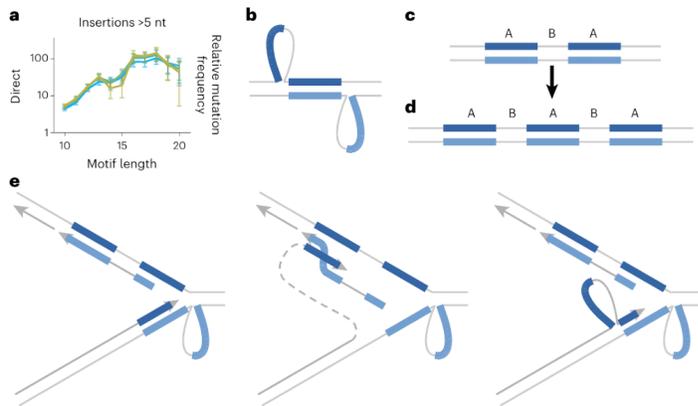


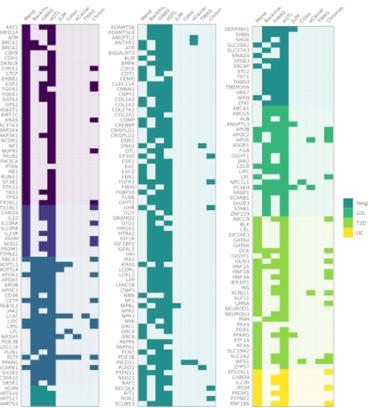
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Revisiting mutagenesis at non-B DNA motifs in the human genome

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

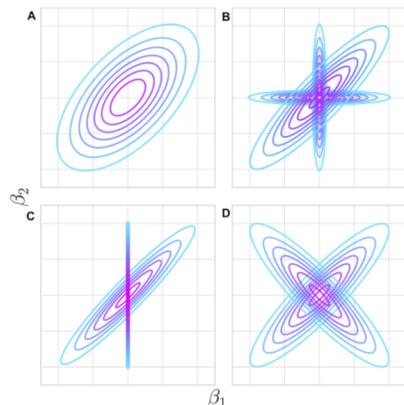
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The missing link between genetic association and regulatory function

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

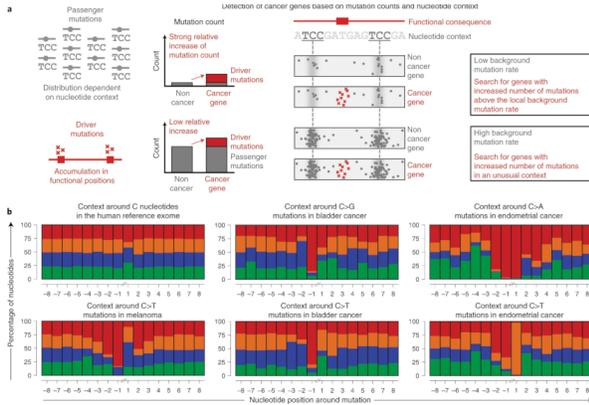
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Maintenance of Complex Trait Variation: Classic Theory and Modern Data

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

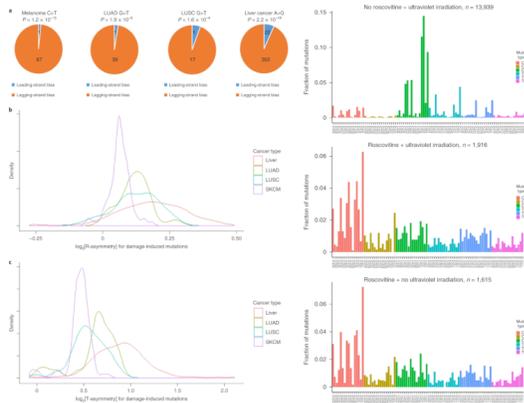
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Identification of Cancer Driver Genes Based On Nucleotide Context

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

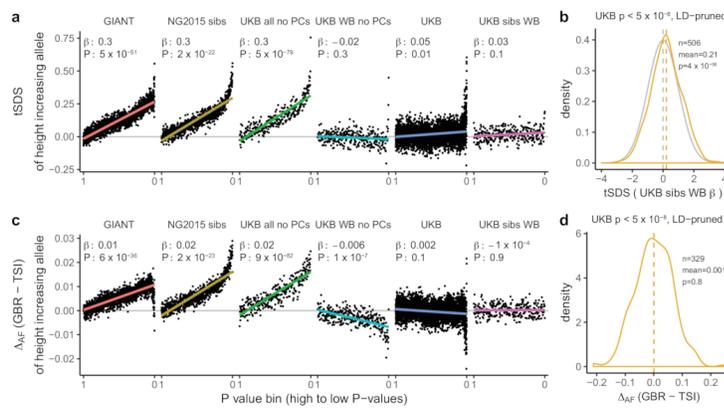
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Error-prone bypass of DNA lesions during lagging-strand replication is a common source of germline and cancer mutations

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

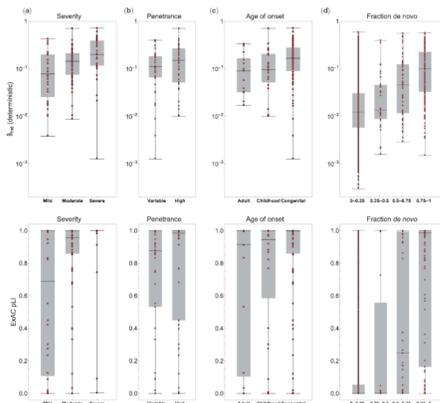
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Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies

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

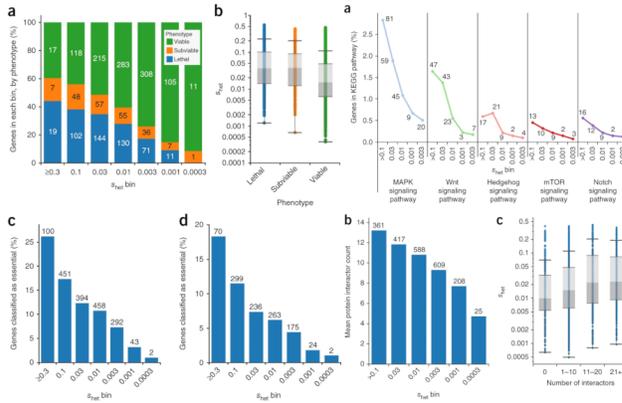
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Applicability of the Mutation-Selection Balance Model to Population Genetics of Heterozygous Protein-Truncating Variants in Humans

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

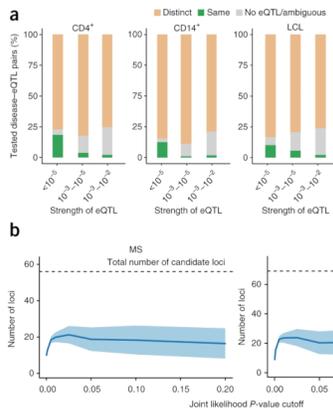
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Estimating the selective effects of heterozygous protein-truncating variants from human exome data

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

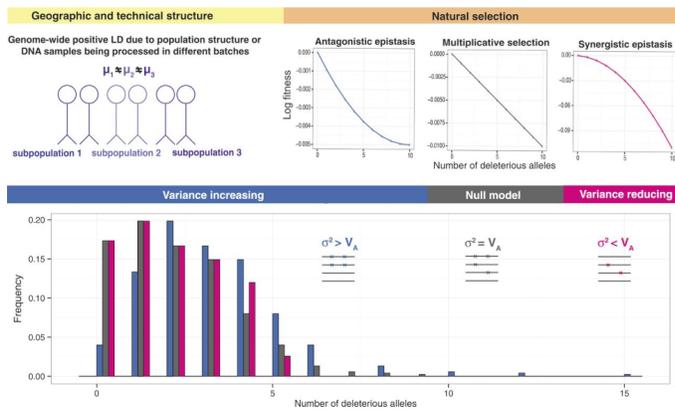
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Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types

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

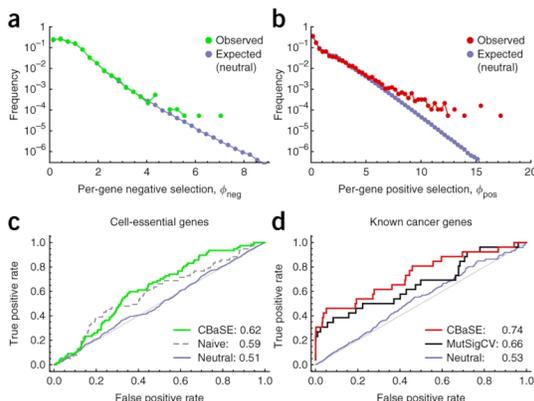
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Negative selection in humans and fruit flies involves synergistic epistasis

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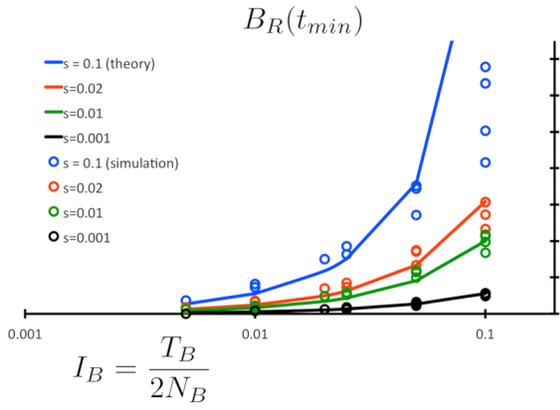
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Bayesian inference of negative and positive selection in human cancers

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

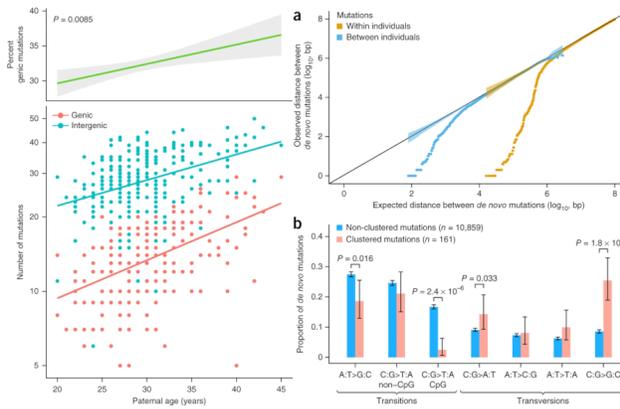
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Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck

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

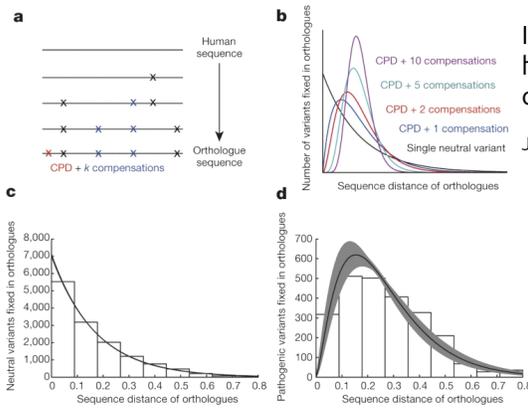
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Genome-wide patterns and properties of de novo mutations in humans

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

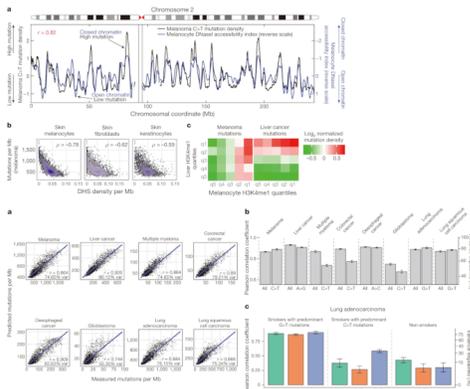
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Identification of cis-suppression of human disease mutations by comparative genomics

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](#)



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Recent Sunyaev Lab social events:



BBQ at Shamil's place, Spring 2023



Vegan-friendly dinner at [Koshari Mama](#), Spring 2022



 [Walden Pond](#), Fall 2021

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