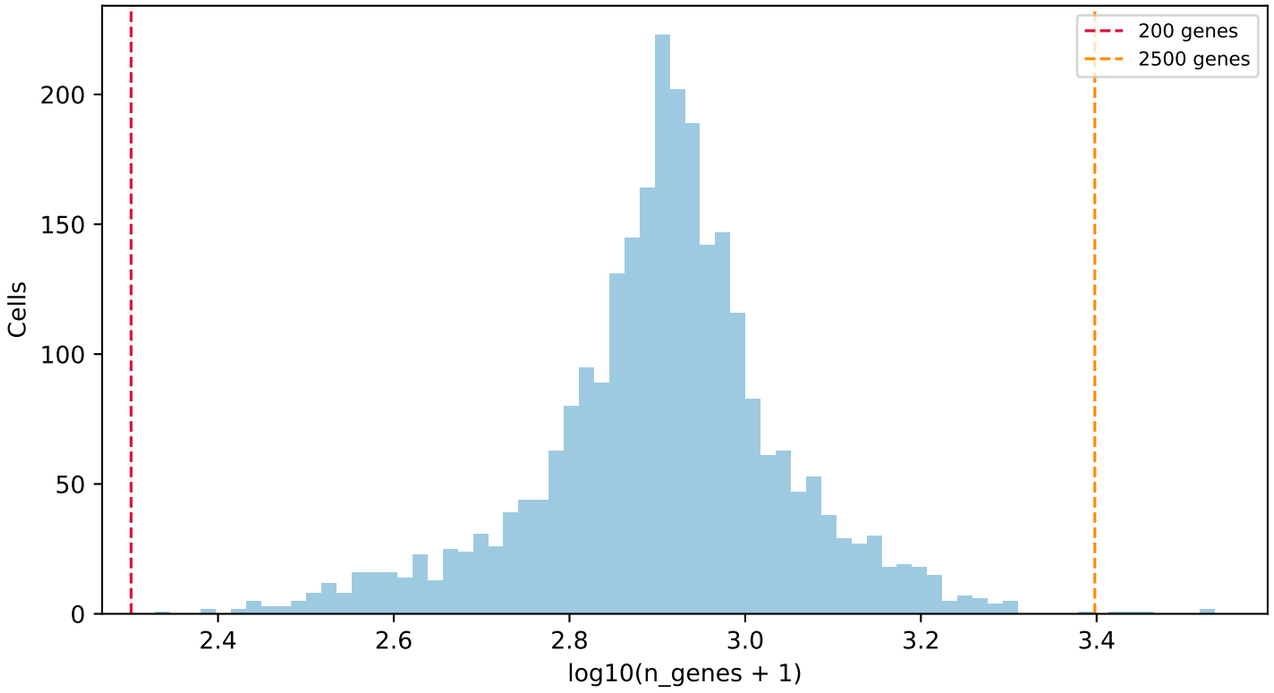
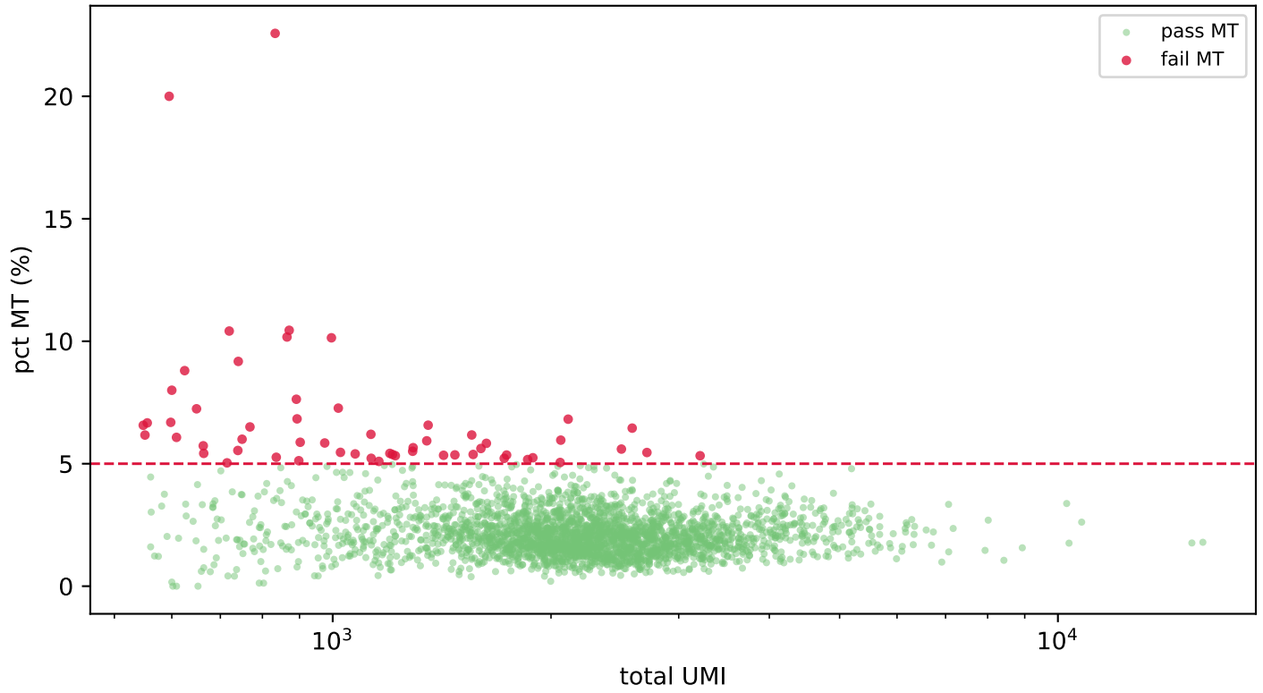
PBMC3k QC trace: which step removed which barcode, and which denominator was used

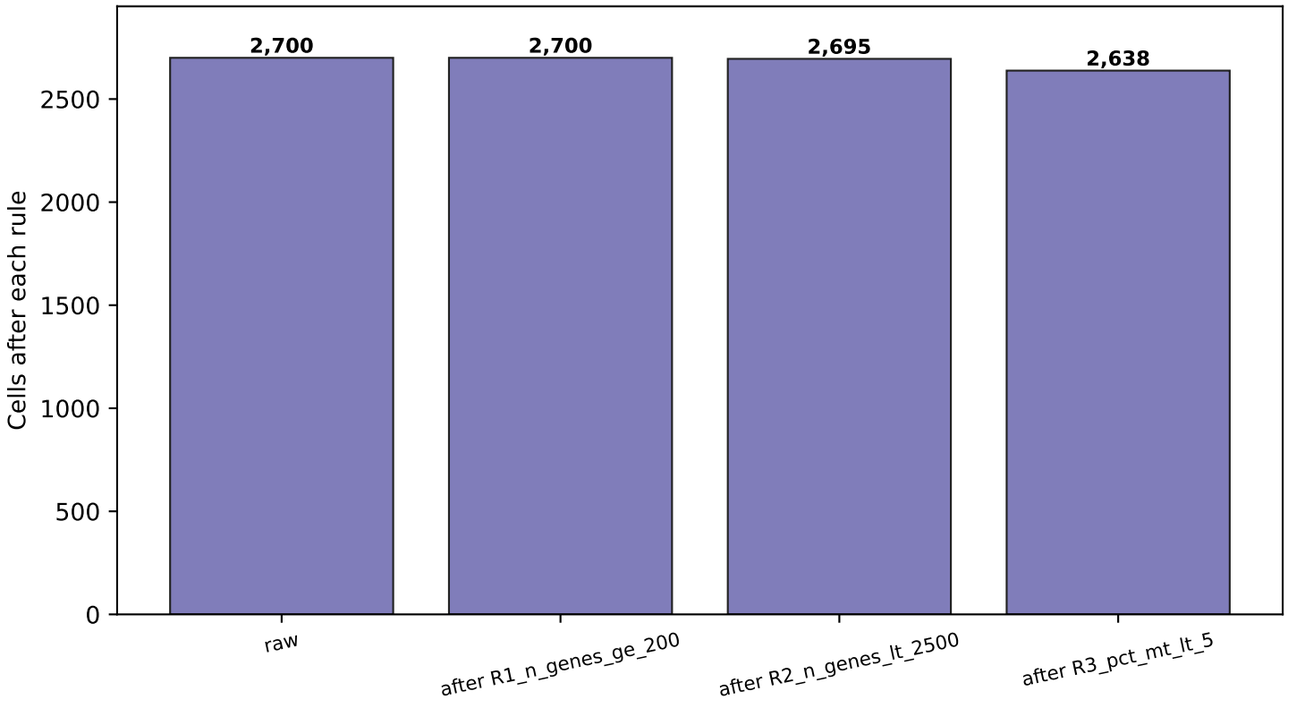
A. Genes per barcode (all 2,700)



B. MT fraction vs depth



C. Sequential removal (observed counts)



D. Field mismatch after gene filtering
1,908 cells differ, max |diff| = 56

