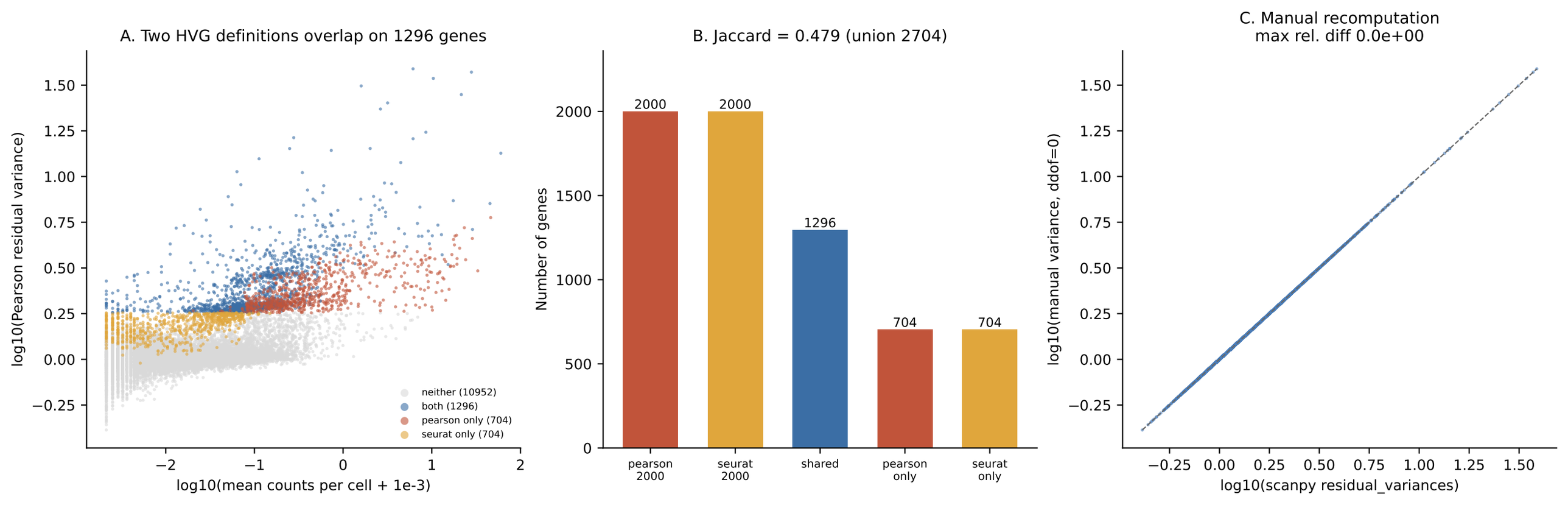
A. Two HVG definitions overlap on 1296 genes
log10(Pearson residual variance)
log10(mean counts per cell + 1e-3)
neither (10952)
both (1296)
pearson only (704)
seurat only (704)
B. Jaccard = 0.479 (union 2704)
Number of genes
2000
2000
1296
704
704
pearson 2000
seurat 2000
shared
pearson only
seurat only
C. Manual recomputation
max rel. diff 0.0e+00
log10(manual variance, ddof=0)
log10(scanpy residual_variances)