CURRICULUM VITAE

Matthew Thomas Maurano

Address: Institute for Systems Genetics and Department of Pathology
NYU Medical Center
Science Building, Room 801
435 East 30th Street
New York, NY 10016
Tel: +1 (646) 501-4576
maurano@nyu.edu
http://www.mauranolab.org

EDUCATION:

2013	Ph.D.	Dept. of Genome Sciences, University of Washington, Seattle, WA, USA Thesis: *Regulatory variation and human disease*, Advisor: Dr. John A. Stamatoyannopoulos
2005	B.A.	Computer Science (with Honors), University of California, Berkeley, CA, USA
2005	B.A.	Molecular & Cell Biology, University of California, Berkeley, CA, USA

FACULTY POSITIONS HELD:

2015– Assistant Professor, Institute for Systems Genetics and Department of Pathology
New York University School of Medicine, New York, NY

OTHER POSITIONS HELD:

2019–	Affiliate, Center for Human Genetics and Genomics, New York University School of Medicine
2017–	Member, Perlmutter Cancer Center, New York University School of Medicine
2013–15	Senior Fellow, University of Washington, Seattle, WA. Advisor: Dr. John A. Stamatoyannopoulos
2008–13	Doctoral research student, Dept. of Genome Sciences, University of Washington, Seattle, WA
2005–08	Project Manager, Professional Services & Software Quality Engineer, Rosetta Biosoftware (Merck), Seattle, WA
2004	Intern, ITC-irst, Univ. of Trento, Italy. Advisors: Drs. Giuseppe Jurman & Cesare Furlanello Thesis: *Microarray missing data reconstruction methods*
2002–03	Undergraduate Researcher, Department of Plant and Microbial Biology, UC Berkeley, CA Advisor: Dr. Steven Brenner. Topic: *Homology of NUDIX proteins in D. Radiodurans*
2002	Intern, AOL/Netscape, Mountain View, CA

HONORS AND AWARDS:

2025	Irma T. Hirschl/Monique Weill-Caulier Research Award
2014	ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Winner
2013	UW Graduate School Fund for Excellence and Innovation Travel Award
2011	UW Graduate School Fund for Excellence and Innovation Travel Award
2000–04	UC Berkeley Regents' Scholarship (awarded to the top <1% of admitted students)
2000–04	Robert C. Byrd Honors Scholarship

PROFESSIONAL ORGANIZATIONS & AFFILIATIONS:

American Society of Human Genetics (2012–)
European Society of Human Genetics (2018–2020)

TEACHING EXPERIENCE:

Fall 2025	A PhD Experience, NYU Vilcek (1 lecture)
Fall 2025	Genetics, NYU Vilcek (2 lectures)
Fall 2024	A PhD Experience, NYU Vilcek (1 lecture)
Spring 2024	Genetics, NYU Vilcek (2 lectures)
Spring 2023	Build-A-Genome, NYU (1 lecture)
Spring 2023	Genetics, NYU Vilcek (2 lectures)

Spring 2022	Genetics, NYU Vilcek (2 lectures)
Fall 2020	Fundamental Discoveries in Biology, NYU Sackler (1 lecture)
Spring 2020	Biomedical Informatics, NYU Sackler (1 lecture)
Fall 2019	Genetics, NYU Sackler (1 lecture)
Fall 2018	Genetics, NYU Sackler (1 lecture)
Fall 2018	Topics in Bioinformatics, NYU Sackler (5 lectures)
Fall 2018	Methods and Applications for Systems & Synthetic Biology, NYU Sackler (4 lectures)
Spring 2018	Grant Writing for Scientists, NYU Sackler (5 lectures)
Fall 2017	Genetics, NYU Sackler (1 lecture)
Fall 2017	Functional Regulatory Genomics, NYU Sackler Research Adventure
Spring 2017	Topics in Bioinformatics, NYU Sackler (5 lectures)
Fall 2016	Genetics, NYU Sackler (1 lecture)
Spring 2016	Molecular Pathology in the Omics Era, NYU Sackler (1 lecture)
Fall 2015	Genetics, NYU Sackler (1 lecture)
2011	Genome 372: Genomics & Proteomics. Graduate teaching assistant.
2011	Genome 361: Fundamentals of Genetics and Genomics. Graduate teaching assistant.
2007–08	Microarray data analysis using Rosetta Resolver (multiple lectures at different sites)

TRAINEES / POSITIONS SUPERVISED:

ADVANCED TRAINEES:

11/2024–present	Raquel Ordoñez Ciriza, Ph.D.
1/2018–4/2023	Ran Brosh, PhD
4/2016–7/2021	Megan Hogan, PhD

POSTDOCTORAL TRAINEES:

6/2025–present	Alejandro Soriano Sexto, Ph.D.	High-throughput approaches to regulatory variation
5/2024–present	Raquel Moya, Ph.D.	Role of calcium channel *CACNA1C* in psychiatric disease
10/2019–11/2024	Raquel Ordoñez Ciriza, Ph.D.	Enhancer selectivity at the *Igf2/H19* imprinted locus
9/2019–9/2024	André Ribeiro-dos-Santos, Ph.D.	High-throughput engineered regulatory variation
11/2018–6/2019	Stepan Grinek, Ph.D.	Efficient approaches for statistical fine mapping
11/2016–5/2018	Jesper Maag, Ph.D.	Modeling regulatory variation

PRE-DOCTORAL TRAINEES:

7/2025–present	Jacob Bernheim	Large-scale analysis of regulatory function
7/2019–5/2024	Raquel Moya	Role of calcium channel *CACNA1C* in psychiatric disease
7/2017–6/2018	Brandon Mannion	Insulator function and long-distance interaction

GRADUATE THESIS COMMITTEES:

10/2024	Jimin Tan	NYU Vilcek (Ad hoc)
4/2021–present	Brianna Berrios	NYU Vilcek
10/2017–5/2020	Sana Badri	NYU Sackler
4/2017–12/2021	Sudarshan Pinglay	NYU Sackler
3/2017–2/2022	Bo Xia	NYU Sackler
2/2017	Esben Eickhardt	Aarhus University (Ad hoc external reviewer)
8/2016–12/2017	Pamela Wu	NYU Sackler Molecular Biophysics
7/2015–12/2017	Harris Lazaris	NYU Sackler Biomedical Informatics

GRADUATE ROTATION STUDENTS:

Spring 2025	Jacob Bernheim	NYU Vilcek
Summer 2020	Brianna Berrios	NYU Sackler
Winter 2019	Raquel Moya	NYU Sackler
Spring 2018	Neil Jethani	NYU MSTP program
Winter 2018	Nicholas Mamrak	NYU Sackler
Winter 2017	Brandon Mannion	NYU Sackler

POSTBAC

7/2024–present	Colleen McLoughlin
7/2023–1/2024	Chloe Palumbo
7/2021–7/2023	Gwen Ellis
11/2019–6/2021	Angela Hitchcock
6/2019–4/2021	Raven Luther
8/2018–7/2021	Emily Huang

OTHER MENTORSHIP OF GRADUATE STUDENTS:

6/2023–8/2023	Nerea Berastegui Zufiaurre	University of Navarra, Pamplona, Spain
6/2020–8/2020	Emily Huang	NYU School of Global Public Health
6/2020–8/2020	William Egan	NYU Center for Data Science
10/2017–6/2019	Raven Luther	NYU Biology
9/2017–8/2018	Nick Vulpescu	NYU Biology
6/2016–8/2016	Yun Yan	NYU Tandon School of Engineering

UNDERGRADUATE MENTORSHIP:

05/2023–08/2023	Milosz Majewski	Maastricht University
6/2019–8/2019	Nora Gilligan	NYU Computer Science
6/2018–8/2018	James Schull	Stanford Computer Science
6/2017–8/2017	Aidan Reilly	Johns Hopkins University
6/2017–8/2017	Maia Stoicovici	NYU Tandon Chemical and Biomolecular Engineering
6/2017–8/2017	Nick Vulpescu	NYU Biology

HIGH SCHOOL STUDENT MENTORSHIP:

7/2025–8/2025	Jacob Gluck	Staten Island Technical High School
7/2025–8/2025	Danielle Brekher	Staten Island Technical High School

TRAINEE AWARDS:

2022	Raquel Ordoñez	FASEB The Genome Engineering Conference travel award
2021	Raquel Moya	MacCracken Award for leadership, attitude & academic achievement

EDITORIAL RESPONSIBILITIES:

Editorial Boards:

Cell Reports

Ad-hoc reviewer for:

American Journal of Human Genetics
BMC Bioinformatics
BMC Genomics
Cell Genomics
Cell Systems
Cell Reports
eLife
Epigenetics & Chromatin
European Journal of Human Genetics
Genome Biology
Genome Research
Human Mutation
Nature Biotechnology
Nature Genetics
Nucleic Acids Research
PLoS Genetics
Review Commons
Science
Trends in Biotechnology

SPECIAL INTERNATIONAL RESPONSIBILITIES:

2024 Reviewer panel, CaixaResearch Health 2025
2024 Ad hoc reviewer, Worldwide Cancer Research 2024
2024 Reviewer panel, CaixaResearch Health 2024
2023 Reviewer panel, CaixaResearch Health 2023
2021 Reviewer panel, CaixaResearch Health 2021
2021 Reviewer panel, CaixaResearch Health 2020
2020 External Reviewer, Mardsen Fund
2018 Reviewer panel, CaixaResearch Health 2018
2018 External Juror, Fondazione Bruno Kessler WebValley
2018 External Reviewer, Wellcome Trust Sir Henry Dale Fellowship
2017 External Reviewer, European Research Council - Starting Grant
2016 External Reviewer, Wellcome Trust Sir Henry Dale Fellowship

SPECIAL NATIONAL RESPONSIBILITIES:

2024 Session Moderator, ASHG Annual Meeting
2024 Abstract Reviewer, ASHG Annual Meeting
2024 External Reviewer, GREGoR Consortium Research Grant proposals
2023 External Reviewer, GREGoR Consortium Research Grant proposals
2016–present Member, GTEx Consortium
2016–present Member, GTEx Analysis Working Subgroup
2015–2017 Member, GTEx Imprinting Analysis Working Subgroup
2013–2014 Member, ENCODE/CHARGE Consortia Joint Workshop Working Group
2013–2017 Member, ENCODE GWAS Analysis Working Group

SPECIAL LOCAL RESPONSIBILITIES:

2025–present NYU ISG Emergency Resilience Program & Business Continuity Committee
2024–2025 Faculty Search Committee, NYU Institute for Systems Genetics/SynBioMed
2023–2024 Faculty Search Committee, NYU Institute for Systems Genetics/SynBioMed
2021–2022 Faculty Search Committee, NYU Institute for Systems Genetics
2016–2017 Faculty Search Committee, NYU Institute for Systems Genetics
2016–present NYUMC High Performance Computing Steering Committee
2016 Reviewer, Making Headway Foundation Pediatric Neuro-Oncology Research
2015–present Interviewer, NYU Vileck Graduate Program
2015–2024 Interviewer, NYU Medical Scientist Training Program
2015–2016 Faculty Search Committee, NYU Institute for Systems Genetics
2014–2015 Faculty Search Committee, NYU Institute for Systems Genetics
2011–2012 Seminar Committee, UW Dept. of Genome Sciences

INVITED AND SELECTED PRESENTATIONS:

2025

- Invited speaker, Solving the human cis-regulatory code Workshop, Toronto, ON (11/25)
- Invited speaker, NYU Langone Center for Human Genetics and Genomics annual retreat, New York, NY (9/25)
- Invited speaker, NYU Langone Pathology Research Day, New York, NY (9/25)
- Invited speaker, ASBMB Symposium "Evolution & Core Processes in Gene Regulation", Stowers Inst., KS (6/25)
- Invited speaker, Dark Genome Target Discovery & Development Summit, Boston, MA (6/25)
- Invited speaker, Department of Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD (4/25)

2024

- Invited speaker, NHGRI CEGS Grantee Meeting, San Diego, CA (10/24)
- Invited speaker, Company of Biologists Workshop, Building to Understand, Buxted Park, UK (7/24)
- Selected speaker, CRISPR and beyond, Wellcome Trust Genome Campus, Cambridge, UK (4/24)

2023

- Invited speaker, Epigenetics & Stem Cell Biology Laboratory, NIEHS, Durham, NC (12/23)
- Invited speaker, MRC Human Genetics Unit and Edinburgh Cancer Research/CRUK-Scotland Centre, Edinburgh, UK (11/23)
- Invited speaker, NHGRI CEGS Grantee Meeting, New York, NY (10/23)
- Keynote speaker, 5th Czech Centre for Phenogenomics conference, Prague, Czech Republic (9/23)

2022

- Selected speaker, American Society of Human Genetics, Los Angeles, CA (10/22)
- Invited speaker, NHGRI CEGS Grantee Meeting, Durham, NC (10/22)
- Selected speaker, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY (3/22)

2021

- Invited speaker, NHGRI CEGS Grantee Meeting, New York, NY (10/21)

2020

- Invited speaker, NYU Translational Progress in Research Seminar Series, New York, NY (11/20)
- Invited speaker, NHGRI CEGS Grantee Meeting, Berkeley, CA (10/20)
- Invited speaker, NYU Cancer Genome Dynamics Research Talk, New York, NY (10/20)
- Invited speaker, NYU Pathology COVID-19 Seminar Series, New York, NY (6/20)
- Invited speaker, New York COVID-19 Genomics Research Network Meeting, New York, NY (4/20)

2019

- Invited speaker, NHGRI CEGS Grantee Meeting, Boston, MA (11/19)
- Invited speaker, American Society of Human Genetics, Houston, TX (10/19)
- Selected speaker, EMBL Symposium: Systems Genetics, Heidelberg, Germany (9/19)
- Invited speaker, NYU Cancer Center Retreat, New York, NY (9/19)
- Selected speaker, CRISPR and beyond, Wellcome Trust Genome Campus, Cambridge, UK (9/19)

2018

- Invited speaker, NHGRI CEGS Grantee Meeting, Chicago, IL (11/18)
- Invited speaker, NYU Cancer Genome Dynamics Program Retreat, New York, NY (9/18)
- Invited speaker, NYU ABL Computational Analysis Forum, New York, NY (9/18)
- Invited speaker, Ewha-Jax symposium, Ewha Womans University, Seoul, South Korea (3/18)
- Invited speaker, Dept. of Biochemistry and Molecular Biology, Penn State University, Hershey, PA (1/18)
- Invited speaker, New York Human Genetics meeting, New York Genome Center, New York, NY (1/18)

2017

- Invited speaker, Horizons in Genomic Sciences, Intl. Lab for Human Genome Research, Cancún, México (9/17)
- Invited speaker, GP-write meeting, Center of Excellence for Engineering Biology, New York, NY (5/17)
- Invited speaker, Department of Biology, University of Copenhagen, Stockholm, Denmark (2/17)
- Invited speaker, Centre for Integrative Sequencing, Aarhus University, Aarhus, Denmark (2/17)

2016

- Invited speaker, Distinguished Seminar, Lady Davis Institute, McGill University, Montreal, QC (10/16)
- Invited speaker, American Society for Bone and Mineral Research Genomics Session, Atlanta, GA (9/16)
- Selected speaker, NY Meeting on Computational and Statistical Genomics, Cold Spring Harbor, NY (7/16)
- Invited speaker, Measuring and modeling quantitative sequence-function relationships, Banbury, Cold Spring, NY (7/16)
- Invited speaker, Department of Medicine Research Day, NYU School of Medicine, New York, NY (5/16)
- Invited speaker, School of Biotech./Biomolecular Sciences, Univ. New South Wales, Sydney, Australia (5/16)
- Keynote speaker, Systems Biology Workshop, La Trobe Ctr. for AgriBioscience, Melbourne, Australia (5/16)
- Selected speaker, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY (3/16)
- Selected speaker, Epigenomics 2016, Rio Mar, PR (2/16)
- Invited speaker, Plant and Animal Genome XXIV Conference, San Diego, CA (1/16)

2015

- Invited speaker, Computational Genomics Seminar, Mt. Sinai School of Medicine, New York, NY (10/15)
- Invited speaker, American Society for Bone and Mineral Research, Seattle, WA (10/15)
- Invited speaker, NYU Science After Hours, New York, NY (10/15)
- Selected speaker, Genomics of Common Disease, Wellcome Trust Genome Campus, Cambridge, UK (9/15)
- Invited speaker, Altius Institute for Biomedical Sciences retreat, Seattle, WA (7/15)
- Invited speaker, AHA ATVB/PVD Next Generation Technology Bootcamp, San Francisco, CA (5/15)
- Selected speaker, ENCODE Consortium Meeting, Cold Spring Harbor, NY (3/15)
- Selected speaker, CSHL Systems Biology: Global Regulation of Gene Expression, Rio Mar, PR (1/15)

2014

- Invited speaker, American Heart Association Annual Meeting, Chicago, IL (11/14)
- Selected speaker, American Society of Human Genetics, San Diego, CA (10/14)
- Invited speaker, Genomics of Common Disease, Potomac, MD (9/14)
- Invited speaker, Dept. of Systems Biology, Columbia University, New York, NY (6/14)
- Invited speaker, Institute for Systems Genetics, NYU School of Medicine, New York, NY (5/14)
- Invited speaker, Dept. of Genetics & Development, Columbia University, New York, NY (5/14)
- Invited speaker, Dept. of Molecular Biology & Genetics, Cornell University, Ithaca, NY (5/14)

2013

- Invited speaker, American Heart Association Annual Meeting, Dallas, TX (11/13)
- Invited speaker, Enhancer Biology in Health and Disease, Banbury Center, Cold Spring Harbor, NY (10/13)
- Invited speaker, Dept. of Genetics, Albert Einstein College of Medicine, Bronx, NY (1/13)

RESEARCH FUNDING:

ACTIVE SUPPORT:

Irma T. Hirschl/Monique Weill-Caulier Research Award (PI: Maurano MT) 2/1/2025–1/31/2030

Title: **Dissection of *Sox2* expression regulation using high-throughput synthetic regulatory genomics**

Description: *Sox2* is a key transcription factor controlling stem cells and involved in various cancers. This proposal will apply the new field of synthetic regulatory genomics to analyze the regulatory architecture of the *Sox2* locus.

R01 MH136353 (PI: Maurano MT) 12/1/2024–11/30/2028

Title: **Dissection of noncoding repeats in psychiatric genetics using synthetic regulatory genomics**

Description: This proposal develops and applies novel genomic technologies to interpret complex genomic regions underpinning psychiatric diseases. Better recognition of the functional consequences of noncoding sequence variation will provide insight into how transcriptional mis-regulation may lead to psychiatric disease in relevant cell and tissue contexts.

RM1 HG009491 (PI: Boeke JD) 06/12/2018–02/29/2028

Title: **CEGS: Center for Synthetic Regulatory Genomics**

Description: This project includes basic mechanistic work utilizing highly efficient DNA assembly to construct thousands of 100 kb gene loci varying in key candidate regulatory sequences to uncover sequence determinants specifying regulation of the gene in question, promising to dramatically improve our ability to interpret variation in non-coding regulatory elements and to decipher genome function.

Role: Co-Investigator

NSF (PI: Boeke JD) 09/01/23–08/31/27

Title: **UKRI/BBSRC-NSF/BIO Building synthetic regulatory units to understand the complexity of mammalian gene expression**

Description: This research will synthesize, deliver, and study a fully functional chromosomal unit (a TAD) that specifies a precise developmental outcome in mammalian cells, and which works independently of position of integration in the genome.

Role: Co-Investigator

Revive and Restore (PI: Boeke JD) 4/01/24–03/31/28
Title: **Winding back the clock – the genome edited re-wilded chicken**
Description: To identify genomic loci and fine-scale regions that distinguish domestic chickens from their wild and feral counterparts. These will then be used to create a genome-edited 'wild' chicken, based on a domestic origin.
Role: Co-Investigator

COMPLETED SUPPORT:

NYU Langone Health CTSI (PI: Maurano MT) 8/26/2024–12/31/2024
Title: "**Single-molecule epigenomic profiling of the schizophrenia-associated tandem repeat at *CACNA1C***"
Description Pilot project to establish feasibility of Fiber-seq to profile a tandem repeat at the *CACNA1C* schizophrenia association locus.

NSF (PI: Boeke JD) 08/01/19–07/31/24
Title: **URoL: Epigenetics 2 Reverse Engineering Human Epigenetic Machinery in Yeast**
Description: This research will reconstitute human epigenetic pathways within the "simple" eukaryote *S. cerevisiae* to provide a bottom-up approach for unraveling principles of chromatin organization and inherited gene expression.
Role: Co-Investigator

NSF (PI: Boeke JD) 08/01/19–07/31/23
Title: **RoL: PAX6 as a model for synthetic hypervariation studies**
Description This project will employ a systematic synthetic genomics-based approach "synthetic hypervariation" that allows such variations to be constructed with great precision in yeasts cells.
Role: Co-Investigator

R35 GM119703 (PI: Maurano MT) 07/22/2016–05/31/2023
Title: **Genomic organization of long-distance gene regulation**
Description: This project aims to probe the sequence determinants of long-distance interaction in mammalian genomes using computational modeling, development of novel transposon probes for regulatory domains, and genome editing of composite regulatory loci.

AMP FNIH (PI: Richards JB) (subaward) 9/3/2020–9/2/2021
Title: **Target gene approach to T2D targets**
Description The objective of this project is to provide a tool, that given a set of genetic associations and genomic landscape features, assigns a probability that a gene is causal for T2D and its complications.
Role: PI of subcontract

Colton Center for Autoimmunity Grant (PI: Abramson S) 05/01/2017–04/30/2018
Source: Colton Family Foundation
Title: **Expanding Capability for Human Cell Line Genomic Engineering for Probing Autoimmune Disease**
Role: Project Co-Lead
Description: This project will address the capability to engineer mouse and human stem cells, ready with specialized "landing pads" to accommodate large pieces of DNA, which can be subsequently differentiated into good models for autoimmune disorders such as lupus.

F31 MH094073 (PI: Maurano MT) 08/16/2012–12/15/2013
Title: **Regulatory Genomics of Human Neurodevelopment**

BIBLIOGRAPHY:

ORCID: 0000-0002-2218-8628
(* corresponding / co-corresponding author; reverse chronological)

PREPRINTS:

1. Ordoñez R, Ribeiro-Dos-Santos AM, McLoughlin C, Ellis G, Ashe HJ, Zufiaurre NB, Brosh R, Majewski M, Camellato B, Boeke JD, and **Maurano MT***. "Synthetic Genomic Dissection of Enhancer Context Sensitivity and Synergy." **bioRxiv** (2025). [Preprint]. August 13, 2025 [cited 2025 Aug 14]. Available from: doi: 10.1101/2025.08.13.669251.
2. Ribeiro-dos-Santos AM, **Maurano MT***. "Iterative improvement of deep learning models using synthetic regulatory genomics." **bioRxiv** (2025). [Preprint]. February 21, 2025 [cited 2025 Feb 22]. Available from: doi: 10.1101/2025.02.04.636130.

PUBLISHED WORK

1. Moya R, Wang X, Tsien RW*, **Maurano MT***. "Structural characterization of a polymorphic repeat at the *CACNA1C* schizophrenia locus." **PNAS**, In press (2025). Available from: doi: 10.1101/2024.03.05.303780.

2. Ordoñez R, Zhang W, Ellis G, Zhu Y, Ashe HJ, Ribeiro-dos-Santos AM, Brosh R, Huang E, Hogan MS, Boeke JD, **Maurano MT***. "Genomic context sensitizes regulatory elements to genetic disruption." **Molecular Cell** 84: 1842-1854.e7 (2024). PMID: 38759624.

3. Camellato B, Brosh R, Ashe HJ, **Maurano MT**, and Boeke JD. "Synthetic reversed sequences reveal default genomic states." **Nature** (2024), 628: 373–380 (2024) PMCID: PMC11006607.

   Commentary: **Nature** 628:271-273 (2024)

4. Xia B, Zhang W, Zhao G, Zhang X, Bai J, Brosh R, Wudzinska A, Huang E, Ashe H, Ellis G, Pour M, Zhao Y, Coelho C, Zhu Y, Miller A, Dasen JS, **Maurano MT**, Kim SY, Boeke JD, and Yanai I. "On the Genetic Basis of Tail-Loss Evolution in Humans and Apes." **Nature** 626: 1042–1048 (2024) doi: 10.1038/s41586-024-07095-8.

   Press: Zimmer C. "How Humans Lost Their Tails". **New York Times**, 9/22/2021.

5. Zhang W, Golynker I, Brosh R, Fajardo A, Zhu Y, Wudzinska AM, Ordoñez R, Ribeiro-Dos-Santos AM, Carrau L, Damani-Yokota P, Yeung ST, Khairallah C, Vela Gartner A, Chalhoub N, Huang E, Ashe HJ, Khanna KM, **Maurano MT**, Kim SY, tenOever BR, and Boeke JD. "Mouse Genome Rewriting and Tailoring of Three Important Disease Loci." **Nature** 623: 423–431 (2023). PMC10632133.

   Commentary: Nature Reviews Genetics doi: https://doi.org/10.1038/s41576-023-00681-y (2023)

   Commentary: Nature Genetics 55:2018 (2023)

6. Brosh R, Coelho C, Ribeiro-dos-Santos AM, Ellis G, Hogan MS, Ashe HJ, Somogyi N, Ordoñez R, Luther R, Huang E, Boeke JD, **Maurano MT***. "Synthetic regulatory genomics uncovers enhancer context dependence at the *Sox2* locus." **Molecular Cell** 83:1140-1152.e7 (2023). PMC10081970.

7. Costanzo MC, von Grotthuss M, Massung J, Jang D, Caulkins L, Koesterer R, Gilbert C, Welch RP, Kudtarkar P, Hoang Q, Boughton AP, Singh P, Sun Y, Duby M, Moriondo A, Nguyen T, Smadbeck P, Alexander BR, Brandes M, Carmichael M, Dornbos P, Green T, Huellas-Bruskiewicz KC, Ji Y, Kluge A, McMahon AC, Mercader JM, Ruebenacker O, Sengupta S, Spalding D, Taliun D, AMP-T2D Consortium, Smith P, Thomas MK, Akolkar B, Brosnan MJ, Cherkas A, Chu AY, Fauman EB, Fox CS, Kamphaus TN, Miller MR, Nguyen L, Parsa A, Reilly DF, Ruetten H, Wholley D, Zaghloul NA, Abecasis GR, Altshuler D, Keane TM, McCarthy MI, Gaulton KJ, Florez JC, Boehnke M, Burtt NP, and Flannick J. "The Type 2 Diabetes Knowledge Portal: An Open Access Genetic Resource Dedicated to Type 2 Diabetes and Related Traits." **Cell Metabolism** 35: 695-710.e6 (2023) PMCID: PMC10231654.

8. Berastegui N, Ainciburu M, Romero JP, Garcia-Olloqui P, Alfonso-Pierola A, Philippe C, Vilas-Zornoza A, San Martin-Uriz P, Ruiz-Hernández R, Abarrategi A, Ordoñez R, Alignani D, Sarvide S, Castro-Labrador L, Lamo-Espinosa JM, San-Julian M, Jimenez T, López-Cadenas F, Muntion S, Sanchez-Guijo F, Molero A, Montoro MJ, Tazón B, Serrano G, Diaz-Mazkiaran A, Hernaez M, Huerga S, Bewicke-Copley F, Rio-Machin A, **Maurano MT**, Díez-Campelo M, Valcarcel D, Rouault-Pierre K, Lara-Astiaso D, Ezponda T, and Prosper F. "The Transcription

Factor DDIT3 Is a Potential Driver of Dyserythropoiesis in Myelodysplastic Syndromes." **Nature Communications** 13: 7619 (2022). PMC9734135.

9. Pinglay S, Bulajić M, Rahe DP, Huang E, Brosh R, German S, Cadley JA, Rieber L, Easo N, Mahony S, **Maurano MT**, Holt LJ, Mazzoni EO, Boeke JD. "Synthetic genomic reconstitution reveals principles of mammalian *Hox* cluster regulation". **Science**, 377: eabk2820 (2022). PMC9648154.

10. Zhang W, Brosh R, McCulloch LH, Zhu Y, Ashe H, Ellis G, Camellato BR, Kim SY, **Maurano MT**, and Boeke JD. "A Conditional Counterselectable Piga Knockout in Mouse Embryonic Stem Cells for Advanced Genome Writing Applications." **IScience** 25: 104438 (2022).

11. Ribeiro-dos-Santos AM, Hogan MS, Luther RD, **Maurano MT***. "Genomic context sensitivity of insulator function." **Genome Research** 32: 425–436 (2022). PMC8896466.

12. Forgetta V, Jiang L, Vulpescu NA, Hogan MS, Chen S, Morris JA, Grinek S, Benner C, McCarthy MI, Fauman E, Greenwood CM*, **Maurano MT***, and Richards JB*. "An Effector Index to Predict Causal Genes at GWAS Loci." **Human Genetics** (2022). PMID35147782.

13. Halvorsen M, Gould L, Wang X, Grant G, Moya R, Rabin R, Ackerman MJ, Tester DJ, Lin PT, Pappas JG, **Maurano MT**, Goldstein DB, Tsien RW, Devinsky O. "De novo mutations in childhood cases of sudden unexplained death that disrupt intracellular Ca2+ regulation". **PNAS** 118:e2115140118 (2021). PMC8719874.

    Press:
    Splete H. "Gene Mutations May Drive Sudden Unexplained Deaths in Children". **Medscape**. 1/4/2022
    Doctrow B. "Genetics of sudden unexplained death in children". **NIH Research Matters**. 1/11/2022.
    Servick K. "Geneticists find clues to sudden unexplained child deaths". **Science**, 2/10/2022.

14. Dellicour S, L S Hong, Vrancken B, Chaillon A, Gill MS, **Maurano MT**, Ramaswami S, Zappile P, Marier C, Harkins GW, Baele G, Duerr R, Heguy A. "Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City". **PLoS Pathogens** 17: e1009571 (2021). PMC8136714.

15. Halow J, Byron R, Hogan MS, Ordoñez R, Groudine M, Bender MA, and Stamatoyannopoulos JA*, **Maurano MT***. "Tissue context determines the penetrance of regulatory DNA variation." **Nat. Communications** 12:2850 (2021). PMC8121920.

16. Brosh R, Laurent JM, Ordoñez R, Huang E, Hogan MS, Hitchcock AM, Mitchell LA, Pinglay S, Cadley JA, Luther RD, Truong DM, Boeke JD, **Maurano MT**. "A versatile platform for locus-scale genome rewriting and verification." **PNAS** 118:e2023952118 (2021). PMC7958457.

    Commentary: CRISPR J 4:163-166 (2021).

17. Mitchell LA, McCulloch LH, Pinglay S, Berger H, Bosco N, Brosh R, Bulajic M, Huang E, Hogan MS, Martin JA, Mazzoni EO, Davoli T, **Maurano MT**, and Boeke JD. "De novo assembly and delivery to mouse cells of a 101 kb functional human gene." **Genetics** 218: iyab038 (2021). PMC Journal – In Progress.

18. Elizondo V, Harkins GW, Mabvakure B, Smidt S, Zappile P, Marier C, **Maurano MT**, Perez V, Mazza N, Beloso C, Ifran S, Fernandez M, Santini A, Perez V, Estevez V, Nin M, Manrique G, Perez L, Ross F, Boschi S, Zubillaga MN, Balleste R, Dellicour S, Heguy A, Duerr R. "SARS-CoV-2 genomic characterization and clinical manifestation of the COVID-19 outbreak in Uruguay." **Emerging Microbes and Infections** 11:1-52 (2020). PMC7832039.

19. **Maurano MT** *, Ramaswami S, Westby G, Zappile P, Dimartino D, Shen G, Feng X, Ribeiro-Dos-Santos AM, Vulpescu NA, Black M, Hogan M, Marier C, Meyn P, Zhang Y, Cadley J, Ordonez R, Luther R, Huang E, Guzman E, Serrano A, Belovarac B, Gindin T, Lytle A, Pinnell J, Vougiouklakis T, Boytard L, Chen J, Lin LH, Rapkiewicz A, Raabe V, Samanovic-Golden MI, Jour G, Osman I, Aguero-Rosenfeld M, Mulligan MJ, Cotzia P, Snuderl M*, and Heguy A*. "Sequencing Identifies Multiple Early Introductions of SARS-CoV-2 to the New York City Region." **Genome Research** 30:1781-1788 (2020). PMC7706732.

    Cover article; Press:
    Zimmer C. "Most New York Coronavirus Cases Came From Europe, Genomes Show". **New York Times**, 4/8/2020.
    Watkins D., Holder J, Glanz J, Cai W, Carey B, White J. "How the Virus Won". **New York Times**, 6/24/2020.

Zimmer C. "One Meeting in Boston Seeded Tens of Thousands of Infections, Study Finds". **New York Times**, 8/26/2020.

20. Laurent JM, Fu X, German S, **Maurano MT**, Zhang K, and Boeke JD. "Big DNA as a Tool to Dissect an Age-Related Macular Degeneration-Associated Haplotype." **Precision Clinical Medicine** 2: 1–7 (2019).

21. Morris JA, Kemp JP, Youlten SE, Laurent L, Logan JG, Chai RC, Vulpescu NA, Forgetta V, Kleinman A, Mohanty ST, Sergio CM, Quinn J, Nguyen-Yamamoto L, Luco A-L, Vijay J, Simon M-M, Pramatarova A, Medina Gómez C, Trajanoska K, Ghirardello EJ, Butterfield NC, Curry KF, Leitch VD, Sparkes PC, Adoum A-T, Mannan NS, Komla-Ebri DSK, Pollard AS, Dewhurst HF, Hassall TAD, Beltejar M-JG, 23andMe Research Team, Adams DJ, Vaillancourt SM, Kaptoge S, Baldock P, Cooper C, Reeve J, Ntzani EE, Evangelou E, Ohlsson C, Karasik D, Rivadeneira F, Kiel DP, Tobias JH, Gregson CL, Harvey NC, Grundberg E, Goltzman D, Adams DJ, Lelliott CJ, Hinds DA, Ackert Bicknell CL, Hsu YH, **Maurano MT**, Croucher PI, Williams GR, Bassett JHD, Evans DM, and Richards JB. "An Atlas of Genetic Influences on Osteoporosis in Humans and Mice." **Nature Genetics** 51: 258–266 (2019). PMC6358485.

22. Wang X, Zhou T, Wunderlich Z, **Maurano MT**, DePace AH, Nuzhdin SV, and Rohs R. "Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection." **Molecular Biology and Evolution** 35: 1958–1967 (2018). PMC6063282.

23. eGTEx Project. "Enhancing GTEx by Bridging the Gaps Between Genotype, Gene Expression, and Disease." **Nature Genetics** 49: 1664–1670 (2017).

24. GTEx Consortium. "Genetic Effects on Gene Expression Across Human Tissues." **Nature** 550: 204–213 (2017).

25. Kemp JP, Morris JA, Medina Gómez C, Forgetta V, Warrington NM, Youlten SE, Zheng J, Gregson CL, Grundberg E, Trajanoska K, Logan JG, Pollard AS, Sparkes PC, Ghirardello EJ, Allen R, Leitch VD, Butterfield NC, Komla-Ebri D, Adoum A-T, Curry KF, White JK, Kussy F, Greenlaw KM, Xu C, Harvey NC, Cooper C, Adams DJ, Greenwood CMT, **Maurano MT**, Kaptoge S, Rivadeneira F, Tobias JH, Croucher PI, Ackert Bicknell CL, Bassett JHD, Williams GR, Richards JB, and Evans DM. "Identification of 153 New Loci Associated with Heel Bone Mineral Density and Functional Involvement of GPC6 in Osteoporosis." **Nature Genetics** 49: 1468–1475 (2017).

26. Medina Gómez C, Kemp JP, Dimou NL, Kreiner E, Chesi A, Zemel BS, Bønnelykke K, Boer CG, Ahluwalia TS, Bisgaard H, Evangelou E, Heppe DHM, Bonewald LF, Gorski JP, Ghanbari M, Demissie S, Duque G, **Maurano MT**, Kiel DP, Hsu YH, C J van der Eerden B, Ackert-Bicknell C, Reppe S, Gautvik KM, Raastad T, Karasik D, van de Peppel J, Jaddoe VWV, Uitterlinden AG, Tobias JH, Grant SFA, Bagos PG, Evans DM, and Rivadeneira F. "Bivariate Genome-Wide Association Meta-Analysis of Pediatric Musculoskeletal Traits Reveals Pleiotropic Effects at the SREBF1/TOM1L2 Locus." **Nature Communications** 8: 121 (2017).

27. Chen L, Ge B, Casale FP, Vasquez L, Kwan T, Garrido-Martín D, Watt S, Yan Y, Kundu K, Ecker S, Datta A, Richardson D, Burden F, Mead D, Mann AL, Fernandez JM, Rowlston S, Wilder SP, Farrow S, Shao X, Lambourne JJ, Redensek A, Albers CA, Amstislavskiy V, Ashford S, Berentsen K, Bomba L, Bourque G, Bujold D, Busche S, Caron M, Chen SH, Cheung W, Delaneau O, Dermitzakis ET, Elding H, Colgiu I, Bagger FO, Flicek P, Habibi E, Iotchkova V, Janssen-Megens E, Kim B, Lehrach H, Lowy E, Mandoli A, Matarese F, **Maurano MT**, Morris JA, Pancaldi V, Pourfarzad F, Rehnstrom K, Rendon A, Risch T, Sharifi N, Simon M-M, Sultan M, Valencia A, Walter K, Wang S-Y, Frontini M, Antonarakis SE, Clarke L, Yaspo M-L, Beck S, Guigó R, Rico D, Martens JHA, Ouwehand WH, Kuijpers TW, Paul DS, Stunnenberg HG, Stegle O, Downes K, Pastinen T, and Soranzo N. "Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells." **Cell** 167: 1398–1414.e24 (2016).

28. Iotchkova V, Huang J, Morris JA, Jain D, Barbieri C, Walter K, Min JL, Chen L, Astle W, Cocca M, Deelen P, Elding H, Farmaki A-E, Franklin CS, Frånberg M, Gaunt TR, Hofman A, Jiang T, Kleber ME, Lachance G, Luan J, Malerba G, Matchan A, Mead D, Memari Y, Ntalla I, Panoutsopoulou K, Pazoki R, Perry JRB, Rivadeneira F, Sabater-Lleal M, Sennblad B, Shin S-Y, Southam L, Traglia M, van Dijk F, van Leeuwen EM, Zaza G, Zhang W, UK10K Consortium, Amin N, Butterworth A, Chambers JC, Dedoussis G, Dehghan A, Franco OH, Franke L, Frontini M, Gambaro G, Gasparini P, Hamsten A, Issacs A, Kooner JS, Kooperberg C, Langenberg C, Marz W, Scott RA, Swertz MA, Toniolo D, Uitterlinden AG, van Duijn CM, Watkins H, Zeggini E, **Maurano MT**, Timpson NJ, Reiner AP, Auer PL, and Soranzo N. "Discovery and Refinement of Genetic Loci Associated with Cardiometabolic Risk Using Dense Imputation Maps." **Nature Genetics** 48: 1303–1312 (2016).

29. van der Harst P, van Setten J, Verweij N, Vogler G, Franke L, **Maurano MT**, Wang X, Mateo Leach I, [145 authors], Chambers JC, Jamshidi Y, Visel A, Christoffels VM, Isaacs A, Samani NJ, and de Bakker PIW. "52 Genetic Loci Influencing Myocardial Mass." **Journal of the American College of Cardiology** 68: 1435–1448 (2016). PMC5478167

    Commentary: **Journal of the American College of Cardiology** 68: 1449-1451 (2016).

30. Boeke JD, Church G, Hessel A, Kelley NJ, Arkin A, Cai Y, Carlson R, Chakravarti A, Cornish VW, Holt L, Isaacs FJ, Kuiken T, Lajoie M, Lessor T, Lunshof J, **Maurano MT**, Mitchell LA, Rine J, Rosser S, Sanjana NE, Silver PA, Valle D, Wang H, Way JC, and Yang L. "The Genome Project-Write." **Science** (2016).

31. **Maurano MT** *, Haugen E, Sandstrom R, Vierstra J, Kaul R, and Stamatoyannopoulos JA *. "Large-scale identification of functional variants impacting human transcription factor occupancy in vivo." **Nat. Genetics** 47: 1393–1401 (2015). PMC4666772.

    Research highlight at **Nature Reviews Genetics** 16: 688 (2015).

32. **Maurano MT** *, Wang H, John S, Shafer A, Canfield T, Lee K, and Stamatoyannopoulos JA *. "Role of DNA Methylation in Modulating Transcription Factor Occupancy." **Cell Reports** 12: 1184–1195 (2015). PMID:26257180

33. Zheng HF, Forgetta V, Hsu YH, Estrada K, Rosello Diez A, Leo PJ, Dahia CL, Park Min KH, Tobias JH, Kooperberg C, [124 authors], **Maurano MT**, [13 authors], Jackson RD, Rowe DW, Loomis CA, Evans DM, Ackert Bicknell CL, Joyner AL, Duncan EL, Kiel DP, Rivadeneira F, and Richards JB. "Whole-Genome Sequencing Identifies EN1 as a Determinant of Bone Density and Fracture." **Nature** 526: 112–117 (2015).

34. **Maurano MT**, and Stamatoyannopoulos JA. "Taking Stock of Regulatory Variation." **Cell Systems** 1: 18–21 (2015).

35. Liu M, **Maurano MT**, Wang H, Song CZ, Navas PA, Emery DW, Stamatoyannopoulos JA and Stamatoyannopoulos G. "Genomic discovery of potent chromatin insulators for human gene therapy." **Nature Biotechnology** 33: 198-203 (2015). PMID:25580597

    Research highlight at **Nature Reviews Genetics** 16: 130-131 (2015).

36. **Maurano MT**, Humbert R, Rynes E, Thurman RE, Haugen E, Wang H, Reynolds AP, Sandstrom R, Qu H, Brody J, Shafer A, Neri F, Lee K, Kutyavin T, Stehling-Sun S, Johnson AK, Canfield TK, Giste E, Diegel M, Bates D, Hansen RS, Neph S, Sabo PJ, Heimfeld S, Raubitschek A, Ziegler S, Cotsapas C, Sotoodehnia N, Glass I, Sunyaev SR, Kaul R, and Stamatoyannopoulos JA. "Systematic Localization of Common Disease-Associated Variation in Regulatory DNA." **Science** 337: 1190–1195 (2012). PMC3771521.

    Cover article and **Perspective** at **Science**. 2012;337(6099):1179-80.

    Research highlight at **Nature Genetics** 2012;44(10):1079.

37. **Maurano MT**, Wang H, Kutyavin T, and Stamatoyannopoulos JA. "Widespread Site-Dependent Buffering of Human Regulatory Polymorphism." **PLoS Genetics** 8: e1002599 (2012). PMC3310774.

    Commentary: **Nature Genetics** 2012;44(5):481; **Nature Reviews Genetics** 2012;13(5):297.

38. Wang H, **Maurano MT**, Qu H, Varley KE, Gertz J, Pauli F, Lee K, Canfield T, Weaver M, Sandstrom R, Thurman RE, Kaul R, Myers RM, and Stamatoyannopoulos JA. "Widespread Plasticity in CTCF Occupancy Linked to DNA Methylation." **Genome Research** 22: 1680–1688 (2012). PMC3431485

39. Vernot B, Stergachis AB, **Maurano MT**, Vierstra J, Neph S, Thurman RE, Stamatoyannopoulos JA, and Akey JM. "Personal and Population Genomics of Human Regulatory Variation." **Genome Research** 22: 1689–1697 (2012).

40. Thurman RE, Rynes E, Humbert R, Vierstra J, **Maurano MT**, Haugen E, Sheffield NC, Stergachis AB, Wang H, Vernot B, Garg K, John S, Sandstrom R, Bates D, Boatman L, Canfield TK, Diegel M, Dunn D, Ebersol AK, Frum T, Giste E, Johnson AK, Johnson EM, Kutyavin T, Lajoie B, Lee B-K, Lee K, London D, Lotakis D, Neph S, Neri F, Nguyen ED, Qu H, Reynolds AP, Roach V, Safi A, Sanchez ME, Sanyal A, Shafer A, Simon JM, Song L, Vong S, Weaver M, Yan Y, Zhang Z, Zhang Z, Lenhard B, Tewari M, Dorschner MO, Hansen RS, Navas PA, Stamatoyannopoulos G, Iyer VR, Lieb JD, Sunyaev SR, Akey JM, Sabo PJ, Kaul R, Furey TS, Dekker J, Crawford GE, and Stamatoyannopoulos JA. "The Accessible Chromatin Landscape of the Human Genome." **Nature** 489: 75–82 (2012). PMC3721348

41. Neph S, Vierstra J, Stergachis AB, Reynolds AP, Haugen E, Vernot B, Thurman RE, John S, Sandstrom R, Johnson AK, **Maurano MT**, Humbert R, Rynes E, Wang H, Vong S, Lee K, Bates D, Diegel M, Roach V, Dunn D, Neri J, Schafer A, Hansen RS, Kutyavin T, Giste E, Weaver M, Canfield T, Sabo P, Zhang M, Balasundaram G, Byron R, MacCoss MJ, Akey JM, Bender MA, Groudine M, Kaul R, and Stamatoyannopoulos JA. "An Expansive Human Regulatory Lexicon Encoded in Transcription Factor Footprints." **Nature** 489: 83–90 (2012). PMC3736582

42. ENCODE Project Consortium. "An Integrated Encyclopedia of DNA Elements in the Human Genome." **Nature** 489: 57–74 (2012).

43. Neph S, Kuehn MS, Reynolds AP, Haugen E, Thurman RE, Johnson AK, Rynes E, **Maurano MT**, Vierstra J, Thomas S, Sandstrom R, Humbert R, and Stamatoyannopoulos JA. "BEDOPS: High-Performance Genomic Feature Operations." **Bioinformatics** 28: 1919–1920 (2012). PMC3389768.

PATENTS:

1. Brosh R, Laurent J, **Maurano MT**, Boeke JD. Big-IN: a versatile platform for locus-scale genome rewriting and verification (PCT/US21/54988) *pending*. Priority date 10/14/2020, Filed: 10/24/2021.

Last updated: 9/11/2025