CURRICULUM VITAE

Matthew Thomas Maurano

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Citizenship: U.S.A.

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. (Honors)	Computer Science, 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 Langone Medical Center, New York, NY.

OTHER POSITIONS HELD:

2019-	Member, New York University Center for Human Genetics and Genomics
2017-	Member, New York University Perlmutter Cancer Center
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 at Rosetta (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 Advisor: Dr. Steven Brenner. Topic: *Homology of NUDIX proteins in D. Radiodurans*
2002	Intern, AOL/Netscape

HONORS AND AWARDS:

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-)

TEACHING EXPERIENCE:

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 and 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:

POSTDOCTORAL TRAINEES:

10/2019-present	Raquel Ordoñez Ciriza, Ph.D.	Enhancer selectivity at the *Igf2/H19* imprinted locus
9/2019-present	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:

7/2019-present	Raquel Moya	Role of calcium channel CACNA1C in psychiatric disease

7/2017-6/2018	Brandon Mannion	Insulator function and long-distance regulatory interaction

GRADUATE THESIS COMMITTEES:

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:

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

OTHER MENTORSHIP OF GRADUATE STUDENTS:

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:

6/2019-8/2019	Nora Gilligan	NYU Computer Science
6/2018-8/2018	James Schull	Stanford Computer Science
6/2017-8/2017	Aidan Reilly	NYU Summer Undergraduate Research Program
6/2017-8/2017	Maia Stoicovici	NYU Tandon Chemical and Biomolecular Engineering
6/2017-8/2017	Nick Vulpescu	NYU Biology

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
Science

SPECIAL INTERNATIONAL RESPONSIBILITIES:

2020	External Reviewer, Mardsen Fund
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:

2016-	Member, GTEx Consortium
2016-	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:

2021-22	Faculty Search Committee, NYU Institute for Systems Genetics
2016-17	Faculty Search Committee, NYU Institute for Systems Genetics
2016-	NYUMC High Performance Computing Steering Committee
2016	Reviewer, Making Headway Foundation Pediatric Neuro-Oncology Research
2015-present	Interviewer, NYU Sackler Graduate Program
2015-present	Interviewer, NYU Medical Scientist Training Program
2015-16	Faculty Search Committee, NYU Institute for Systems Genetics
2014-15	Faculty Search Committee, NYU Institute for Systems Genetics
2011-12	Seminar Committee, UW Dept. of Genome Sciences

INVITED AND SELECTED PRESENTATIONS:

2022

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

2020

- Invited speaker, NYU Translational Progress in Research Seminar Series, New York, NY (11/20)
- 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, 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, 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)
- 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:

R35 GM119703 (PI: Maurano MT)	07/22/2016 - 05/31/2022
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.
RM1 HG009491 A1 (PI: Boeke JD)	06/12/2018 - 03/31/2023
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) 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

NSF (PI: Boeke JD) 08/01/19-07/31/23
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

COMPLETED SUPPORT:

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) 2012-13
Title: **Regulatory Genomics of Human Neurodevelopment**

BIBLIOGRAPHY:

ORCID: 0000-0002-2218-8628

(* corresponding / co-corresponding author; reverse chronological)

PREPRINTS:

1. 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." **bioRxiv** (2022) doi: 10.1101/2022.06.20.495832.
2. Camellato B, Brosh R, Maurano MT, and Boeke JD. "Genomic Analysis of a Synthetic Reversed Sequence Reveals Default Chromatin States in Yeast and Mammalian Cells.". **bioRxiv**, (2022). doi: 10.1101/2022.06.22.496726.

3. Zhang W, Golynker I, Brosh R, Wudzinska AM, Zhu Y, Carrau L, Damani-Yokota P, Khairallah C, Chalhoub N, Huang E, Ashe H, Khanna KM, Maurano MT, Kim SY, tenOever BR, and Boeke JD. "Mouse Genomic Rewriting and Tailoring: Synthetic Trp53 and Humanized ACE2." **bioRxiv** (2022). doi: 10.1101/2022.06.22.495814v1.

4. Xia B, Zhang W, Wudzinska A, Huang E, Brosh R, Pour M, Miller A, Dasen JS, **Maurano MT**, Kim SY, Boeke JD, Yanai I. "The genetic basis of tail-loss evolution in humans and apes." **bioRxiv** (2021). doi: 10.1101/2021.09.14.460388.

5. Berastegui N, Ainciburu M, Romero JP, Alfonso-Pierola A, Philippe C, Vilas-Zornoza A, San Martin P, Ordoñez R, Alignani D, Sarvide S, Castro L, Lamo-Espinosa JM, San-Julian M, Jimenez T, López F, Muntion S, Sanchez-Guijo F, Molero A, Montoro J, Tazón B, Serrano G, Diaz-Mazkiaran A, Hernaez M, Huerga S, Copley F, Rio-Machin A, **Maurano MT**, Díez-Campelo M, Valcarcel D, Rouault-Pierre K, Lara-Astiaso D, Ezponda T, Prosper F. "Transcriptional regulation of HSCs in Aging and MDS reveals DDIT3 as a Potential Driver of Transformation." **bioRxiv** (2021). doi: 10.1101/2021.09.08.459384.

PUBLISHED WORK

1. 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).

2. 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).

3. Ribeiro-dos-Santos AM, Hogan MS, Luther RD, **Maurano MT***. "Genomic context sensitivity of insulator function." **Genome Research** gr.276449.121 (2022).

4. 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).

5. 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).

6. 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.

7. 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.

8. 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).

9. 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.

10. 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.

11. **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

12. 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).

13. 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.

14. 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.

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

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

17. 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).

18. 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).

19. 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).

20. 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).
21. 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).
22. 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).
23. **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.

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