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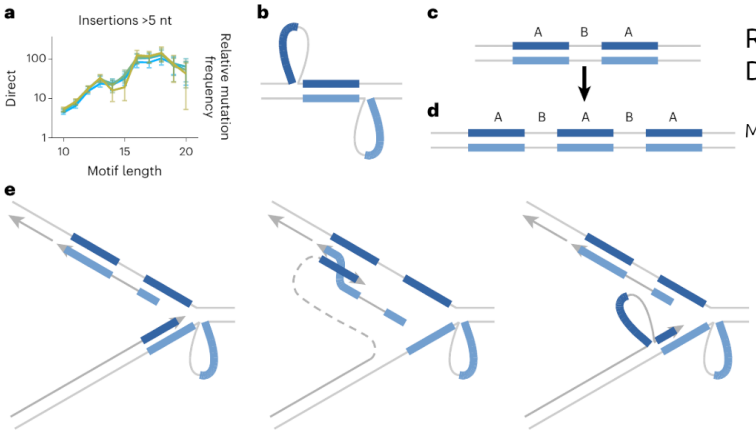
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NERINE reveals rare variant associations in gene networks across phenotypes and implicates an SNCA-PRL-LRRK2 subnetwork in Parkinson's disease

Nazeen S et al. (2026) Cell Genom 6(7):101284

On the cover: Nazeen et al. present NERINE, an algorithm used to study gene networks. The image depicts a nerine flower and the spatial structure of the VDAC protein, which the program NERINE links with Parkinson's disease. Artist: Rauf Sunyaev.

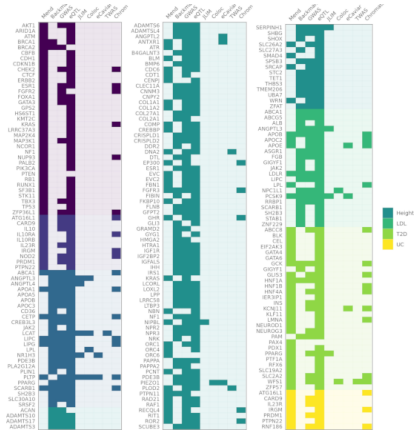
DOI:10.1016/j.xgen.2026.101284

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Revisiting mutagenesis at non-B DNA motifs in the human genome

McGinty RJ, Sunyaev SR (2023) Nat Struct Mol Biol

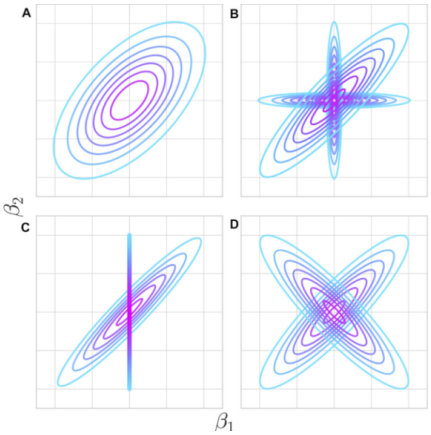
DOI:10.1038/s41594-023-00936-6

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The missing link between genetic association and regulatory function

Connally NJ et al. (2022) Elife 11:e74970

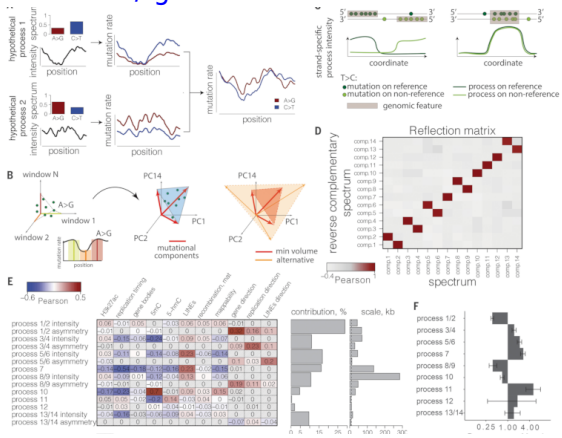
DOI:10.7554/eLife.74970



- Maintenance of Complex Trait Variation: Classic Theory and Modern Data

  Koch EM, Sunyaev SR (2021) Front Genet 12:763363

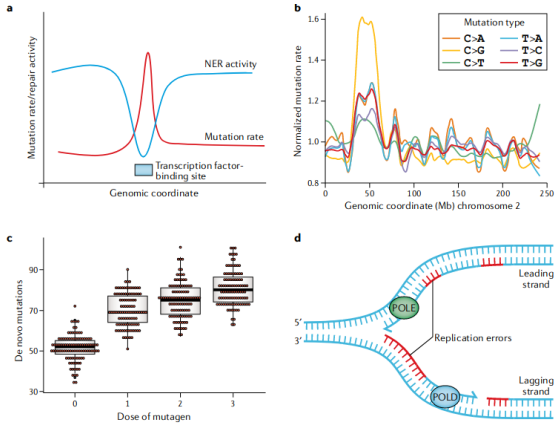
  DOI:10.3389/fgene.2021.763363



- Population sequencing data reveal a compendium of mutational processes in the human germ line

  Seplyarskiy VB et al. (2021) Science 373(6558):1030-1035

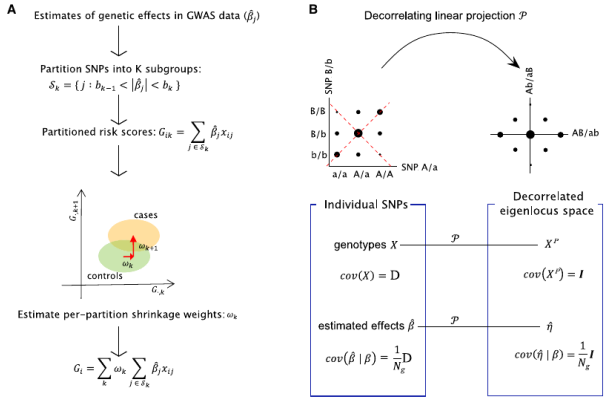
  DOI:10.1126/science.aba7408



- The origin of human mutation in light of genomic data

  Seplyarskiy VB, Sunyaev S (2021) Nat Rev Genet 10:672-686

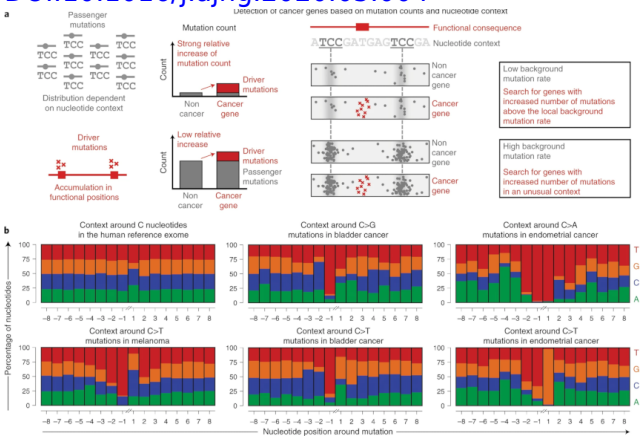
  DOI:10.1038/s41576-021-00376-2



- Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics

  Chun S. et al. (2020) Am J Hum Genet 107:46-59

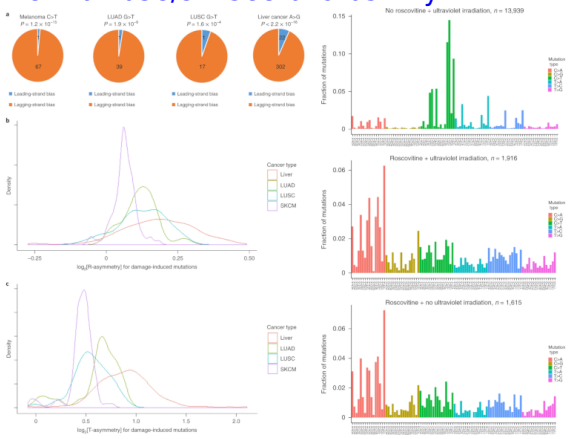
DOI:10.1016/j.ajhg.2020.05.004



Identification of Cancer Driver Genes Based On Nucleotide Context

Dietlein F, Weghorn D et al. (2020) Nat Genet. 52(2):208-218

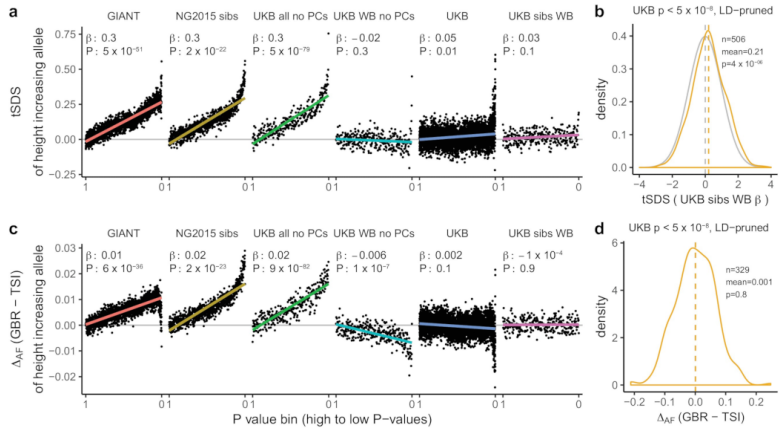
DOI:10.1038/s41588-019-0572-y



Error-prone bypass of DNA lesions during lagging-strand replication is a common source of germline and cancer mutations

Seplyarskiy VB et al. (2019) Nat Genet 51(1):36-41

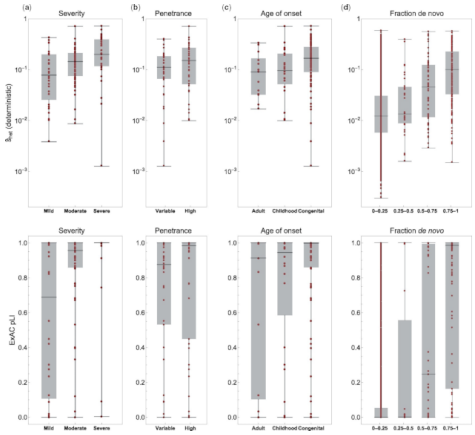
DOI:10.1038/s41588-018-0285-7



Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies

Sohail M et al. (2019) Elife 8:e39702

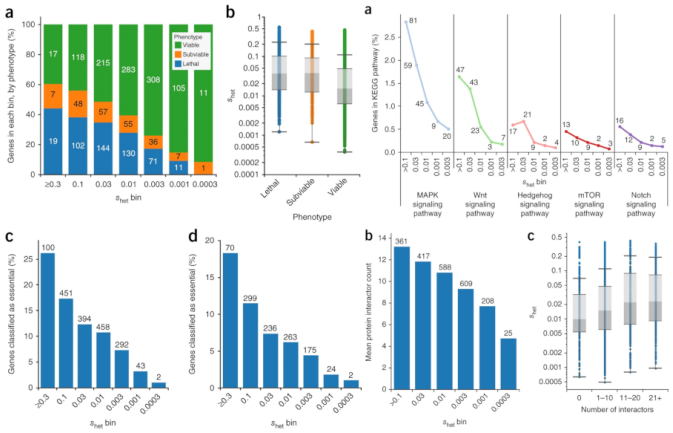
DOI:10.7554/eLife.39702



Applicability of the Mutation-Selection Balance Model to Population Genetics of Heterozygous Protein-Truncating Variants in Humans

Weghorn D et al. (2019) Mol Biol Evol 36(8):1701-1710

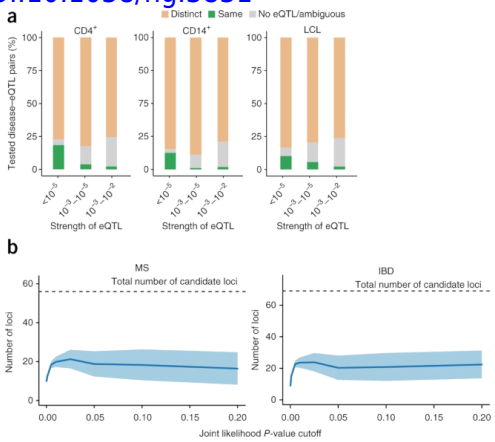
- DOI:10.1093/molbev/msz092



Estimating the selective effects of heterozygous protein-truncating variants from human exome data

Cassa CA et al (2017) Nat Genet 49(5):806-810

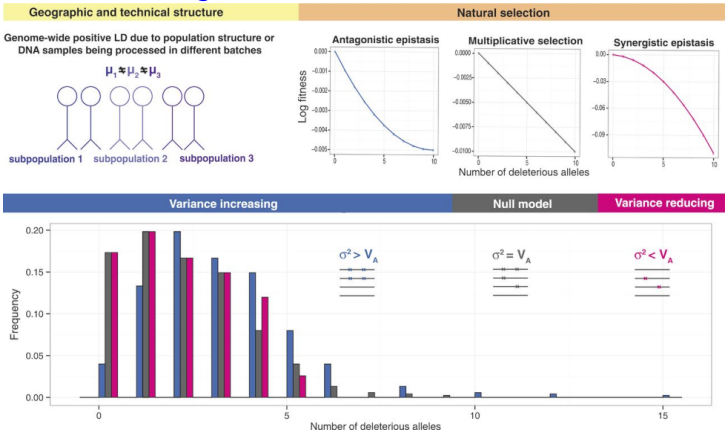
- DOI:10.1038/ng.3831



Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types

Chun S et al. (2017) Nat Genet 49(4):600-605

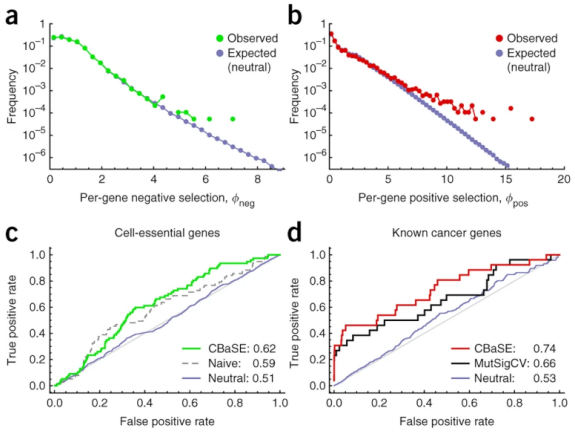
- DOI:10.1038/ng.3795



Negative selection in humans and fruit flies involves synergistic epistasis

Sohail M et al. (2017) Science 356(6337):539-542

DOI:10.1126/science.aah5238

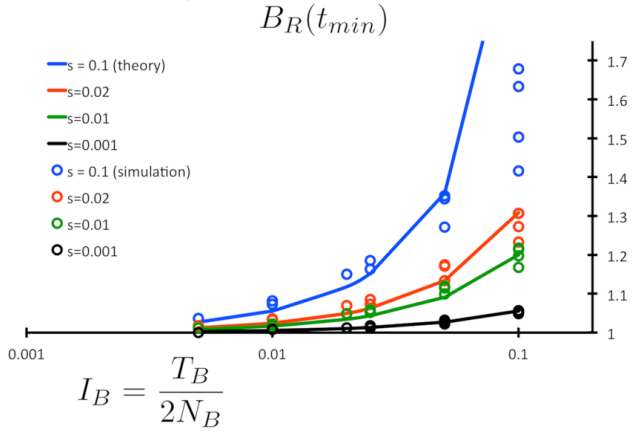


Bayesian inference of negative and positive selection in human cancers

Weghorn D, Sunyaev S (2017) Nat Genet 49(12):1785-1788

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DOI:10.1038/ng.3987

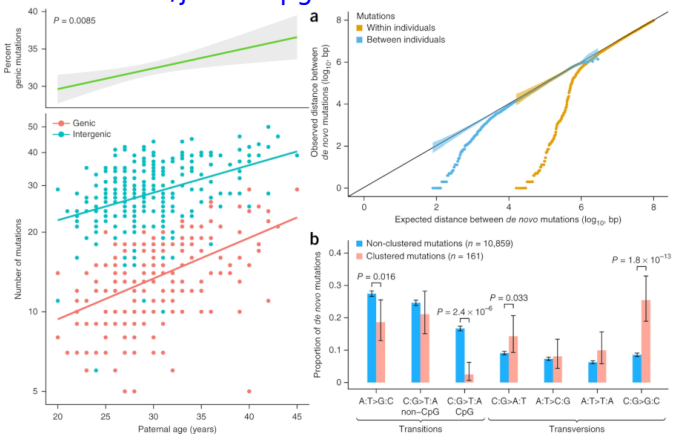


Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck

Balick DJ et al. (2015) PLoS Genet 11(8):e1005436

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DOI:10.1371/journal.pgen.1005436

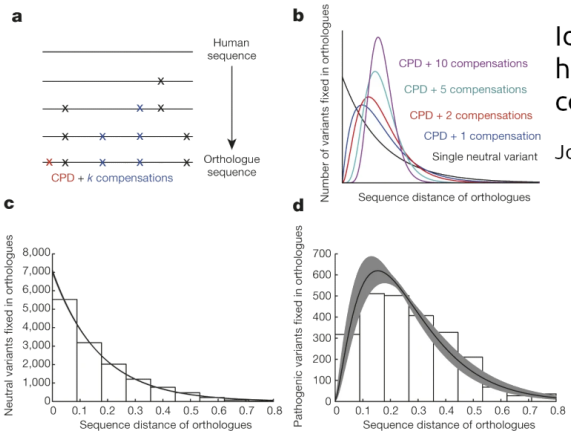


Genome-wide patterns and properties of de novo mutations in humans

Francioli et al. (2015) Nature Genetics, 47(7):822-826

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DOI:10.1038/ng.3292



Identification of cis-suppression of human disease mutations by comparative genomics

Jordan DM et al. (2015) Nature 524(7564):225-229

- DOI:10.1038/nature14497

The Sunyaev Lab is a computational genomics laboratory at Department of Biomedical Informatics, Harvard Medical School and Division of Genetics, Brigham & Women's Hospital. The primary focus of research in the lab is on genetic variation, including the biology and evolution of mutation, the effect of variation on molecular function and structure, population genetics as a lens on evolution, and the maintenance and allelic architecture of complex traits. We develop computational and statistical methods for sequencing studies. We also have projects in cancer genomics and applied human genetics. The lab encompasses a wide range of skills, backgrounds, and interests spanning these topics.

We are involved in the following graduate programs:

- Biological & Biomedical Sciences Program at the Division of Medical Sciences, Harvard Medical School
- Harvard Biophysics Program
- Harvard Bioinformatics and Integrative Genomics Program
- Program in Quantitative Genomics at the Harvard School of Public Health

We participate in:

- Medical and Population Genetics Program at the Broad Institute of MIT and Harvard
- Boston Evolutionary Genomics Supergroup

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Brigham and Women's Hospital
Founding Member, Mass General Brigham

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Sunyaev Lab intranet (login required)

Sunyaev Lab social events:



Boston Red Sox ONE PIECE Theme Night at Fenway Park, Spring 2026



Vegan-friendly dinner at Koshari Mama, Spring 2022



Walden Pond, Fall 2021

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