

Professional status: research fellow at Dana-Farber Cancer Institute studying the role of germline genetics in cancer predisposition using large-scale genomic data science; co-advised by Drs. Eli Van Allen, Sasha Gusev, and Kevin Haigis.

Career objective: to maximize the potential of genomic data science to improve our understanding of basic biology and our ability to predict, prevent, and treat human disease, ideally by leading an independent research group.

Scientific interests: genome biology, structural variation, genome organization, data science, gene regulation, statistics, predictive modeling, variant interpretation sequencing technologies, chromatin, bioinformatics, and medical genetics.

EDUCATION

DEGREES

Ph.D. Harvard University, *Cambridge, MA, USA*

2016-2022 Division of Medical Sciences: Bioinformatics and Integrative Genomics

Thesis Title *The landscape and consequences of structural variation in the human genome*

Advisor Michael E. Talkowski, Ph.D.

A.B. Dartmouth College, *Hanover, NH, USA*

2009-2013 Department of Biological Sciences: Computational Genetics

Research Focus *Models of genetic epistasis in common disease risk*

Advisor Jason H. Moore, Ph.D.

COURSEWORK

Harvard Medical School Principles of Molecular Biology; Principles of Genetics; Clinical Genetics; Computational and Functional Genomics; Advanced Topics in Gene Regulation; Conduct of Science; Analysis of Biological Literature

Massachusetts Institute of Technology (MIT) Quantitative Genomics; Machine Learning

Dartmouth College Molecular Genetics of Eukaryotes; Computational Molecular Biology; Experimental Genetic Analysis; Gene Expression & Inheritance; Biostatistics; Multivariate Calculus; Discrete Probability; Hazardous Data; General Physics; Cell Structure & Function; Physiology; Art of Science Writing; General Chemistry

RESEARCH EXPERIENCE

Research Fellow Laboratory of Eli Van Allen, M.D.

2022-Present Dana-Farber Cancer Institute | Boston, MA, USA

Team Leader Population Genetics & Genome Biology Team, Broad-SV Group

2018-2022 Broad Institute of MIT and Harvard | Cambridge, MA, USA

Ph.D. Candidate Laboratory of Michael E. Talkowski, Ph.D.

2017-2022 Massachusetts General Hospital | Boston, MA, USA

Ph.D. Rotation Student Laboratory of Eric S. Lander, Ph.D. (co-supervised by Jesse Engreitz, Ph.D.)

2017 Broad Institute of MIT and Harvard | Cambridge, MA, USA

Ph.D. Rotation Student Laboratory of Daniel G. MacArthur, Ph.D.

2016 Broad Institute of MIT and Harvard | Cambridge, MA, USA

Bioinformatics Specialist II Laboratory of Michael E. Talkowski, Ph.D., and MGH Genomics and Technology Core

2013-2016 Massachusetts General Hospital | Boston, MA, USA

Student Research Assistant Laboratory of Jason H. Moore, Ph.D.

2011-2013 Geisel School of Medicine at Dartmouth College | Hanover, NH, USA

Student Research Assistant Department of Orthopedic Medicine

2010 Dartmouth Hitchcock Medical Center | Lebanon, NH, USA

Student Research Assistant Laboratory of Thomas P. Jack, Ph.D.

2009 Dartmouth College | Hanover, NH, USA

PROFESSIONAL ACTIVITIES

TEACHING

Teaching Assistant Clinical Genetics (GEN288; Instructor: David Sweetser, M.D.)

2020 Harvard Medical School | Boston, MA, USA

Invited Lecturer Human Genetics (GEN202; Instructor: Matthew Warman, M.D.)

2018 Harvard Medical School | Boston, MA, USA

Invited Lecturer Short Course on Rare Variant Interpretation in Mendelian Diseases

Teaching Assistant Gene Expression and Inheritance (BIOL013; Instructor: Thomas Jack, Ph.D.)
2012-2013 Dartmouth College | Hanover, NH, USA

Volunteer Tutor Calculus and Advanced Mathematics
2010-2011 Hanover High School | Hanover, NH, USA

MENTORSHIP

2019-2022	Isaac Wong, B.S.	Bioinformatics Specialist	Co-supervised with Drs. Michael Talkowski & Harrison Brand
2018-2022	Jack Fu, Ph.D.	Postdoctoral Fellow	Co-supervised with Drs. Michael Talkowski & Harrison Brand
2020-2021	Selin Everett	Undergraduate Researcher	Co-supervised with Drs. Michael Talkowski & Harrison Brand

ACADEMIC SERVICE

Invited Referee 6 articles for 6 journals, including: *Cell Genomics*; *Human Genetics*; *iScience*, *npj Genomic Medicine*; *Trends in Genetics*; *Scientific Data*
2020-Present

Ad Hoc Referee 16 articles for 13 journals, including: *American Journal of Human Genetics*; *BMC Genomics*; *Cell*; *Clinical Genetics*; *Human Molecular Genetics*; *Molecular Genetics & Genomic Medicine*; *Molecular Psychiatry*; *Nature*; *Nature Communications*; *Nature Genetics*; *Nature Reviews Genetics*; *New England Journal of Medicine*; *PLOS Genetics*
2013-Present
All *ad hoc* referee activities conducted with Michael Talkowski, Ph.D.

Organizer Bioinformatics and Integrative Genomics Student Research Seminar Series
2019-2020 Harvard Medical School | Boston, MA, USA

Session Moderator American Society for Human Genetics Annual Meeting
2018 San Diego, CA, USA

Admissions Interviewer PhD Student Admissions, Program in Bioinformatics and Integrative Genomics
2018 Harvard Medical School | Boston, MA, USA

Keynote Session Chair Gordon Research Seminar: Human Genetics and Genomics
2017 Stowe, VT, USA

Invited Panelist The Future of Genome Sequencing in Rare Diseases, NIH Center for Mendelian Genomics
2017 Broad Institute of MIT and Harvard | Cambridge, MA, USA

Student Representative Dresden School Board
2008-2009 School Administrative Unit (SAU) 70 | Hanover, NH & Norwich, VT, USA

OUTREACH

Invited Panelist Prospective Graduate Student Panel
2019 Massachusetts General Hospital Research Institute | Boston, MA, USA

Volunteer Reviewer *Journal of Emerging Investigators*
2016-2019 Cambridge, MA, USA

Contributing Author *The Nascent Transcript* (American Society for Human Genetics Periodical)
2016-2017 USA

Contributing Author Science in the News
2016-2017 Harvard University | Cambridge, MA, USA

Invited Panelist Dartmouth College Young Alumni Panel on Biotechnology Careers
2015 Boston, MA, USA

Alumnus Mentor Dartmouth Externship Program for Professional Exploration
2015 Boston, MA, USA

SELECTED CONSORTIA

Representative publications listed below each consortium, where applicable

- 2016-Present** Genome Aggregation Database (gnomAD), Broad Institute of MIT and Harvard
In May 2020, seven gnomAD papers were published in *Nature*, *Nat. Med.*, and *Nat. Commun.*, and featured on the cover of *Nature*
- 2015-2022** Core Analysis Group, Autism Sequencing Consortium
Fu et al., Nat. Genet. (2022); *Satterstrom, et al., Cell* (2020); *An et al., Science* (2018); *Werling et al., Nat. Genet.* (2018)
- 2015-2022** Structural Variation Group (Broad-SV), Broad Institute of MIT and Harvard
Collins et al., Cell (2022); *Collins et al., Genome Biol.* (2017)
- 2013-2022** Developmental Genome Anatomy Project / International Breakpoint Mapping Consortium
Lowther et al., medRxiv (2022); *Redin et al., Nat. Genet.* (2017)
- 2015-2019** Human Genome Structural Variation Consortium (1000 Genomes Project phase 4)
Zhao et al., Am. J. Hum. Genet. (2021); *Chaisson et al., Nat. Commun.* (2019)
- 2015-2017** Collaborative Center for X-Linked Dystonia Parkinsonism, Massachusetts General Hospital
Aneichyk et al., Cell. (2018)

OTHER AFFILIATIONS

- 2021-Present** European Society for Human Genetics
- 2017-Present** Sigma Xi Honors Society for Scientific Research
- 2015-Present** Program in Population and Medical Genetics, Broad Institute of MIT and Harvard
- 2014-Present** American Society of Human Genetics

FELLOWSHIPS & FUNDING

FELLOWSHIPS

- 2017-2021** \$138,000 NSF Graduate Research Fellowship Program (GRFP; NSF #2017240332)
- 2016-2018** \$92,086 NIH/NHGRI Institutional National Research Service Award (T32; 4T32HG002295-14; PI: Park)

AWARDS & HONORS

MAJOR

- 2021** European Society for Human Genetics Early Career Award for Outstanding Science
€500 prize; one of five winners among 950 trainee applicants at the European Society of Human Genetics Annual Meeting 2021
- 2021** Massachusetts General Hospital Executive Committee on Research Celebration of Science Award
\$1,000 prize; given to MGH Martin Prize finalists; awarded for work on mapping structural variation in the human population
- 2021** European Society for Human Genetics Conference Fellowship of Excellence
Awarded to each of the five top-rated abstracts submitted by trainees to the European Society of Human Genetics Annual Meeting 2021
- 2018** Charles J. Epstein Trainee Award for Excellence in Human Genetics Research
\$2,000 prize; one of three predoctoral winners among 670 applicants at the American Society of Human Genetics Annual Meeting 2018
- 2017** Associate Member, Sigma Xi Honors Society for Scientific Research
- 2014** Clinical Research Team Award, Massachusetts General Hospital
\$2,500 team prize awarded to best entry among 386 teams for work on complex structural variation in neuropsychiatric disorders

MINOR

- 2022** Annual Most Valuable Member (Second Place), Talkowski Laboratory
- 2020** Charles J. Epstein Trainee Award for Excellence in Human Genetics Research (Semifinalist)
\$750 prize; one of 30 predoctoral semifinalists among 433 applicants at the American Society of Human Genetics Annual Meeting 2020
- 2020** Annual Most Valuable Member, Talkowski Laboratory
- 2020** Reviewer's Choice Poster Award, American Society for Human Genetics
Distinction given to top 10% of best-scoring abstracts at the American Society of Human Genetics Annual Meeting 2020
- 2019** Charles J. Epstein Trainee Award for Excellence in Human Genetics Research (Semifinalist)
\$750 prize; one of 30 predoctoral semifinalists among 511 applicants at the American Society of Human Genetics Annual Meeting 2019
- 2019** Trainee & Staff Abstract Award, Center for Genomic Medicine, Massachusetts General Hospital
\$750 travel award; one of three top submitted abstracts for a Center-wide talk competition
- 2019** Travel Award, Center for Genomic Medicine, Massachusetts General Hospital
\$1,500 travel award; one of three winners from a Center-wide competition based on submitted abstract, CV, and travel proposal
- 2018** Travel Award, Harvard University Graduate School of Arts and Sciences Professional Development Fund
\$600 travel award; awarded to present research at American Society of Human Genetics Annual Meeting 2018 in San Diego, CA
- 2018** Annual Most Valuable Member (Third Place), Talkowski Laboratory
- 2018** Selected for the American Society of Human Genetics (ASHG) Trainee Paper Spotlight
Described by ASHG: "The Trainee Paper Spotlight is a quarterly feature highlighting outstanding papers written by ASHG trainees"
Selected paper: Collins *et al.*, *Genome Biol.* (2017). Highlight [available online via ASHG](#).
- 2016** Annual Most Valuable Member (Third Place), Talkowski Laboratory
- 2015** Annual Most Valuable Member, Talkowski Laboratory
- 2014** Annual Most Valuable Member (Second Place), Talkowski Laboratory
- 2009** Robert Stone Memorial Award, Hanover High School
- 2009** Tom Hanlon Cup, Hanover High School

RESEARCH PRESENTATIONS

All presentations were intramural unless marked as [E], which designates an extramural presentation. **Bold** indicates highlighted presentations of note.

A cross-disorder dosage sensitivity map of the human genome

	November 2022	Invited Speaker	Boston Children's Hospital Digital Science Seminar Series	<i>International (Virtual)</i>
	October 2022	Invited Speaker	ClinGen Dosage Sensitivity Curation Working Group	<i>International (Virtual)</i>
	November 2021	Invited Speaker	MGH Analytical and Translational Genetics Unit Seminar Series	<i>Boston, MA, USA</i>
	October 2021	Invited Speaker	Broad Institute Stanley Center for Psychiatric Research Seminar Series	<i>Cambridge, MA, USA</i>
[E]	June 2021	Selected Plenary Speaker	European Society for Human Genetics Annual Meeting	<i>International (Virtual)</i>
[E]	May 2021	Invited Panel Speaker	International Society for Autism Research Annual Meeting	<i>International (Virtual)</i>
	April 2021	Invited Speaker	Broad Institute Medical and Population Genetics Seminar	<i>Cambridge, MA, USA</i>
	January 2021	Invited Speaker	Broad Institute Structural Variation Group	<i>Cambridge, MA, USA</i>
[E]	October 2020	Poster Presentation	American Society of Human Genetics Annual Meeting	<i>International (Virtual)</i>
[E]	March 2018	Poster Presentation	NHGRI Research Training and Career Development Annual Meeting	<i>Los Angeles, CA, USA</i>
	December 2017	Poster Presentation	Broad Institute Scientific Retreat	<i>Boston, MA, USA</i>
	September 2017	Poster Presentation	Massachusetts General Hospital Center for Genomic Medicine Annual Retreat	<i>Cambridge, MA, USA</i>

gnomAD-SV: an open resource of structural variation for medical and population genetics

[E]	August 2021	Invited Speaker	Garvan Institute Computational Biology Seminar Series	<i>Australia (Virtual)</i>
[E]	May 2021	Invited Speaker	UK NHS Southwest Genomic Laboratory Hub Seminar Series	<i>United Kingdom (Virtual)</i>
	April 2021	Invited Speaker	Massachusetts General Hospital Executive Committee on Research Meeting	<i>Boston, MA, USA</i>
[E]	October 2020	Invited Speaker	Boston Children's Hospital Virtual Seminar Series	<i>Boston, MA, USA</i>
[E]	September 2020	Invited Speaker	OpenBox Science Virtual Symposium	<i>International (Conf. Call)</i>
[E]	February 2020	Invited Speaker	ClinGen CNV Interpretation Webinar	<i>International (Conf. Call)</i>
	January 2020	Invited Speaker	Harvard Medical School BIG Ph.D. Recruitment Informational Session	<i>Boston, MA, USA</i>
	December 2019	Invited Plenary Speaker	Broad Institute 15th Annual Retreat	<i>Boston, MA, USA</i>
[E]	December 2019	Invited Speaker	Yale Genetics Walter J. Burdette Trainee Symposium	<i>New Haven, CT, USA</i>
[E]	October 2019	Selected Platform Speaker	American Society of Human Genetics Annual Meeting	<i>Houston, TX, USA</i>
[E]	July 2019	Selected Platform Speaker	Gordon Research Seminar: Human Genetics & Genomics	<i>Waterville Valley, NH, USA</i>
[E]	July 2019	Invited Speaker	ClinGen Biocurator Working Group Monthly Conference Call	<i>International (Conf. Call)</i>
[E]	May 2019	Invited Speaker	NHGRI Genome Sequencing Program Methods Group Conference Call	<i>International (Conf. Call)</i>
[E]	May 2019	Poster Presentation	Cold Spring Harbor Laboratory Biology of Genomes Annual Meeting	<i>Cold Spring Harbor, NY, USA</i>
	May 2019	Selected Platform Speaker	Massachusetts General Hospital CGM Annual Trainee & Staff Seminar	<i>Boston, MA, USA</i>
	March 2019	Invited Speaker	Massachusetts General Hospital Reproductive Endocrine Unit Seminar	<i>Boston, MA, USA</i>
	January 2019	Invited Speaker	Broad Institute Data Sciences Platform Methods & Applications Seminar	<i>Cambridge, MA, USA</i>
	November 2018	Invited Speaker	Broad Institute Medical and Population Genetics Seminar	<i>Cambridge, MA, USA</i>
[E]	February 2018	Invited Speaker	gnomAD Consortium Monthly Analysis Conference Call	<i>International (Conf. Call)</i>
	January 2018	Invited Speaker	Harvard Medical School BIG Ph.D. Recruitment Informational Session	<i>Boston, MA, USA</i>
	August 2017	Selected Speaker	Talkowski Laboratory Retreat	<i>Portsmouth, NH, USA</i>

Methods for structural variation discovery from whole-genome sequencing

	December 2018	Invited Speaker	Broad Institute Data Sciences Platform Methods Primer	<i>Cambridge, MA, USA</i>
	January 2018	Invited Speaker	Broad Institute Data Sciences Platform Methods Seminar	<i>Cambridge, MA, USA</i>

Convergence of copy-number variants and point mutations in neurodevelopmental disorders

[E]	October 2018	Selected Platform Speaker	American Society of Human Genetics Annual Meeting	<i>San Diego, CA, USA</i>
	October 2018	Invited Speaker	Broad Institute Medical and Population Genetics Seminar	<i>Cambridge, MA, USA</i>

Complex structural variation in neurodevelopmental disorders

[E]	July 2017	Poster Presentation	Gordon Research Conference: Human Genetics & Genomics	<i>Stowe, VT, USA</i>
[E]	July 2017	Poster Presentation	Gordon Research Seminar: Human Genetics & Genomics	<i>Stowe, VT, USA</i>
[E]	April 2017	Selected Platform Speaker	NHGRI Research Training and Career Development Annual Meeting	<i>St. Louis, MO, USA</i>
	December 2016	Poster Presentation	Broad Institute Scientific Retreat	<i>Boston, MA, USA</i>
[E]	May 2016	Poster Presentation	Cold Spring Harbor Laboratory Biology of Genomes Annual Meeting	<i>Cold Spring Harbor, NY, USA</i>
[E]	May 2016	Invited Speaker	Human Genome Structural Variation Consortium Semiannual Meeting	<i>Cold Spring Harbor, NY, USA</i>
[E]	October 2015	Poster Presentation	American Society of Human Genetics Annual Meeting	<i>Baltimore, MD, USA</i>
	April 2015	Poster Presentation	Massachusetts General Hospital Scientific Advisory Council Meeting	<i>Boston, MA, USA</i>
	April 2015	Poster Presentation	Massachusetts General Hospital Center for Human Genetics Research Retreat	<i>Cambridge, MA, USA</i>

Limited contribution of rare, noncoding variation to autism spectrum disorders

	April 2017	Invited Speaker	Massachusetts General Hospital Analytical and Translational Genetics Unit	<i>Boston, MA, USA</i>
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Understanding dosage biases in the analysis of whole-genome sequencing datasets

	February 2016	Invited Speaker	Broad Institute Structural Variation and Assembly Group	<i>Cambridge, MA, USA</i>
	December 2016	Invited Speaker	Broad Institute Medical and Population Genetics Seminar	<i>Cambridge, MA, USA</i>
	May 2015	Invited Speaker	Massachusetts General Hospital Molecular Neurogenetics Unit Seminar	<i>Boston, MA, USA</i>

Structural rearrangements in genome editing with CRISPR-Cas9 and TALENs

	January 2015	Invited Speaker	Massachusetts General Hospital Center for Human Genetics Research Seminar	<i>Boston, MA, USA</i>
[E]	October 2014	Selected Platform Speaker	American Society of Human Genetics Annual Meeting	<i>San Diego, CA, USA</i>
	April 2014	Poster Presentation	Massachusetts General Hospital Center for Human Genetics Research Retreat	<i>Cambridge, MA, USA</i>
	April 2014	Invited Speaker	Massachusetts General Hospital Molecular Neurogenetics Unit Seminar	<i>Boston, MA, USA</i>

Articles are grouped based on the extent of contributions to each (primary/major/minor/group) and ordered chronologically thereafter.

- **Primary contributions** include principal leadership roles in conducting and/or overseeing the overall study.
- **Major contributions** include core roles in conducting and/or managing one or more main components of the study.
- **Minor contributions** include supporting or secondary roles in conducting or otherwise facilitating the study.
- **Group authorship** indicates a general involvement as part of a larger consortium that facilitated the study.

Specific details of the contributions to each publication are enumerated below each citation (grey text)

Key: */°/† equal contributions

§ publication highlight

! highly cited (≥100 citations)

Citation statistics from [Google Scholar](#)

REFEREED SCIENTIFIC ARTICLES

Articles authored as a primary contributor

- 2022 § [44] **Collins RL***, Glessner JT, Porcu E, Lepamets M, Brandon R, Lauricella C, Han L, Morley T, Niestroj L, Ulirsch J, Everett S, Howrigan DP, Boone PM, Fu J, Karczewski K, Kellaris G, Lowther C, Lucente D, Mohajeri K, Nõukas M, Nuttle X, Samochoa KE, Trinh M, Ullah F, Võsa U, Hurles ME, Aradhya S, Davis EE, Finucane H, Gusella JF, Janze A, Katsanis N, Matyakhina L, Neale BM, Sanders D, Warren S, Hodge JC, Lal D, Ruderfer DM, Meck J, Mägi R, Esko T, Reymond A, Kutalik Z, Hakonarson H, Sunyaev S, Brand H*, Talkowski ME*. A cross-disorder dosage sensitivity map of the human genome. *Cell* (2022), 185(16): 3041-3055. PMID: [35917817](#). DOI: [10.1016/j.cell.2022.06.036](#).
Conceived of study, curated all data, developed all methods, performed all analyses, and drafted manuscript and figures
§ *Winner of the 2021 ESHG Early Career Award for Outstanding Science (see Awards & Honors)*
§ *Highlighted by Spectrum News, Genome Web, Nature Reviews Genetics, and in a Preview in Cell.*
- 2020 § ! [43] **Collins RL***, Brand H*, Karczewski KJ, Zhao X, Alfoldi J, Khera AV, Francioli LC, Gauthier LD, Wang H, O'Donnell-Luria A, Solomonson M, Baumann A, Munshi R, Walker M, Whelan C, Huang Y, Brookings T, Sharpe T, Stone MR, Tiao G, Laricchia KM, Watts NA, Fu J, Valkanas E, Lowther C, Stevens C, Gupta N, Cusick C, Margolin L, The gnomAD Production Team, The gnomAD Consortium, Spertus JA, Taylor KD, Psaty BM, Rich SS, Post W, Chen YI, Rotter JI, Nusbaum C, Philippakis A, Lander E, Gabriel S, Neale BM, Kathiresan S, Daly MJ, Banks E, MacArthur DG, Talkowski ME. A structural variation reference for medical and population genetics. *Nature* (2020), 581: 444-451. PMID: [32461652](#). DOI: [10.1038/s41586-020-2287-8](#).
Led and conducted all analyses for duration of study (2016-2020); co-led all methods development; wrote manuscript & created all figures
§ *Featured by Nature in an editorial, a News & Views commentary, and on the cover of the May 28, 2020 issue*
§ *Highlighted in Nature Reviews Genetics, GenomeWeb, The Broad Institute, Yahoo! News, Science Daily, and others*
§ *Semifinalist for the 2019 ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics (see Awards & Honors)*
§ *Winner of a Travel Award and a Trainee & Staff Abstract Award from the Massachusetts General Hospital (see Awards & Honors)*
- 2017 § ! [42] **Collins RL**, Brand H, Redin CE, Hanscom C, Antolik C, Stone MR, Glessner JT, Mason T, Pregno G, Dorrani N, Mandrile G, Giachino D, Perrin D, Walsh C, Cipicchio M, Costello M, Stortchevoi A, An J, Currall BB, Seabra CM, Ragavendran A, Margolin L, Martinez-Agosto JA, Lucente D, Levy B, Sanders SJ, Wapner RJ, Quintero-Rivera F, Kloosterman W, Talkowski ME. Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid human genome. *Genome Biology* (2017), 18(36): 1-21. PMID: [28260531](#). DOI: [10.1186/s13059-017-1158-6](#).
Led study design, methods development, and analysis for duration of study (2014-2017); wrote manuscript & created all figures
§ *Selected for the American Society of Human Genetics Trainee Paper Spotlight.*
§ *Highlighted by GenomeWeb, The Broad Institute, the 10X Genomics Blog.*
§ *Selected by the editors of Genome Biology as one of their favorite articles from 2017.*
- 2015 § [41] Brand H*, **Collins RL***, Hanscom C, Rosenfeld JA, Pillalamarri V, Stone MR, Kelley F, Mason T, Margolin L, Eggert S, Mitchell E, Hodge J, Gusella JF, Sanders SJ, Talkowski ME. Paired duplications mark cryptic inversions and are a common signature of complex structural variation. *American Journal of Human Genetics* (2015), 97(1): 170-176. PMID: [26094575](#). DOI: [10.1016/j.ajhg.2015.05.012](#).
Co-designed study and co-led all analyses; created all figures; led manuscript writing
§ *Highlighted by Spectrum News.*
- 2013 [40] **Collins RL**, Hu T, Wejse C, Sirugo G, Williams SM, Moore JH. Multifactor dimensionality reduction reveals a three-locus epistatic interaction associated with susceptibility to pulmonary tuberculosis. *BioData Mining* (2013), 6(1): 4. PMID: [23418869](#). DOI: [10.1186/1756-0381-6-4](#).
Performed all analyses; interpreted all results; assisted in statistical methods development; wrote manuscript & created all figures

Articles authored as a major contributor

- 2022 § [39] Fu JM*, Satterstrom FK*, Peng M*, Brand H*, **Collins RL**, Dong S, Klei L, Stevens CR, Cusick C, Babadi M, Banks E, Collins B, Dodge S, Gabriel SB, Gauthier L, Lee SK, Liang L, Ljungdahl A, Mahjani B, Sloofman L, Smirnov A, Barbosa M, Brusco A, Chung BH, Cuccaro ML, Domenici E, Ferrero GB, Gargus JJ, Herman GE, Hertz-Picciotto I, Maciel P, Manoch DS, Passos-Bueno MR, Persico AM, Renieri A, Tassone F, Trabetti E, Campos G, Chan MC, Fallerini C, Giorgio E, Girard AC, Hansen-Kiss E, Lee SL, Lintas C, Ludena Y, Nguyen R, Pavinato L, Pericak-Vance M, Pessah I, Riberi E, Schmidt R, Smith M, Souza CI, Trajkova S, Wang JY, Yu MH, The Autism Sequencing Consortium, Broad Center for Common Disease Genomics, iPSYCH-BROAD Consortium, Cutler DJ, Rubeis SD, Buxbaum JD°, Daly MJ°, Devlin B°, Roeder K°, Sanders SJ°, Talkowski ME°. Rare coding variation illuminates the allelic architecture, risk genes, cellular expression patterns, and phenotypic context of autism. *Nat. Genet.* (2022), online ahead of print. PMID: TBD. *medRxiv* DOI: [10.1101/2021.12.20.21267194](#).
Contributed to methods development and CNV callset generation; contributed to manuscript writing & revising; co-created Figure 2

- 2021 § [38] Zhao X, **Collins RL**, Lee W, Weber AM, Jun Y, Zhu Q, Weisburd B, Huang Y, Audano PA, Wang H, Walker M, Lowther C, Fu J, Gerstein MB, Devine SE, Marschall T, Korbel JO, Eichler EE, Chaisson MJ, Lee C, Mills RE, Brand H, Talkowski ME. Expectations and blind spots for structural variation detection from short-read alignment and long-read assembly. *American Journal of Human Genetics* (2021), 108(5): 919-928. PMID: [33789087](#). DOI: [10.1016/j.ajhg.2021.03.014](#).
Assisted in study design; contributed to analysis of short-read vs. long-read comparisons; assisted in manuscript & figure preparation
§ Highlighted by [GenomeWeb](#)
- 2020 § ! [37] Karczewski KJ, Francioli LC, Tiao G, Cummings BB, Alföldi J, Wang Q, **Collins RL**, Laricchia KM, Ganna A, Birnbaum DP, Gauthier LD, Brand H, Solomonson M, Watts NA, Rhodes D, Singer-Berk M, Seaby EG, Kosmicki JA, Walters RK, Tashman K, Farjoun Y, Banks E, Poterba T, Wang A, Seed C, Whiffin N, Chong JX, Samocha KE, Pierce-Hoffman E, Zappala Z, O'Donnell-Luria AH, Minikel EV, Weisburd B, Lek M, Ware JS, Vittal C, Armean IM, Bergelson L, Cibulskis K, Connolly KM, Covarrubias M, Donnelly S, Ferriera S, Gabriel S, Gentry J, Gupta N, Jeandet T, Kaplan D, Llanwarne C, Munshi R, Novod S, Petrillo N, Roazen D, Ruano-Rubio V, Saltzman A, Schleicher M, Soto J, Tibbetts K, Tolonen C, Wade G, Talkowski ME, The gnomAD Consortium, Neale BM, Daly MJ, MacArthur DG. Variation across 141,456 human exomes and genomes reveals the spectrum of loss-of-function intolerance across human protein-coding genes. *Nature* (2020), 581. PMID: [32461654](#). DOI: [10.1038/s41586-020-2308-7](#).
Led generation of structural variation callset from whole-genome sequencing of 14,891 samples; designed Figure 3B
§ Winner of the 2018 ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics
§ Highlighted by Nature in an [editorial](#), a [News & Views](#) commentary, and on [the cover](#)
§ Highlighted by [GenomeWeb](#), [The Broad Institute](#), [Yahoo! News](#), [Science Daily](#), and others
- § ! [36] Satterstrom FK*, Kosmicki JA*, Wang J*, Breen M, Rubeis SD, An J, Peng M, **Collins RL**, Grove J, Klei L, Stevens C, Reichert J, Mulhern M, Artomov M, Gerges S, Sheppard B, Xu X, Bhaduri A, Norman U, Brand H, Schwartz G, Nguyen R, Guerrero E, Dias C, Aleksic B, Anney RJ, Barbosa M, Bishop S, Brusco A, Bybjerg-Grauholm J, Carracedo A, Chan MC, Chiochetti A, Chung B, Coon H, Cuccaro M, Curró A, Bernardina BD, Doan R, Domenici E, Dong S, Fallnerini C, Fernández-Prieto M, Ferrero GB, Freitag CM, Fromer M, Gargus JJ, Geschwind D, Giorgio E, González-Peñas J, Guter S, Halpern D, Hassen-Kiss E, He X, Herman G, Hertz-Picciotto I, Hougaard DM, Hultman CM, Ionita-Laza I, Jacob S, Jamison J, Jugessur A, Kaartinen M, Knudsen GP, Kolevz'n A, Kushima I, Lee SL, Lehtimäki T, Lim ET, Lintas C, Lipkin WI, Lopergolo D, Lopes F, Ludena Y, Maciel P, Magnus P, Mahjani B, Maltman N, Manoach DS, Meiri G, Menashe I, Miller J, Minshew N, De Souza EM, Moreira D, Morrow E, Mors O, Mortensen PB, Mosconi M, Muglia P, Neale B, Nordentoft M, Ozaki N, Palotie A, Parellada M, Passos-Bueno MR, Pericak-Vance M, Persico A, Pessah I, Puura K, Reichenberg A, Renieri A, Riberi E, Robinson E, Samocha KE, Sandin S, Santangelo SL, Schellenberg G, Scherer S, Schlitt S, Schmidt R, Schmitt L, Silva IM, Singh T, Siper P, Smith M, Soares G, Stoltenberg C, Suren P, Susser E, Sweeney J, Szatmari P, Tang L, Tassone F, Teufel K, Trabetti E, Trelles MD, Walsh C, Weiss L, Werge T, Werling D, Wigdor EM, Wilkinson E, Willsey JA, Yu T, Yu MH, Yuen R, Zachi E, Betancur C, Cook EH, Gallagher L, Gill M, Lehner T, Senthil G, Sutcliffe JS, Thurm A, Zwick ME, Børglum AD, State MW, Cicek AE, Talkowski ME, Cutler DJ, Devlin B, Sanders SJ°, Roeder K°, Buxbaum JD°, Daly MJ°. Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism. *Cell* (2020), 80(3):568-584.e23. PMID: [31981491](#). DOI: [10.1016/j.cell.2019](#).
Led integration of *de novo* point mutations and autism risk genes with copy-number variation data; created Figure 2F-G
§ Winner of the 2018 ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics (see Awards & Honors)
- 2019 ! [35] Chaisson MJ*, Sanders AD*, Zhao X*, Malhotra A°, Porubsky D°, Rausch T°, Gardner EJ°, Rodriguez O°, Guo L°, **Collins RL**°, Fan X°, Wen J°, Handsaker RE°, Fairley S°, Kronenberg ZN°, Kong X°, Hormozdiari F°, Lee D°, Wenger AM°, Hastie A°, Antaki D°, Audano P, Brand H, Cantsilieris S, Cao H, Cerveira E, Chen C, Chen X, Chin C, Chong Z, Chuang NT, Church DM, Clarke L, Farrell A, Flores J, Galeev T, Gorkin D, Gujral M, Guryev V, Heaton WH, Korfach J, Kumar S, Kwon JY, Lee JE, Lee J, Lee W, Lee SP, Li S, Marks P, Viaud-Martinez K, Meiers S, Munson KM, Navarro F, Nelson BJ, Nodzak C, Noor A, Kyriazopoulou-Panagiotopoulou S, Pang A, Qiu Y, Rosanio G, Ryan M, Stütz A, Spierings DC, Ward A, Welch AE, Xiao M, Xu W, Zhang C, Zhu Q, Zheng-Bradley X, Yakneen S, McCarroll S, Jun G, Ding L, Koh CL, Ren B, Flicek P°, Chen K°, Gerstein MB°, Kwok P°, Lansdorp PM°, Marth G°, Sebati J°, Shi X°, Bashir A°, Ye K°, Devine SE°, Talkowski M°, Mills RE°, Marschall T°, Korbel J°, Eichler EE°, Lee C°. Multi-platform discovery of haplotype-resolved structural variation in human genomes. *Nature Communications* (2019), 10(1):1784. PMID: [30992455](#). DOI: [10.1038/s41467-018-08148-z](#).
Led analysis of long-insert jumping whole-genome libraries; assisted in cross-platform inversion discovery, analysis, and validation
- ! [34] Khera AV*, Chaffin M*, Zekavat SM, **Collins RL**, Roselli C, Natarajan P, Lichtman JH, D'Onofrio G, Matterna J, Dreyer R, Spertus JA, Taylor KD, Psaty BM, Rich SS, Post W, Gupta N, Gabriel S, Lander E, Chen YI, Talkowski ME, Rotter JJ, Krumholz HM°, Kathiresan S°. Whole genome sequencing to characterize monogenic and polygenic contributions in patients hospitalized with early-onset myocardial infarction. *Circulation* (2019), 139(13): 1593-1602. PMID: [30586733](#). DOI: [10.1161/CIRCULATIONAHA.118.035658](#).
Conducted all structural variation discovery and related disease association analyses; created Figure 2; assisted in revising manuscript
- 2018 § ! [33] Werling DM*, Brand H*, An J*, Stone MR*, Zhu L*, Glessner JT, **Collins RL**, Dong S, Layer RM, Markenscoff-Papadimitriou E, Farrell A, Schwartz GB, Wang HZ, Currall BB, Zhao X, Dea J, Duhn C, Erdman C, Gilson M, Handsaker RE, Kashin S, Klei L, Mandell JD, Nowakowski TJ, Liu Y, Pochareddy S, Smith L, Walker MF, Waterman MJ, He X, Kriegstein AR, Rubenstein JL, Sestan N, McCarroll SA, Neale BM, Coon H, Willsey Ajeremy, Buxbaum JD, Daly MJ, State MW, Quinlan A, Marth GT, Roeder K, Devlin B°, Talkowski ME°, Sanders SJ°. An analytical framework for whole genome sequence data and its implications for autism spectrum disorder. *Nature Genetics* (2018), 50(5): 727-736. PMID: [29700473](#). DOI: [10.1038/s41588-018-0107-y](#).
Assisted in study design; assisted in statistical & computational methods development; assisted in structural variant analyses & interpretation
Designed & created Figure 4; assisted in writing of manuscript
§ Highlighted in a [News and Views](#) commentary in [Nature Genetics](#).
- § ! [32] Aneichyk T*, Hendriks WT*, Yadav R*, Shin D*, Gao D*, Vaine CA, **Collins RL**, Domingo A, Currall B, Stortchevoi A, Mulhaupt-Buell T, Penney EB, Cruz L, Dhakal J, Brand H, Hanscom C, Antolik C, Dy M, Ragavendran A, Underwood J,

Cantsilieris S, Munson KM, Eichler EE, Acuña P, Go C, Jamora RDG, Rosales RL, Church DM, Williams SR, Garcia S, Klein C, Müller U, Wilhelmson KC, Timmers HTM, Ballouz S, Gillis J, Lyon GJ, Sapir Y, Wainger BJ, Henderson D, Ito N, Weisenfeld N, Jaffe D, Sharma N, Breakefield XO, Ozelius LJ, Bragg DC^o, Talkowski ME^o. Dissecting the causal mechanism of X-linked dystonia-parkinsonism by integrating genome and transcriptome assembly. *Cell* (2018), 172(5): 897-909.e21. PMID: [29474918](https://pubmed.ncbi.nlm.nih.gov/29474918/). DOI: [10.1016/j.cell.2018.02.011](https://doi.org/10.1016/j.cell.2018.02.011).

Led initial genotyping experiments; discovered initial recombination on disease haplotype; advised secondary studies & manuscript drafting

§ **Highlighted in a Preview commentary in *Cell* and by *Massachusetts General Hospital*.**

- 2017 ! [31] Redin C, Brand H, **Collins RL**, Kammin T, Mitchell E, Hodge JC, Hanscom C, Pillalamarri V, Seabra CM, Abbott M, Abdul-Rahman OA, Aberg E, Adley R, Alcaraz-Estrada SL, Alkuraya FS, An Y, Anderson M, Antolik C, Anyane-Yeboah K, Atkin JF, Bartell T, Bernstein JA, Beyer E, Bongers EMHF, Brilstra EH, Brown CW, Brüggewirth HT, Callewaert B, Corning K, Cox H, Cuppen E, Currall BB, Cushing T, David D, Deardorff MA, Dheedene A, D'hooghe M, de Vries BBA, Earl DL, Ferguson HL, Fisher H, FitzPatrick DR, Gerrol P, Giachino D, Glessner JT, Gliem T, Grady M, Graham BH, Griffis C, Gripp KW, Gropman AL, Hanson-Kahn A, Harris DJ, Hayden MA, Hochstenbach R, Hoffman JD, Hopkin RJ, Hubshman MW, Innes AM, Irons M, Irving M, Janssens S, Jewett T, Johnson JP, Jongmans MC, Kahler SG, Koolen DA, Korzelius J, Kroisel PM, Lacassie Y, Lawless W, Lemyre E, Leppig K, Levin AV, Li H, Li H, Liao EC, Lim C, Lose EJ, Lucente D, Macera MJ, Manavalan P, Mandriole G, Marcelis CL, Margolin L, Mason T, Masser-Frye D, McClellan MW, Mendoza CZ, Menten B, Middelkamp S, Mikami LR, Moe E, Mohammed S, Mononen T, Mortenson ME, Moya G, Nieuwint A, Ordule Z, Parkash S, Pauker SP, Pereira S, Perrin D, Phelan K, Piña-Aguilar RE, Poddighe PJ, Pregno G, Raskin S, Reis L, Rhead W, Rita D, Renkens I, Roelens J, Ruliera J, Rump P, Schilit SLP, Shaheen R, Sparkes R, Spiegel E, Stevens B, Stone MR, Tague J, Thakuria JV, van Bon BW, van de Kamp J, van der Burgt I, van Essen T, van Ravenswaaij-Arts CM, van Roosmalen MJ, Vergult S, Volker-Touw CML, Warburton DP, Waterman MJ, Wiley S, Wilson A, Vega M, Zori RT, Levy B, Brunner HG, de Leeuw N, Kloosterman WP, Thorland EC, Morton CC, Gusella JF, Talkowski ME. The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. *Nature Genetics* (2017), 49(1): 36-45. PMID: [27841880](https://pubmed.ncbi.nlm.nih.gov/27841880/). DOI: [10.1038/ng.3720](https://doi.org/10.1038/ng.3720).

Led development of structural variation discovery methods; analyzed ~10% of all samples; assisted in manuscript drafting & figure design

- 2014 § ! [30] Mandal PK*, Ferreira LMR*, **Collins RL**, Meissner TB, Boutwell CL, Friesen M, Garrison BS, Stortchevoi A, Bryder D, Musunuru K, Brand H, Allen TM, Talkowski ME, Rossi DJ^o, Cowan CA^o. Efficient ablation of genes in human hematopoietic stem and effector cells using CRISPR/Cas9. *Cell Stem Cell* (2014), 15(5): 643-652. PMID: [25517468](https://pubmed.ncbi.nlm.nih.gov/25517468/). DOI: [10.1016/j.stem.2014.10.004](https://doi.org/10.1016/j.stem.2014.10.004).

Designed targeted capture sequencing experiments; executed all analyses associated with CRISPR on- and off-target efficiencies

Designed and created Figure 4; assisted in writing of manuscript

§ **Featured by *TIME Magazine* and on the cover of *Cell Stem Cell***

- § [29] Brand H*, Pillalamarri V*, **Collins RL**, Eggert S, O'Dushlaine C, Braaten EB, Stone M, Chambert K, Doty ND, Hanscom C, Ditmars H, Blais J, Mills R, Lee C, Gusella JF, McCarroll S, Smoller JW, Talkowski ME^o, Doyle AE^o. Cryptic and complex chromosomal aberrations in early onset neuropsychiatric disorders. *American Journal of Human Genetics* (2014). 95:4, 454-461. PMID: [25279985](https://pubmed.ncbi.nlm.nih.gov/25279985/). DOI: [10.1016/j.ajhg.2014.09.005](https://doi.org/10.1016/j.ajhg.2014.09.005).

Led development of structural variation discovery methods; assisted in study design & writing of manuscript; led design for all figures

§ **Recipient of 2014 Massachusetts General Hospital Clinical Research Team Award (see Awards & Honors)**

- ! [28] Veres A, Gosis BS, Ding Q, **Collins RL**, Ragavendran A, Brand H, Erdin S, Talkowski ME, Musunuru K. Low incidence of off-target mutations in individual CRISPR-Cas9 and TALEN targeted human stem cell clones detected by whole-genome sequencing. *Cell Stem Cell* (2014), 15:1, 27-30. PMID: [24996167](https://pubmed.ncbi.nlm.nih.gov/24996167/). DOI: [10.1016/j.stem.2014.04.020](https://doi.org/10.1016/j.stem.2014.04.020).

Led structural variation discovery analyses; assisted in writing of manuscript

Articles authored as a minor contributor

- 2022 [27] Tai DJC*, Razaz P*, Erdin S*, Gao D*, Wang J, Nuttle X, de Esch CE, Collins RL, Currall BB, O'Keefe K, Burt ND, Yadav R, Mohajeri K, Anechik T, Ragavendran A, Stortchevoi A, Morini E, Ma W, Lucente D, Hastie A, Kelleher RJ, Perlis RH, Talkowski ME^o, Gusella JF^o. Tissue and cell-type specific molecular and functional signatures of 16p11.2 reciprocal genomic disorder across mouse brain and human neuronal models. *American Journal of Human Genetics* (2022), online ahead of print. PMID: [36152629](https://pubmed.ncbi.nlm.nih.gov/36152629/). DOI: [10.1016/j.ajhg.2022.08.012](https://doi.org/10.1016/j.ajhg.2022.08.012).

Conducted analyses of genomic properties of 16p11.2 CNV locus.

- 2021 ! [26] Nasser J*, Bergman DT*, Fulco CP*, Guckelberger P*, Doughty BR*, Patwardhan T, Jones TR, Nguyen TH, Ulirsch JC, Natri HM, Weeks EM, Munson G, Kane M, Kang HY, Cui A, Ray JP, Eisenhaure TM, Mualim K, **Collins RL**, Dey K, Price A, Epstein CB, Kundaje A, Xavier RJ, Daly MJ, Huang H, Finucane HK, Hacohen N, Lander ES^o, Engreitz JM^o. Genome-wide maps of enhancer regulation connect risk variants to disease genes. *Nature* (2021), 593: 238-243. PMID: [33828297](https://pubmed.ncbi.nlm.nih.gov/33828297/). DOI: [10.1038/s41586-021-03446-x](https://doi.org/10.1038/s41586-021-03446-x).

Contributed to development of enhancer prediction model (ABC-Max) in 16 immune cell types

- [25] Gudmundsson S, Karczewski KJ, Francioli LC, Tiao G, Cummings BB, Alfoldi J, Wang Q, **Collins RL**, Laricchia KM, Ganna A, Birnbaum DP, Gauthier LD, Brand H, Solomonson M, Watts NA, Rhodes D, Singer-Berk M, England EM, Seaby EG, Kosmicki JA, Walters RK, Tashman K, Farjoun Y, Banks E, Poterba T, Wang A, Seed C, Whiffin N, Chong JX, Samochoa KE, Pierce-Hoffman E, Zappala Z, O'Donnell-Luria AH, Vallabh-Minikel E, Weisburd B, Lek M, Ware JS, Vittal C, Armean IM, Bergelson L, Cibulskis K, Connolly KM, Covarrubias M, Donnelly S, Ferreira S, Gabriel S, Gentry J, Gupta N, Jeandet T, Kaplan D, Llanwarne C, Munshi R, Novod S, Petrillo N, Roazen D, Ruano-Rubio V, Saltzman A, Schleicher M, Soto J, Tibbetts K, Tolonen C, Wade G, Talkowski ME, Neale BM, Daly MJ, MacArthur DG. Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature* (2021), online ahead of print. PMID: [34373650](https://pubmed.ncbi.nlm.nih.gov/34373650/). DOI: [10.1038/s41586-021-03758-y](https://doi.org/10.1038/s41586-021-03758-y).

Contributed to the production of the Genome Aggregation Database (gnomAD)

- [24] Wahlster L*, Verboon JM*, Ludwig LS, Black SC, Luo W, Garg K, Voit RA, **Collins RL**, Garimella K, Costello M, Chao KR, Goodrich JK, DiTroia SP, O'Donnell-Luria A, Talkowski ME, Michelson AD, Cantor AB, Sankaran VG. Familial

Thrombocytopenia Due to a WAC-ANKRD26 Gene Fusion. *Journal of Experimental Medicine* (2021), 218 (6): e20210444. PMID: [33857290](https://pubmed.ncbi.nlm.nih.gov/33857290/).

Assisted in sequencing data analysis to identify the causal complex inversion underlying this Mendelian blood disorder

- [23] Jung R, Lee Y, Barker D, Correia K, Shin B, Loupe J, **Collins RL**, Lucente D, Ruliera J, Gillis T, Mysore JS, Rodan L, Picker J, Lee J, Howland D, Lee R, Kwak S, MacDonald ME., Gusella JF., Seong IS. Mutations causing Lopes-Maciel-Rodan Syndrome are huntingtin hypomorphs. *Human Molecular Genetics* (2021), online ahead of print. PMID: [33432339](https://pubmed.ncbi.nlm.nih.gov/33432339/). DOI: [10.1093/hmg/ddaa283](https://doi.org/10.1093/hmg/ddaa283).
Curated information on the presence of Huntington loss-of-function mutations in the general population
- 2020 [22] Han L*, Zhao X*, Benton ML, Perumal T, **Collins RL**, Hoffman G, Johnson JS, Sloofman L, Consortium C, Brennand KJ, Brand H, Sieberts SK, Marengo S, Peters MA, Lipska BK, Roussos P, Capra JA, Talkowski M, Ruderfer DM. Functional annotation of rare structural variation in the human brain. *Nature Communications* (2020), 11:2990, 1-13. PMID: [32533064](https://pubmed.ncbi.nlm.nih.gov/32533064/). DOI: [10.1038/s41467-020-16736-1](https://doi.org/10.1038/s41467-020-16736-1).
Contributed to structural variation discovery analyses and statistical methods development; assisted in manuscript drafting & figure design
- [21] Lillväli H, Pajusalu S, Wojcik MH, Goodrich J, **Collins RL**, Murumets U, Tammur P, Blau N, Lillväli K, Öunap K. Genome sequencing identifies a homozygous inversion disrupting *QDPR* gene as a cause for dihydropteridine reductase deficiency. *Molecular Genetics & Genomic Medicine* (2020), 5:e1154. PMID: [32022462](https://pubmed.ncbi.nlm.nih.gov/32022462/). DOI: [10.1002/mgg3.1154](https://doi.org/10.1002/mgg3.1154).
Assisted in variant interpretation and manuscript editing
- 2019 [20] Toomer K*, Yu M*, Fulmer D, Guo L, Moore K, Moore R, Drayton K, Glover J, Peterson N, Ramos-Ortiz S, Drohan A, Catching BJ, Stairley R, Wessels A, Lipschutz JH, Delling FN, Jeunemaitre X, Dina C, **Collins RL**, Brand H, Talkowski ME, del Monte F, Mukherjee R, Awgulewitsch A, Body S, Hardiman G, Da Silveira W, Wang B, Leyne M, Durst R, Markwald R, Le Scouranec S, Hagege A, Le Tourneau T, Kohl P, Rog-Zielinska E, Schott J°, Levine RA°, Milan D°, Bouatia-Naji N°, Slangenaupt S°, Norris RA°. Primary cilia defects causing mitral valve prolapse. *Science Translational Medicine* (2019), 11(493). PMID: [31118289](https://pubmed.ncbi.nlm.nih.gov/31118289/). DOI: [10.1126/scitranslmed.aax0290](https://doi.org/10.1126/scitranslmed.aax0290).
Conducted exome sequencing analysis that identified missense variants in *DZ1P1* as a likely causal gene for mitral valve prolapse
- 2018 ! [19] An JY*, Lin K*, Zhu L*, Werling DM*, Dong S, Brand H, Wang HZ, Zhao X, Schwartz GB, **Collins RL**, Currall BB, Dastmalchi C, Dea J, Duhn C, Gilson MC, Klei L, Liang L, Markenscoff-Papadimitriou E, Pochareddy S, Ahituv N, Buxbaum JD, Coon H, Daly MJ, Kim YS, Marth GT, Neale BM, Quinlan AR, Rubenstein JL, Sestan N, State MW, Willsey AJ, Talkowski ME°, Devlin B°, Roeder K°, Sanders SJ°. Genome-wide *de novo* risk score implicates promoter variation in autism spectrum disorder. *Science* (2018), 362(6420). PMID: [30545857](https://pubmed.ncbi.nlm.nih.gov/30545857/). DOI: [10.1126/science.aat8464](https://doi.org/10.1126/science.aat8464).
Contributed to genome annotations, burden testing design, promoter-proximal analysis framework, and figure design
- [18] Halgren C, Nielsen NM, Nazaryan-Petersen L, Silahtaroglu A, **Collins RL**, Lowther C, Kjaergaard S, Frisch M, Kirchhoff M, Brøndum-Nielsen K, Lind-Thomsen A, Mang Y, El-Schich Z, Boring C, Mehrjouy MM, Jensen PKA, Fagerberg C, Krogh LN, Hansen J, Bryndorf T, Hansen C, Talkowski ME, Bak M, Tommerup N*, Bache I*. Risk and recommendations in prenatally detected *de novo* balanced chromosomal rearrangements from assessment of long-term outcomes. *American Journal of Human Genetics* (2018). PMID: [29805044](https://pubmed.ncbi.nlm.nih.gov/29805044/). DOI: [10.1016/j.ajhg.2018.04.005](https://doi.org/10.1016/j.ajhg.2018.04.005).
Led phenotype-blinded analysis of 27 prenatal WGS cases, including functional interpretation and phenotype prediction
- 2017 [17] Pedersen B, **Collins RL**, Talkowski ME, Quinlan A. Indexcov: fast whole-genome coverage quality-control from BAM or CRAM indexes. *GigaScience* (2017), 6(11), 1-6. PMID: [29048539](https://pubmed.ncbi.nlm.nih.gov/29048539/). DOI: [10.1093/gigascience/gix090](https://doi.org/10.1093/gigascience/gix090).
Contributed to study design, analyses, and manuscript drafting
- § ! [16] Shaw ND*, Brand H*, Kupchinsky ZA, Bengani H, Plummer L, Jones TI, Erdin S, Williamson KA, Rainger J, Stortchevoi A, Samooha K, Currall BB, Dunican DS, **Collins RL**, Willer JR, Lek A, Lek M, Nassan M, Pereira S, Kammin T, Lucente D, Silva A, Seabra CM, Chiang C, An Y, Ansari M, Rainger JK, Joss S, Smith JC, Lippincott MF, Singh SS, Patel N, Jing JW, Law JR, Ferraro N, Verloes A, Rauch A, Steindl K, Zweier M, Scheer I, Sato D, Okamoto N, Jacobsen C, Tryggestad J, Chernausk S, Schimmenti LA, Brasseur B, Cesaretti C, García-Ortiz JE, Buitrago TP, Silva OP, Hoffman JD, Mühlbauer W, Ruprecht KW, Loeyls BL, Shino M, Kaindl AM, Cho C, Morton CC, Meehan RR, van Heyningen V, Liao EC, Balasubramanian R, Hall JE, Seminara SB, Macarthur D, Moore SA, Yoshiura K, Gusella JF, Marsh JA, Graham Jr JM, Lin AE, Katsanis N, Jones PL, Crowley Jr WF, Davis EE°, FitzPatrick DR°, Talkowski ME°. *SMCHD1* mutations associated with a rare muscular dystrophy can also cause isolated arhinia and Bosma arhinia microphthalmia syndrome. *Nature Genetics* (2017), 49(2): 238-248. PMID: [28067909](https://pubmed.ncbi.nlm.nih.gov/28067909/). DOI: [10.1038/ng.3743](https://doi.org/10.1038/ng.3743).
Analyzed the initial set of 18/40 whole-exomes that primed discovery of *SMCHD1* as pleiotropic contributor to arhinia
§ Highlighted in a News and Views commentary in *Nature Genetics* and reviewed in *Trends in Genetics*.
- § [15] Maussion G*, Cruceanu C*, Rosenfeld JA, Bell SC, Jollant F, Szatkiewicz J, **Collins RL**, Hanscom C, Kolobova I, de Champfleury NM, Blumenthal I, Chiang C, Ota V, Hultman C, O'Dushlaine C, McCarroll S, Alda M, Jacquemont S, Ordlu Z, Marshall CR, Carter MT, Shaffer LG, Sklar P, Girirajan S, Morton CC, Gusella JF, Turecki G, Stavropoulos DJ, Sullivan PF, Scherer SW, Talkowski ME, Ernst C. Implication of LRRC4C and DPP6 in neurodevelopmental disorders. *American Journal of Medical Genetics* (2017), 173(2): 395-406. PMID: [27759917](https://pubmed.ncbi.nlm.nih.gov/27759917/). DOI: [10.1002/ajmg.a.38021](https://doi.org/10.1002/ajmg.a.38021).
Led copy number variation analyses to quantify neurodevelopmental disorder liability conferred by alterations to the netrin gene family
§ Featured on the cover of *The American Journal of Medical Genetics*
- 2016 [14] Ordlu Z, Kammin T, Brand H, Pillalamarri V, Redin CE, **Collins RL**, Blumenthal I, Hanscom C, Pereira S, Bradley I, Crandall BF, Gerrol P, Hayden MA, Hussain N, Kanengisser-Pines B, Kantarci S, Levy B, Macera MJ, Quintero-Rivera F, Spiegel E, Stevens B, Ulm JE, Warburton D, Wilkins-Haug LE, Yachevich N, Gusella JF, Talkowski ME, Morton CC. Structural chromosome rearrangements require nucleotide level resolution: lessons from next-generation sequencing in prenatal diagnosis. *American Journal of Human Genetics* (2016), 99(5): 1015-1033. PMID: [27745839](https://pubmed.ncbi.nlm.nih.gov/27745839/). DOI: [10.1016/j.ajhg.2016.08.022](https://doi.org/10.1016/j.ajhg.2016.08.022).
Performed structural variation analyses for 20% of samples presented in study

- [13] Schilit S, Currall B, Yao R, Hanscom C, **Collins RL**, Pillalamarri V, Lee DYD, Kammin T, Zepeda-Mendoza CJ, Mononen T, Nolan LS, Gusella JF, Shen J, Talkowski M, Morton CC. Estrogen-related receptor gamma implicated in a case of syndromic hearing loss and mild developmental delay. *European Journal of Human Genetics* (2016), 24(11): 1622-1626. PMID: [27381092](https://pubmed.ncbi.nlm.nih.gov/27381092/). DOI: [10.1038/ejhg.2016.64](https://doi.org/10.1038/ejhg.2016.64).
Co-led analysis of whole-genome sequencing of patient in study
- [12] Macakova M, Bohuslavova B, Vochozkova P, Pavlok A, Sedlackova M, Vidinska D, Vochoyanova K, Liskova I, Valekova I, Baxa M, Ellederova Z, Klima J, Juhas S, Juhasova J, Klouckova J, Haluzik M, Klempir J, Hansikova H, Spacilova J, **Collins RL**, Blumenthal I, Talkowski M, Gusella JF, Howland DS, DiFiglia M, Motlik J. Mutated Huntingtin causes testicular pathology in transgenic minipig boars. *Neurodegenerative Diseases* (2016), 16(3-4): 245-259. PMID: [26959244](https://pubmed.ncbi.nlm.nih.gov/26959244/). DOI: [10.1159/000443665](https://doi.org/10.1159/000443665).
Performed whole-genome analysis of chromosomal integrity in germline samples to validate genome structure of transgenic animal models
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