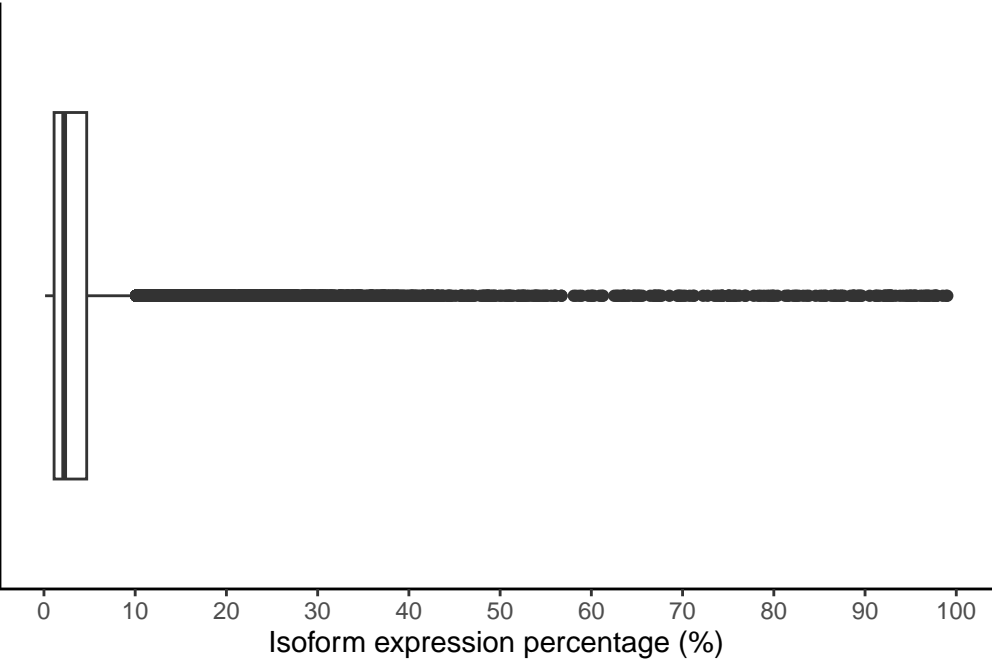
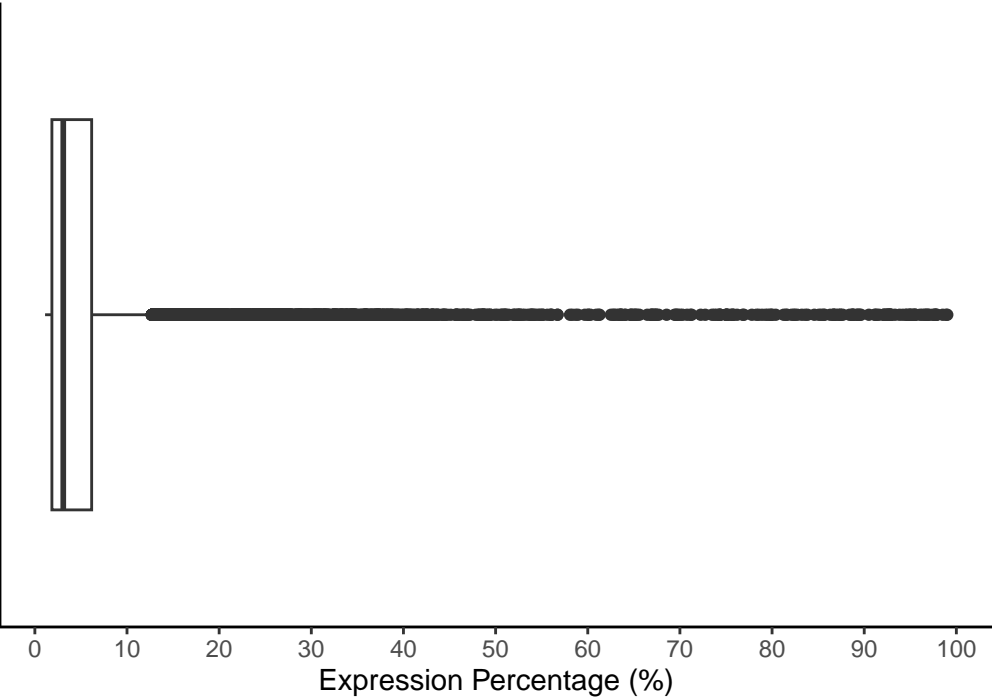


CHECK THAT DISTRIBUTION OF READS AND ISOFORMS
ARE GOOD AFTER FILTERING FEATURES
(to reduce false positives from FLAMES isoform quantification)

BEFORE removing isoforms
expressed in =<1% of cells



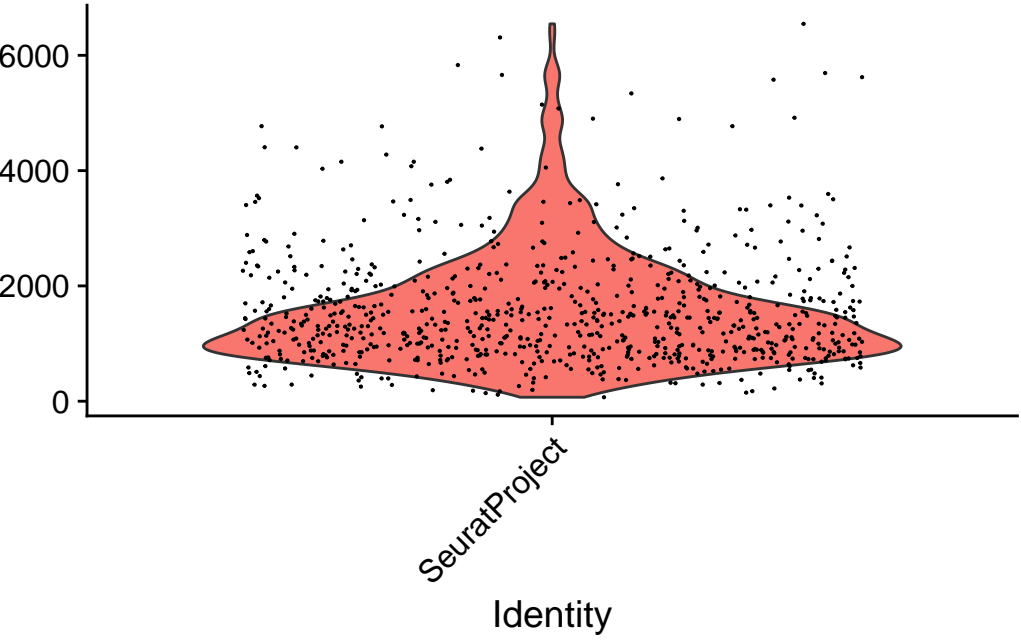
AFTER removal



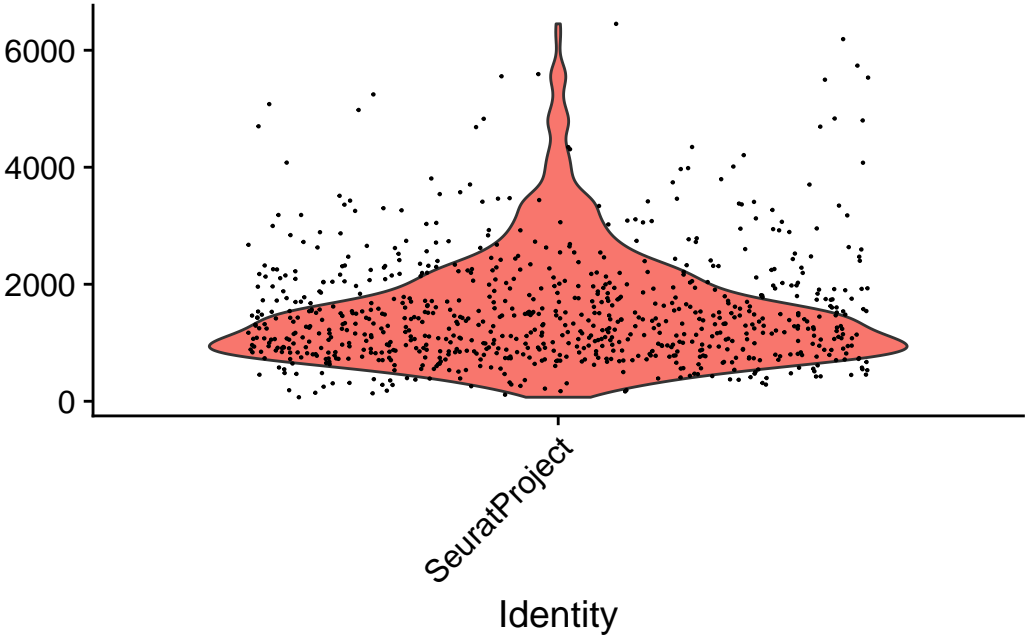
| | |
|--|---------|
| <i>Number.of.Isoforms.Removed</i> | 4436 |
| <i>Total.Reads.Before.Filtering</i> | 1261683 |
| <i>Total.Reads.After.Filtering</i> | 1241617 |
| <i>Number.of.Raw.Read.Counts.Removed</i> | 20066 |

| | Isoform expression frequency across cells (%) BEFORE Filtering (%) | Isoform expression frequency AFTER filtering (%) |
|---|--|---|
| 1 | Min. : 0.1233 | Min. : 1.110 |
| 2 | 1st Qu.: 1.1097 | 1st Qu.: 1.850 |
| 3 | Median : 2.2195 | Median : 3.083 |
| 4 | Mean : 5.0080 | Mean : 6.463 |
| 5 | 3rd Qu.: 4.6856 | 3rd Qu.: 6.165 |
| 6 | Max. : 99.0136 | Max. : 99.014 |

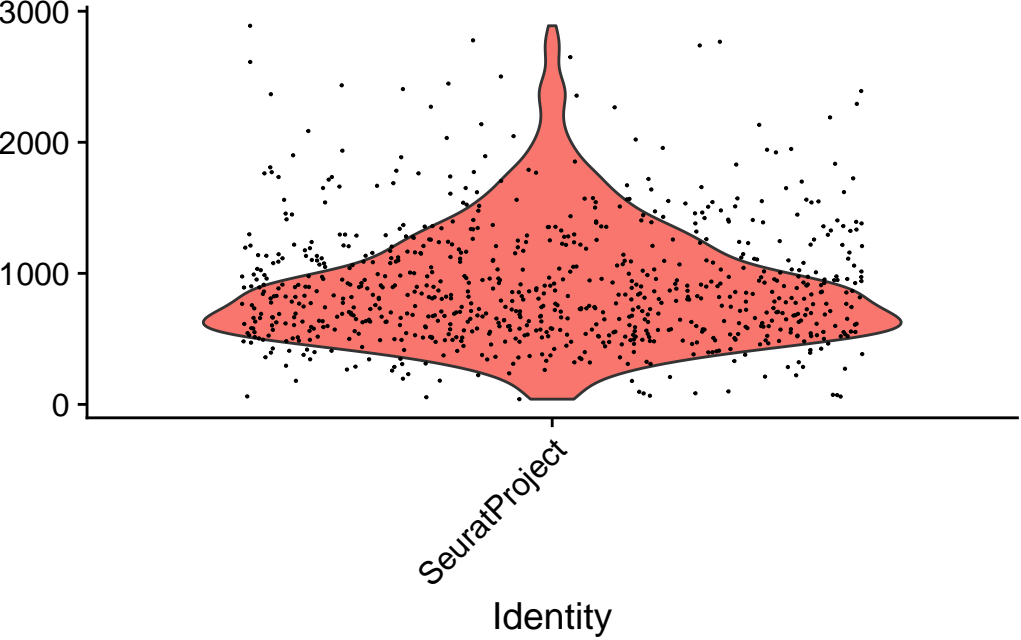
Total RNA molecules (reads)
per cell BEFORE filtering



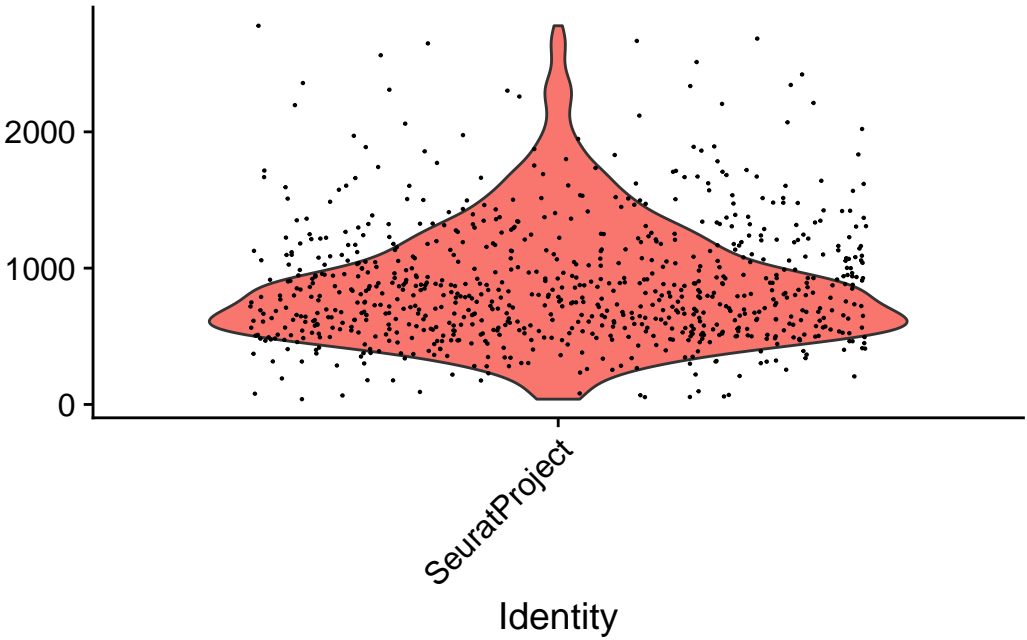
Total RNA molecules (reads)
per cell AFTER filtering



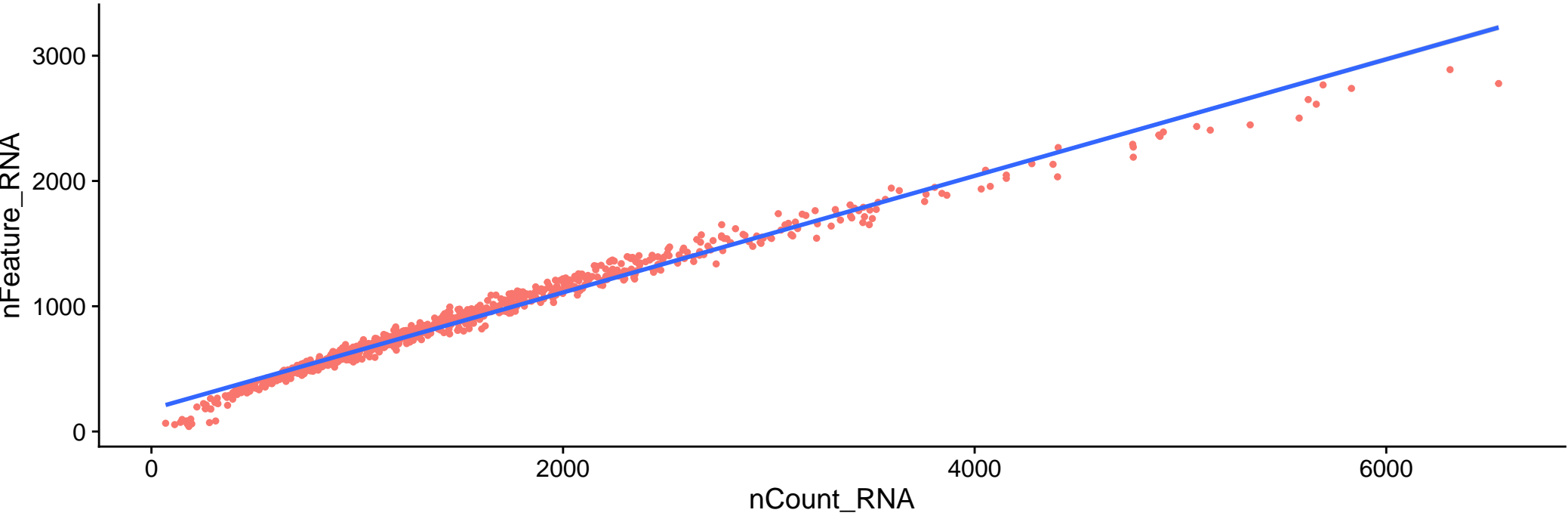
Total unique isoforms
per cell BEFORE filtering



Total unique isoforms
per cell AFTER filtering



Correlation plot of RNA molecules and distinct transcripts per cell BEFORE filtering



Correlation plot of RNA molecules and distinct transcripts per cell AFTER filtering

