



Fastq read 1

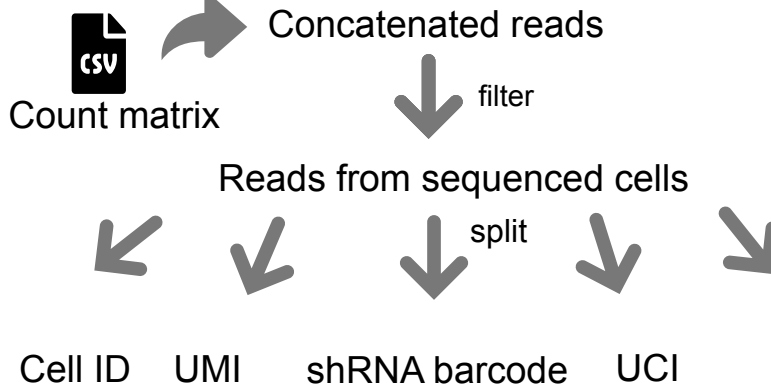
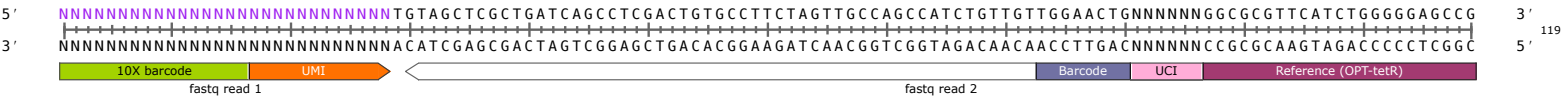


Fastq read 2

Reverse and complement
read 2

Concatenate reads

catcher_10Xcatch
catcher_scicatch
wrapper functions



CTTCTTTC, CHD7.1
GTACTCAA, CHD7.2
AGGCGAGA, GATA4.1
...

rc_barcodes_genes.csv

Filter for correct
reference and barcode

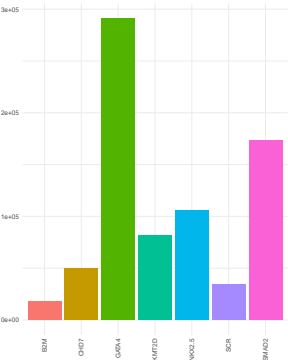
Add name of the perturbation
and KD gene

Plots

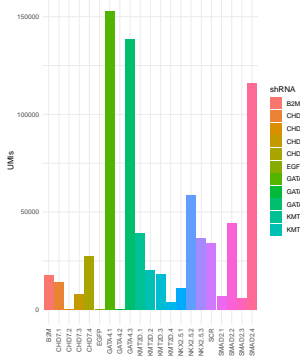
catcher_10XcatchQC
catcher_scicatchCQ

percentage of UMIs
supporting a UCI over
total UMIs of integration
in a cell

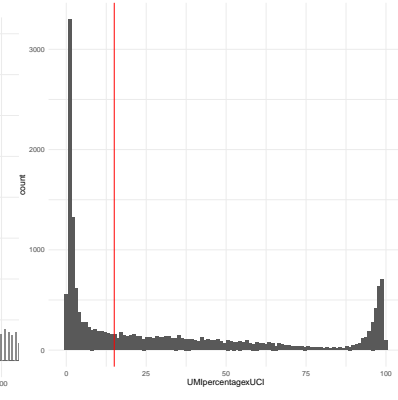
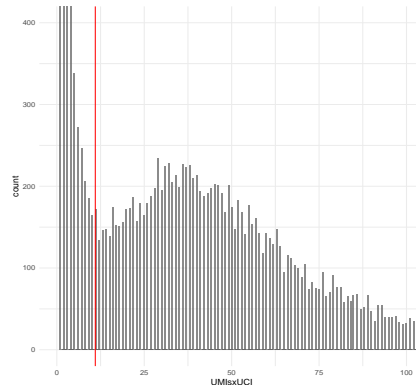
gene distribution



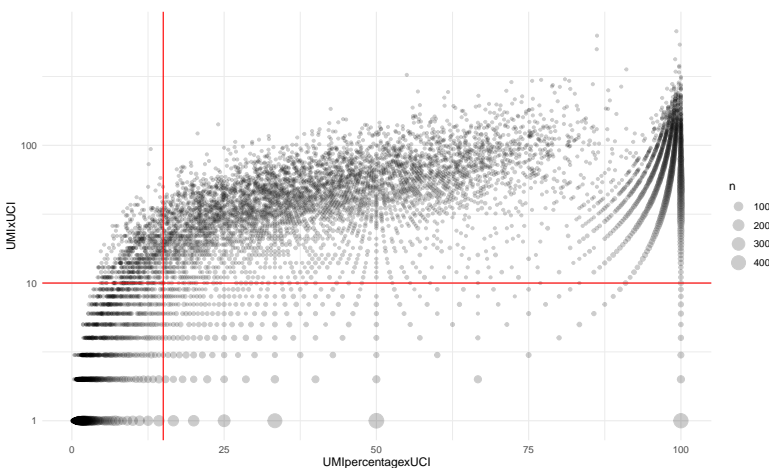
barcode distribution



UMIs per UCI



2D plot of UMI count and percentage



UMIs per UCI

- Automated
- Bimodal mode
- Noise mode

Percentage

- Automated
- 15%

Choose thresholds based on plots