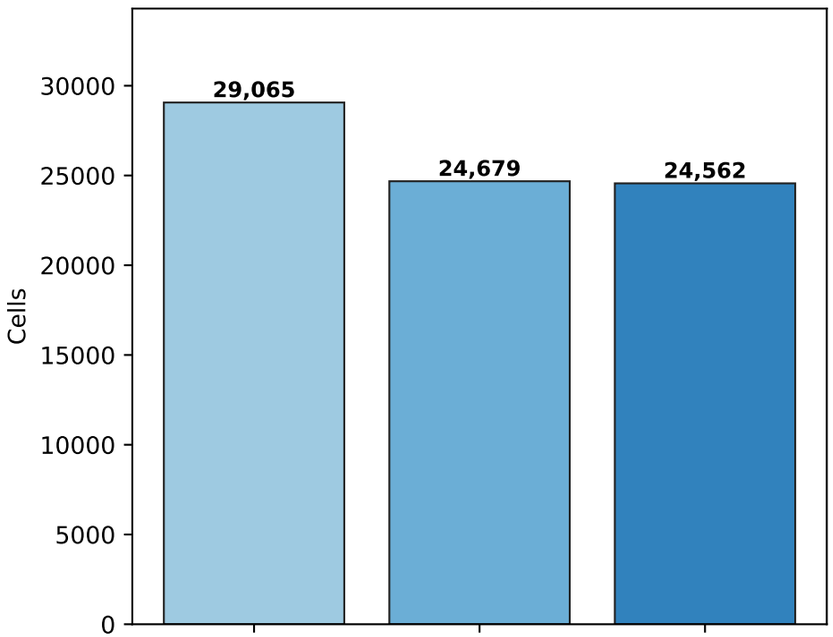
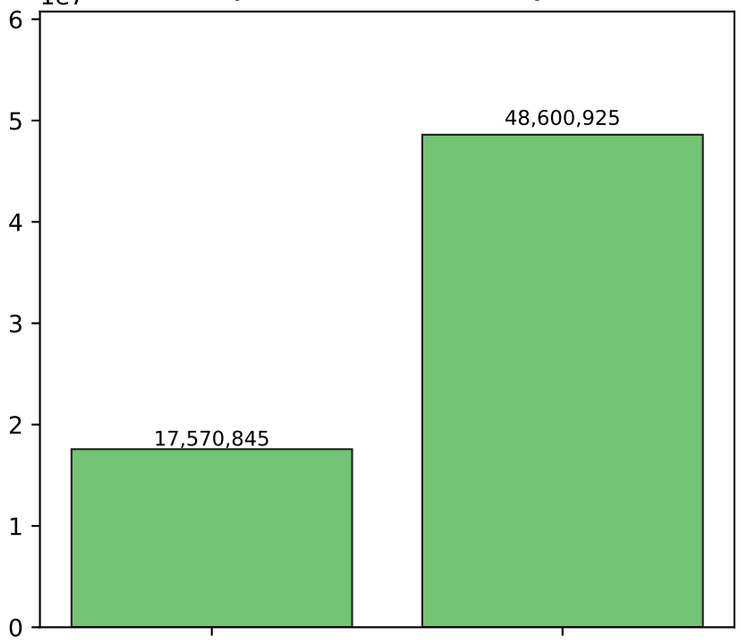
Kang 2018 (GSE96583) merge: source tracking and input conservation

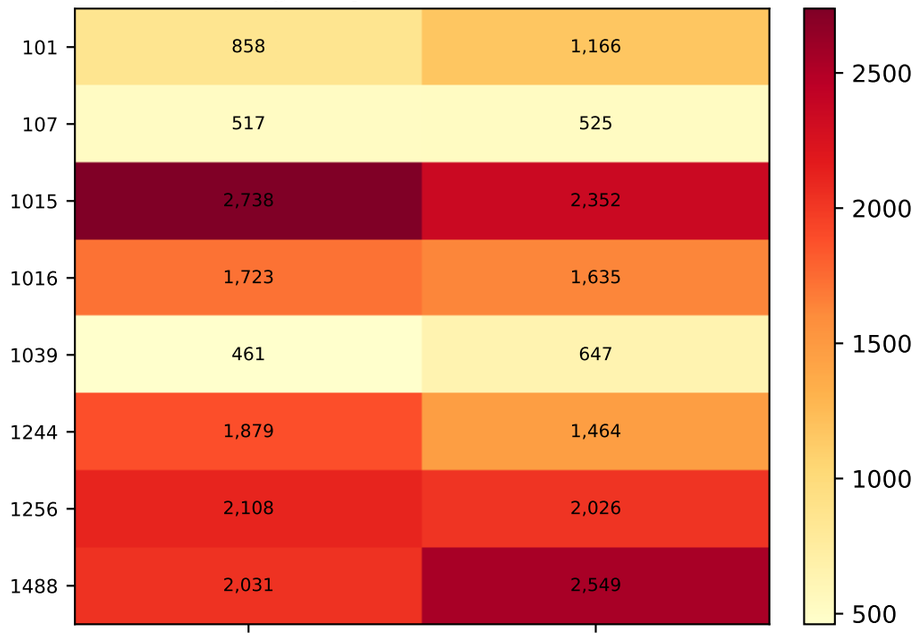
A. Cell ledger



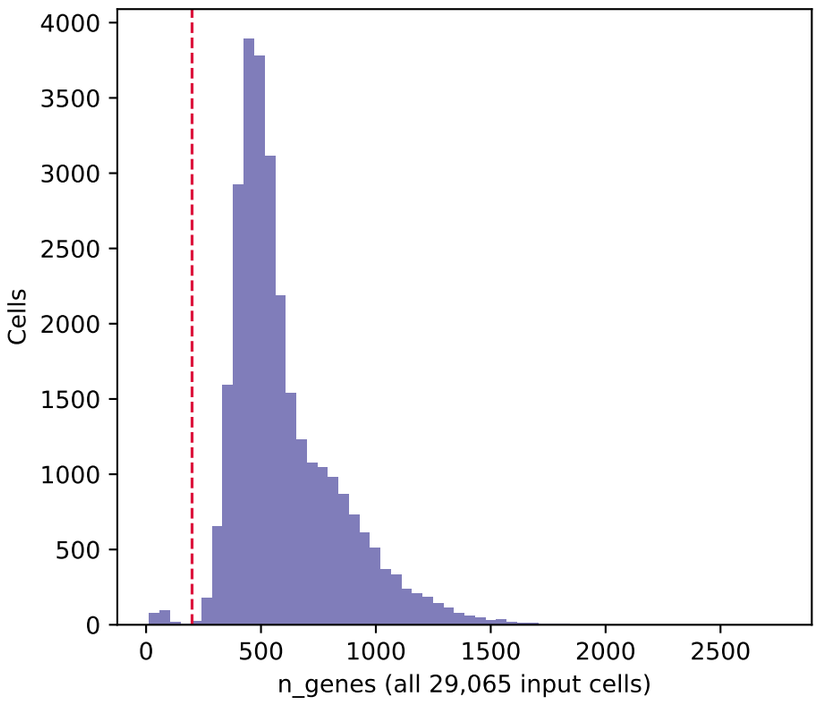
B. Rebuild == original (elementwise diff = 0)



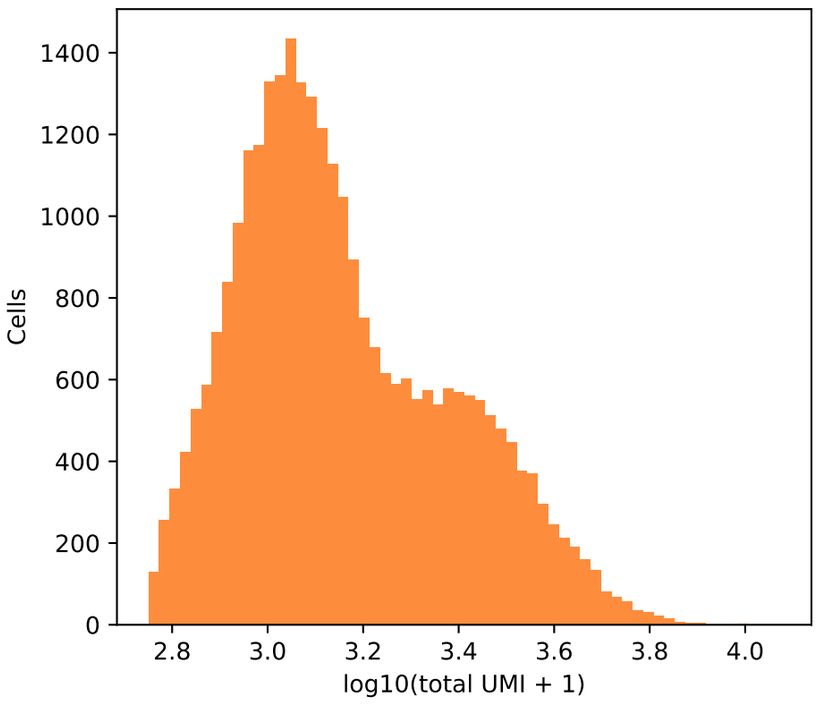
C. Singlets per donor x condition



D. Genes per cell median 533



E. Depth: all 29,065 input cells



F. What this design can and cannot answer

Structural boundaries of this design

capture libraries: 2 (2.1 = ctrl only, 2.2 = stim only)
donor x condition units: 16
donors: 8

condition is fully confounded with
capture library -> library effect and
stimulation effect cannot be separated.

Each donor was split into two aliquots
measured under the two conditions:
a paired observation, NOT a crossover
design. The 16 units are NOT 16
independent replicates.

MT genes present: 13; total MT counts: 0
-> the 10% MT rule removes nothing here.