

Genome-wide CRISPR insights at single-cell resolution

Illumina Single Cell CRISPR Prep

Connect genotype to phenotype in single cells at unprecedented scale

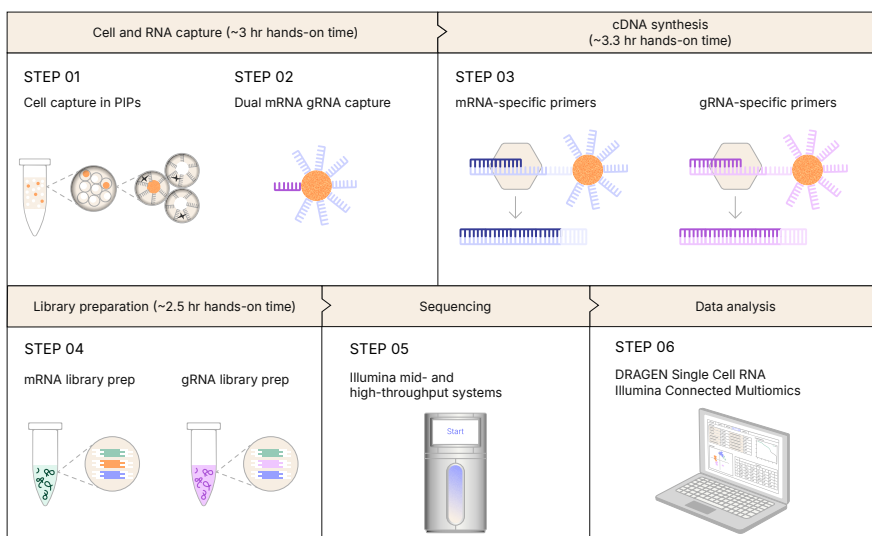
Illumina Single Cell CRISPR Prep combines direct capture of CRISPR guide RNA (gRNA) with the high resolution of single-cell RNA sequencing to reveal the impacts of gene perturbations across the transcriptome, one cell at a time. The assay can be scaled to analyze millions of cells and thousands of genes simultaneously, maximizing insights from genome-wide CRISPR screens.

Genome-scale CRISPR analysis within budget

Illumina Single Cell CRISPR Prep eliminates the need for complex microfluidic equipment and upfront capital expenses, offering a low cost of entry and user-friendly workflow so more labs can access insights from genome-wide CRISPR screening.

Simple, proven workflow

Illumina Single Cell CRISPR Prep uses innovative PIPseq™ chemistry for dual capture of gRNA and mRNA from the same cell. The workflow integrates seamlessly with Illumina sequencing systems and data analysis to provide a streamlined end-to-end solution for large single-cell CRISPR screens.



Simple

Use a vortexer-based method with an intuitive manual workflow to conduct single-cell studies on your benchtop



Scalable

Process from 100s up to 10M cells per sample based on experimental goals and get the most out of your data



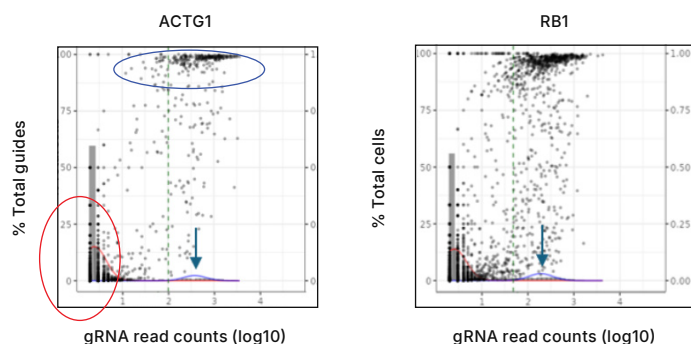
Affordable

Perform single-cell CRISPR screens in your lab with the lowest cost per cell on the market*

*Cost per cell calculated for library preparation and sequencing only and does not include gRNA libraries.

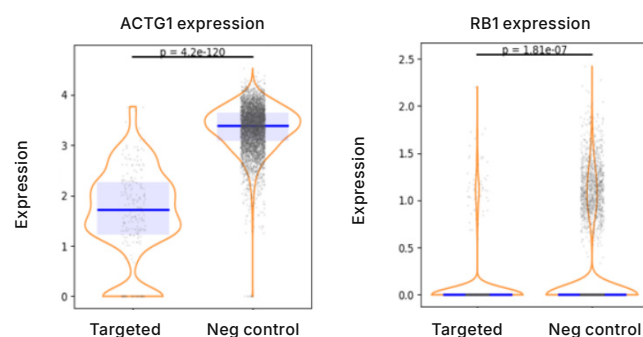
Highly sensitive guide detection

Guide thresholding



Positive CRISPR gRNA expression (blue circle) can be reliably differentiated from background reads (red circle), enabling sensitive perturbation assignment as shown for two genes, *ACTG1* and *RB1*.

Targeted gene expression



Identified CRISPR perturbations can be directly correlated to knock-down of targeted genes (*ACTG1* and *RB1*) compared to non-targeted negative controls.

Exceptional performance in > 1M cells

Gene expression mRNA performance*

Number of cells	Capture rate (%)	Reads in cells (%)	Mean reads/cell	Median transcripts/cell	Median genes/cell
1,002,506	71.1%	87.9%	9612	4337	2528

CRISPR gRNA performance*

rTag-matched reads	CRISPR valid reads in cells	Cells with $\geq$ gRNA	Cells with 1 gRNA	Median gRNA (read) counts per cell	Median features per cell	% guides detected
82.79%	74.6%	71.3%	60.4%	261	1	100%

*Gene expression and CRISPR gRNA detection were assessed using 1.4M cells from a CRISPR-edited cell line loaded on to the Illumina Single Cell CRISPR Prep M1 kit. Libraries were sequenced on the NovaSeq™ X System 10B flow cell at a read depth of ~9800 reads/cell for gene expression and ~1300 reads/cell for the CRISPR gRNA libraries. Data were analyzed with DRAGEN v4.4.4. Guide assignments were performed using a custom implementation of Gaussian mixture modeling with gRNA counts. Targeted gene perturbations were examined only for cells with single guide assignments.

Expand your single-cell CRISPR studies today

Conduct your genome-wide CRISPR screens with confidence, backed by the expertise of the global leader in genomics.



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