(a) Client (Web browser) — Study design, JSON File, FASTA library, Sequence Counter, FASTQ samples, Trimmer; AWS EC2 — Web server, e-mail sender; AWS S3 (Temporal storage); Notify the analysis ended; Retrieve data; Notify new job; AWS SQS (Global job queue); Notify new job; Analytics Server — Internal job queue, Run analysis scripts; Notify a job ended; Store result

(b) Study Design — Survival and Dropout screens (REFERENCE CONDITIONS, TEST CONDITIONS, Infect cells); Enrichment-based screens (Lentiviral pool of sgRNAs or shRNAs, Selection of cells by FACS, GFP high (upper quartile), Unsorted, GFP low (lower quartile)); Select

(c) sgRNA extraction from RNA-seq reads

(d) Correlation heatmap (Pearson's Correlation); Single gene visualization GENE

sgRNA	High.fc	High.pval	High.padj
GENE_1	0.5	2.00E-01	8.00E-01
GENE_2	0.3	1.00E-01	7.00E-01
GENE_3	1.2	5.00E-06	3.00E-04