic domains of Science and Technology that will determine the future position and competitiveness of the United States in Science and Technology.

In my view, based on direct observations, he is the most accomplished American scientist today with the breadth of experience, track record, credibility and vision to assume this critical role for the Nation.

With my utmost respect

A handwritten signature in black ink, appearing to read 'Elias A. Zerhouni', with a stylized flourish at the end.

Elias A. Zerhouni, MD
Former director NIH, 2002-2008



Harold Varmus, M.D.
 Lewis Thomas University Professor of Medicine
 Joan & Sanford I. Weill Department of Medicine
 Tel 646-962-6873 Fax 646-962-0675
varmus@med.cornell.edu

March 10, 2021

Senator Maria Cantwell
 Chair, United States Committee on Commerce Science and Transportation
 Hart Senate Office Building, 420A
 Washington, DC 20510

Dear Madam Chairperson:

I am writing to express my enthusiasm for the nomination of Professor Eric Lander to be the Director of the Office of Science and Technology Policy (OSTP).

I have known Eric well for over thirty years, beginning at a time when he was a mathematician teaching at the Harvard Business School, and I have followed his career closely as he played a central role in the Human Genome Project (when I was Director of the NIH and he was a faculty member at the Whitehead Institute at MIT), as he founded and ran the extraordinary Broad Institute at Harvard and MIT (and I served on his advisory board), and as he co-chaired (with John Holdren and me) the President's Advisory Council on Science and Technology (PCAST) in the Obama Administration. In these and many other venues, Eric has performed with vision, energy, and deep knowledge of many fields of science. His contributions to public welfare and to the success of our scientific enterprise have been immense, and he has vigorously nurtured the careers of all of the members of the Broad Institute and its collaborating institutions, especially women and minority scientists, with a sense of fairness and justice.

Eric has already made history by being the first biologist nominated for the Directorship at OSTP and by being offered a seat in the White House cabinet if he is confirmed as Director. At a time when science is so critical to the future of our country and our species, it is imperative to have a scientist with his skills and stature in those positions. I urge you to bring his confirmation proceedings to a swift and successful outcome.

Sincerely,

Harold Varmus MD
 Lewis Thomas University Professor, Weill Cornell Medicine
 Senior Associate Member, New York Genome Center
 Former Director, NIH (1993-1999) and NCI (2010-2015)
 Nobel Laureate in Physiology or Medicine (1989)
 National Medal of Science (2003)

Cc: David Strickland, Majority Staff Director, United States Committee on Commerce Science and Transportation

Catherine E. Woteki, Ph.D.

143 Kentucky Avenue SE

Washington, DC 20003

April 8, 2021

Senator Maria Cantwell, Chair
Committee on Commerce, Science and Transportation
U.S. Senate
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker, Ranking Member
Committee on Commerce, Science and Transportation
U.S. Senate
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to support the nomination of Dr. Eric Lander as Director of the Office of Science and Technology Policy and Science Advisor to the President of the United States. Having served as the Chief Scientist and Under Secretary for Research, Education and Economics at the U.S. Department of Agriculture, I understand how critical it is to have an experienced scientist at the helm of US science policy and providing guidance to the President when science can inform important decisions. And, having had the opportunity to work with Dr. Lander, I know he has the experience and leadership to be an outstanding chief scientist for the nation.

Dr. Lander combines a deep understanding of science with administrative skills and policy experience. He is well known and highly respected in the science community for his pioneering work in the Human Genome Project. He will bring broad knowledge of mathematics, genetics and biological science to the role of OSTP Director along with entrepreneurial and administrative experience as the founding director of the Broad Institute. He will also bring experience in science policy from his 8-year tenure on President Obama's Council of Advisors on Science and Technology and a broad network of contacts in other scientific disciplines.

We as a nation will be well-served by Dr. Lander as our chief scientist and I urge you to move forward on his confirmation.

Sincerely yours,

. Catherine E. Woteki

Catherine E. Woteki, Ph.D.

Professor of Food Science and Human Nutrition, Iowa State University

Distinguished Visiting Institute Professor, Biocomplexity Institute, University of Virginia

President, Charles Valentine Riley Memorial Foundation



6120 Executive Blvd., #750,
Rockville, MD 20852
Office Phone (301) 347-9309
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Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

On behalf of the Coalition for the Life Sciences (CLS), I write to support with our highest enthusiasm the appointment of Eric Lander, Ph.D., as the Director of the Office of the Science and Technology Policy (OSTP). At this critical time in our nation's history, we face existential challenges, in public health (including the ongoing COVID-19 pandemic) and health care, in the environment (including climate change), in food and water security, and in energy production, utilization and storage. Each of these challenges can be addressed only by dramatic advances in science and technology motivated and coordinated by the nation's next OSTP Director.

The CLS strongly endorses Dr. Lander as OSTP Director. He will bring to the position scientific brilliance, proven leadership, government experience, and communications skills to meet these challenges. His extraordinary capacity to assimilate and evaluate the full spectrum of science and technology will empower OSTP to make evidence-based recommendations that will strengthen the US science and technology endeavor writ large. Dr. Lander has demonstrated his leadership skills on a small scale in his own lab, at a larger level in his creation and leadership of the Broad Institute at Harvard and MIT, and at an enterprise level during his co-chairmanship of PCAST. These qualities are rare, and they are exactly what are needed in the next OSTP Director.

Dr. Lander's scientific brilliance cannot be understated. His seminal research was the sequencing and interpretation of the human genome, a massive undertaking that changed the course of biomedical research. He was a principal leader on the Human Genome Project – a 13-year endeavor involving hundreds of scientists from around the world whose collected efforts culminated in sequencing human DNA from end to end. When the Human Genome Project ended in 2003, Dr. Lander founded and then led the Broad Institute, which was uniquely open, collaborative, cross-disciplinary, and able to organize projects from small to grand scales.

The American Society for Cell Biology (301) 347-9300 www.ascb.org	Chan Zuckerberg Initiative www.chanzucke.org	Genentech, a Member of the Roche Group (650) 467-6617 www.gene.com	The Genetics Society of America (301) 634-7500 www.genetics-gsa.org	Howard Hughes Medical Institute (301) 215-8500 www.hhmi.org	Johnson & Johnson Institute for Biotechnology (256) 327-0425 www.jhuisonalp-ha.org	Novartis Institutes for Biomedical Research (617) 871-4110 www.nibr.org	Society for Neuroscience (202) 962-4000 www.sfn.org
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Dr. Lander's scientific resume encapsulates only one facet of his impressive abilities. As OSTP Director, Dr. Lander will be called upon to make science, and its societal roles, more accessible to the American public. Dr. Lander is a superb spokesperson for science, and his experience in science policy qualifies him as an exceptional leader for OSTP, advisor to the administration and communicator to America's residents.

As chair of the CLS Dr. Lander was eloquent in unpacking and developing informed context for science and technology policies, opportunities and issues, and a fierce advocate for scientific innovation and discovery. As co-chair of PCAST, he oversaw the development and release of over 30 reports that aided President Obama's decision making on issues ranging from STEM education, nanotechnology, and climate change.

Dr. Lander is the right person to lead the OSTP, at a time when the opportunities for science to advance society are vast, and when science must be at the table for critical societal decisions. We urge you to rapidly and enthusiastically confirm his appointment, allowing him to begin the crucial work of coordinating interagency science and technology policy efforts.

Sincerely,



Keith R. Yamamoto, Ph.D.
Chair, Coalition for the Life Sciences
Vice Chancellor for Science Policy and Strategy, UCSF
Director, UCSF Precision Medicine
Vice Dean for Research, School of Medicine
Professor, Cellular & Molecular Pharmacology



MASSACHUSETTS INSTITUTE OF TECHNOLOGY

L. Rafael Reif, President

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March 12, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

I write to strongly endorse President Biden's nomination of Eric Lander to serve as the next director of the Office of Science and Technology Policy (OSTP).

From Covid-19 to climate change, cybersecurity to U.S. competitiveness in innovation, the nation faces urgent challenges whose solutions depend on a broad and deep understanding of the frontiers of science and technology.

As a scientist, executive and policy maker, Dr. Lander meets this moment with a rare combination of skills and qualities, including his remarkable record as a global scientific pioneer, his broad and sophisticated understanding across the landscape of science and innovation, his decades of experience in management and negotiation at the highest levels of American science, and his established record in shaping national science policy.

At MIT, we also know him as a brilliant teacher who has inspired generations of students; his skill at making scientific concepts vivid and memorable will also be of great service to the nation now.

For more than a century, America's strength in science and technology has been central to America's strength, period. Today, if we hope to keep the nation safe, inspire innovation, create new industries and more and better jobs for Americans; reverse growing inequality; restore the environment; combat and adapt to climate change; find sustainable ways to rebuild our infrastructure and to power and connect our modern society; feed our people; overcome and prevent pandemics; heal the sick; and deepen our understanding of the universe, the nation needs leaders at the highest level who are prepared to lead the way in sustaining and enhancing the nation's scientific and technological leadership.

Massachusetts Institute of Technology

Senator Maria Cantwell
Senator Roger Wicker
March 12, 2021
Page 2

Eric Lander is such a leader. And I am also confident that – in coordination with the superb new leaders of PCAST, Dr. Frances Arnold and Dr. Maria Zuber – Dr. Lander will take full advantage of this moment to draw on the rich diversity of America's scientific talent in building the strength of the government's science advising team.

As you consider Dr. Lander's nomination, I would be pleased to answer any questions you may have.

Sincerely,

A handwritten signature in black ink, appearing to read "L. Rafael Reif". The signature is fluid and cursive, with the first name "L." and last name "Reif" clearly distinguishable.

L. Rafael Reif

LRR/mes

CC:
David Strickland, Majority Staff Director, United States Committee on Commerce Science and Transportation

John Keast, Minority Staff Director, United States Committee on Commerce Science and Transportation



Phillip A. Sharp
Institute Professor
psharppa@mit.edu
617-253-6421
617-253-3867

March 12, 2021

Dear Members of the U.S. Senate Committee on Commerce, Science, and Transportation:

This is a letter strongly supporting the nomination of Dr. Eric Lander to become the next Director of the Office of Science and Technology Policy. Dr. Lander is one of the most important and dynamic leaders in contemporary science. He has innovated in science with the development of the genomic mapping of multi-genetic risk factors for human dysfunction. He led and helped to organize the human genome project, which propelled science dramatically over the last two decades. He then founded the Broad Institute, which has uniquely advanced identification of genes that increase the risk of medical traits and thus is accelerating the understanding and treatment of disease. Throughout his career, he has championed openness, collaboration, and integrity in science. Further, he has served the country in many capacities—most obviously as co-chair of the OSTP Science Advisory Committee. For all of the reasons and many more, I strongly support his appointment as Director of the Office of Science and Technology Policy.

The following is a more detailed presentation of the above summary:

Dr. Lander has made outstanding contributions in science through his own writing and in mentoring a large community of outstanding scientists. The major theme of his research is the extension of genomic concepts and technology to human genetics. This began as a collaboration with Dr. David Botstein when Dr. Lander first entered life sciences that developed the mathematical formulation of mapping multiple gene contributions to phenotype. It was continued by Dr. Lander in the realization of a SNP map for the human and mouse genomes. Please note that throughout this period, Dr. Lander promoted the public release of the results as soon as possible. The high point of the research came with the GWAS mapping of many specific alleles in a population with disease phenotypes. Skepticism about the importance of this population-based approach by the leading human geneticists in the country was powerful. Without Dr. Lander's talented commitment and leadership, these studies would not have happened. They have been funded primarily by philanthropic sources. It is becoming clearer every day that the approach has contributed uniquely to many critical insights.

The sequencing of the human genome and its associated technology and computational advances is an incredible, transformative advance. There are tens—if not hundreds—of great scientists who had a significant role in making this happen. Without question, Dr. Lander ranks among the most important in this group. He helped to formulate the approach in the human genome initiative, led the development of the SNP map to allow linkages between segments sequenced by short tracts, rapidly expanded the technology of the public effort to complete the draft sequence in 2001, then drafted the publication of the “finished sequence” in 2003. If the deletion test is applied—how would the human genome sequencing initiative have advanced if

Dr. Lander had not been involved?—the answer would be “disaster.” Without the leadership and scientific contributions of Dr. Lander, the public effort by NIH and DOE would not have been successful in the same timeframe; nor would the private effort have advanced as rapidly as it did. At the end in 2003, the two efforts complimented one another, and science benefitted greatly. Dr. Lander continues to build on this foundation.

Dr. Lander’s creation of the Broad Institute will also greatly impact life sciences for decades, if not centuries. Its charter is to facilitate collaboration between many scientists and institutes to investigate genomics and cellular biology of both normal and disease physiology. The Institute is freestanding in terms of finances and space, with primary faculty appointments at both MIT and Harvard. However, most faculty active in research at the Broad Institute are associated through collaborations based on its unique strengths in technology and computation. The Broad Institute is singular in the breadth and depth of this IT and genomic technology. It is the model for the future of a large segment of research in life sciences. Here again, the deletion test shows that the Broad Institute would not exist without Dr. Lander. Its contributions over the past decades have been outstanding—even revolutionary. They will become more so in the future.

Dr. Lander’s national leadership through co-chairing the President’s Council of Advisors for Science and Technology (PCAST) from 2009–2017 was also remarkable. It certainly benefited from President Obama’s openness to highlighting national challenges and the importance of science and technology in meeting those challenges. I served on this council for a number of years during President Clinton’s administration and the range of policy questions considered were related mostly to international security. During Dr. Lander’s leadership, PCAST formulated science-based policy recommendations on many critical domestic and international issues. I admired its elevation of science in consideration of important policies for the country. Similarly, Dr. Lander’s continued commitment to bring science into judicial decisions is highly commendable. Recently, this has focused on amicus briefs to the Supreme Court. In validation of their impact, the Court has recognized these briefs as significant intellectual contributions by an important scientific leader.

In conclusion, Dr. Lander’s science and policy leadership over the past thirty years is unique and certainly merits his appointment. I enthusiastically recommend this action.

Sincerely yours,



Phillip A. Sharp

Phillip A. Sharp is an Institute Professor (highest academic rank) at MIT and member of the Department of Biology and the Koch Institute for Integrative Cancer Research. He joined the MIT

Center for Cancer Research in 1974 and served as its director 1985–91, before heading the Department of Biology, 1991–99. He was founding director of the McGovern Institute, 2000–04. His research interests center on the molecular biology of gene expression relevant to cancer and the mechanisms of RNA splicing. His work in 1977 provided the first indications of discontinuous genes in mammalian cells and earned Dr. Sharp the 1993 Nobel Prize in Physiology or Medicine. Dr. Sharp has authored over 430 papers. He is an elected member of the National Academies of Science and of Medicine, the AAAS, the American Philosophical Society, and the Royal Society, UK. Dr. Sharp is a co-founder of Biogen and Alnylam Pharmaceuticals, Inc.



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11 March 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I am writing to heartily support the naming of Dr. Eric Lander as head of the White House Office of Science and Technology Policy.

I have known Eric since he first got interested in genetics after a degree in mathematics and a stint teaching at Harvard Business School. He teamed up with David Botstein when we were both at MIT to investigate methods of using human genetic markers to discover disease associations. This so intrigued Eric that he decided to make a career in mammalian genetics. I offered him a position as a Whitehead Fellow, he came, and the rest is history. Eric proved to be the fastest learner I have ever seen and soon was teaching genetics.

When the idea of the Human Genome Project started to be discussed, it was natural for Eric to think about whether he could play any role. He first put a toe in but that rapidly became total immersion. The remarkable thing about Eric's involvement was that he did not just contribute to the theory, where his training provided him with special tools, he soon took on the actual production of sequence and his became the lead unit in providing sequence data as well as its analysis. Eric became a scientific entrepreneur for this work, bringing together people with various talents, teaching them, coordinating them and ultimately acting as the spokesman for the work. This was one of the great contributions to modern science.

For Eric, sequencing was not a goal; it was a step on the road to a new genomic science. Thus, Eric has not been devoted to only human sequencing but has been involved in deriving many other genomic sequences. And he has not cared only about sequencing but has used the sequences to find genes for particular diseases and particular traits. And he has not been satisfied to do only genetics, he has led the way to using sequence

.../continued



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data as a new tool in medicine. And he has not just concentrated on sequence data but has developed technology for other scans of the genome, like scanning with RNAi to examine gene function.

In his role as institution builder, Eric has created the Broad Institute, a unique institution in the biomedical world. It has built upon the style and substance of genomic science to illuminate the problems of medicine from new perspectives. He has provided a home where the brightest young medical scientists can realize their dreams and become central contributors to progress in medical science. His ability to convince Eli and Edythe Broad to support the Broad Institute brought \$600 million of new resources to medicine.

Eric is everything; a great thinker, a great organizer, a great motivator and a great speaker. He puts all of talents at the service of reaching scientific goals. He has done this for the human genome but more recently has devoted much of his energy to developing a new type of research institute, one that uses sequencing and other platform technologies as tools for creating new types of medical understanding and application. Further, I know from working with him on a PCAST report, how much energy and commitment he has put into advising the Executive on matters of science.

Eric is one of the finest geneticists of this generation. Although still with more to give to science and to his country, he is a stellar choice to head the White House Office of Science and Technology Policy. He would be one of the most accomplished scientists to ever serve in this role but his previous experience in PCAST in the Obama administration provided him with the background needed to head OSTP and advise the President on all matters of science.

Sincerely,

David Baltimore, Ph.D.
President Emeritus and Distinguished Professor of Biology
Department of Biology & Biological Engineering
California Institute of Technology

cc: David Strickland, Majority Staff Director, United States Committee on Commerce
Science and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and
Transportation

JOHNS HOPKINS
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Peter Agre, MD
Bloomberg Distinguished Professor and Director
Johns Hopkins Malaria Research Institute

12 March 2021

Senator Maria Cantwell, Chair
Senator Roger Wicker, Ranking Member
United States Senate Committee on Commerce, Science, and Transportation.
Washington, DC 20510

c/o
David Strickland, Majority Staff Director,
David_strickland@commerce.senate.gov
John Keast, Minority Staff Director,
John_keast@commerce.senate.gov

re: Eric S. Lander, PhD

Dear Chair Cantwell and Ranking Member Wicker:

I am writing to convey my absolutely highest level of support for Eric S Lander, PhD as President Joe Biden's choice to become Director of the Office of Science and Technology Policy (PCAST) and Presidential Science Advisor. I have known Dr. Lander both personally and professionally for more than 20 years, and I consider him the best possible individual for this extremely important position in our government.

A brilliant computational scientist and geneticist with a wide range of expertise and a skillful administrator, Dr. Lander is Professor of Biology at the Massachusetts Institute of Technology. Among his multiple unique qualifications:

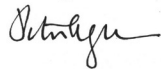
- a principal leader of the sequencing of the Human Genome Project;
- founder of the renowned Broad Institute at MIT/Harvard;
- eight years of previous service on the President's Council of Advisors on Science and Technology;
- four years of previous service on the Department of Defense Innovation Board.

Dr. Lander has also exhibited his genuine social conscience contributing to development of the DNA sequencing methodology for the Innocence Project, as author of a friend of the court to the United States Supreme Court concerning unwarranted patenting of the human breast cancer gene *BRCA1*, and for establishing low cost of diagnostic methods employed for diagnosis of COVID.

Dr. Lander is an eloquent communicator who always displays the highest level of integrity. In addition to all of his professional successes and achievements, Dr. Lander is a warm-hearted American who loves his country.

Please consider Dr. Lander carefully, for I believe you will never find a better candidate.

Sincerely,

A handwritten signature in black ink, appearing to read "Peter Agre", with a stylized flourish at the end.

Peter Agre, M.D.
Bloomberg Distinguished Professor and Director
Johns Hopkins Malaria Research Institute
2003 Nobel Laureate in Chemistry

Cc: Melissa_porter@commerce.senate.gov

Cc: Crystal_tully@commerce.senate.gov

March 15, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce
Science and Transportation, Hart Senate Office
Building, 420A Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on
Commerce Science and Transportation, 555 Dirksen
Senate Office Building, Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I write to support the nomination of Dr. Eric Lander as Director of the Office of Science and Technology Policy. Many others will speak to his strong scientific background, so I will speak to his skills at communicating science to the public and his support of basic research, which is the wellspring of technological innovation.

Global competition is at an all time high for this nation. Other nations are vying for leadership in the industries that will shape our future, industries that may be powered by AI and quantum networking, biotechnology, and new ways to cheaply generate energy. They are investing in scientific research, realizing that it underlies the technological innovations that are needed to address their national challenges. At such a time, our own nation needs an articulate, inspiring spokesperson for the benefits of scientific research, and its intimate connection to health, national security, and the economy. Dr. Lander's leadership and his many public talks about the benefits of a wide range of science show that he is that person. I refer you to a talk he gave (attached) about the way the "Miracle Machine" of basic research works, and the great return on investment it has given.

Dr. Lander has identified two superb co-chairs of the President's Committee on Science and Technology: Professor Frances Arnold at Caltech, winner of the Nobel Prize in Chemistry, and Professor Maria Zuber, Vice President for Research at MIT, astrophysicist and former chair of the National Science Board. This leadership team will serve the nation well.

Dr. Lander has the background, the skills, and the perspective to take American science forward at a most critical time for our country. I hope the Senate will look favorably upon his nomination as OSTP Director.

Sincerely,



France A. Cordova
Former Director, National Science Foundation
President Emerita Purdue University
Chancellor Emerita University of California, Riverside
Former Chief Scientist, NASA
Former Chair, Smithsonian Institution Board of Regents

Cc: David Strickland, Majority Staff Director, U.S. Committee on Commerce Science and Transportation
Cc: John Keast, Minority Staff Director, U.S. Committee on Commerce Science and Transportation



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April 9, 2021

Dear Chair Cantwell and Ranking Member Wicker,

I enthusiastically support Dr. Eric Lander's appointment as Head of OSTP and Science Advisor to the President of the United States. Dr. Lander is the founding director of the Broad Institute (Harvard/MIT), which has led national efforts in genome sequencing, human genetic mapping, cancer genome sequencing, and many other areas.

Dr. Lander also has experience in advisory roles in the federal government, having been the co-chair of the President's Council of Advisors on Science and Technology (PCAST). He has extensive experience in communicating complex scientific concepts to non-scientists.

Dr. Lander has a strong commitment to diversity, which is important to me in general and also as a female scientist. Many of the group leaders at the Broad Institute are female. I have not worked with Dr. Lander directly, but I know many of the female scientists at the Broad Institute. My impression is that women scientists have had good experiences in working with Dr. Lander and have a high regard for him.

The entire scientific community will benefit greatly from having Dr. Lander serve in the Cabinet. It is likely that he will lead the nation in an effort to effectively use science to advance material and social progress.

Sincerely,

A handwritten signature in cursive script, reading "Pamela J. Bjorkman".

Pamela J. Bjorkman
David Baltimore Professor of Biology
and Biological Engineering
Merkin Institute Professor

National Math Festival. Gala dinner at the Library of Congress, 4/16/2015

(Introduction by David Eisenbud)

First, thanks to Jim Simons, to David Eisenbud, to Robbert Dijkgraaf, to Bob Tjian, and everyone who put together this first-ever National Math Festival. It's about time!

My assignment, from David, was to make the case for basic research. Now, looking around the room, I have to confess, I'm not sure to whom I need to make the case. But that was the assignment. And so, I'm going to do it. Because the truth is, we *all* have to be able to make the case for basic research. It is very important for us to be able to articulate the case for basic research.

We have in this room people who have been tremendous forces for the importance of basic research. I want to thank former Representative Bart Gordon, who was Chairman of the House Committee on Science and Technology from 2007 until 2011, and former Representative Rush Holt, who is a research physicist and former professor and current CEO of the American Association for the Advancement of Science. We have Representative Jerry McNerney, who has the distinction of being the only mathematician serving in Congress. We had, until a moment ago, Leader Nancy Pelosi, who has also been a great supporter of research. So, even within the Congress, I preach to the converted and, indeed, from some of them, I have learned much about how to make the case for basic research. But, let's get down to it.

My title is, The Miracle Machine. I'll come back to what that means in a moment.

Because we are in Washington, DC, though, I want to start by talking about responsible public policy. As David says, I co-chair the President's Council of Advisors on Science and Technology for the White House, and I've come, over the six years I've been doing that, to appreciate the importance of responsible public policy. I've been aware that, since 2008, we've been living through a great recession. We're now climbing out, but it's been slow. As you heard from President of the European Central Bank Mario Draghi, Europe is climbing out much more slowly, if at all. Budgets are tight everywhere. We have not the surplus of the late 1990s, but deficits. Understandably, our elected officials want to ensure that with respect to public spending, we're getting the maximum bang for the buck—or euro, as the case may be. Before committing money, they want to see clear objectives, short-term outcomes, and avoidance of waste. No line item in the national budgets has escaped this scrutiny. And that includes research.

Looking to the north, Canada, in 2013, decided to radically shift the focus of its National Research Council. It announced the transformation of a 98-year-old agency, which had been the leading force for basic research in Canada, into essentially a one-stop concierge service to bolster technological innovation by industry and generate jobs. To increasingly focus the Canadian National Research Council on industry issues, they describe themselves now as a strategic R&D organization for industry that aims to be directly responsive to those short-term goals. I can understand why a government might choose to do that.

In Europe, we've seen similar things. In 2011, Ireland's government substantially changed how it thinks about funding science—to focus predominantly on research with clear potential to grow the economy and create jobs. The European Commission recently announced a plan to cut nearly 3 billion euros from the Horizon 2020 program—which includes funding for the European Research Council, which is the premier, frontier research organization directed at fundamental research—in order to move money into a new Strategic Investment Fund for Europe, a short-term focused stimulus program. They plan to cut about 5 percent of the European Research Council's budget.

Here in the United States, we are not immune from this kind of thinking. There are bills in Congress to ensure the accountability of taxpayer dollars invested in science, to ensure that dollars are stretched efficiently and effectively—I quote from websites here—to ensure “accountability” and “transparency”. There are proposals that the National Science Foundation be required to publish a justification of each and every grant's scientific merits and relevance to the broad national interest—that is, to the economy or defense. Now, how could you possibly disagree with such prudent investing of American dollars? How could you possibly disagree with accountability, transparency? If I'm investing in real estate, I want to see a clear path to a return on my investment. If I'm investing in a start-up company, I might be willing to wait for a few years before I get my return, but I want to see a clear business plan. If investing in building roads and bridges for a country, I'd like a clear connection between social investment and social return. So what can possibly

be wrong with wanting to have a clear case for precisely how investments in basic research will pay off?

The answer is: absolutely everything! Everything is wrong with it. Applying this kind of filter to basic research is a terrible strategy. It'll guarantee that you will have ordinary returns—projects that pay off, at an ordinary rate. In the short term, you'll get outputs. But you will miss the extraordinary returns. Fundamental research is fundamentally different than any other kind of investment. We're all still struggling to understand it, but it is a remarkable thing: because time and time again, we've found that basic research can pay huge, out-of-proportion returns. Basic research can completely transform for the better our society, our economy, our defense.

From a mathematical point of view, you'd say that the distribution of returns from basic research has a very fat tail. That is, you can get 10:1 returns, and 100:1 returns, and 1000:1 returns, and 10,000:1 returns out of that tail. It doesn't fall off like an exponential; it has very fat tails. And, indeed, as the mathematicians here know, there are even distributions with fat tails where the *expected* return is infinite. Basic research is probably closer to that than to some normally distributed return for typical kinds of investments.

The problem is that transformative ideas and discoveries often come out of left field. Try as you might, you cannot predict where they come from. We're dealing with something pretty remarkable here. I've started to call this thing the Miracle Machine. It is miraculous, and it is a machine, because it's quite reproducible; it works again and again. More and more, I want to understand how this Miracle Machine works. It is a challenge to explain it to people. Maybe the best way to explain it is through example. So I'm going to pick some examples, and tell you about them. Some of them you'll all know, because it's a highly mathematical crowd. Some of them you're not going to know very much about, because I'll pick some biological examples; they'll be kind of fun. These examples are at the heart of the case we need to make.

So, let's start with math. As you know, I am by training a pure mathematician: a Princeton undergraduate, Oxford graduate student. I studied algebraic number theory and topology at Princeton, and then wrote my Ph.D. thesis at Oxford on group representation theory and algebraic coding theory. What got me most excited about math first in high school and in college was number theory. I love number theory—how can you not love number theory at that age?

In high school, I read and loved G.H. Hardy's *Introduction to the Theory of Numbers*. The book conveyed the essential beauty of number theory, especially of prime numbers. Hardy loved number theory, precisely because it was both beautiful and completely useless. In his famous essay, "A Mathematician's Apology", Hardy likened pure mathematics to painting and poetry; he was proud that it had no practical applications. In the essay, he wrote that no one had found any practical applications—he actually said, any "war-like" applications; that was what was on his mind at the time—to be served by number theory or by general relativity. And, he said it seemed unlikely that anyone will do so for many, many years. Well, Hardy must be turning in his grave. Because number theory—prime numbers—lie at the heart of national security and communications. Public-key cryptography is fundamentally based on the question of decomposing numbers into their prime factors. So, number theory is central to commerce and defense.

The other thing that Hardy said had no foreseeable application was relativity. [Laughter]

Relativity itself has its roots in mathematics. You know, if you were explaining to, let's say, a Congressional committee in the 1800s why you were funding a grant on non-Euclidean geometry, you'd be saying: yes, yes, Mr. Congressman, I realize that for 2000 years we've known that parallel lines never meet, but let's just imagine that what we know isn't true, and let's fund someone to study what would happen in a counterfactual world where all lines intersected and there were no parallel lines.

You could imagine that this would not be looked on with great favor. It would be viewed as some kind of mind game, because it didn't describe the real world, and it therefore wasn't practical. Except, of course, it turns out that it *does* describe the real world. It just was that the math was ahead of our understanding of the real world—to the curved space-time of general relativity.

Now, to return Hardy's question, is relativity practical? Well, anybody who used their iPhone to get here tonight was using GPS, and anybody who's using GPS is using general relativity, because you actually need to correct for the time dilation of the satellites in order to get accurate GPS positioning. Your iPhone has general relativity built into it. Hardy was a great number theorist, but, I think, a very bad predictor of the ultimate impact of mathematics.

Let me switch to physics. When Charles Townes invented lasers, he was advised by many people that it was a solution looking for a problem. What were you going to do with these lasers? It was a curiosity. People had masers and he wanted to know whether he could do a similar thing at the frequency of light, I don't think I would have wanted to defend its utility in advance based on that rationale. But lasers did turn out to be useful—for cutting, welding, printing, CDs, bar codes, scanners, treating acne, treating kidney stones, eye surgery, dentistry, fingerprint analysis, holograms, and laser light shows.

What about huge particle accelerators? Those giant machines built to study obscure sub-atomic particles that you will never meet in your everyday life: quarks and leptons, and things like that. What excuse do we have for investing public money to build large particle accelerators to pursue this curiosity at this scale?

Well, it kind of turns out that, when you build those things, it ends up giving us the technology to make synchrotron light sources that are used for x-ray crystallography, which used to study the structures of human proteins and which are central to all drug development efforts. Any good drug-development effort needs to have the structures of protein targets, and they have solved these structures using synchrotron light sources. It's very hard to predict that things like quark investigations will be useless—because they have this uncanny way of turning out, just when you'd least expect it, to be enormously useful.

And then there's Andre Geim, the physicist who had Friday sessions in the lab where they deliberately worked on wacky things. They studied how geckos can climb up and stick to very smooth surfaces; it might not sound very important. But it led to the development of a super-sticky adhesive able to stick to the smoothest surfaces.

He was also very interested in magnetic levitation and famously developed in his lab a system to levitate a frog. For this he won, in my fair City of Cambridge, Mass., an Ig Nobel prize for frog levitation. The Ig Nobels, if you've not been to the ceremony (I've actually been a speaker at the Ig Nobels) are a parody of the Nobel Prize.

Geim, also in his lab, used Scotch tape to peel off very thin layers of graphite, then used tape on those layers to peel off thinner layers, and then thinner layers and thinner layers—until he got to layers of graphite that were just one atom thick. That is to say, *graphene*—a single monolayer of carbon atoms. For

this work, he received not an Ig Nobel prize, but a Nobel Prize. Graphene is the thinnest material, incredibly strong, incredibly transparent, totally impervious, you can't even get helium through it. The same curiosity that levitated the frog produced the graphene. It's very hard to figure out in advance which ideas will turn into floating frogs and which will turn into graphene.

Now these stories are just not a fluke. In the United States, we have this thing that I am increasingly thinking of as the Miracle Machine: a reproducible system for making miracles come to pass, for making dreams into reality.

Vannevar Bush, the famous dean of engineering at MIT who directed research for the United States government during World War II, wrote a famous essay after the war about an imaginary device that he called a Memex. The essay was about the idea of a device that would give you access to all human knowledge. He imagined it with lots of microfilm and ways of accessing all that microfilm, whereby people could trace paths through all of human knowledge—a very appropriate image for the building in which we sit today, the Library of Congress. The Memex would contain all of the Library of Congress, all of human knowledge. It was . . . kind of crazy in 1945 to dream about such a thing. Well, along the way, as more people thought about such ideas, computers were developed. The field of computer science, built very much on mathematics, was developed. Hundreds of playful projects and algorithms, all sorts of things; the Internet was born. All of these things flowed one after another, after another.

In 1993, the National Science Foundation gave a 3.6 million-dollar grant to some investigators at Stanford. According to the abstract of the grant application, the purpose was to work on an integrated virtual library that will provide uniform access to the large number of emerging networked information sources and collections that will link everything to personal information collections to collections found today in conventional libraries to large data collection. Two students working on this . . . you know where this is going . . . were Sergey Brin and Larry Page. This work gave rise to Google.

On my iPhone, I just checked the market cap of Google today. It is 360 billion dollars, which is a very, very precise 100,000-fold return on NSF's investment in a 3.6 million dollar grant. One hundred thousand-fold is a good return, if you can get it. Of course, the problem is, you don't know in advance precisely *where* to get it.

Now, to get Google took more than just that public investment. You had a public investment from the NSF in basic science, and then, as these ideas proved more and

more practical a few years later, the other part of the great Miracle Machine swung into action—private investment, from venture capitalists, from capital markets, to launch and sustain businesses, like Google. What we have in this country is an amazing partnership between a public good—publicly-funded, basic research, where we don't know precisely what it will deliver, or on what time frame—and then private investment. It's a fabulous partnership. Now, America is not the only country that does this. The Miracle Machine is not unique to the United States, but nowhere is it operating better than in the United States. And no place has reaped greater return from this Miracle Machine. So, it's important to understand how the pieces work together.

What about biology? While I am trained as an algebraic combinatorialist, I have migrated over the years into biology (although I still use mathematics throughout biology). Biology is very fertile territory for some crazy-sounding studies. Let me tell you about some of the truly wacky things that have been done in biology.

Biologists went and used Federal dollars to go to Yellowstone to look at bacteria that grow in hot springs. Pretty obscure. Who cares? Sounds like just butterfly collecting. Why hot springs . . . don't we have enough bacteria everywhere else? Well, it turns out that bacteria that grow in hot springs are remarkable, because all their enzymes are stable against extremely high temperatures. And a particular enzyme in these bacteria, a DNA polymerase, turned out to be a crucial component in the DNA amplification technology called polymerase chain reaction, PCR, that is used millions of times around the world every day. We have PCR in its current working form because somebody *did* go to the hot springs, although they didn't go for the purpose of enabling PCR.

Biologists also wondered why jellyfish glow green. It's a cool question, but why should you waste public funding figuring out why they glow green? Well, it turns out the answer is a certain protein, now called Green Fluorescent Protein (GFP). It can be attached, via genetic engineering, to other proteins that will now be marked by glowing green. With some modifications, you can also change the protein to glow red, and yellow, and other colors. And, with these tutti-frutti tags on proteins, you can study the internal architecture of cells in exquisite detail. It turns out that wondering why jellyfish glow green gave rise to tools that are used in tens of thousands of labs around the world and was worth a Nobel Prize.

Here's another one: there are weird bacteria that can grow in amazingly salty conditions, such as in incredibly salty lakes in Egypt and Sudan. Scientists were curious about how bacteria can grow in five-molar salt solutions. Somebody decided to investigate this seemingly ridiculous question, and figured out that they have a light-driven ion pump that uses sunlight to transport ions. Now, this was just a curiosity, until some investigators realized that if you put light-driven ion pumps into neurons, you could get the neurons to fire whenever you shined a light on them. This gave rise to optogenetics—the optical control of neurons—which is now used all over neurobiology. By the way, one of the applications that people are working on is inserting those optically-responsive ion channels into the retina to restore the sight of people with certain kinds of blindness. I could go on and on with examples from bacteria.

But, let's move from bacteria to fruit flies. Politicians love to beat up on fruit fly research. Geneticists collect strange mutant fruit flies with weird defects; there's one called hedgehog, and it's got all these little funny spikes on it. It sounds like a silly thing to do—except that the FDA just approved a hedgehog inhibitor in humans that treats basal cell carcinoma. It turns out that the same pathway the fruit fly uses for early development is a pathway operative in your skin cells. Evolution has conserved it over the course of hundreds of millions of years.

Now, some politicians, including Republicans and Democrats over time, have sought to sound reasonable by ridiculing Federal grants that sound silly—at least if you only read their abstracts. William Proxmire, a Democrat of Wisconsin, famously gave the Golden Fleece awards in the 1970s for projects that he thought were frivolous, a waste of the taxpayers' money. In 1975, he gave the Golden Fleece to a study of the sex life of screwworms. You couldn't pick a better title than that: the sex life of screwworms. The U.S. Department of Agriculture gave a quarter of a million dollars to study the sex life of screwworms! Ridiculous! Except it turns out, the sex life of screwworms is pretty important. The screwworms are parasites. And scientists found out that females lay their eggs immediately after the first time they mate with a male. And it occurred to them: if one were to release a very large number of sterile males, they would overwhelm the fertile males and mate with the females, who would lay eggs that weren't fertilized, and one would be able to control the pest. This strategy was implemented and it has saved about twenty billion dollars in livestock costs and reduced the cost of beef by five percent. To his enormous

credit, Senator Proxmire apologized, acknowledging that he blew that one. It tells you that you ought to read more than the abstract.

Now, not all basic research in life sciences is bizarre-sounding or curiosity-driven. Sometimes critical research is about collecting lots of information, because you have a hunch that it's going to be useful, but you don't exactly know how.

To explain this, let me turn to another great example of the Miracle Machine. In 1953, Crick and Watson discovered the double helical structure of DNA and inferred how life encoded information in these two strands of DNA—with a sequence of DNA bases on one strand and a complementary sequence on the other strand. At the time, they had no idea that you would ever be able to read those sequences. I know, because I asked each of them. They said, not a chance, we never imagined that we'd be able, in our lifetime, to be able to read out all that information.

But the information was there, and maybe you could find a way to read it. So the Miracle Machine got to work, with tens of scientists, and then hundreds of scientists, and then thousands of scientists, chipping away at bits of this really great puzzle. And they began to work out how DNA is copied in cells. And how it's turned into RNA, and it's interpreted to make proteins, and then how we might be able to take some of those tricks and do it in the laboratory to actually clone DNA and sequence DNA. First a few letters, then hundreds of letters, then thousands of letters, then millions of letters and then this idea of a Human Genome Project, which started about 1985 and was, at first, considered pretty nuts. Some thought it was a total waste of money, because it was going to cost billions of dollars. But the scientific community debated it, and the Congress decided to fund it. By 1990, there was work underway. And by April 25, 2003, we had a finished sequence of the human genome. April 25, 2003—we actually chose that date on purpose. It was the 50th anniversary to the day of the publication of the Watson-Crick paper. That's what you can do in a half a century: you can go from a crazy idea that you might be able to somehow read out all that information to actually accomplishing it.

So, what did we get out of it? Well, we got many of the things we expected. But, the most interesting things we got were the things we *hadn't* expected. The Human Genome turned out to be an amazing font of information for understanding the genetic basis of disease. For example, this past week, I was talking to a colleague who has been working out the genetics of early heart disease. We all know that lipids play an important role in heart disease—for example, LDL, the bad cholesterol, and HDL, the good cholesterol. But, he's using the human genome to discover entirely *new* pathways—for example, a pathway that has nothing to do with lipids at all; it looks like that's going to be very important. Similar things are happening for diabetes. And, for schizophrenia, genetics is starting to tell us that the disease is being driven by excessive pruning of neuronal outgrowth in adolescence. For autism, we have a great collaboration with Jim Simons that is helping to unravel the biological basis of autism. For cancer, the genome is revealing a tremendous amount of information about the cellular basis of the disease, and has led to hundreds of drugs that are in clinical development.

Beyond these applications to disease, there are many amazing fundamental discoveries about how genes are regulated, about how DNA is folded in the nucleus of the cell, about evolution, and about human populations and how they spread about the world. And, a complete surprise, about how humans interbred with Neanderthals—which we can read out from the DNA, using a heavy dose of mathematical analysis.

In fact, all of this discovery has depended on a heavy dose of mathematical analysis. For example, suppose we scan the human genome to find genes for heart disease or schizophrenia. How do we know if a correlation is significant? If you're going to do only one test, you can use the classic significance level of $p = 0.05$. But, what if you're looking across an entire continuous genome of three billion bases? What's a significant result? Only math can tell us. It turns out you need to know the extreme valuable distribution of certain stochastic process called an Ornstein Uhlenbeck diffusion. In simpler terms, it turns out that figuring out whether a genetic finding is significant is equivalent to considering the behavior of a particle undergoing Brownian motion while coupled to the origin by a Hookean spring and asking how far it can get from the origin in a certain amount of time. This is just one of many unexpected connections between math and biology.

Here's another: We study how the genome folds up in a cell. We recently studied a paper showing that—to a first-order approximation—the genome folds up as a fractal. Actually, we now have enough data to say that it's not quite a fractal. It's almost a fractal and we can now see how it differs from a fractal. We learn this by combining molecular biology and mathematics to study the distribution of distances between points in the genome.

So, what's been the economic impact of the Human Genome Project? Well, it's only been a little while so far, but the Battelle Institute calculated that the billions of dollars of investment that the Federal government put into the project has returned approximately 140:1, so far. That's a pretty good return. They estimate the total return is in the neighborhood of about a trillion dollars.

All right, you get the point. When economists try to figure out the return on investment of basic research, the numbers vary because it's hard to measure precisely. But, the estimated ROI ranges from 20 percent per annum and 60 percent per annum. Now, as my friend and PCAST colleague Bill Press points out, you might say: "With returns like that, I should invest my whole retirement fund in basic research!"

The problem is, of course, as the economists say, the returns are not appropriate—they can't be captured by a private investor. The investor in basic research can't fully capture the economic returns, because the fruits are largely knowledge that accrues to society at large. You can file patents, but this applies to only a very small fraction of knowledge. You can't patent laws of nature, and a good thing, that.

So this Miracle Machine has these two components. The first component is *public* investment in basic research. It has to be public. Private investors won't invest if they can't own the fruits, but the public can invest because it gets its return in the form of benefits for society and in greater tax revenues from the economic activity. The second component is private investment that comes along to enable commercialization.

We need every person in Congress, we need every American to understand how this Miracle Machine works—that it has these (and other) essential parts and they work together to produce social good.

If you think you can improve social returns by moving money from long-term basic research to short-term investments, you fundamentally misunderstand the Miracle Machine. You will end up with modest returns, at best.

Now, basic research investments pose a problem for our elected officials. For other kinds of investments, they expect that *they* should be allocating the funds to specific projects. But, we're saying: No, you shouldn't pick the projects. And, we're saying: Please don't ask researchers to explain how their work is directly connected to the national interest. Please don't ask them to be explicit, because it will cause them to focus on the short-term—in which case the game is lost.

So, how should funds be allocated? I hate to say it, because it sounds elitist, but, you need to rely on expert taste and expert judgment as to what's a great question to study. In a democratic society, it is hard to say that the right answer is to rely on experts. You don't want to have to say that. But it *is* the right answer.

Now, we shouldn't ask for unbounded trust. As Reagan said, "trust, but verify". The right way to monitor basic research, instead of asking what the payoff is *going* to be over the *next* 25 years, is to look backward and ask what my payoff has been over the *last* 25 years. If you continue to see that you've been doing amazingly well over these last 25 years (which has been the case), you should continue to invest in basic research! I suppose there is always the risk that, at some point the high returns on basic research will cease, but it hasn't happened yet!

We need to keep the Miracle Machine functioning, we need to train amazing young minds, we need to fund the best ideas, because, at least so far, no one has invented any system that has had a greater impact on human welfare. Thank you very much.



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April 8, 2021

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to offer my strongest support for Dr. Eric Lander's appointment as Head of OSTP and Science Advisor to the President of the United States. Dr. Lander is a visionary scientist who created the Broad Institute joint between Harvard and MIT, which has pioneered important genomic discoveries that launched the biological sciences into the 21st century.

Dr. Lander has broad leadership experience including eight years on PCAST and 4 years on the DoD Innovation Board. He is an excellent communicator of science with the ability to explain difficult concepts to a lay audience. Thus, he has all of the attributes that make him the ideal candidate for this position.

Dr. Lander is a brilliant scientist who has exhibited strong leadership throughout his career. Our country faces many challenging problems and scientific leadership is key to helping solve these and to provide a roadmap for navigating the country on the right path. As case in point, the unprecedented rapidity of vaccine development during the pandemic is based on excellent and timely implementation of basic science principles. Dr. Lander's expertise and insights will help rebuild the public's trust in science at this critical juncture in our history.

The scientific community is excited about the role that Dr. Lander will play in the White House, where he will provide an important link between government and science and communicate important ideas to the public. I enthusiastically endorse his appointment, as he is the ideal person for the job.

Sincerely,

A handwritten signature in cursive script that reads "Marianne Bronner".

Marianne Bronner, Ph.D.
Distinguished Professor
Director of the Beckman Institute



April 7, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

Please accept this letter as my strongest possible support of Eric Lander for the position of director of the Office of Science and Technology Policy. I have known Eric since 1998, when he hired me to join the MIT/Whitehead Center for Genome Research, and he has been the most important mentor and champion of my career as a professional scientist, helping to propel me to the position I currently hold as the Senior Director of the Genomics Platform at the Broad Institute of MIT and Harvard, and a member of the Institute's Executive Leadership Team.

Eric's decision to hire me fresh out of graduate school was an unusual one—then and now. Most Ph.D. graduates are expected to spend several years as a postdoctoral fellow in order to climb the academic ladder. But I was tremendously excited about the developments in genomics and the Human Genome Project, and eager to jump straight into this work and start to build my career as a professional scientist. Eric recognized my hunger, potential, and drive—and not only did he provide me with the opportunity to prove myself, but he also has continued to mentor, support, and advise me in the 23 years that we have known each other.

Indeed, Eric's influence on my career—and that of countless scientists, especially female scientists—has been immense. Guided by his vision, leadership, and mentorship, my team and I have turned the Broad's Genomics Platform into a world-leading center of excellence of genomics. (We currently sequence one whole human genome every 8 minutes.) His encouragement and coaching empowered me to take on ever greater challenges, and to imagine that no problem is too big to solve.

A recent example of this has been the Broad's experience in Covid-19 viral diagnostics. Eric helped guide my team and me in our quest to establish and rapidly scale up the Broad's first-ever viral diagnostics lab. The lessons I learned from Eric—how to pivot quickly, how to think creatively to surmount challenges, and how to imagine what might at first seem unimaginable—provided crucial inspiration and ultimately led to our success in standing up what is now one of the largest testing facilities in the U.S. with a daily capacity of >150,000 tests.

Most of all, Eric has taught me and all his mentees the need step up and serve the public when called upon to do so. Starting with the Human Genome Project, he has always argued forcefully that science should be for the public good. At a time when we desperately need scientists to rise to the

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great challenges of our time—such as climate change, future pandemics, and antibiotic resistance—I can think of no better person to rally the scientific community and engage the public in science.

I hope the Senate will quickly confirm this brilliant, extraordinary scientist, who will devote his considerable intellect and talents to serve the American people. Thank you for your time and consideration.

Yours sincerely,



Stacey Gabriel, Ph.D.
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Massachusetts
General Hospital



Deborah T. Hung, M.D., Ph.D.

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Professor of Medicine
Harvard Medical School
Massachusetts General Hospital
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April 8, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I want to thank you for your critical leadership on the Senate Committee on Commerce, Science, and Transportation. As you are overseeing the confirmation process of Dr. Eric Lander for the Cabinet-level position of Director of the Office of Science and Technology Policy, I wanted to write to express my enthusiastic support of Eric and the impact that he could have in serving our country in this position.

To provide context, I am currently a Professor of Genetics and Medicine at Harvard Medical School, Massachusetts General Hospital, and the Broad Institute of MIT and Harvard, as well as the Co-Director of the Infectious Disease and Microbiome Program at the Broad Institute and a practicing infectious disease and critical care physician at the Brigham and Women's Hospital in Boston. I first met Eric in 2006 as I was transitioning from my position as a postdoctoral fellow to an independent academic position and was hired as an assistant professor at the Broad Institute by Eric in his role as the director of the institute.

You will no doubt have heard from many other sources regarding Eric's transformative role in changing the fundamental trajectory of biomedical research through his championing of the human genome project and the subsequent leveraging of this map to understand health and disease; I will thus leave those perspectives to numerous others. I am writing specifically to share my own personal experiences not only with the content of his scientific expertise, but importantly, with his deeply held belief in the potential of the scientific endeavor to impact our world, as manifest in his mentoring and championing of the next generation of scientists. *Quite simply, I am the professor and scientist that I am today because of Eric's belief in and commitment to me over the past 14 years. He has empowered me to ask important and relevant questions to human health and to dare to think and act creatively and ambitiously in trying to tackle them, with resources that he marshalled to support my vision.* Our early conversations were filled with his encouraging me to articulate what I deemed to be the critical questions in infectious diseases and what was needed to answer them. I cannot overstate how this advice flies in the face of the conventional wisdom that is typically given to young faculty members who are instead encouraged to take the next, safe, incremental step in their work. I know that Eric has shared

similar advice to a whole generation of early-career scientists who came under his watch at the Broad Institute and are now disseminated world-wide. *Through the years, Eric took me to places that I never envisioned being part of my scientific journey and gave me a voice to champion those issues about which I cared most deeply.* He brought me to influential forums to speak about tuberculosis (another pandemic which is the leading infectious disease cause of death world-wide) and drew attention to the antibiotic resistance crisis while at the White House in his previous role as co-chair of the President's Council of Advisors on Science and Technology.

I consider myself incredibly fortunate to have had the opportunity to pursue my scientific career at the Broad Institute, not only because of the collaborative and vibrant research culture established by Eric, but because it is an extremely supportive environment of professional women and even young mothers, which was critical to my professional path. As you may know, the Broad Institute was recognized by *Working Mother* magazine for four straight years as one of the 100 Best Companies for leadership in creating progressive programs in the areas of advancement of women, mentoring, flexibility, childcare, and paid parental leave. Like every institution, the Broad still has work to do. Nevertheless, the institution-wide recognition of the importance of women to the scientific endeavor is a tone that was set from above, in smaller rooms and smaller discussions led by Eric. As I now sit on different leadership committees and scientific advisory boards across academia, private foundations, and industry, often as one of a very few if not the sole woman at the table, I am constantly sadly reminded that it is a luxury to work in this environment. I am struck by the relative uniqueness of working at an academic institution where 4 of the first 7 assistant professor faculty hires made by Eric were women. I do not believe that this was a consequence of intentionally prioritizing gender balance; instead, I believe that *while Eric recognizes the need to support gender balance and diversity more generally, he was actually simply seeking to recruit the very best scientists that he possibly could and recognizing that the very best candidates are often women.*

Importantly, I know that I am not alone. I am completely confident that my view of Eric and his creation of a culture where young women scientists can thrive is widely shared by many who have had the good fortune of being mentored by him. About 18 months ago, at a particularly poignant moment in our cultural history when the need to hear women's voices was acknowledged, several of Eric's mentees recognized the uniqueness of his support of women in science and his belief in the role of the next generation in the pursuit of scientific excellence. In honor of this specific trait that distinguishes Eric from far too many scientific leaders, we established the Eric S. Lander Award in Scientific Excellence to be given yearly to the Broad Institute postdoctoral fellow who demonstrates the greatest scientific excellence, with a commitment to promoting women in science and their inclusion in the scientific community. Because of the overwhelming enthusiasm from dozens of scientists who had benefitted from his mentorship, we raised the endowment for this award *literally* in less than 24 hours.

Given the uniqueness of these days, please permit me to end with some simple reflections on my interactions with Eric during the COVID-19 pandemic. At the end of February and early March 2020, as the uncertainty of COVID-19 was descending, I recall speaking candidly with Eric from my perspective as an infectious disease physician. Despite what seemed at-the-time an absurd notion of shutting down the entire research institute, he respected my expertise and ultimately empowered me to take the necessary steps to prepare for the uncertainty. Within weeks, as case numbers were climbing in the United States, a single phone call from me was all that was needed for Eric to trust me enough to pivot the entire Broad Institute to take up COVID-19 testing, becoming the largest non-commercial COVID-19 testing laboratory in the United States. As the weeks and months progressed and numerous other COVID-19 research efforts were launched at the Broad in an effort to play our role in the crisis, I recall Eric introducing the key leaders of these efforts at a meeting of the Broad Institute Board of Directors. Recognizing that all of the leaders were women scientists, *Eric movingly gave credit to us and said unequivocally that it was "because we were all women", that he believes that the Broad Institute was successful in responding to the pandemic.* I believe that this anecdote encapsulates the spirit of

Eric and his belief that the future of science lies in the hands of young, more junior scientists, the likes of whom he has committed a lifetime to mentoring and who he is now proud both to give credit and to call his trusted advisors. If confirmed, I am confident that he will bring that same spirit to the Office of Science and Technology Policy.

Sincerely,

A handwritten signature in dark ink, appearing to read 'D. Hung', with a stylized flourish at the end.

Deborah T. Hung, M.D.-Ph.D.
Co-Director, Infectious Disease & Microbiome Program
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March 11th, 2021

To Whom It May Concern

I am writing to express my strong support for Dr. Eric Lander' nomination for the position of Director of the Office of Science and Technology Policy. In my opinion, Eric will do a great job and will represent science well in this position.

Yours sincerely,

A handwritten signature in black ink that reads "R.J. Roberts". The signature is fluid and cursive, with a long horizontal stroke extending to the right.

Sir Richard Roberts Ph.D., F.R.S.
1993 Nobel Laureate in Physiology or Medicine
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April 9, 2021

Dear Senator and Chairman Cantwell and Ranking Member Wicker,

Today I write to you with a sense of urgency regarding the confirmation of Dr. Eric Lander as the Presidential Science Advisor and Head of the OSTP. Science is a critical part of the recovery of our nation's health and its economy, and scientific principles are key to solutions to climate change, environmental hazards, and sustainable practices in energy and agriculture. Importantly, having strong and well-informed science leadership will be critical to our nation's future success.

Eric Lander holds forth the principles of science applied toward the solution of the critical problems of humankind. His work in founding the Broad Institute set forth the path of the genetic revolution that has impacted our understanding and treatment of human disease. In creating this highly interdisciplinary Institute, he has also worked to ensure diversity in the sciences; for example, the Broad Summer Science Program that targets underserved and underrepresented young people to introduce them to the sciences. He has been an ally and supporter of women in science, including many top women faculty members.

Dr. Lander carries a broad perspective of science and technology, an infinite learner who seeks to understand and address complex problems, and engages in creative solutions. He is a true visionary with an incredible dedication to our nation. It is critical that we move forward with a powerful science agenda as quickly as possible as the nation works toward recovery, and Eric Lander's confirmation will be a first step towards that goal.

Thank you and Best Regards,

A handwritten signature in cursive script that reads "Paula T. Hammond".

Paula T. Hammond



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ktfaber@caltech.edu

April 11, 2021

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to offer my firmest support for the appointment of Dr. Eric Lander as the Director of the Office of Science and Technology Policy and Presidential Science Advisor. Our nation is fortunate to have a scientist of Dr. Lander's caliber nominated for these positions. He will bring broad experience across the sciences and mathematics to the roles. Moreover, he is both a leader and a visionary, as evidenced by his founding directorship of the Broad Institute, the joint undertaking between MIT and Harvard focused on human health through biomedical and genomic research. His leadership extends to the greater scientific and technological communities through his service to the President's Council of Advisors on Science and Technology and the DoD Innovation Board.

At a time when a good fraction of the American public has lost faith in science, it is particularly important to have an individual as OSTP Director and Presidential Science Advisor who is an eminent scientist, a inspired leader, and an outstanding communicator of science. Dr. Lander will bring well-principled and sound advice to the many health, science, and technology challenges we now face. I encourage you to move forward with all necessary speed to confirm Dr. Lander's Cabinet appointment.

Thank you for your consideration.

Most sincerely,

A handwritten signature in cursive script, reading "Katherine T. Faber".

Katherine T. Faber
Simon Ramo Professor of Materials Science

* Please note that the opinions expressed here are my own, and not those of the California Institute of Technology.



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March 11, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

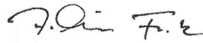
I'm writing in enthusiastic support of Dr. Eric Lander's appointment as Director of the Office of Science and Technology Policy.

I regard Dr. Lander as a superb choice for this position as he is one of the most accomplished scientists in the world, with a distinctive record of research achievements, public service and intellectual leadership. He is uniquely qualified to provide leadership in the highest office at a time marked by unprecedented challenges to our civilization -- foremost global warming and the galloping pandemics -- that require rational evidence-based solutions and the kind of ingenuity that Dr. Lander displayed in tackling the Human Genome Project.

As one who has greatly benefited from generous funding by the National Institutes of Health for the past 40 years, I can appreciate the value of continuous basic science funding and the crucial importance of science policy in helping the nation to keep up with the changing world.

In conclusion, I don't believe President Biden could have nominated a scientist better qualified for this position.

Sincerely,

A handwritten signature in black ink, appearing to read 'J. Frank'.

Joachim Frank, Ph.D.
2017 Chemistry Nobel Prize

cc:
David Strickland, Majority Staff Director, United States Committee on Commerce Science
and Transportation

John Keast, Minority Staff Director, United States Committee on Commerce Science and
Transportation

BIG DATA INSTITUTE

Li Ka Shing Centre for Health Information and Discovery



Professor Cecilia Lindgren

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April 12th, 2021- Oxford, UK

*Senator Maria Cantwell**Chair, United States Committee on Commerce Science and Transportation**Hart Senate Office Building, 420A**Washington, DC 20510**Senator Roger Wicker**Ranking Member, United States Committee on Commerce Science and Transportation**555 Dirksen Senate Office Building,**Washington, DC 20510*

Dear Chair Cantwell and Ranking Member Wicker,

Please accept this letter as my unequivocal support of Dr. Eric Lander for the position of director of the Office of Science and Technology Policy.

I have known and worked with Eric for over 20 years, stretching back to when I was a Ph.D. candidate at Lund University. My supervisor at the time, Dr. Groop, was a long-term collaborator of Eric's and starting in 1999, I regularly visited the Whitehead/MIT Center for Genome Research, which he directed, to work on a number of collaborative projects. This led to a generous invitation to spend almost 18 months with Eric and his team during my Ph.D. training. It was the most exhilarating time of my career. The genome was being sequenced, we identified the first robust genetic association to age related diabetes, and we had discussions about what audacious goals we could try to reach – what the key seminal unanswered questions were. Eric has the extraordinary capacity to make his team and people around him feel that everything is possible. He often pressed that the true challenge is to figure out what the important questions are – if you manage that how to answer them will follow naturally. Because of his mentorship I fell in love with science and the scientific process.

Most recently, I had the opportunity to return and spent almost three years at the Broad Institute of MIT and Harvard (2012-2015) as a Scholar in Residence in the Medical and Population Genetics Program. During this time, we again started to discuss what the barriers to the next wave of scientific breakthrough are and how we would overcome them. Out of these discussions, which Eric drove, the International Common Disease Alliance was born, a world-wide forum of scientists coming together to accelerate the pace of discovery of genetic risk predisposition of common diseases, into

deep understanding of the mechanisms associated with this genetic risk and how the knowledge of the genetics and mechanisms can lend itself to accelerated therapeutic advances. I have had the opportunity to chair ICDA together with Eric over the last few years where he has generously offered his precious time, treated me as a peer and provided deep and insightful mentorship. This experience instilled in me the courage to reach for my goal of taking on the leadership of Oxford Big Data Institute and I was appointed earlier this year.

As many of us, his students and postdoctoral fellows, will testify, Eric is an extraordinary teacher and mentor. He both challenges his students and mentees to strive higher—to think of bigger questions and bolder solutions—and provides the support and encouragement they need to learn and, ultimately, to succeed. And, he has always been a genuine supporter and dedicated mentor of female scientists—there is a long list of women in human genetics and the life sciences who I know count Eric as one of the most important influences in their career and I am proud to be one of them.

Eric is a master communicator. He is exceptionally adept at not only conveying complex ideas and concepts to an audience far beyond Ph.D. graduate students in biology but also the thrill and excitement of scientific discovery. More than 72,000 people around the world have enrolled in his free online "Introduction to Biology — The Secret of Life" course on edX, the online educational platform, underscoring how accessible and exciting he has made biology in particular, but also science in general, to a wide swath of people.

In the challenging times that we find ourselves in, the U.S. and indeed the entire world needs to rebuild public trust and interest in science, especially as we face global challenges such as pandemics and climate change. We urgently need leadership with those skills— a passion for teaching and science, clearly and well communicated, and perhaps most importantly based on a deep compassion for fellow men and women no matter their origin.

As it has become clear that the future of our world rests on such public acceptance and engagement in science, I can think of no better person than Eric Lander to serve as a bridge between science and the public.

Yours sincerely,



Cecilia Lindgren, Ph.D.
 Director of the Oxford Big Data Institute
 Li Ka Shing Centre for Health Information and Discovery
 University of Oxford



Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building, Washington, DC 20510

cc: David Strickland, Majority Staff Director, US Committee on Commerce Science and Transportation
John Keast, Minority Staff Director, US Committee on Commerce Science and Transportation

March 13, 2021

Dear Chair Cantwell and Ranking Member Wicker:

I am writing to express my enormous enthusiasm for Eric Lander as Director of OSTP. He is arguably, the best possible choice for the country. I can think of no one better!

Eric is both brilliant and wise. When I came to Princeton as a freshman, I had heard tales of this brilliant mathematician who was four years older than me named Eric Lander. Of the years, I would learn of his fundamental contributions to the human genome project, his important scientific papers and his role in building one of the most important new scientific institutions in the US, the Broad Institute.

Eric has a long record of public service. He served for 8 years on PCAST and for the past four years was part of the DOD Defense Innovation Board. He has a deep commitment to science and has fought hard for justice and access to health care.

I strongly encourage you to confirm this superb scientist!

Sincerely,

David Spergel
Founding Director, Center for Computational Astrophysics, Flatiron Institute, NY
Charles Young Professor of Astronomy Emeritus, Princeton University, NJ
After July 1, President, Simons Foundation

Publishers Support Innovative and Sustainable Public Access

Publishers are critical to advancing science, innovation, and public health by producing and broadly disseminating high-quality journals, books, databases, and other content. The ongoing public health crisis demonstrates the importance of this work and publishers' commitment to promoting scientific discovery. Publishers are working around the clock to rapidly validate and provide access to reliable and accurate information to guide our decisions as we respond to the COVID-19 pandemic.

Peer-reviewed journals play a crucial role in ensuring the integrity of science and providing rigorous, validated information that doctors, scientists, engineers, and researchers from all fields can rely upon. Hundreds of non-profit scientific and medical societies, university presses, and commercial publishers across the country make significant investments to advance research. This includes reviewing and curating submitted articles, managing the peer-review process, editing and improving content, investing in digital infrastructure and workflows, and disseminating these important works to readers around the world.

Publishers, in partnership with researchers, universities, federal agencies, and policymakers, are advancing access to high-quality publications and other information. A sustainable policy framework is essential to support and uphold our nation's world-leading system of scientific and scholarly communication. In particular, the following are key:

- **Promoting Equity and Choice for Researchers**
 - Publishers strongly support efforts to promote a more inclusive research community, and public access policies must reflect the diverse needs of researchers. Many researchers—whether due to their discipline, early career stage, institution, or personal circumstances—do not have funding to finance publication costs.
 - Public access policies should support choice for researchers in where and how to publish their works. This should continue to include publisher-financed open access models which may carry an embargo period to support publishers' investments. Failing to do so could exacerbate current inequalities in the research ecosystem, forcing authors with fewer resources to limit how and when they publish articles, or to publish in outlets investing less in article quality.
- **Supporting Diverse and Innovative Publishing Models**
 - Publishers are continuously innovating to ensure broad access to reports on the latest discoveries and new tools to enhance the dissemination and impact of publications. The result is clear: an ever-increasing array of options for researchers to communicate their ideas and discoveries to the world. Publishers are delivering these options through a diverse range of business models and a variety of open science initiatives, including making data and pre-prints more widely available.
 - Public access policies should support, not constrain, this innovation, which is critical to meeting the diverse needs of authors, readers, and publishers across a wide spectrum of disciplines and organizations.
- **Protecting Academic Freedom**
 - Freedom to publish is a fundamental principle of academic freedom. It is essential for researchers to share their views, foster debate, and advance knowledge. Researchers should be able to choose to publish in the outlets where their research will have the most impact and best meet their needs. Key to this is ensuring authors have adequate information and funding to make this choice.
 - Public access policies should be flexible, allowing authors to choose where to publish regardless of the business model of the publication, and allowing authors to choose license terms that ensure the integrity of their work, rather than create new barriers and burdens for researchers. In particular, public access policies should avoid compulsory license terms or other one-size-fits-all approaches, as they undermine the basic benefits of copyright and reduce incentives for market investment and innovation.



Tuesday, April 27, 2021

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building
Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker,

I am writing to offer my strongest support for Dr. Eric Lander's appointment as the Head of OSTP and Science Advisor to the President of the United States. With Dr. Lander's experience in transforming the scientific field and creation of the remarkable Broad Institute, I am confident he will bring exceptional leadership and insight to the country.

Dr. Lander served as co-chair of the President's Council of Advisors on Science and Technology for former President Barack Obama and has won numerous awards in creating a new era of genomics-based precision medicine and healthcare that has transformed the field of genomics. Furthermore, Dr. Lander's efforts in creating more inclusive research and medicine demonstrates his attunement to both the public and scientific needs. As a world-renowned visionary and groundbreaking scientific leader, I am confident he will be an effective public servant.

There truly is no one better for the job, and I, as well as the entire scientific community, will applaud his smooth and swift confirmation.

Sincerely,
Hongli Sun
Director, Engineering
Illumina Inc

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
Washington, DC 20510

Senator Roger Wicker
Ranking Member, United States Committee on Commerce Science and Transportation
555 Dirksen Senate Office Building,
Washington, DC 20510

LETTER IN SUPPORT OF THE NOMINATION OF DR. ERIC LANDER AS DIRECTOR OF THE OFFICE OF
SCIENCE AND TECHNOLOGY POLICY.

From William C. Campbell, FRS, PhD
NOBEL PRIZE IN PHYSIOLOGY OR MEDICINE 2015, WITH SATOSHI OMURA,

Dear Chair Cantwell and Ranking Member Wicker:

Dr. Lander is extraordinarily well qualified for the position, being an outstanding scientist,
supremely gifted in its basic and applied applications, and in matters of policy and the
formulation of advice for governmental decision-makers.

Expert communication is vital to the position of Director of the Office of Science and
Technology Policy. Having watched and listened to Lander talking to students, I can attest to
his brilliance as a communicator.

Sincerely,

William Campbell.

William C. Campbell FRS, PhD
27 Samuel Way, North Andover, MA 01845, USA
wcampbel@drew.edu
wcampbellwc2@gmail.com
cc:

David Strickland, Majority Staff Director, United States Committee on Commerce Science and
Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and
Transportation

Senator Maria Cantwell
Chair, United States Committee on Commerce Science and Transportation
Hart Senate Office Building, 420A
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Ranking Member, United States Committee on Commerce Science and Transportation
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LETTER IN SUPPORT OF THE NOMINATION OF DR. ERIC LANDER AS DIRECTOR OF THE OFFICE OF
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Sincerely,

William Campbell.

William C. Campbell FRS, PhD
27 Samuel Way, North Andover, MA 01845, USA
wcampbel@drew.edu
wcampbellwc2@gmail.com
cc:

David Strickland, Majority Staff Director, United States Committee on Commerce Science and
Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and
Transportation

From: H Robert Horvitz <horvitz@mit.edu>
Date: March 12, 2021 at 9:15:03 AM EST

Senator Maria Cantwell
 Chair, United States Committee on Commerce Science and Transportation
 Hart Senate Office Building, 420A
 Washington, DC 20510

Senator Roger Wicker
 Ranking Member, United States Committee on Commerce Science and Transportation
 555 Dirksen Senate Office Building
 Washington, DC 20510

Dear Chair Cantwell and Ranking Member Wicker:

I am writing to endorse with the strongest support possible the nomination of Dr. Eric Lander for the position of director of the Office of Science and Technology Policy (OSTP). Dr. Lander is exceptional, and I am confident that he will perform exceptionally in this position. Dr. Lander is a world-renowned scientist, an outstanding institution builder and leader, a deeply experienced public servant, an advocate for justice and equity, a highly successful biotechnology entrepreneur, and a communicator extraordinaire. In short, Dr. Lander is brilliant, with a dazzling breadth and depth of knowledge that has repeatedly left me in awe. Dr. Lander is strikingly quick to learn about new areas and issues, to perceive the nuances of difficult problems, and to develop novel and practical ways to solve those problems.

I have known Dr. Lander since he joined my biomedical research laboratory at MIT in 1984 as a visiting scientist. I helped recruit Dr. Lander to join the MIT faculty in 1989 and have worked closely with him since in many contexts, including (1) The Human Genome Project, which he helped propel; (2) the Coalition for the Life Sciences, which provides guidance about biomedical issues to members of Congress, (e.g., via the Congressional Biomedical Research Council); and (3) our joint MIT course in graduate Genetics (in which Dr. Lander discusses the fundamentals of and ethical issues surrounding human genetics and genetic disease as well as ways to use knowledge about human genetics to develop novel medicines). I have followed Dr. Lander's stellar career with deep admiration as he co-led The Human Genome Project, founded and led the world-renowned Broad Institute of MIT and Harvard, co-chaired PCAST (the President's Council of Advisors on Science and Technology) for 8 years during the administration of President Obama, and proved himself a highly successful biotechnology entrepreneur by founding multiple companies that have developed novel diagnostics and therapeutics now improving the lives of patients worldwide.

In short, Dr. Lander is an exceptionally talented and broad scientist. I cannot imagine a better choice to be director of OSTP. I support Dr. Lander for this position without reservation and with unequivocal enthusiasm.

Sincerely yours,
H. Robert Horvitz
Professor of Biology, MIT
Investigator, Howard Hughes Medical Institute
Member, U.S. National Academy of Sciences
Member, U.S. National Academy of Medicine
Nobel Prize in Physiology or Medicine, 2002

cc:
David Strickland, Majority Staff Director, United States Committee on Commerce Science and Transportation
John Keast, Minority Staff Director, United States Committee on Commerce Science and Transportation

RESPONSE TO WRITTEN QUESTIONS SUBMITTED BY HON. MARIA CANTWELL TO
DR. ERIC S. LANDER

Financial Conflicts of Interest. Given the considerable authority granted to the Director of the Office of Science and Technology Policy, it is critical that you avoid any actual or apparent conflicts of interest. According to your financial disclosures, you hold investments in entities that may be affected by the work you would perform as Director, including companies in the medical, biotechnology, and pharmaceutical industries. As a part of your ethics agreement, you have said that you will divest from these investments.

Question 1. If confirmed, will you commit to divesting from any investments you hold in entities that may present an actual or apparent conflict of interest, including but not limited to entities operating in the medical, biotechnology, and pharmaceutical industries?

Answer. Yes.

Question 2. Will you commit to complying with all of the provisions in the Ethics Agreement you signed on February 19, 2021?

Answer. Yes.

Conflicts of Interest in Future Employment. The OSTP's mission has direct interaction with research institutions like the Broad Institute. During your confirmation hearing you expressed an interest in returning to work at the Broad Institute after your tenure as Director of the OSTP is complete.

Question 1. Please detail the steps that you will take as Director of OSTP to ensure that any decision the impacts the Broad Institute does not present a conflict of interest or the appearance of a conflict of interest with your previous work at the Broad Institute and your intended return to that same institution.

Answer. I will not participate personally or substantially in any particular matter that, to my knowledge, would have a direct and predictable effect on the financial interests of the Broad Institute. I will not participate in any particular matter involving specific parties in which the Broad Institute is a party or represents a party. Furthermore, in the event that an actual or potential conflict arises with regard to Broad or any other entity or person, I will consult with an agency ethics official and take whatever steps are needed to resolve such conflict, including immediate recusal and/or divestiture.

Question 2. Will you commit to providing this Committee, upon request, information regarding funding, contracts, or support directed towards the Broad Institute and your involvement in the decision to send funding, contracts, or support to that institution?

Answer. I have resigned from my position as CEO of the Broad Institute and I am on an unpaid leave of absence from my position as tenured professor there. If confirmed as OSTP Director, if requested, I commit to working with this Committee to provide information regarding funding, contracts, or support directed towards the Broad Institute by OSTP while I serve in this capacity. Moreover, I commit to this Committee that I will recuse myself from any and all decisions that could potentially or actually direct funding, contracts, or support towards the Broad Institute.

Diversity in STEM. The nation has struggled to increase STEM diversity. Congress has authorized a number of programs to broaden participation in STEM, but we have yet to see any significant progress.

Question 1. If confirmed as Director of OSTP, what concrete steps will you take that would garner additional support for and expand participation in STEM?

Answer. I understand that we are not drawing upon the full potential of our country's talent, owing the long-term underrepresentation of various groups, including women and people of color. Increasing diversity and advancing equity in STEM is critical to our success in science and technology, and it requires a systematic approach.

We need to invite and engage more people in STEM, embrace and lift up more role models, give more students amazing hands-on opportunities to learn and engage in the scientific enterprise, create more inclusive and diverse learning and working environments, and monitor, measure, evaluate and report on progress towards these goals.

If confirmed, I'm committed to working with educators, community thought leaders, science and technology stakeholders, public and private institutions, agencies, and Congress to develop a plan to carry out the President's vision of a more inclusive and equitable nation.

Question 2. How do you address concerns that your decision to toast Dr. Watson, and your failure to include recognition for two notable female scientists is evidence

that you will perpetuate stereotypes and not take active steps to promote the work of minorities and women in STEM if you are confirmed?

Answer. I believe that supporting women and people of color in STEM is critical. I understand that science has not always been welcoming—and has often been hostile—to individuals from underrepresented groups. This is such an important issue because the lack of inclusion is not only deeply unfair, but is also one of the greatest risks to America's success. Throughout my career, I have worked to improve diversity and inclusion in science.

If confirmed, I am committed to making full inclusion and equitable outcomes a high priority, including building the most diverse OSTP and PCAST in history and developing a plan to increase the numbers of women and people from underrepresented groups in the science and technology professions by 50 percent. I would welcome the opportunity to work with you on this.

RESPONSE TO WRITTEN QUESTIONS SUBMITTED BY HON. RAPHAEL WARNOCK TO
DR. ERIC S. LANDER

Inclusion of Underserved Communities. In my home state, Georgia Tech, Morehouse College, and PRENEURology Global have launched the Southeast Minority Business Development Agency—Business Growth Hub, which will serve as a network of entrepreneur spaces, education pathways, and engagement programs—specifically focused on minority entrepreneurs and students.

Question. How can OSTP better work with agencies, Congress, and the university and startup ecosystem to bring research out of the lab and into underserved, underrepresented localities that need more opportunities for new businesses and new jobs?

Answer. I understand how important it is for agencies, STEM ecosystems, Congress, and OSTP to work together to turn research into business and job opportunities for those in underserved communities.

As indicated in the American Jobs Plan, the Administration is calling on Congress to invest in workforce training that prioritizes underserved communities and communities hit hardest by our transforming economy. It asks for the support of investments that ensure those from underserved groups have greater access to new infrastructure jobs. The President's plan also calls for support of community college partnerships that build capacity to deliver job training programs based on in-demand skills. I am also in full support of the President's *Executive Order On Advancing Racial Equity and Support for Underserved Communities Through the Federal Government*.

If confirmed, I am committed to working with agencies, such as the National Science Foundation, the Department of Education, and the Department of Labor to support the development of policies and programs that deliver resources and benefits equitably to all. Likewise, I am committed to working with agencies, STEM education ecosystems, and Congress to support economic and scientific growth in underserved communities. I am also personally interested to learn more about the Southeast Minority Business Development Agency—Business Growth Hub, to understand ways in which it may be a useful model for other underserved communities.

Innovation and Efficiency. Our most serious global challenges are increasingly at the intersection of scientific disciplines with significant societal impacts. Our vulnerable populations and disadvantaged communities are and will withstand the worst of health and environmental challenges. Unfortunately, our Federal research agencies are often siloed both internally and across agencies in their approaches and missions. The researchers in our universities in Georgia often want to tackle challenges at this intersection—such as the health impacts of energy technology—but are stymied by the current bureaucratic structures of our research agencies.

Question. How will you work to bring our agencies together to make real change that spurs new discoveries and innovation?

Answer. I understand how important it is for the success of our research community that the Federal government take a holistic approach in supporting new discoveries and innovation. And, I know that this does not always occur.

Optimizing interagency collaboration is central to OSTP's mission and OSTP is uniquely positioned to carry out this goal, through its leadership of National Science and Technology Council (NSTC), which helps to coordinate science and technology across the Federal agencies and support collaborative initiatives and activities across agencies.

If confirmed, I am committed to utilizing the NSTC to its full capacity, supporting agencies that model convergent approaches to their work, and identifying and sup-

porting other ways that agencies can support the intersection of scientific disciplines with the potential of significant societal impact.

Improved Screening Technology. As we have seen throughout the Covid-19 pandemic, America's seniors went without preventive health services for far too long. One major consequence of this is the substantial reduction in cancer screenings among those at greatest risk for cancer: adults over age 65. The risks are further exacerbated by the health inequities we face in the U.S. that continue to disproportionately impact African-Americans. In August 2020, NCI Director Dr. Sharpless warned of an increase in late-stage cancer diagnosis due to missed screenings.

Question. As the Director of OSTP, what would you do to ensure that the Administration pursues policies that promote innovative screening technology to reduce the number of late-stage cancer diagnoses?

Answer. As a life scientist who has worked on cancer and other diseases, I appreciate the importance that screening plays in reducing late-stage cancer diagnoses. I know that recent advances in science and technology offer new opportunities to detect cancers earlier and to ensure access that is broader and equitable to all. I understand how important it is to support policies that promote such technology.

I know the President supports advanced research and screening efforts found through the Centers for Disease Control and Prevention's National Comprehensive Cancer Control and the National Breast and Cervical Cancer Early Detection Programs, and the Food and Drug Administration's Oncology Center of Excellence, for example. I am also in full support of the President's *Executive Order On Advancing Racial Equity and Support for Underserved Communities Through the Federal Government*. The pandemic has disproportionately impacted African-Americans and others who have been historically underserved, marginalized, and adversely affected by persistent poverty and inequality.

If confirmed, I will work with agencies to support the development of policies and programs that promote innovative technologies to improve medical diagnoses and care and deliver resources and benefits equitably to all.

Reliable and accurate scientific information. These days, as we deal with the worst public health crisis in generations, it's more important than ever to have reliable and accurate scientific information. We clearly need rigorous, peer-reviewed analyses of research to guide our decisions.

Question. Dr. Lander, how would you work with the scientific societies and publishers to produce high-quality scientific analyses and articles while ensuring policymakers, community leaders, and the greater scientific community has access to potentially lifesaving and life-improving information?

Answer. I understand the importance of ensuring that we have reliable and accurate scientific information, especially on topics with lifesaving and life-improving implications. I also recognize that it is important that information is rapidly and fully accessible to policymakers, community leaders, and the greater scientific community.

To execute on these goals, there needs to be funding and collaboration mechanisms to generate critical data related to public health as well as mechanisms and norms for ensuring rapid and open sharing of data sets and publications. The pandemic has led to innovation in these areas and it will be important to capture and evaluate the learnings and see how they might be reflected in policy.

These goals also relate the importance of scientific integrity, including within the Federal government. OSTP is in full support of the President's *Memorandum on Restoring Trust in Government Through Scientific Integrity and Evidence-Based Policymaking*. To implement this policy, OSTP recently launched a multi-agency Scientific Integrity Task Force. As noted in a recent press release, "the Task Force will review existing Federal scientific-integrity policies to identify effective solutions that will help improve the lives of the American people, inform innovative and equitable policy, and revitalize the confidence of the American public in its government."

If confirmed, I am committed to supporting efforts to capture and evaluate the learnings during the pandemic about innovative scientific practices; supporting the Scientific Integrity Task Force; and exploring additional ways in cooperation with the scientific community to ensure scientific information used in decisions is of the highest quality and publicly available.

RESPONSE TO WRITTEN QUESTIONS SUBMITTED BY HON. ROGER WICKER TO
DR. ERIC S. LANDER

Question 1. Dr. Lander, nearly half of Federal research dollars over the last 20 years went to just six states, and more than one third went to just two states, Cali-

ifornia and Maryland. U.S. world leadership in science and technology is dependent on tapping into the potential of all Americans as we build the workforce of the future.

- What steps should we take to better spread science and technology research and expertise across the entire nation?

Answer. If confirmed, I'm committed to working with Congress, Federal science agencies, and my White House colleagues to make sure that all Americans have the opportunities to do science and technology research and benefit from the results of research.

I believe we can learn from and build on existing programs such as the Established Program to Stimulate Competitive Research (EPSCoR), the Institutional Development Award (IDeA) program at the National Institutes of Health (NIH), U.S. Department of Agriculture (USDA) programs supporting research across the country, Federal STEM-education programs, and other capacity-building programs to build research infrastructure and capacity in all states and jurisdictions throughout the United States.

Question 2. According to FBI Director Christopher Wray, "the greatest long-term threat to our Nation's information and intellectual property, and to our economic vitality, is the counterintelligence and economic espionage threat from China."

- What steps can universities and industry take to protect our valuable research from foreign espionage?

Answer. I understand the importance of protecting against foreign espionage, including espionage that targets non-public information and intellectual property. Government, academia, and industry must work together to strengthen and protect our innovation enterprise. This includes increased understanding and awareness of risks, identification of technological vulnerabilities, cyber security measures and training, and openness and transparency with respect to research and development collaborations.

If confirmed, I look forward to working with academic research institutions, industry, and with Congress to identify and implement appropriate measures to safeguard prepublication research and intellectual property, and build our competitiveness in science and technology.

Question 3. Dr. Lander, although basic research in universities and government agencies is important, more than 70 percent of R&D in our Nation is funded and conducted by industry.

- How can our Federal research agencies work to ensure industry is at the table in technology development so we can cross the so-called "valley of death" between conducting research and actually developing commercially viable products?

Answer. I understand the importance of ensuring that Federal research agencies are involved in technology development to address the "valley of death" that exists between research and developing commercially viable products.

Public-private partnerships can be a valuable tool for addressing the "valley of death" challenge. For example, on April 27, the White House announced that the National Science Foundation (NSF), in partnership with the Department of Defense Office of the Undersecretary of Defense for Research and Engineering, the National Institute of Standards and Technology (NIST), and nine leading companies, launched a program to accelerate research on next-generation networking and computing systems. This partnership joins our great Federal research institutions with nine leading companies including Apple, Ericsson, Google, IBM, Intel, Microsoft, Nokia, Qualcomm, and VMware. Together, they will partner to tackle society's future needs for connectivity, maintain U.S. leadership in critical technologies, and upgrade the Nation's digital infrastructure.

If confirmed I commit to supporting the administration's efforts in this area and to working with you to explore other strategies.

Question 4. U.S. leadership in R&D is critical. Our near peer competitors like China are investing significant resources in these fields. I was proud to champion the recently enacted Industries of the Future Act, which directs OSTP to develop a plan to continue U.S. leadership in industries of the future.

- What will you do at OSTP to enable U.S. advancements in technology, such as artificial intelligence and quantum science, so that we can maintain a competitive advantage over countries like China?

- Follow-up: If confirmed, will you commit to swift implementation of the Industries of the Future Act?

Answer. I understand the importance of U.S. leadership in research and development in order to enable U.S. advancements in technology so that we can maintain an international competitive advantage.

OSTP, as part of the Biden-Harris Administration, strongly supports increased funding for emerging technologies. Notably, as indicated in the American Jobs Plan, the Administration is calling on Congress to “make an \$180 billion investment that will advance U.S. leadership in critical technologies and upgrade America’s research infrastructure. U.S. leadership in new technologies—from artificial intelligence to biotechnology to computing—is critical to both our future economic competitiveness and our national security.”

If confirmed, I commit to working with you to support U.S. leadership in research and development and to implement the Industries of the Future Act.

Question 5. Dr. Lander, FY 2018 marked the first increase in Federal science and engineering obligations to HBCUs since FY 2014. Unfortunately, this remains only a small fraction of the total Federal dollars awarded to all U.S. institutions of higher education. HBCUs play a critical role in education and scientific research. As we discussed in our meeting, Jackson State University was a pioneer in researching the environmental and genetic factors associated with heart, kidney and lung diseases among African Americans through the Jackson Heart Study.

- If confirmed, what will you do to increase the amount of Federal R&D spending at HBCUs like those in my home state of Mississippi?

Answer. I understand the important role that HBCUs play in education and scientific research. The *National Center for Science and Engineering Statistics (NCSES)* of the National Science Foundation recently released an update on *Women, Minorities, and Persons with Disabilities in Science and Engineering*, reporting that 23 percent of African American or Black graduates who earned an S&E doctorate between 2015 and 2019 earned their bachelor’s degree from an HBCU.

As indicated in the American Jobs Plan, the Administration is calling on Congress “to make a \$10 billion R&D investment at HBCUs and other MSIs.” The Plan also calls on Congress “to invest \$15 billion in creating up to 200 centers of excellence that serve as research incubators at HBCUs and other MSIs to provide graduate fellowships and other opportunities for underserved populations, including through pre-college programs.”

As indicated in the American Families Plan, the Administration is calling on Congress to support a \$400 million investment “in teacher preparation programs at HBCUs, TCUs, and MSIs” and a \$5 billion investment “to expand existing institutional aid grants to HBCUs, TCUs, and MSIs,” which would include creating or expanding “educational programs in high-demand fields (*e.g.*, STEM, computer sciences, nursing, and allied health).” As further noted in the American Families Plan, “these proposed investments, combined with the \$45 billion proposed in the American Jobs Plan targeted to these institutions, will enable America’s HBCUs, TCUs, and MSIs to help advance underrepresented students and make the U.S. more competitive on the global stage.”

If confirmed, I am committed to working with agencies to support the development of policies and programs that deliver resources and benefits equitably to all and with Congress to support greater Federal R&D spending at HBCUs.

Question 6. Dr. Lander, In February, NASA successfully landed the Perseverance rover on the surface of Mars. Even more remarkably, this was the 9th time NASA has accomplished such a feat. Space science and technology inspires us and has enriched our lives. As director of OSTP, you will have a role in maintaining U.S. progress in this critical area.

- How do you plan to ensure continued focus on space science and exploration? Will you work with the National Space Council to advance this effort?

Answer. I understand the importance of space as a national and international source of inspiration, which reminds us of the boldness of the human spirit through feats like flying the first helicopter on Mars and launching a new space telescope, and scientific and technological knowledge.

If confirmed, I will ensure the United States remains at the vanguard of space science and technology with ground-breaking achievements, like the deployment of the Perseverance rover and the use of American-made rockets to transport Americans safely into space. If confirmed, I look forward to working closely with the National Space Council because much work remains to advance the future of space

science and technology. I commit to working with this committee, if confirmed, to advance our national space policy objectives in service to the American people.

Question 7. Dr. Lander, last Congress this Committee passed several bipartisan bills focused on at OSTP. This Congress, I continued that work by introducing the Ocean Exploration Act, along with Senators Cantwell, Schatz, Murkowski, and Whitehouse.

- Can you speak to the importance of bipartisan work for our oceans? And what do you see as the role of OSTP in fostering ocean exploration?

Answer. Covering more than 70 percent of the Earth's surface and over 97 percent of its inhabitable volume, the ocean is critical to our Nation's health, prosperity, and security. All Americans benefit from the services the ocean provides, such as commerce, food production, energy, tourism and recreation, environmental protection, conservation, and national and homeland security.

I applaud this committee's leadership on ocean issues, and its strong support for ocean observations, stewardship, and ocean exploration, and recognize that the recently codified Ocean Policy Committee (OPC) provides an effective way to coordinate and advance these interests.

If confirmed, I look forward, with my colleague and OPC co-chair Brenda Mallory, Chair of the Council on Environmental Quality, to convening the OPC.

I greatly appreciate this committee's continuing support for the important work of exploring, observing, and predicting ocean processes. These activities are currently undertaken by numerous Federal agencies, the private sector, non-governmental organizations, and academic institutions. Meeting ambitious goals to map, explore, and characterize the ocean requires engaging these partners to facilitate effective partnerships and working with agencies to minimize barriers to external participation.

As co-chair of the OPC and the National Science and Technology Council's Subcommittee on Ocean Science and Technology, OSTP will play an important role in coordinating and supporting the continued advancement of ocean science and technology, and I commit to working with you to do so.

RESPONSE TO WRITTEN QUESTIONS SUBMITTED BY HON. MIKE LEE TO
DR. ERIC S. LANDER

Question 1. During the hearing you stated that you "have been on record supporting a moratorium on the use of germline genome editing to create designer babies." A moratorium is only a temporary restriction on this type of research and last year, you coauthored a report on Heritable Human Genome Editing that charts a potential path forward on this research.

- Do you support a permanent ban on germline genetic engineering to create designer babies? If so, why? If not, what parameters do you believe must be put in place before a moratorium should be lifted?

Answer. This is an extremely important issue: genome editing technology is a powerful tool with potential applications to improve human health and very worrying potential consequences. I am against the use of genome editing technology to create "designer babies." I believe that the unintended consequences and ethical issues are not yet adequately understood and that germline editing is not yet safe or effective enough to justify any use in the clinic.

A moratorium on heritable gene editing is an important first step—there are scientific, technical, medical, ethical and social issues that will need to be addressed before a decision can be made about whether to lift, extend, or make permanent a moratorium. The decision is not mine alone to make. I believe these discussions will require broad societal input.

If confirmed, I would welcome the opportunity to hear your thoughts and work with you on this critical issue.

Question 2. The Biden Administration recently lifted restrictions on the use of fetal tissue for medical research. These new rules would allow scientists to use tissue derived from abortions for medical research. Recently, news broke from a series of FOIA requests that showed how the Food and Drug Administration paid an estimated \$2,000 per individual baby and sometimes up to \$12,000 per box of harvested organs. Some documents have even showed that the FDA bought body parts from babies that were 24 weeks old as well as the skulls of second trimester babies.

- With the Biden Administration's lifting restrictions on use of fetal tissue, do you support the trafficking of aborted human body parts?

- If confirmed to be OSTP Director, a role that involves the coordination and establishment of research and development goals across Federal agencies, will you oppose this type of scientific research being conducted at the FDA or any Federal agency?

Answer. I understand the importance of this issue, which raises sensitive ethical and moral concerns.

The administration's policy keeps in place all of the rigorous expectations, regulations, and applicable laws for conducting this type of research that were adopted by previous administrations, including the most recent. In particular, every researcher will still have to clear the very high bar to demonstrate that the research goals cannot be accomplished in any other way and that robust informed-consent procedures are in place.

If confirmed, I would advise the President on the scientific underpinnings—for example, what advances might result from the development of alternative models to the use of human fetal tissue—and I look forward to working with Congress on continuing to ensure ethical and moral issues are fully considered.

Question 3. It's anticipated that the Senate will soon take up the Endless Frontier Act, which places a great deal of responsibility on the OSTP Director and National Science Foundation for implementation of a \$100+ billion government R&D effort to counter China's threat to the U.S. homeland. As I stated during the hearing, I'm concerned that in this conversation that we are only trying to respond to the CCP threat with more government spending.

- Are there structural changes that we need to make in order to better mobilize the United States to meet the challenges posed by the Chinese government? How about regulatory changes? Tax code changes? Workforce changes?
- Will U.S. spending be less effective without making these structural changes?

Answer. I understand the urgent need to counter the competitive threat that China poses. Our strategic response and competition with China will require an all-of-government effort, as President Biden has recognized. To address this critical issue, it is important to carefully consider the full range of challenges that American industry may face in competition with China and the full range of levers that might be applied to maximize American competitiveness, including regulatory, tax, and workforce policies.

If confirmed, I look forward to working with you to explore all the tools we will need to meet the challenge, including which regulatory, tax, and workforce policies may be the most effective.

Question 4. What is the appropriate role of the Federal government for the categories of "basic research", "applied research", or "development"? And what should be left to the private sector?

Answer. I understand the importance of investments from the Federal and private sector to ensure that all the categories of scientific research in the United States research and development ecosystem will thrive. In each category, the Federal support should focus primarily on driving critical R&D that would not otherwise be done—at all, at adequate scale, or at adequate speed—by the private sector, owing to insufficient private return on investment.

If confirmed, I commit to working with you to exploring this balance so that all aspects of scientific research can be supported and thrive.

Question 5. The OSTP under the Trump Administration was influential in the formation of the UAS Integration Pilot Program (IPP). The IPP is now completed and the FAA is now transitioning into their next program called BEYOND. A big question in drone policy is the scope of Federal preemption. A September 2020 GAO report noted that both DOT and DOJ will soon be issuing a joint opinion on the scope of FAA preemption in the context of low altitude drone operations. The FAA has taken the position that they control the airspace from the ground up.

- Do you think the Federal government has the ability to regulate the airspace a couple of feet above your lawn? What about inches above the blades of grass? Is this a problematic position to take?
- Do you think full and safe drone integration is possible without shared responsibility between the Federal government and state and local governments?

Answer. I understand the important role that Unmanned Aerial Systems play now and will play in the future and thus the importance of ensuring that the United States has balanced guidelines and regulations. I recognize it is important to weigh the considerations of individual property rights and Federal authority. It is also im-

portant to work together at all levels of government to develop the best possible solutions to these complex issues.

If confirmed, I pledge to work with you to address these important matters.

Question 6. Access to additional spectrum is critical for future technological innovation. Unfortunately, the Federal government sits on a lot of a valuable spectrum bands, particularly mid-band spectrum which is the best suited for 5G wireless networks.

- Do you think Federal agencies currently use their spectrum efficiently?
- Should government agencies be immune from oversight of their use of the electromagnetic spectrum?
- I think Congress and Executive Branch agencies need the best available data to identify inefficiencies in both the commercial and government contexts. Will you support my legislation, the Government Spectrum Valuation Act, which would require NTIA to calculate the value or the “opportunity costs” associated with Federal spectrum so that we can make more informed decisions?

Answer. I understand the tremendous need to use spectrum efficiently. The demand on our spectrum for uses like 5G and other applications is growing exponentially. Because spectrum is a finite resource, we need to continuously evaluate how it is allocated and used and how to devise ways to squeeze all the value out of it for the American people, including for our economy and national security.

If confirmed, I pledge to work with you to address these important balancing considerations.

Question 7. Congress is in the midst of a debate about Federal legislation related to data privacy.

- What is the role of the Federal government when it comes to data privacy?
- Some believe the FTC should be given greater authority to prescribe data privacy rules, including broad APA authority. What are your views on this?

Answer. I understand the importance of addressing data privacy issues. We cannot maximize the benefits of technology without ensuring privacy.

If confirmed, I will work with Federal agencies and the Congress to develop effective ways to protect personal data and to build trust among the American people that personal data about them are protected, while also helping America reap the benefits of innovation and the Internet economy.

Question 8. Regulatory red tape is likely the single largest barrier to deployment of wired and wireless broadband. It can be especially difficult for small rural providers to invest the time, money, and effort to build a network that is on or crosses Federal lands. Because 2/3 of Utah’s land is owned by the Federal government, Utah broadband providers more urgently feel the need for Federal permitting reform for broadband infrastructure.

- What would you recommend to agencies to help streamline the permitting process so we can lower the cost, as well as more efficiently allow, for companies to deploy broadband on Federal land?

Answer. Americans depend on the Internet for education, work, healthcare, and commerce.

Without broadband, it will be impossible for people to fully participate in the American economy in the 21st Century.

High-speed Internet connectivity needs to be readily, affordably, equitably, and reliably available to every American household. However, millions of Americans lack access to broadband service. These unserved and underserved Americans are disproportionately rural Americans, people on Tribal reservations, people of color, Americans who are older, or those with low-incomes, or with disabilities.

If confirmed, I commit to working with you to explore options to lower the costs of deployment and streamline the deployment of broadband so that more Americans can reap the benefits of connectivity.

Question 9. What is the role of the Federal government in regulation of tech companies and tech censorship generally? How would you approach this issue as you advise the President?

Answer. If confirmed, I will approach the issue of advising on technology governance the same way I approach all science and technology policy issues: with curiosity and an open mind; by calling on the best minds throughout the country for their advice; engaging with companies, organizations, Congress, and academia for their insights and experiences; and relying on our best-available scientific and technical research.

Question 10. Is the Internet a public utility? Should it be regulated as such?

Answer. The past year has made it that clear that Americans depend on Internet access for education, work, healthcare, and commerce.

If confirmed, I will work with Congress to identify appropriate approaches for Internet governance. Whatever legal approach is adopted should support affordable and equitable access for all Americans.

RESPONSE TO WRITTEN QUESTION SUBMITTED BY HON. DAN SULLIVAN TO
DR. ERIC S. LANDER

Question. As you know, the Office of Science and Technology has previously played a critical role in spectrum policy, which is obviously crucial for leadership in 5G—especially in our race with China. If confirmed, what role do you see your OSTP taking in spectrum policy, and what more can be done to help the U.S. lead in 5G?

Answer. I understand the critical need for U.S. leadership in 5G—both for U.S. economic growth and our national security.

United States policies that create easier access to spectrum will not only spur the domestic economy, but will help us maintain international leadership in this crucial area of modern technological innovation and commerce.

If confirmed, I pledge to work with stakeholders, including civil society, government, and industry to optimize and advance efficient spectrum use and American competitiveness.

