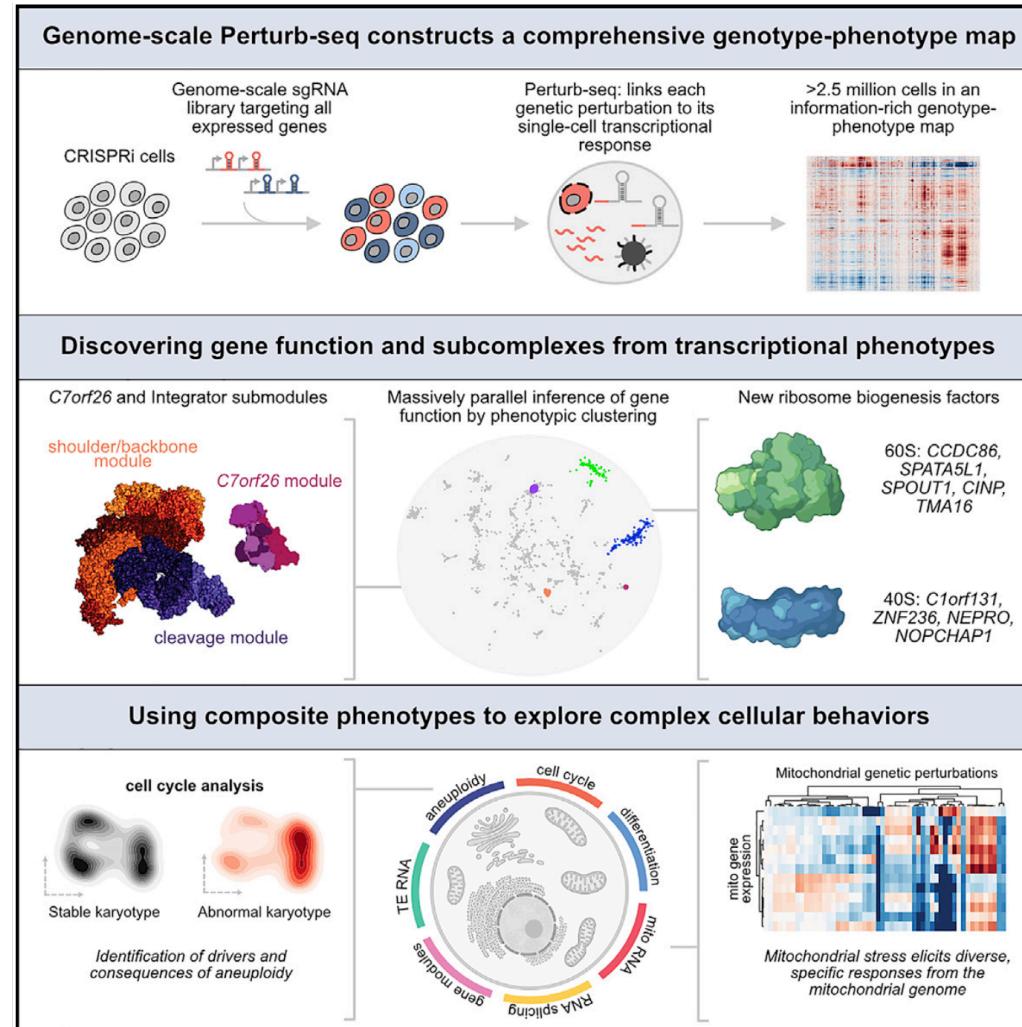
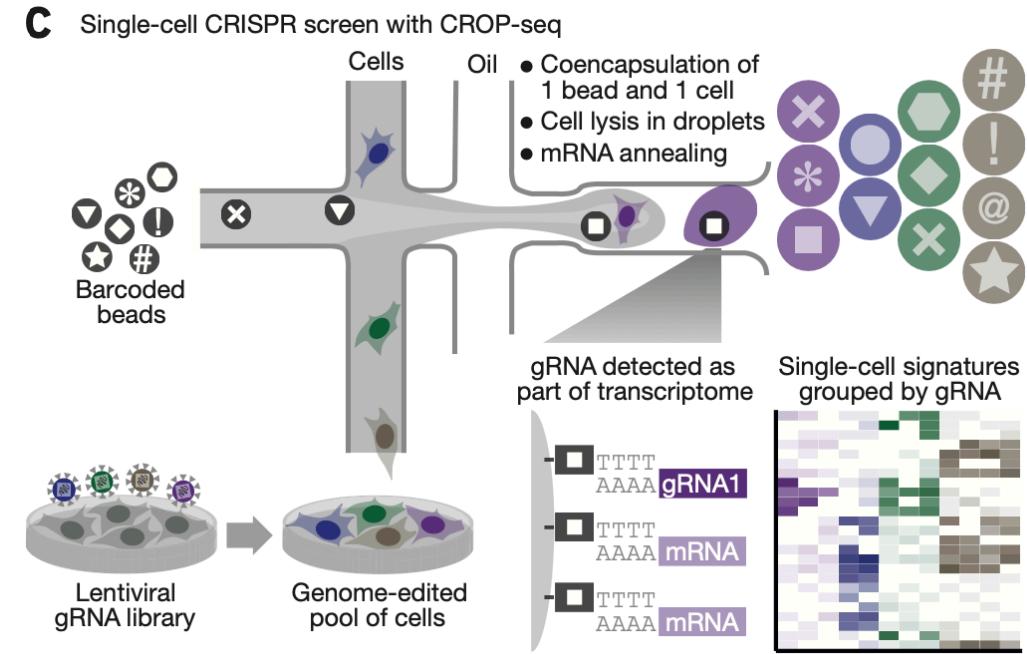
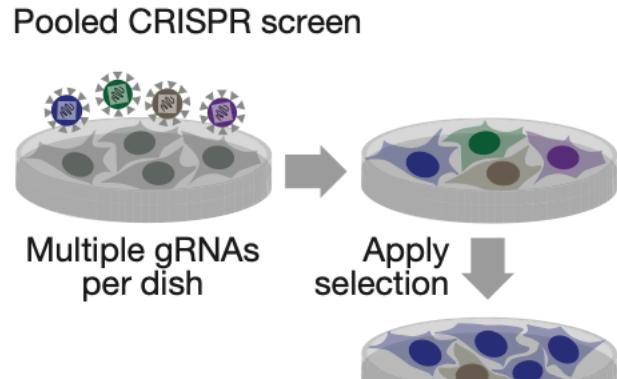


EP03: Genome-wide CRISPR screens with single-cell transcriptome readout

bioinforbricklayer
Papers of the week



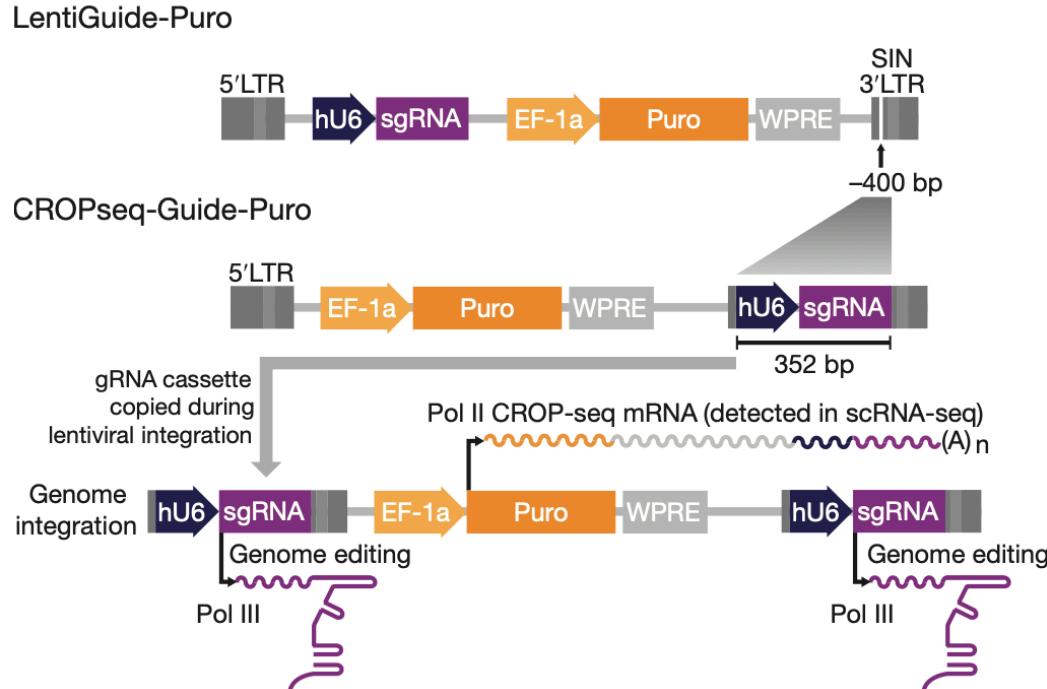
Why single-cell CRISPR screen is necessary?



Datlinger et al., Nature Methods, 2017

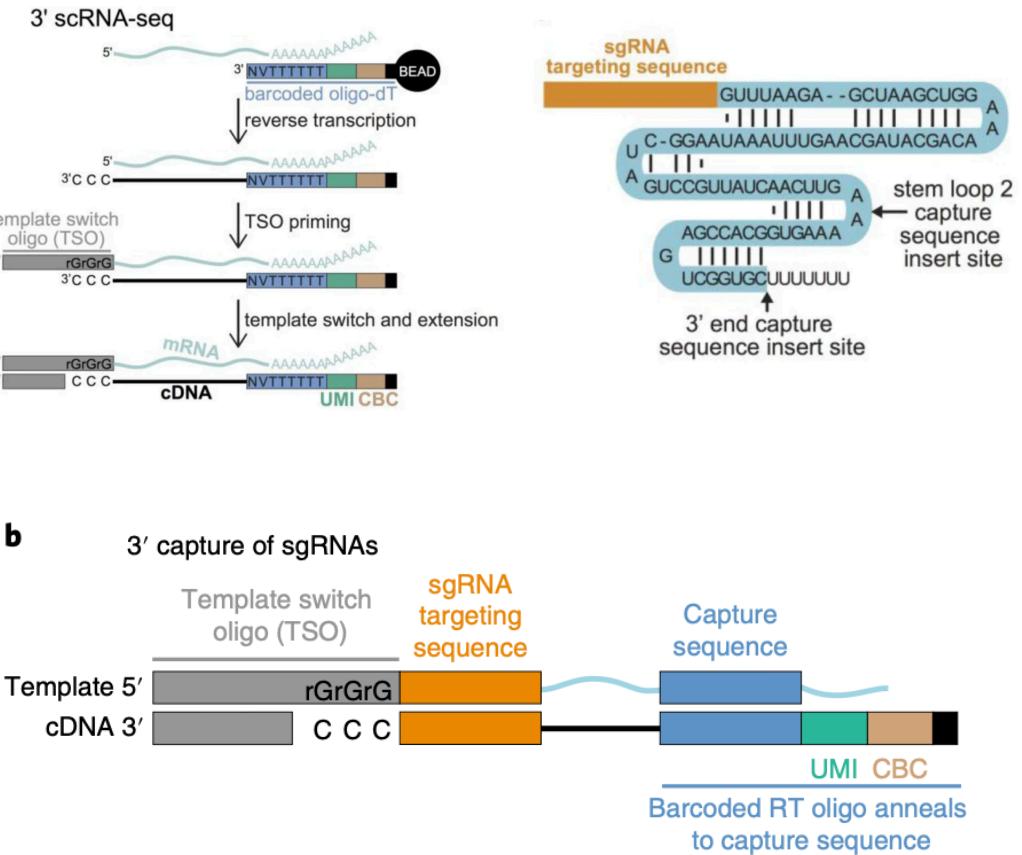
Two different approaches to perform single-cell CRISPR screen

CROP-seq



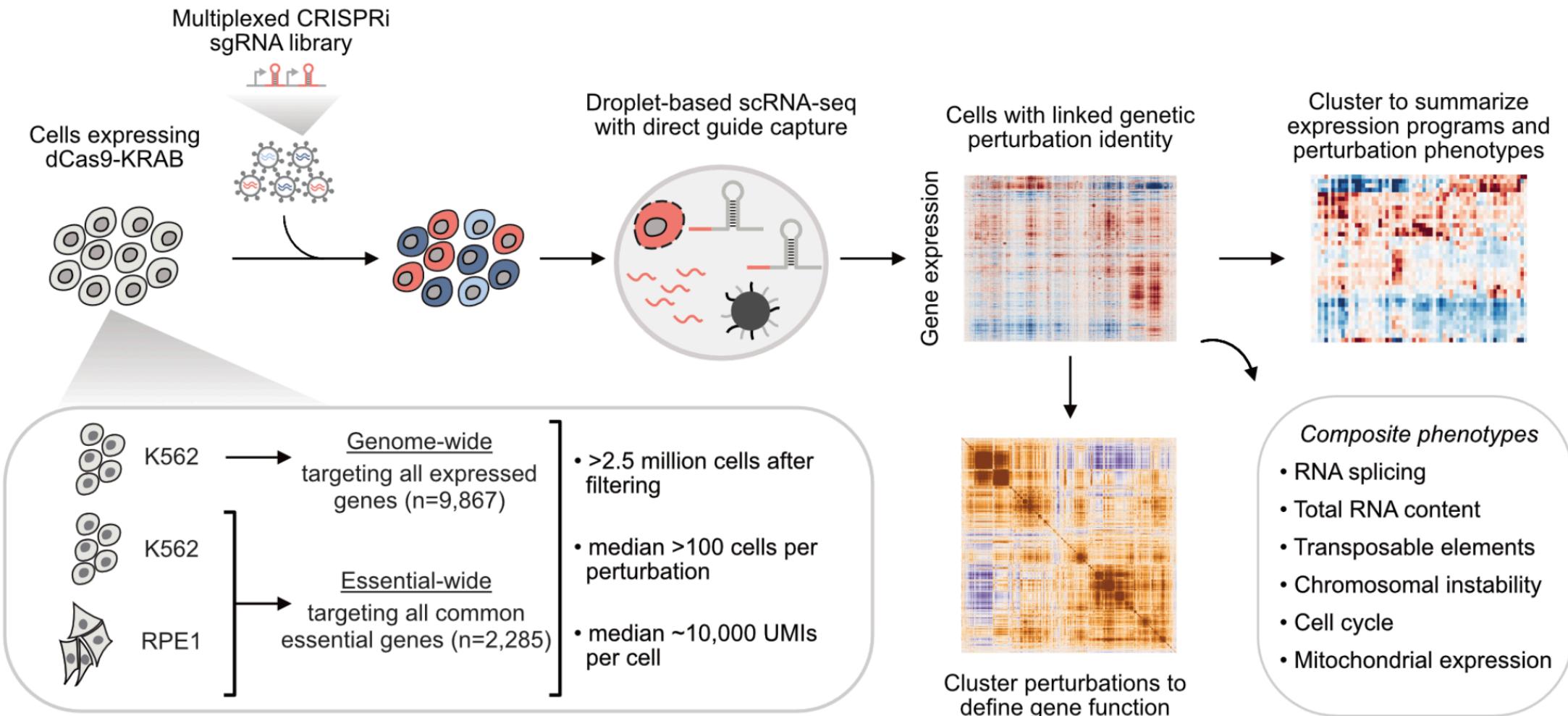
Datlinger et al., Nature Methods, 2017

Perturb-seq

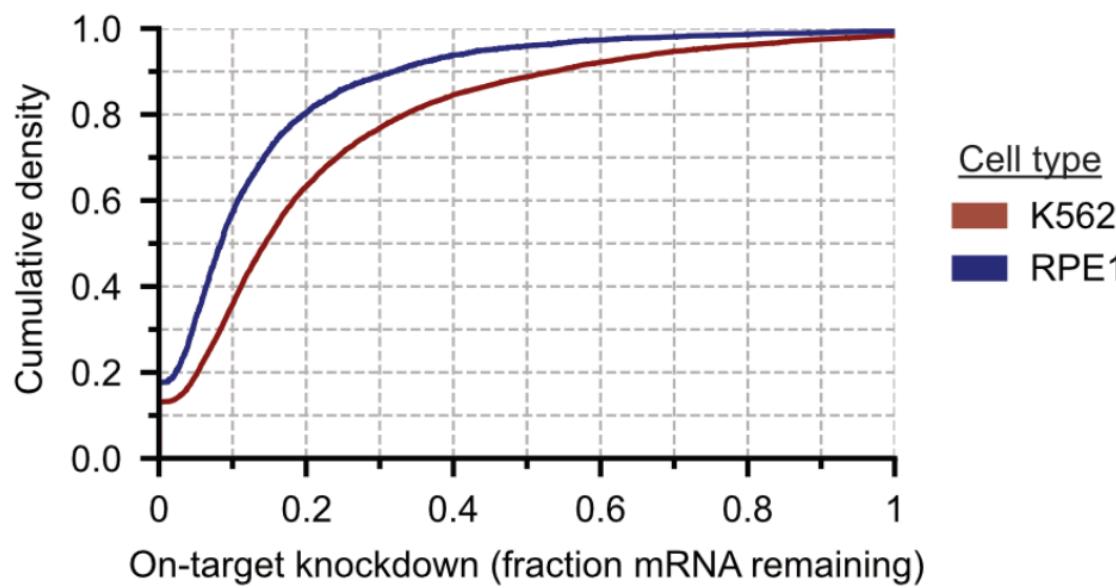


Reprogle et al., Nature Biotechnology, 2020

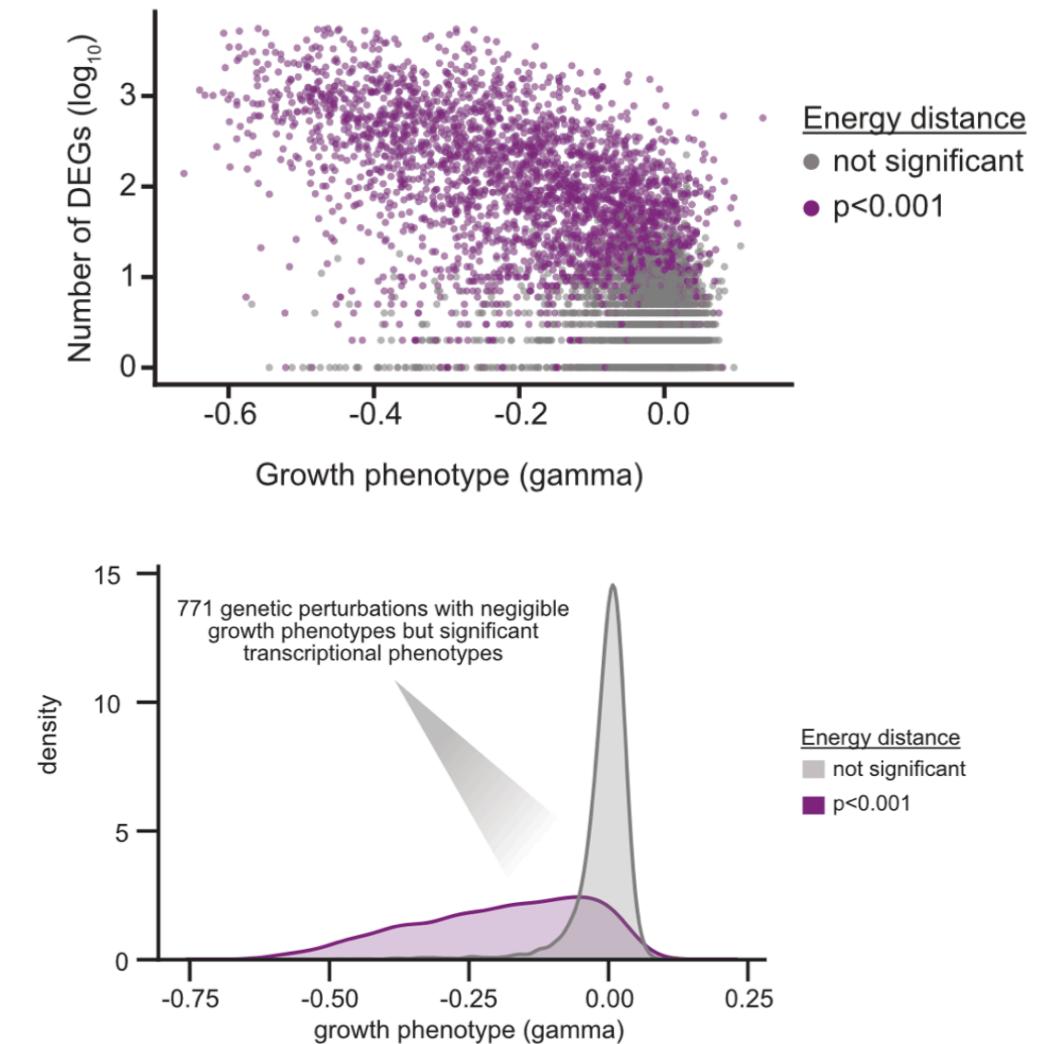
Experimental procedure of genome-wide perturb-seq screen

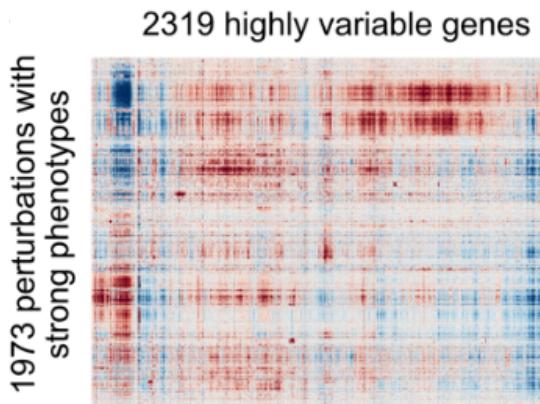


The global efficacy of CRISPRi knockdown



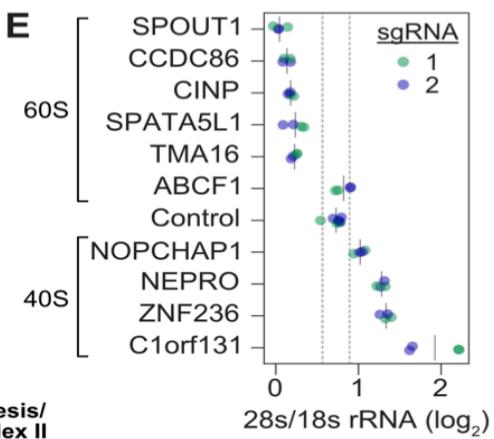
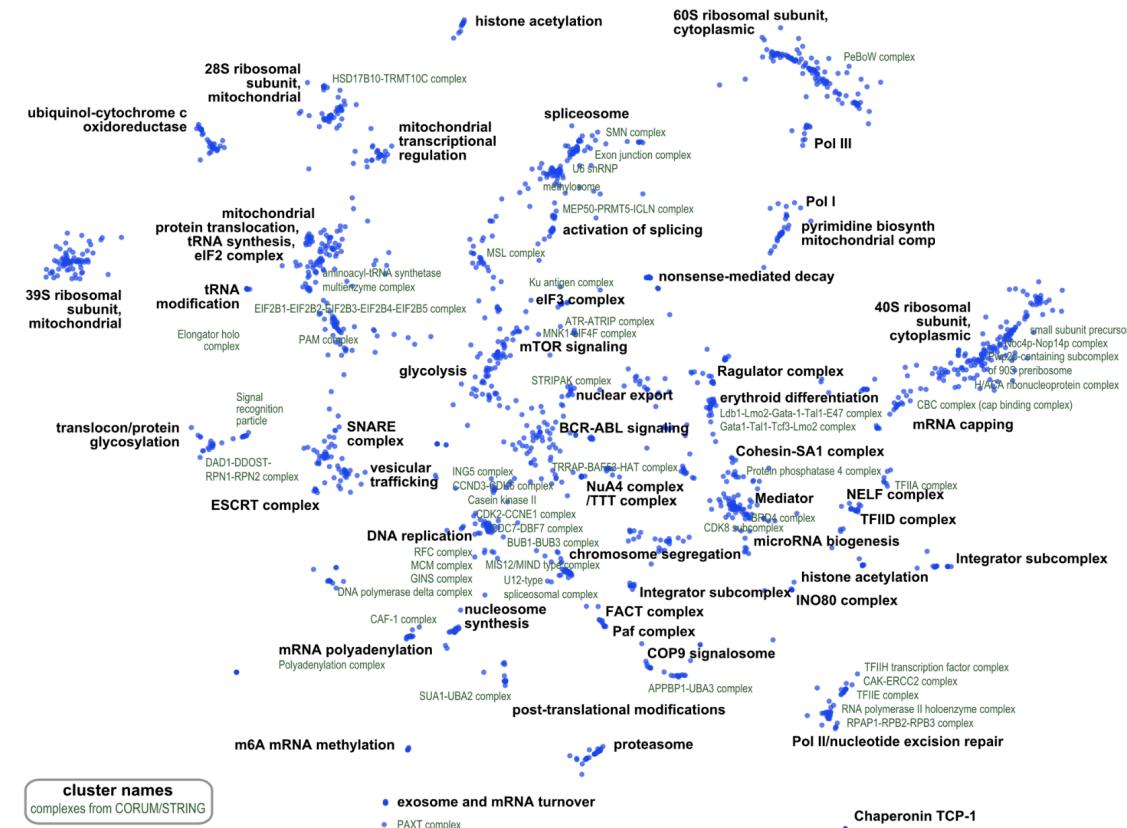
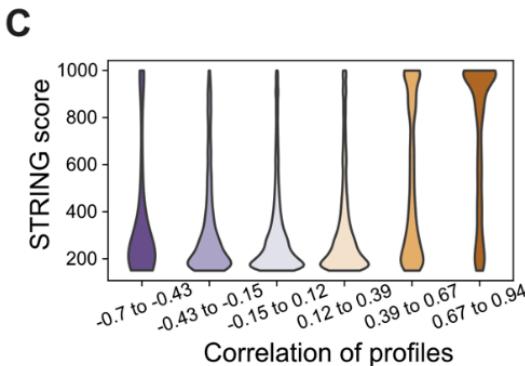
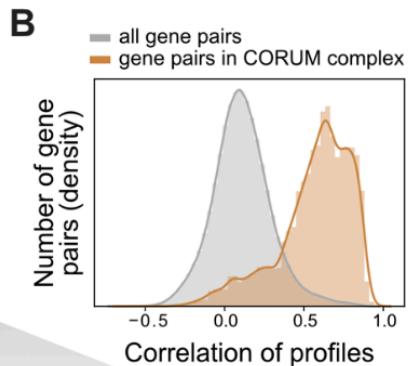
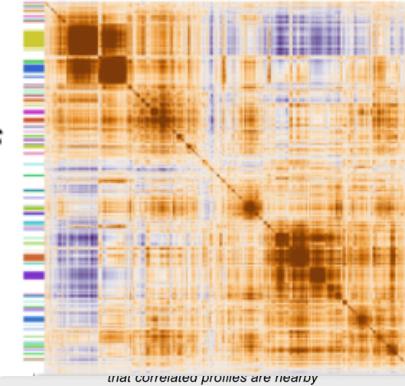
To detect individual differentially expressed genes, we applied the Anderson-Darling (AD) test to compare the distribution of expression levels for each gene in cells bearing each genetic perturbation against control cells.



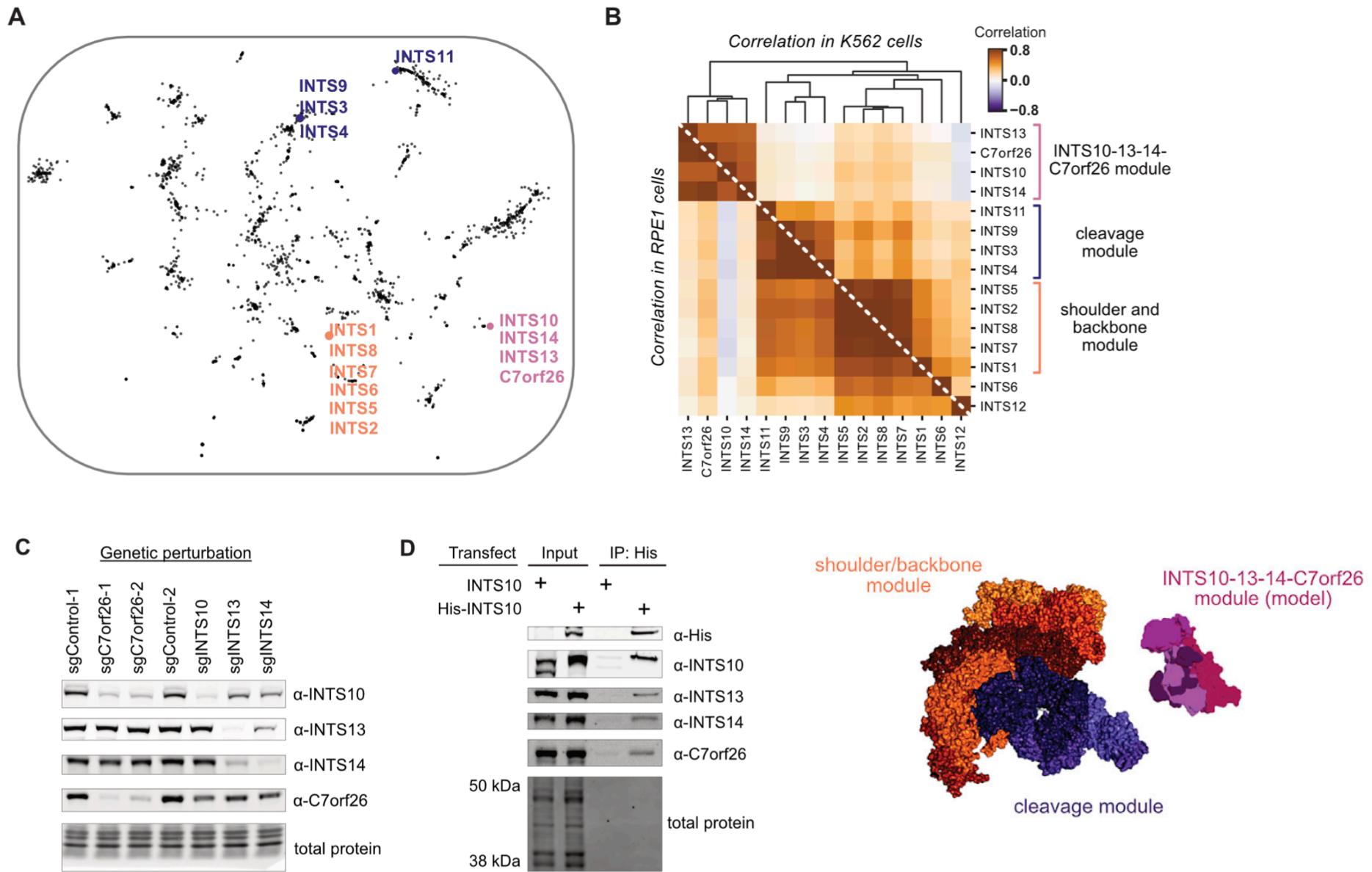


Compare perturbations using correlation of expression profiles

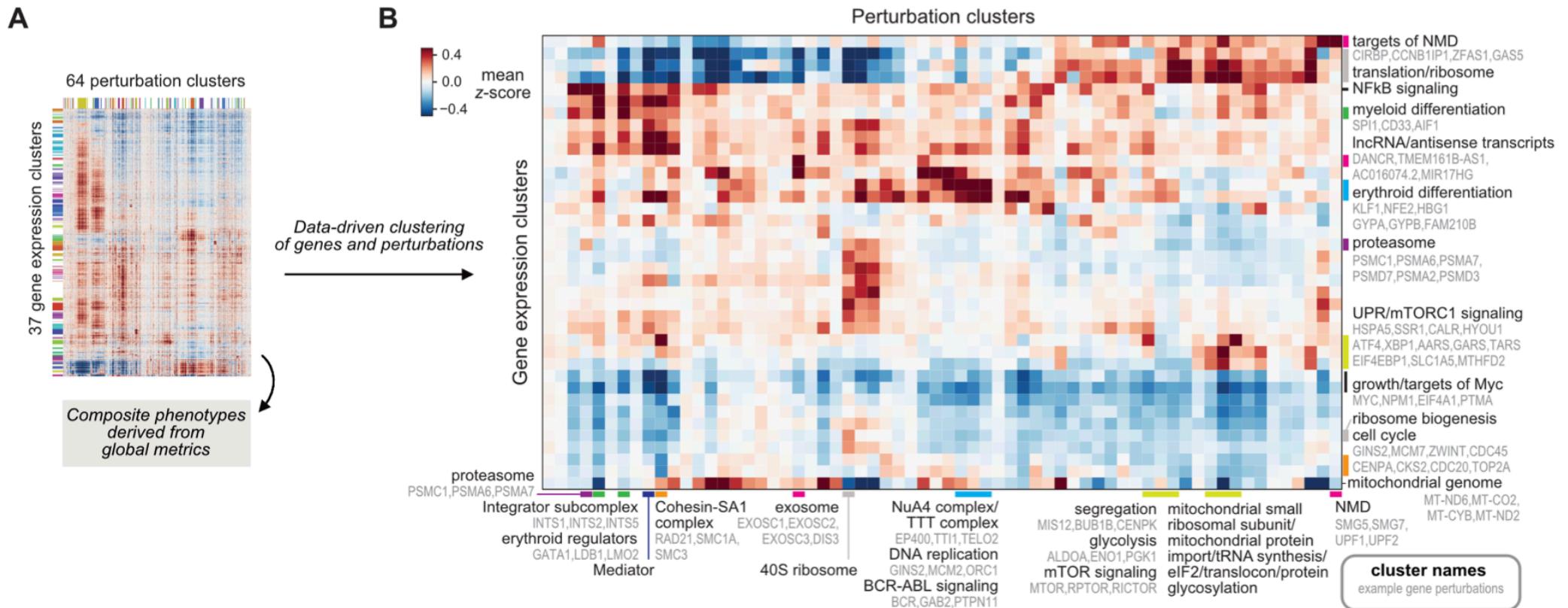
perturbation-perturbation correlation matrix



Identification of novel component in Integer complex

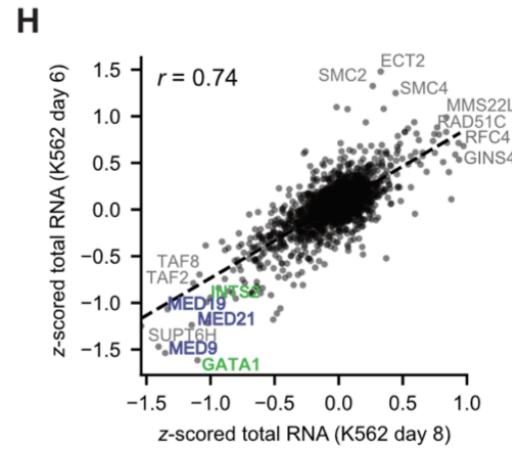
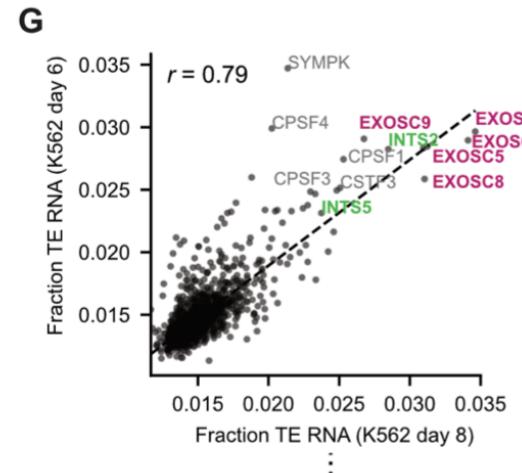
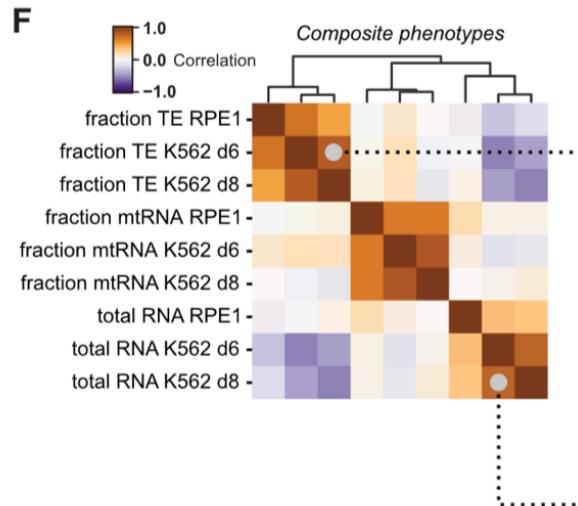
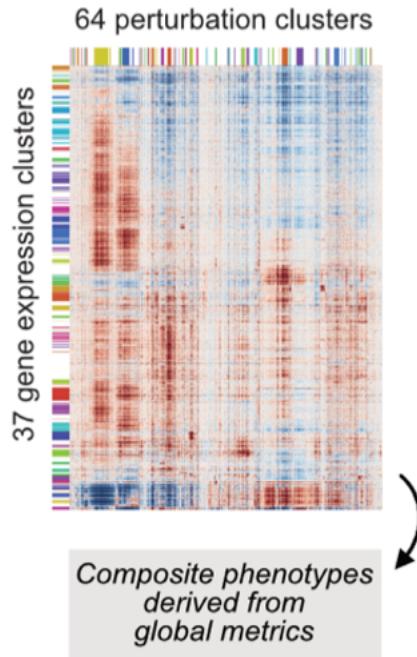


Summarizing genotype-phenotype relationships with Perturb-seq



Unfolded protein response (UPR), activated by the loss of ER-resident chaperones and translocation machinery, and integrated stress response (ISR), activated by loss of mitochondrial proteins, aminoacyl-tRNA synthetases, and translation initiation factors

Hypothesis-driven study of composite phenotypes



Exploring genetic drivers and consequences of aneuploidy in single cells

