STEPHEN B. MONTGOMERY

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EDUCATION

Doctor of Philosophy, Genetics Sep/2002 – Oct/2006
University of British Columbia, Vancouver, Canada

Bachelor of Applied Science, Engineering Physics Sep/1997 – Apr/2002
Electrical Engineering Option
University of British Columbia, Vancouver, Canada

PROFESSIONAL EXPERIENCE

Assistant Professor
Stanford University School of Medicine, Stanford, California, USA Jul/2011 – *present*
Department of Pathology
Department of Genetics
Department of Computer Science, by courtesy
Director of Genome Informatics, Department of Pathology

Postdoctoral Researcher Nov/2009 – Jun/2011
University of Geneva, Geneva, Switzerland
Department of Genetic Medicine and Development
Prof. Emmanouil T. Dermitzakis Laboratory

Postdoctoral Researcher Nov/2006 – Oct/2009
Wellcome Trust Sanger Institute, Cambridge, United Kingdom
Human Genetics programme
Prof. Emmanouil T. Dermitzakis Laboratory

Graduate Student Sep/2002 – Oct/2006
Canada's Michael Smith Genome Sciences Centre, Vancouver, Canada
Bioinformatics group
Prof. Steven J.M. Jones Laboratory

Instructor Sep/2002 – Oct/2006
Canadian Bioinformatics Workshops
Bioinformatics, Genomics and Developing the Tools

PREPRINT PUBLICATIONS*

***Underlined highlights myself or people in my laboratory.**

1. Gottlieb, A., Daneshjou, R., DeGorter, M., **Montgomery, S.B.**, Altman, R. (2017) Population-specific imputation of gene expression improves prediction of pharmacogenomic traits for African Americans**,** bioRxiv link, Bioinformatics, *submitted*

PEER-REVIEWED PUBLICATIONS*

***Underlined highlights myself or people in my laboratory.**

1. Li, X. [1], Kim, Y. [1], Tsang, E.K. [1], Davis, J.R. [1], Damanai, F.N., Chiang, C., Hess, G.T., Zappala, Z., Strober, B.J., Scott, A.J., Li, A., Ganna, A., Bassik, M.C., Merker, J.D., GTEx Consortium, Hall, I.M., Battle, A. [*], **Montgomery, S.B.** [*] (2016) The impact of rare variation on gene expression across tissues [1]joint first authors [*]joint corresponding authors, bioRxiv link, Nature, *in press*, *will appear Oct 12th, 2017*
2. The GTEx Consortium (2017) Genetic effects on gene expression across 44 human tissues. bioRxiv link, Nature, *in press, will appear Oct 12th, 2017* (**Montgomery,S.B.**, joint corresponding author)
3. The eGTEX Project (2017) Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics, *in press, will appear Oct 12th, 2017* (**Montgomery,S.B**., joint corresponding author)
4. Ioannidis, N.M., Davis, J.R., DeGorter, M.K., Larson, N.B., McDonnell, S.K., French, A.J., Battle, A., Hastie, T.J., Thibodeau, S.N., **Montgomery, S.B.**, Bustamante, C.D., Sieh, W., Whittemore, A.S. (2017) FIRE : Functional inference of genetic variants that regulate gene expression, Bioinformatics, Aug 24th, 2017
5. Merker, J.D., Wenger, A.M., Sneddon, T., Grove, M., Zappala, Z., Frésard, L., Waggot, D., Utiramerur, S., Hou, Y., Smith, K.S., **Montgomery, S.B.**, Wheeler, M., Buchan, J.G., Lambert, C.C., Eng, K.S., Hickey, L., Korlach, J., Ford, J., Ashley, E.A., (2017) Long-read genome sequencing identifies causal structural variation in a Mendelian disease. Genetics in Medicine, Jun 2017
6. Knowles, D.A., Davis, J.R., Edgington, H., Raj, A., Favé, M-J., Zhu, X., Potash, J.B., Weissman, M.M., Shi, J., Levinson, D.F., Awadalla, P., Mostafavi, S., **Montgomery, S.B.**[*], Battle, A[*] (2017) Allele-specific expression

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7. Steri, M., Orrù, V., Idda, M.L., Pitzalis, M., Pala, M., Zara, I., Faà, V., Floris, M., Deiana, M., Asunis, I., Sidore, C., Porcu, E., Mulas, A., Marongiu, M., Serra, V., Lobina, M., Piras, M.G., Marongiu, M., Sole, G., Busonero, F., Maschio, A., Cusano, R., Cuccuru, G., Deidda, F., Poddie, F., Farina, G., Dei, M., Lai, S., Virdis, F. Olla, S., Satta, M.A., Pani, M, Cocco, E., Frau, J., Coghe, G., Lorefice, L., Fenu, G., Ferrigno, P., Ban, M., Barizzone, N., Leone, M., Guerini, F.R., Piga, M., Firinu, D., Kockum, I., Bomfim, I.L., Olsson, T., Alfredsson, L., Suarez, A., Carreira, P., Castillo-Palma, M.J., Marcus, J.H., Congia, M., Angius, A., Melis, M., Gonzalez, A., Riquelme, M.E.A., Da Silva, B.M., Marchini, M., Danieli, M.G., Del Giacco, S., Mathieu, A., Pani, A., **Montgomery, S.B.**, Rosati, G., Hillert, J., Sawcer, S., D´Alfonso, S., Todd, J.A., Novembre, J., Abecasis, G.R., Whalen, M.B., Marrosu, M.G., Meloni, A., Sanna, S., Gorospe, M., Schlessinger, D., Fiorillo, E., Zoledziewska, M., Cucca, F. (2017) Evolutionarily selected overexpression of the cytokine BAFF raises autoimmunity risk, [1]joint first authors NEJM, Apr 27;376(17):1615-1626.

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9. Chiang, C., Scott, A.J., Davis, J.R., Tsang, E.K., Li, X., Kim, Y., Hadzic, T., Damani, F., Ganel, L., GTEx Consortium, **Montgomery, S.B.**, Battle, A., Conrad, D.F., Hall, I.M. (2017) The impact of structural variation on human gene expression, Nature Genetics, May;49(5):692-699.

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PEER-REVIEWED REVIEWS*

***Underlined highlights myself or people in my laboratory.**

1. Ritchie, M.D.[*], Davis, J.R., Aschard, H., Battle, A., Conti, D., Mengmeng, D., Eskin, E., Fallin, M.D., Hsu, L., Kraft, P., Moore, J.H., Pierce, B.L., Bien, S., Thomas, D.C., Wei, P., **Montgomery, S.B.**[*] (2017) Incorporation of Biological Knowledge into the Study of Gene-Environment Interactions, [*]joint corresponding authors, AJE, Volume 186, Issue 7, 1 October 2017, Pages 771–777

2. McAllister, K., Mechanic, L.E., Amos, C., Aschard, H., Blair, I., Chatterjee, N., Conti, D., Gauderman, W.J., Hsu, L., Hutter, C.M., Jankowska, M., Kerr, J., Kraft, P., **Montgomery, S.B.**, Mukherjee, B., Papanicolaou, G.J., Patel, C.J., Ritchie, M.D., Ritz, B.R., Thomas, D.C., Wei, P., Witte, J.S. (2017) Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases, AJE, Volume 186, Issue 7, 1 October 2017, Pages 753–761

3. Zappala, Z., **Montgomery, S.B.** (2016) Non-Coding Loss-of-Function Variation in Human Genomes, Human Heredity 2016;81(2):78-87

4. Kukurba, K.R., **Montgomery, S.B.** (2015) RNA-Sequencing and Analysis, Cold Spring Harb Protoc., Apr 13;2015(11):951-69

5. Battle, A., **Montgomery, S.B.**, (2014) Determining causality and consequence of expression quantitative trait loci, Human Genetics, 2014, Jun ;133(6) :727-35

6. Miller, C.L., Assimes, T.L., **Montgomery, S.B.,** Quertermous, T., Investigation of causal genetic mechanisms for coronary heart disease genome-wide associations, Curr Atheroscler Rep, 2014;16:406

7. Li, X., **Montgomery, S.B.**, Detection and impact of rare regulatory variants in human disease, Frontiers in Statistical Genetics and Methodology, May 31 ;4 :67
8. **Montgomery, S.B.,** Dermitzakis, E.T., From Expression QTLs to Personalized Transcriptomics. Nature Reviews Genetics, 2011, Apr ; 12(4) :277-82
9. **Montgomery, S.B.,** Dermitzakis, E.T.,The resolution of the genetics of gene expression. Human Molecular Genetics, 2009, R(2):R211-5

NON-PEER-REVIEWED PUBLICATIONS*

***Underlined highlights myself or people in my laboratory.**

1. Karczewski, K.J., **Montgomery, S.B.**, The performance of genomic medicine Genome Biology, 2013, 14:316
2. Morin, R. **Montgomery, S.B.**, Cancer Transcriptome Sequencing and Analysis (Chapter 5), Cancer Genomics: From Bench to Personalized Medicine, 2013
3. Ning, Z., **Montgomery, S.B.,** Out of the sequencer and into the wiki as we face new challenges in genome informatics, Genome Biology, 2010, 11:308
4. **Montgomery, S.B.,** Kasaian, K., Jones, S.J.M., Griffith, O.L. Annotating the Regulatory Genome (Chapter 20). Computational Biology of Transcription Factor Binding. Methods Mol Biol. 2010;674:313-49.
5. **Montgomery S.B.** Current computational methods for prioritizing candidate regulatory polymorphisms. Methods in Molecular Medicine. Humana Press. 2009, 569 :89-114

TRAINEES

Konrad Karczewski, Ph.D. student, BMI, now a postdoc at Broad Institute	2012-2013
Olga Sazonova, Ph.D., Postdoctoral Researcher, now a scientist at 23andme	2013-2014
Eric Wu, SIMR/high-school student, now a grad student at Stanford	2012-2013
Tony Jiang, SIMR/high-school student, now an undergrad at Yale	2013-2014
Hoon Cho, Undergraduate Student, now a grad student at MIT	2012-2013
Mauro Pala, Ph.D., Visiting Graduate Student, now a scientist CNRS (Sardinia)	2012-2013
Tracy Nance, Ph.D., Postdoctoral Researcher, now at Epinomics	2012-2014
Kim Kukurba, Ph.D. student, Genetics, now at Raytheon	2012-2015
Xin Li, Ph.D., Postdoctoral Researcher, on professional break	2012-2017
Zach Zappala, current Ph.D. student, Genetics, now a postdoc at Broad Institute	2013-2017
Marianne DeGorter, Ph.D., Postdoctoral Researcher, Banting Fellow	2013-
Emily Tsang, current Ph.D. student, BMI, obtained PhD August 2017	2013-
Joe Davis III, current Ph.D. student Genetics, obtained PhD August 2017	2013-
Bosh Liu, current Ph.D. student, Biology	2014-
Laure Fresard, Ph.D., Postdoctoral Researcher, CEHG Fellow	2015-
Brunilda Balliu, Ph.D., Postdoctoral Researcher	2015-
Nathan Abell, current Ph.D. student, Genetics	2016-
Michael Gloudemans, current Ph.D. student, BMI	2016-
Abhiram Rao, current Ph.D. student, Bioengineering, co-mentor Erik Ingelsson	2016-
Craig Smail, current Ph.D. student, BMI	2017-
Nicole Ferraro, current Ph.D. student, BMI	2017-
Matt Durant, current Ph.D. student, Genetics, co-mentor Ami Bhatt	2017-
Olivia de Goede, current Ph.D. student, Genetics, co-mentor Karla Kirkegaard	2017-

Rotation students : Rhea Richardson (Genetics), Michael Haney (Genetics), Michael Sikora (Genetics), Erin Mitsunaga (Genetics), David Moskowitz (BMI), Jessica Ribado (Genetics), Eli Moss (Genetics), Rachel Agoglia (Genetics), Siming Zhang (Genetics), Cameron Prybol (Genetics), Nikki Teran (Genetics), Tyler Shimko (Genetics), Anna Shcherbina (BMI)

Thesis advisory/qualifying/defense commitees : Michael Sikora (Genetics), Julian Homburger (Genetics), Nora Yucel (Genetics), Helio Costa (Genetics), Alicia Martin (Genetics), Gokul Ramaswami (Genetics), Sofia Kyriazopoulou-Panagiotopoulou (CS), Oana Ursu (BMI), Shaila Musharoff (Genetics), Trevor Martin (Biology), Yi Liu (BMI), David Poznik (BMI), Azad Raiesdana (Medicine), Kimberley McManus (Genetics), Zoe Assaf (Biology), Ryosuke Kita (Biology), Linda Szabo (BMI), Tyler Shimko (Genetics), Rachel Agoglia (Genetics), Emily Glassberg (Biology), Ariel Yablonovitch (Genetics), Jessica Ribado (Genetics), Weizhuang Zhou (Bioengineering)

AWARDS AND SPECIAL RECOGNITION

- 2011 Genome Technology Magazine Rising PI (December 2011 issue)
- 2010 A-Star New Investigator Award (not accepted)
- NSERC (Natural Sciences and Engineering Research Council) postdoctoral fellowship.
- NSERC UK Millennium Research Award.
- EMBO (European Molecular Biology Organization) Long-term postdoctoral fellowship.
- Co-PI on Genome BC funding for "The Regcreative Workshop" in Ghent, Belgium.
- Co-PI on Genome Canada funding for "The Regcreative Workshop" in Ghent, Belgium.
- BC Cancer Agency Lloyd Skarsgard Research Excellence Prize (awarded annually to single BC Cancer Agency graduate student)
- NSERC PGS-Doctoral Scholarship.
- Invited to attend "Encoding Information in DNA Sequences" conference in Okinawa, Japan (40 students of 400 selected)
- BCNET Best Overall winner for Chinook project.
- MSFHR (Michael Smith Foundation for Health Research) Senior Studentship Award.
- UBC PhD Tuition Fee Award.
- EBI Travel Grant for EnsEMBL Developers Day.

PROFESSIONAL AND VOLUNTEER SERVICE

Editorial service: American Journal of Human Genetics, Associate Editor, 2018-2021
PLoS Computational Biology, *ad hoc* Guest Editor, 2014-
PLoS Genetics, *ad hoc* Guest Editor, 2012-
BMC Genomics, Associate Editor, 2012-2015
eLife, *ad hoc* Guest Editor, 2016-

NIH Study Sections: Meeting 2018/01 GHD (CSR)
Meeting 2017/10 GVE (CSR)
Meeting 2017/05 ZDK1-GRB-N-M2 (NIDDK)
Meeting 2017/05 ZRG1-ETTN-G-02 (CSR)
Meeting 2017/01 GVE (CSR)
Meeting 2016/05 ZAI1-LAR-I-M1 (NIAID)
Meeting 2016/01 ZHG1-HGR-M-J1 (NHGRI)
Meeting 2015/05 ZGM1-PPBC-Y-PG (NIGMS)
Meeting 2014/01 ZAI1-LAR-I-S1 (NIAID)
Meeting 2013/05 ZAI1 LAR-I-M2 (NIAID)

Grant reviewer: Marsden Fund, Royal Society of New Zealand, 2017
NASA, TRI Omics Study Section, 2017
Genome Canada, Disruptive Innovation in Genomics Competition, 2015
Research Foundation Flanders (Belgium), 2015
Medical Research Council (UK), 2014
Israeli Science Foundation, 2014
Stanford Child Health Research Institute, 2012-
Genome Quebec / Genome Canada, 2012
Natural Sciences and Engineering Research Council, 2013
Ministry of Health, Singapore, 2011

Ad hoc reviewer: AJHG, Bioinformatics, Cell Systems, Cell Stem Cell, Database, eLife, Genome Biology and Evolution, Frontiers in Genetics, Genome Research, Human Genetics, Human Molecular Genetics, Human Mutation, Molecular Systems Biology, Nature, Nature Biotechnology, Nature Genetics, Nature Immunology, Nature Reviews Genetics, Nucleic Acids Research, PLoS Comp Bio, PLoS Genetics, PLoS One, PNAS, Science

Other service: BIRS 2017 organizer http://www.birs.ca/events/2017/5-day-workshops/17w5131
BIRS 2015 organizer https://www.birs.ca/events/2015/5-day-workshops/15w5142
BIRS 2013 organizer https://www.birs.ca/events/2013/5-day-workshops/13w5083
European Conference of Computational Biology 2012, 2014, 2016 – PC member
ASHG Mentor/Trainee Luncheon 2015, 2016, 2017
Stanford Genetics Graduate Student Admission committee
Stanford Center for Genomics and Personalized Medicine Advisory Committee
Stanford Medicine and Hospitals Genome Sequencing Advisory Committee
Department Senator, Stanford School of Medicine
Faculty of 1000, Associate Member, 2011-2012
Education outreach, STIMULUS Cambridge

Conference organizer, The Regcreative Jamboree, Ghent Belgium
Education outreach, UBC Let's Talk Science Partnership Program
Conference organizer, Vancouver Bioinformatics User Group, www.vanbug.org.
Education outreach, Java and bioinformatics article series for O'Reilly and Associates. "Java for Bioinformatics" and "Java APIs for Bioinformatics"

Group memberships: ClinGen, NESCENT cisevol working group, 1000 Genomes Project, MoTrPAC, Hapmap 3 Consortium, GEUVADIS project, GTEx project, MuTHeR project SardiNIA project, Alspac analysis group and Canadian Data Integration Centre.

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PRESENTATIONS/INVITED MEETINGS (since 2011)

Mount Sinai, Dept of Genetics and Genomic Sciences (Invited Speaker)	2017
University of Pittsburgh, Dept of Human Genetics (Invited Speaker)	2017
ADA 77th Scientific Meeting, San Diego, USA (Invited Speaker)	2017
BioConductor Meeting, Stanford, USA, (Invited Speaker)	2016
Sardinia Summer School in Genomics , Pula, Italy (Invited Speaker)	2016
FIMM Think Different Seminar Series, Helsinki, Finland (Invited Speaker)	2016
2nd Barbados Workshop on Population Epigenomics (Invited Speaker)	2016
EMBL|Stanford Conference : Personalized Health, Heidelberg, Germany (Invited Speaker)	2015
American Society of Human Genetics Meeting, Baltimore, USA (Invited Speaker)	2015
BIRS, Banff, Canada (Conference Organizer, Speaker)	2015
Winter School in Mathematics and Computational Biology, Australia (Invited Speaker)	2015
Sardinia Summer School in Genomics, Pula, Italy (Invited Speaker)	2015
Symposium on Advances in Genomics, Epi and Stats, UPenn, USA (Invited Speaker)	2015
Cartagene Conference, Montreal, Canada (Invited Speaker)	2015
"Rare regulatory variation in individuals, families and populations"	
UCSF Institute of Human Genetics Seminar, San Francisco, USA (Invited Speaker)	2015
University of Chicago Human Genetics Seminar, Chicago, USA (Invited Speaker)	2015
CSHL Systems Biology of Gene Regulation, Rio Mar, Puerto Rico (Speaker)	2015
European Union FP7 Syscol Workshop, Wolfenbuttel, Germany (Invited Speaker)	2014
Wellcome Trust Genome Informatics Meeting, Cambridge, UK (Speaker)	2014
ICSB Regulatory Genetics SIG, Boston, USA (Invited Speaker)	2014
Big Data in Biomedicine, San Francisco, USA (Session host)	2014
TriCon Molecular Medicine, San Francisco, USA (Invited Speaker)	2014
UC Davis Guest Lecturer, Davis, USA (Invited Speaker)	2013
UC Berkeley Guest Lecturer, Berkeley, USA (Invited Speaker)	2013
CSHL Precision Medicine, Cold Spring Harbor, USA (Speaker)	2013
"Interpreting the impact of rare, deleterious and loss-of-function variants from transcriptome data"	
American Society of Human Genetics Meeting, San Francisco, USA (Invited Speaker)	2013
International Genetic Epidemiology Society, Chicago, USA (Invited Speaker)	2013
Sardinia Summer School in Genomics, Pula, Italy (Invited Speaker)	2013
Canadian Institute for Advanced Research, Banff, Canada (Invited Speaker)	2013
BIRS, Banff, Canada (Conference Organizer, Speaker)	2013
Sardinia Summer School in Genomics , Pula, Italy (Invited Speaker)	2012
International Conference on Systems Biology, Toronto, Canada (Invited Speaker)	2012
"Analysis of gene expression patterns in a single extended family"	
Capita Select in Complex Disease Analysis, Liege, Belgium (Invited Speaker)	2012
Personalized Medicine World Congress, Mountain View, USA (Invited Speaker)	2012
Swedish Medical Genetics Society, Uppsala, Sweden (Invited Speaker)	2011
"Transcriptome sequencing and diagnostics"	
International Conference on Systems Biology, Mannheim, Germany (Invited Speaker)	2011
Sardinia Summer School in Genomics, Pula, Italy (Invited Speaker)	2011
European Society of Human Genetics, Amsterdam, Netherlands (Invited Speaker)	2011
Gordon Conf. on Quantitative Genetics and Genomics, Galveston, USA (Invited Speaker)	2011

ADVANCED TRAINING

Stanford Grant Writing Course (R01 Countdown Pilot)
CITI Group 1 training certificate #8919278
NIH Protecting Human Research Participants certificate # 422835
UBC Advanced Molecular Biology Laboratories "Molecular Biology Techniques Workshop"
UBC Professional Training Workshop "Leadership and Management Workshop"

MEDIA

MIT Technology Review, A DNA App Store Is Here But Proceed With Caution 2017
https://www.technologyreview.com/s/608313/a-dna-app-store-is-here-but-proceed-with-caution/
GenomeWeb, Parody Genomics 2017
https://www.genomeweb.com/scan/parody-genomics
Gizmodo, "Scientists Push Back Against Booming Genetic Pseudoscience Market" 2017
http://gizmodo.com/scientists-push-back-against-booming-genetic-pseudoscie-1796923059
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http://www.radionz.co.nz/national/programmes/thiswayup/audio/201795485/how-genes-define-us
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GenomeWeb, Stanford Team to Use Targeted RNA-seq for Allele-Specific Expression 2014
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GRANTS

ACTIVE

1R01HG008150 (Montgomery, Stephen B., PI) 08/01/2015-06/30/2018 1.20 calendar
National Institutes of Health
Predicting Casual Non-Coding Variants in a Founder Population
Major Goals: The main goal of this project is to develop methods which integrate genome, transcriptome and trait data to identify and validate impactful non-coding variants. Funding for Stanford is split between 3 PIs.

1R33HL120757 (Quertermous, Thomas) 03/05/2014-02/28/2019 0.60 calendar
National Institutes of Health
Identification of Causal Coronary Heart Disease Variation in Smooth Muscle Cells
Major Goals: The main goal of this project is to apply genome, transcriptome and epigenome sequencing to identify causal regulatory variants underlying coronary heart disease-associated variation.

Grant 02/01/2016-01/31/2019 0.00 calendar*
Glenn Center for Biology of Aging Research Stanford University
Genetics of Gene Expression in an Elderly, Longitudinal Cohort
Major Goals: Main goals are longitudinal transcriptome profiling of elderly individuals; and identification of gene regulatory changes in advanced age.
*PI effort may not be billed to Glenn Center grant.

1R01DK107437 (Quertermous, Thomas) 01/01/2016-12/31/2019 0.84 calendar
National Institutes of Health

Molecular Mechanisms of Insulin Resistance Associated Loci
Major Goals: The main goal of this project is to apply genome, transcriptome and epigenome sequencing to identify causal regulatory variants underlying insulin resistance-associated variation.

1U01HG00908001 (Bustamante, Carlos D.) 05/02/2016-03/31/2020 0.60 calendar
National Institutes of Health
Center for Multi- and Trans-ethnic Mapping of Mendelian and Complex Diseases
Major Goals: The goal of this GSPAC Center grant is to analyze common and rare variants in 250,000 genomes across a range of ethnicities. Dr. Montgomery shares a postdoc with Dr. Bustamante on this grant.

1U01HG009431 (Pritchard, Jonathan) 02/01/2017-01/31/2021 0.60 calendar
National Institutes of Health
Decoding the Regulatory Architecture of the Human Genome Across Cell Types, Individuals and Disease
Major Goals: This project focuses on analysis of ENCODE data to identify regulatory variants involved in human disease.

1U24DK112348 (MPI: Snyder, M./Montgomery, S.) 12/13/2016 – 11/30/2022 1.20 calendar
National Institutes of Health
Stanford/Salk MoTrPAC Site for Genomes, Epigenomes and Transcriptomes
Major Goals: The Stanford/Salk MoTrPAC site is designed to provide genomes, transcriptomes and epigenomes for the MoTrPAC to elucidate molecular changes in response to physical activity.

COMPLETED

1R01MH101814 (Bustamante, Carlos D.) 08/01/2013-06/30/2017 0.84 calendar
National Institutes of Health University of Geneva
Methods for High-Resolution Analysis of Genetic Effects on Gene Expression
Major Goals: This project is for the second phase of statistical analyses as part of GTEx.

5U01HG007436 (Bustamante, Carlos D.) 09/23/2013-07/31/2017 0.60 calendar
National Institutes of Health Clinically Relevant Genome Variation Database
Major Goals: The main goal of this project is to create a unified, public and freely available database of genetic alterations relevant to clinical care. Our ultimate goal is to empower clinicians, genetic counselors, and patients to make informed decisions based on DNA testing.

1U01HG007593-03 (Li, Jin Billy) 04/22/2014-03/31/2017 1.80 calendar
National Institutes of Health
High Resolution Allele Specific Expression Assays

54341548 (Montgomery, Stephen) 09/11/2014 - 05/31/2016 0.60 calendar
Prime Sponsor: National Institutes of Health
University of California, San Diego
Single-cell Sequencing and in situ Mapping of RNA Transcripts in Human Brains

N/A (Montgomery, Stephen) 10/01/2012 - 09/30/2015 1.44 calendar
Edward Mallinckrodt, Jr. Foundation
Expression Response to Environment in Coronary Artery Smooth Muscle Cells

The Fred Hutchinson Cancer Research Center 03/01/2015 – 08/31/2015 0.12 calendar
Pilot RNA-seq Study Among Long Life Study Participants of the WHI