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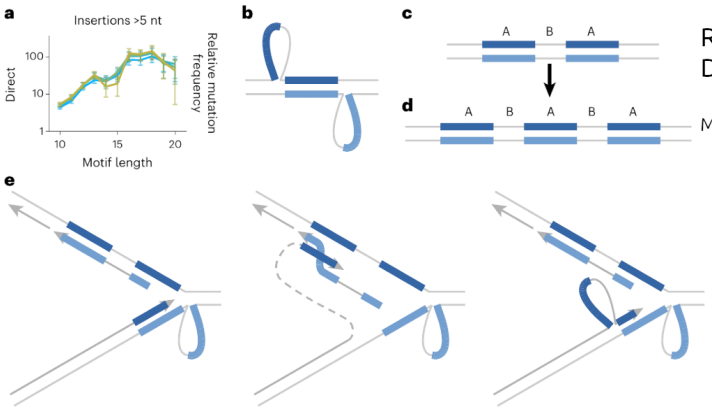
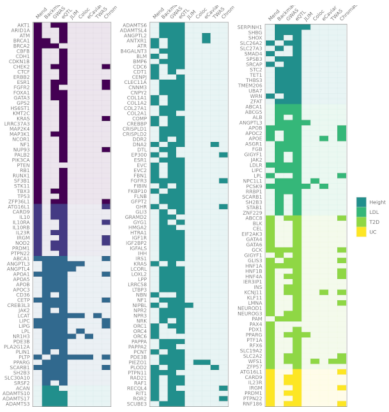


Revisiting mutagenesis at non-B DNA motifs in the human genome

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

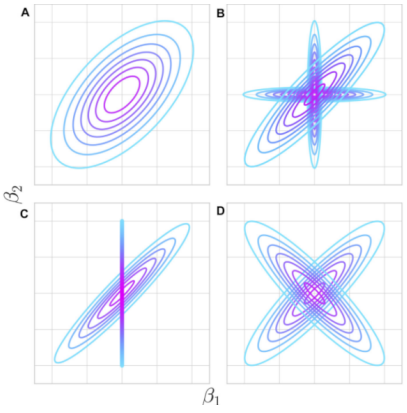
- DOI:10.1038/s41594-023-00936-6



The missing link between genetic association and regulatory function

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

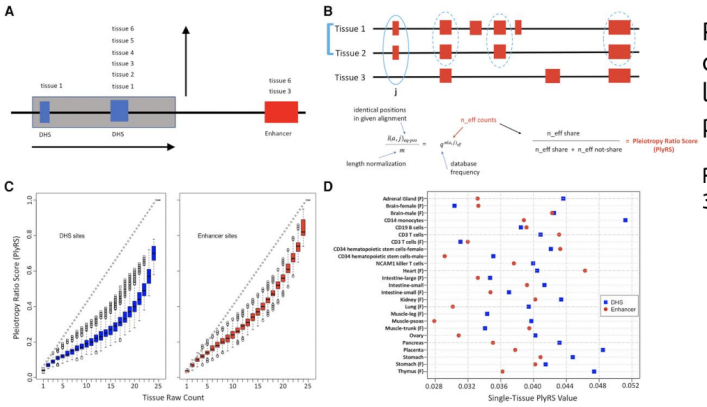
- DOI:10.7554/eLife.74970



Maintenance of Complex Trait Variation: Classic Theory and Modern Data

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

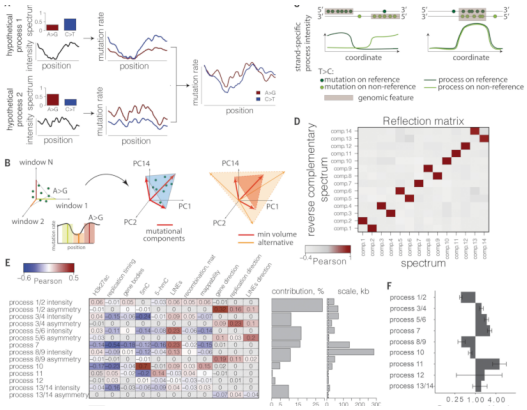
- DOI:10.3389/fgene.2021.763363



Purifying selection on noncoding deletions of human regulatory loci detected using their cellular pleiotropy

Radke DW et al. (2021) Genome Res 31(6):935-946

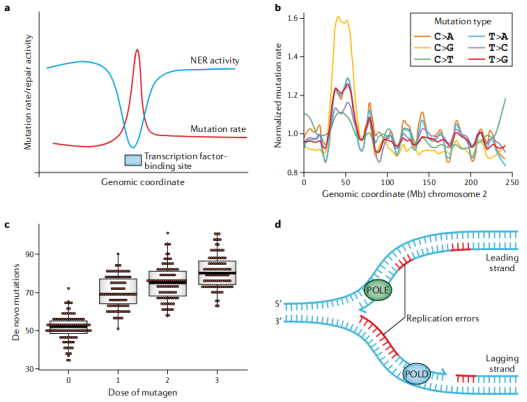
- DOI:10.1101/gr.275263.121



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

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

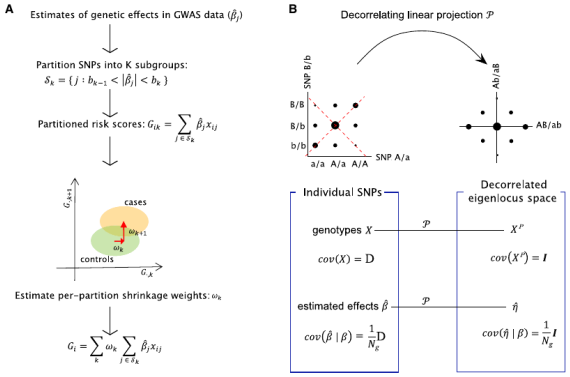
- DOI:10.1126/science.aba7408



The origin of human mutation in light of genomic data

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

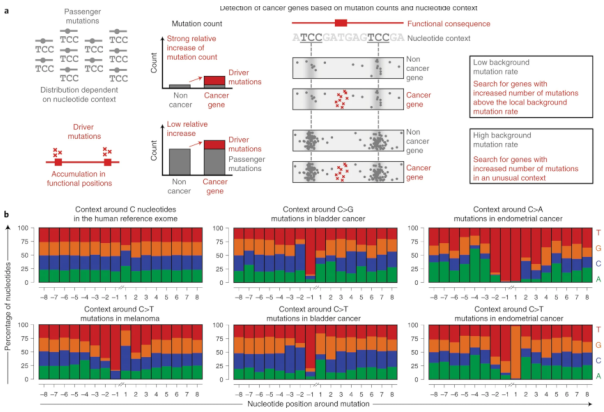
- DOI:10.1038/s41576-021-00376-2



Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics

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

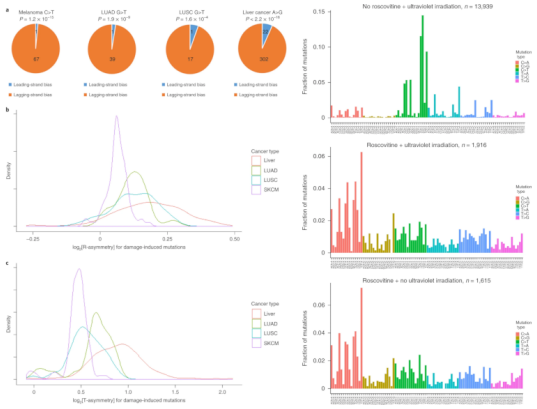
- DOI:10.1016/j.ajhg.2020.05.004



Identification of Cancer Driver Genes Based On Nucleotide Context

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

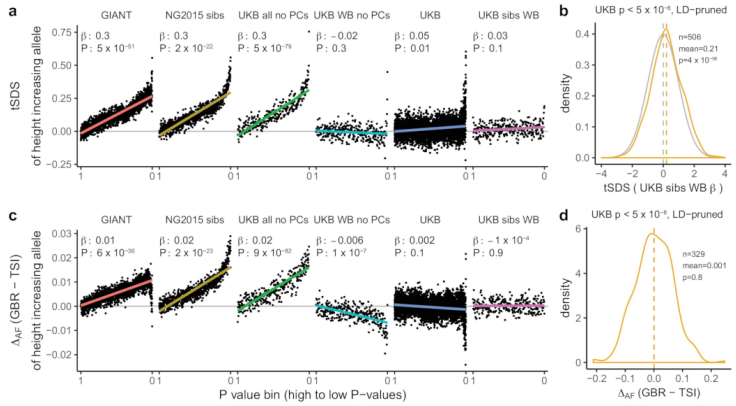
DOI:10.1038/s41588-019-0572-y



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

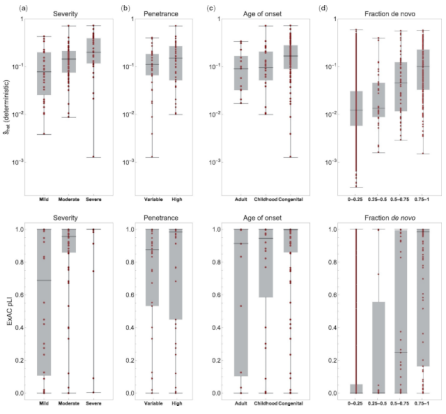
DOI:10.1038/s41588-018-0285-7



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

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

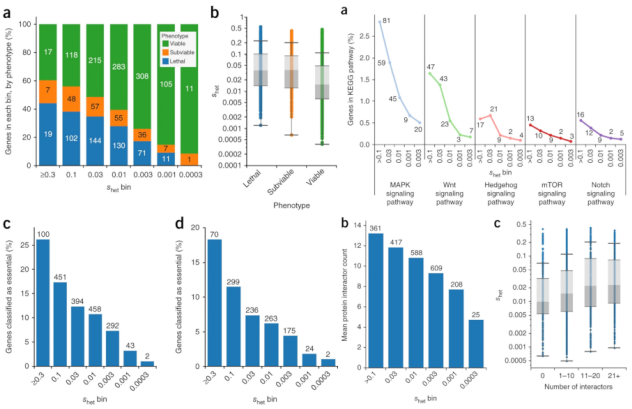
DOI:10.7554/eLife.39702



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

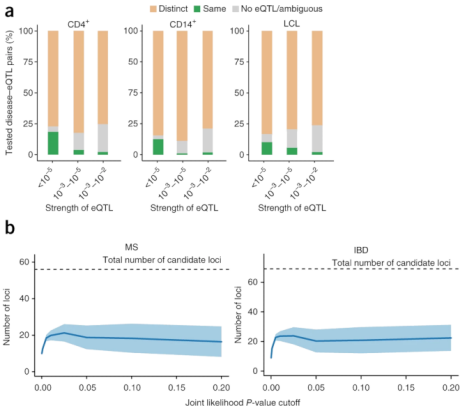
DOI:10.1093/molbev/msz092



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

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

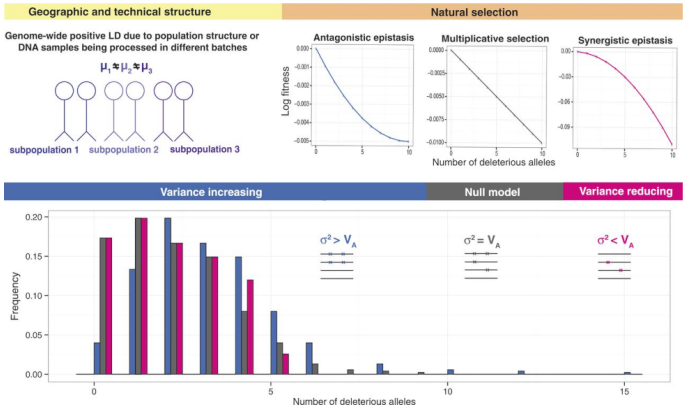
- DOI:10.1038/ng.3831



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

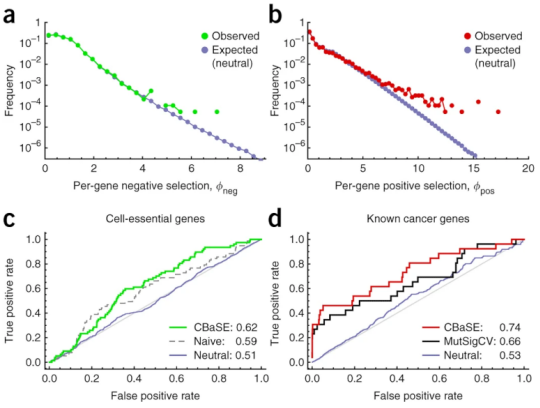
- DOI:10.1038/ng.3795



Negative selection in humans and fruit flies involves synergistic epistasis

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

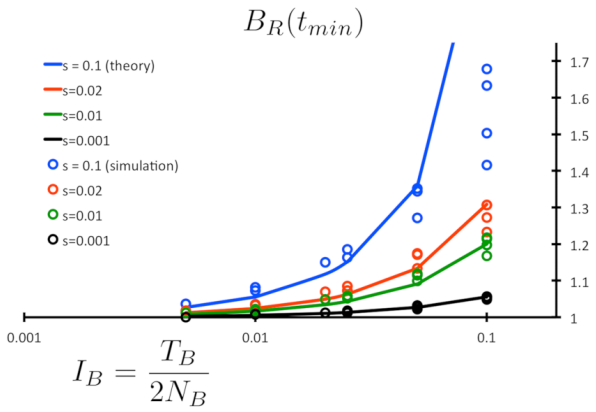
- DOI:10.1126/science.aah5238



Bayesian inference of negative and positive selection in human cancers

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

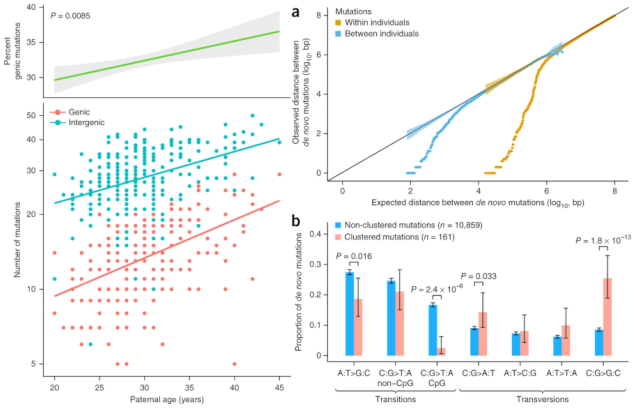
- DOI:10.1038/ng.3987



- Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck

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

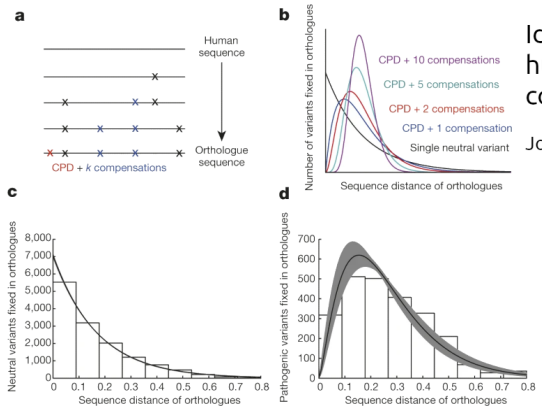
  DOI:10.1371/journal.pgen.1005436



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

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

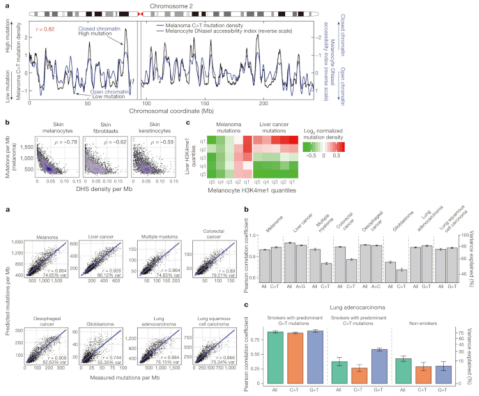
  DOI:10.1038/ng.3292



- 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



- Cell-of-origin chromatin organization shapes the mutational landscape of cancer

  Polak P et al. (2015) Nature 518(7539):360-364

  DOI:10.1038/nature14221

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

HARVARD MEDICAL SCHOOL

BLAVATNIK INSTITUTE
BIOMEDICAL INFORMATICS

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

BROAD INSTITUTE

Sunyaev Lab intranet (login required)

Recent Sunyaev Lab social events:

BBQ at Shamil's place, Spring 2023

Vegan-friendly dinner at Koshari Mama, Spring 2022

Walden Pond, Fall 2021