PRODUCT SHEET
CRISPR DETECT

Single Cell CRISPR Screening at Unprecedented Scale

Pair guide RNA detection with the whole transcriptome in individual cells

By linking individual CRISPR perturbations with gene expression signatures, single cell pooled CRISPR screening enables analysis of complex phenotypes and has been applied to developmental biology, drug development, and understanding treatment response. Wider adoption of this approach is constrained by the feasibility of processing a sufficient number of cells for large single guide RNA (sgRNA) libraries. CRISPR Detect brings the scalability of Evercode technology to single cell pooled CRISPR screens, enabling analysis of 100s to 10,000s of perturbations in each experiment.

- **Genome-wide screens made feasible**
  Screen large guide RNA libraries in up to 1 million cells in a single experiment
- **Detect more cells with one sgRNA**
  Confidently detect a single guide from more cells with efficient enrichment
- **Analyze more samples**
  Evaluate up to 96 samples or treatments with a single Evercode WT Mega

Scalability of Evercode Applied to CRISPR Screening

Analyze the whole transcriptome and paired sgRNAs expressed from CROP-seq vectors

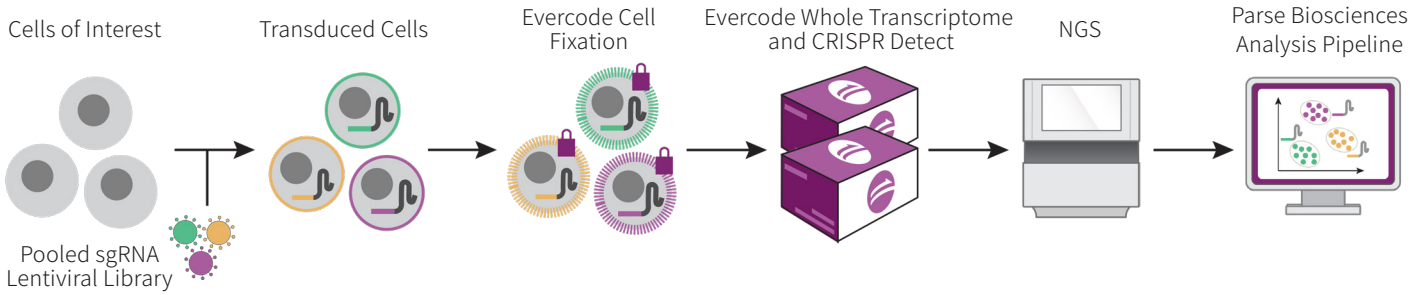

Figure 1. Single Cell CRISPR Screening Overview. A pooled lentiviral library is prepared by cloning sgRNA sequences into a vector, which is packaged into lentiviral particles. Target cells are transduced with this lentiviral sgRNA library, and cells expressing sgRNAs are selected with an antibiotic or fluorescent marker. sgRNA expressing cells are then fixed with Evercode Fixation and processed with Evercode Whole Transcriptome and CRISPR Detect for gene expression and sgRNA detection. After sequencing, the Parse analysis pipeline assigns sgRNAs and associated whole transcriptomes to individual cells.

Analyze More Perturbations in Fewer Runs

Scale easily from 100s to 10,000s of sgRNAs with CRISPR Detect and Evercode technology

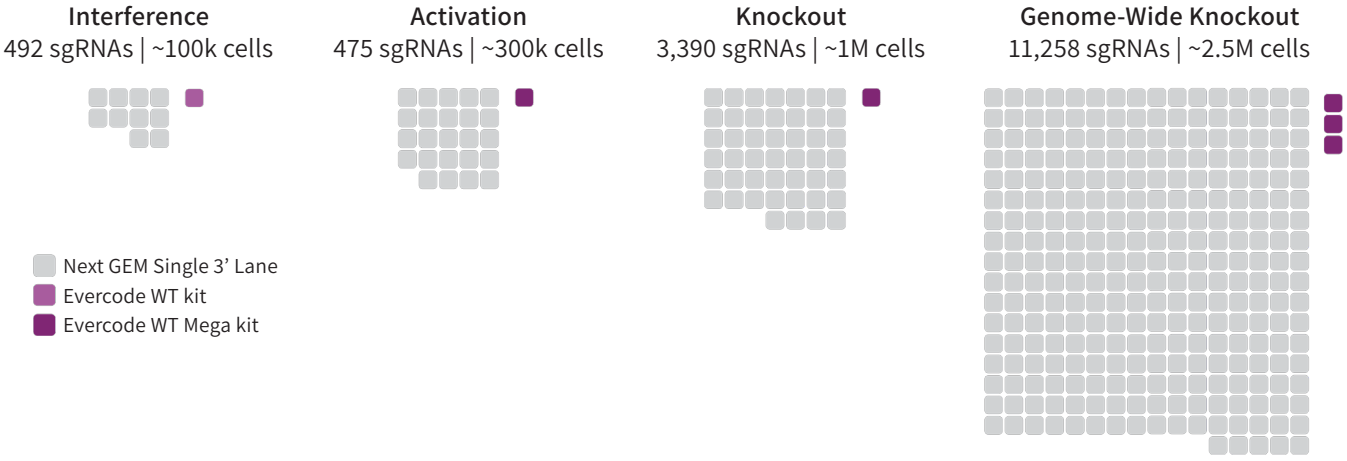

Figure 3. Size of Recently Published CRISPR Screens. The published number of 10x Genomics Chromium Next GEM Single 3' Kit (Next GEM Single 3') lanes and projected Evercode Whole Transcriptome kits to obtain the same number of cells from published CRISPR screens. From left to right, the PubMed IDs of these studies are 36381608, 32634384, 36747789, and 35688146.

Detect More Cells with Just One Guide

Avoid underpowered analysis and wasted sequencing data

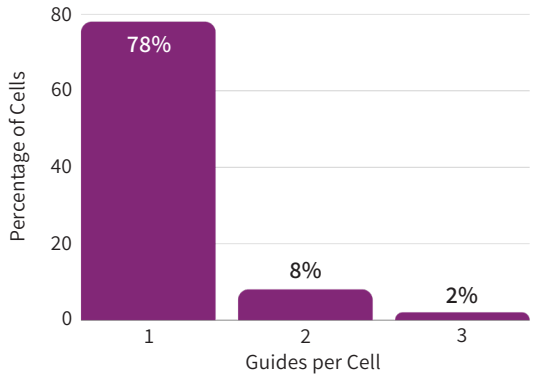

Figure 2. Sensitive sgRNA Detection. LN18 cells were prepared such that each cell expressed exactly one sgRNAs from a CROP-seq vector. Fixed cells were processed with Evercode WT Mega v2 and CRISPR Detect. One sublibrary was analyzed and sgRNAs were assigned to cells with the default Parse analysis settings.

PRODUCT ORDERING INFORMATION

PRODUCT	PART NUMBER
CRISPR Detect Guide RNA enrichment sufficient for 16 sublibraries	CRS1010
Evercode WT Mega v2 Up to 1,000,000 cells or nuclei and 96 samples	ECW02155
Evercode WT v2 Up to 100,000 cells or nuclei and 48 samples	ECW02135
Evercode Cell Fixation v2 Up to 4 samples	ECF2001

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