Leveraging Large iPSC Cohorts and Population Scale Stem Cell Models to Study the Effect of Genetic Variation on Cellular Phenotypes

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The CIRM-CDI iPSC Repository

SAMPLE COLLECTION



Liver Disease

Lung Disease

Heart disease

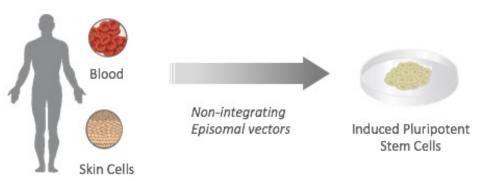
disorders

disorders

Blinding eye disease

Neurodegenerative

Childhood neurological



Generating the world's largest induced pluripotent stem cell (iPSC) bank

A COLLABORATIVE ENDEAVOR



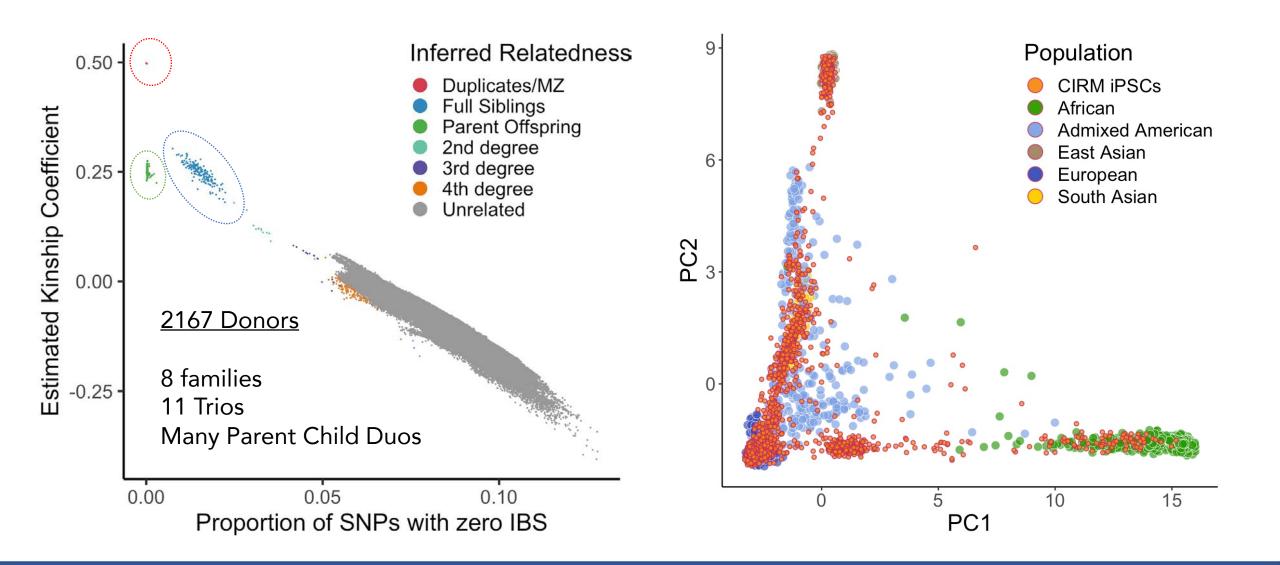


Organoid

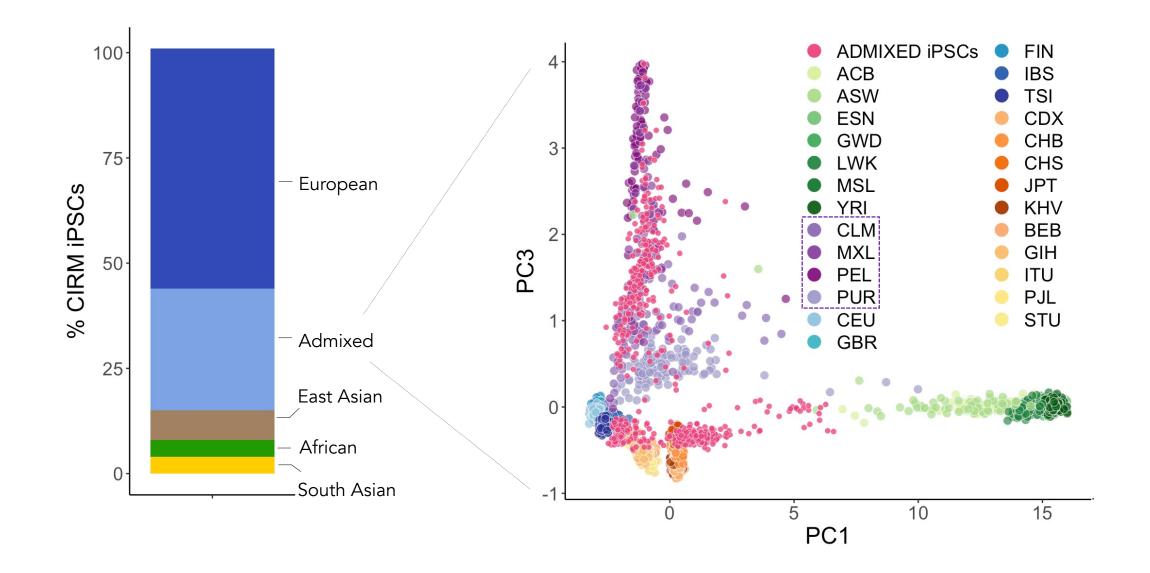
CELL & REGENERATIVE BIOLOGY

Schizophrenia Bipolar Disorder Autism

CIRM iPSCs have Diverse Genetic Ancestries



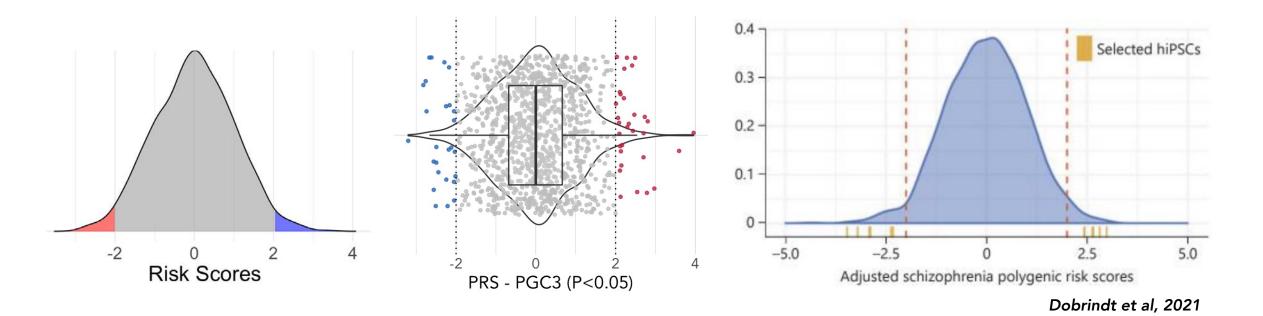
CIRM iPSCs have Diverse Genetic Ancestries



Enabling Rational Selection of Lines for Disease Modeling

The value of genotyped cell lines:

- o Design experiments informed by ancestry, relatedness and polygenic risk
- o Identify lines harboring genetic variants or haplotypes of interest
- o Enable identification and validation of cell lines across laboratories



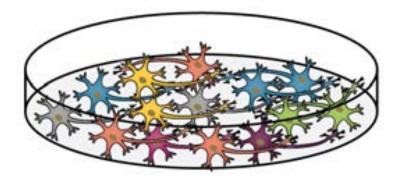
Population-scale stem cell models

Linking genetic variants to cellular phenotypes

The "Village-in-a-Dish" Experimental Paradigm

Grow cells from 100s of people together, then measure their phenotypes

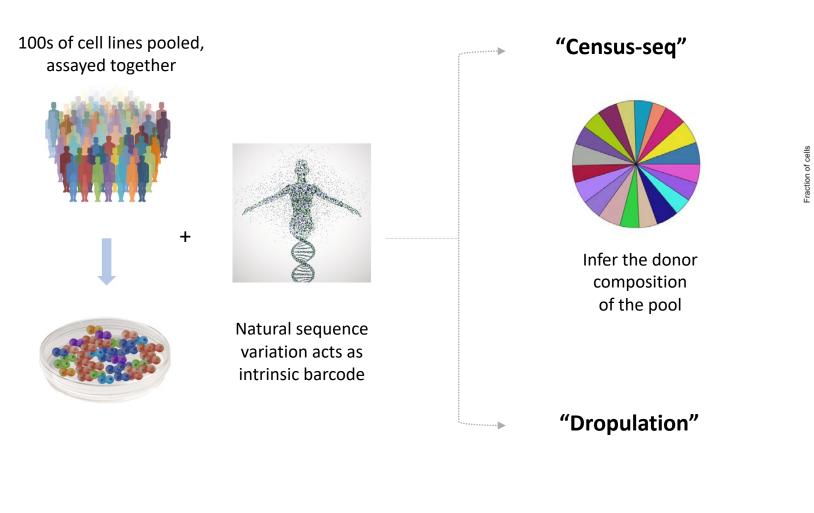
- Cell environments identical
- Cells processed identically, simultaneously
- Reduce noise from technical variation



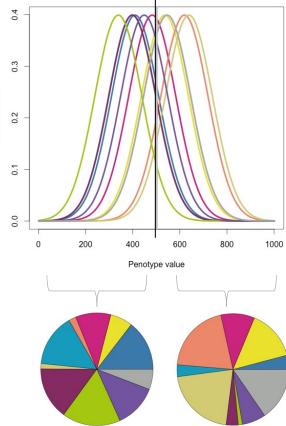




Linking Donor Genotypes to Cellular Phenotypes



Sorting or selecting cells (based on phenotype) changes the pool's donor composition



Linking Donor Genotypes to Cellular Phenotypes

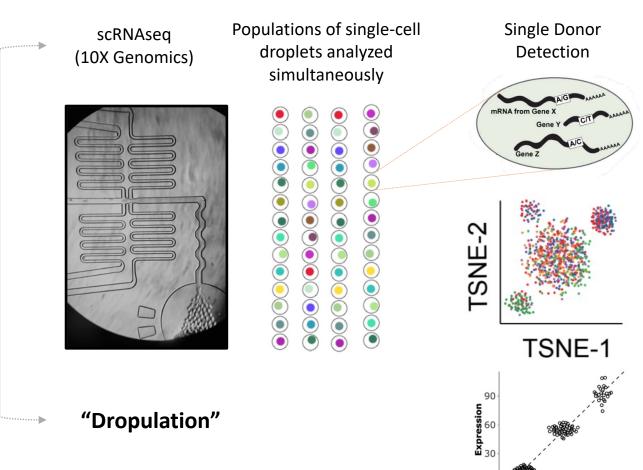
100s of cell lines pooled, assayed together







Natural sequence variation acts as intrinsic barcode



C/C

C/T

Genotype

T/T

Applications of Pooled Experimental Systems



HE PREPRINT SERVER FOR BIOLOGY

Mapping genetic effects on cellular phenotypes with "cell villages"

Jana M. Mitchell, James Nemesh, Sulagna Ghosh, Robert E. Handsaker, Curtis J. Mello, Daniel Meyer, Kavya Raghunathan, Heather de Rivera, Matt Tegtmeyer, Derek Hawes, Anna Neumann, D Ralda Nehme, Kevin Eggan, Steven A. McCarroll

doi: https://doi.org/10.1101/2020.06.29.174383

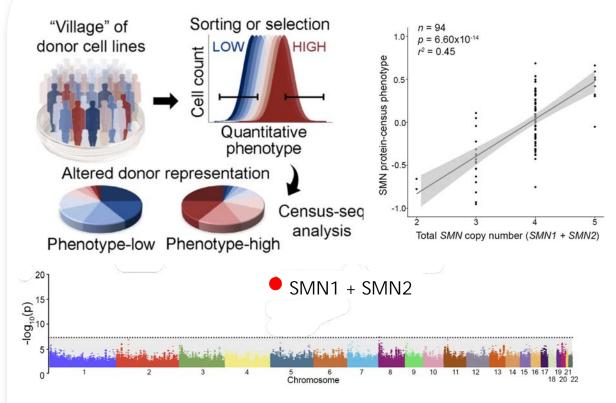


THE PREPRINT SERVER FOR BIOLOGY

Natural variation in gene expression and Zika virus susceptibility revealed by villages of neural progenitor cells

Michael F. Wells, James Nemesh, Sulagna Ghosh, Jana M. Mitchell, Curtis J. Mello, Daniel Meyer, Kavya Raghunathan, Matthew Tegtmeyer, Derek Hawes, Anna Neumann, Kathleen A. Worringer, Joseph J. Raymond, Sravya Kommineni, Karrie Chan, Daniel Ho, Brant K. Peterson, Federica Piccioni, Balda Nehme, Kevin Eggan, Steven A. McCarroll

Census: GWAS in a dish



- High throughput association of donor genotypes to cellular phenotypes at low cost
- Pharmacogenetic profiling

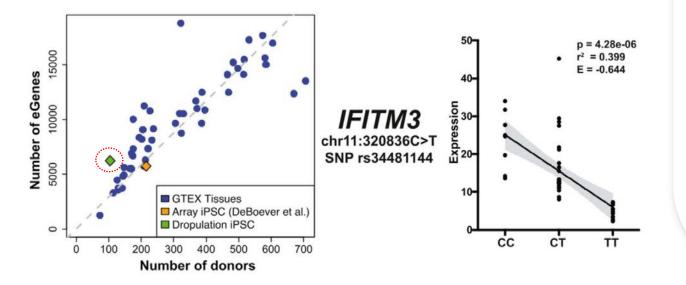
Applications of Pooled Experimental Systems



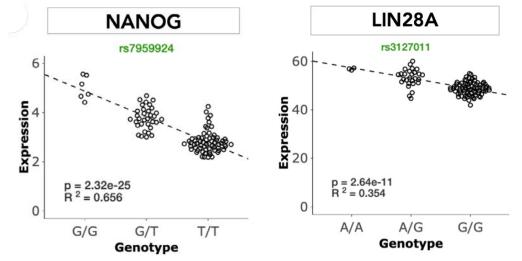
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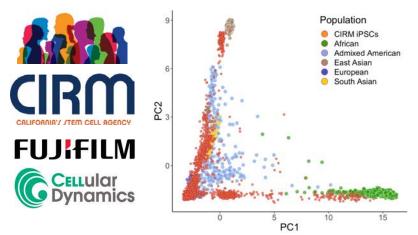
Dropulation: Interindividual Variation



- Discover eQTLs across multiple donors in a dish
- Uncover cell type/state specific eQTLs
- Link disease relevant variants to cellular phenotypes
- Study genetic basis of inter-individual variation

The CIRM-CDI Collection and Cell Villages provide new opportunities for Population-Scale Models of Disease

Publicly accessible genetic data



Linked Donor Metadata

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Cell Villages



eQTL discovery and colocalization with risk variants

Cellular and Genetic Perturbations

Drug Screens and Pharmacogenomic Profiling