Fig. S1

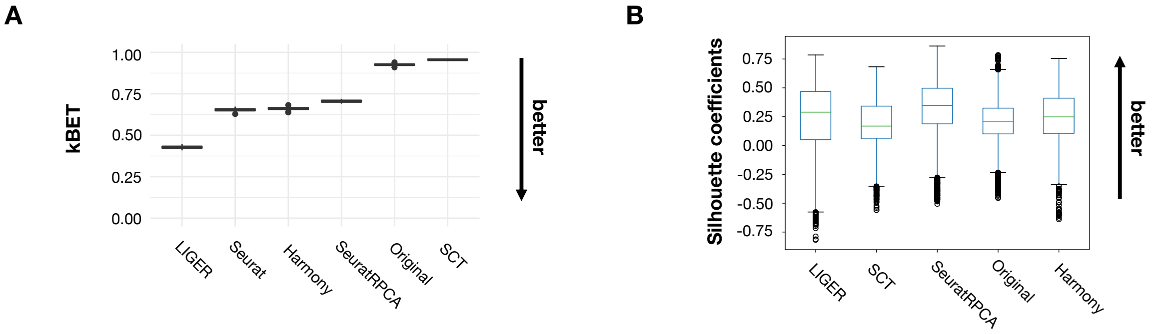

Fig. S1 Evaluation metrics for harmonization.
(A) Batch correction performance evaluation by plots of kBET metrics and (B) Silhouette coefficients. For our demo dataset, LIGER was identified as the best batch correction method.

Fig. S2

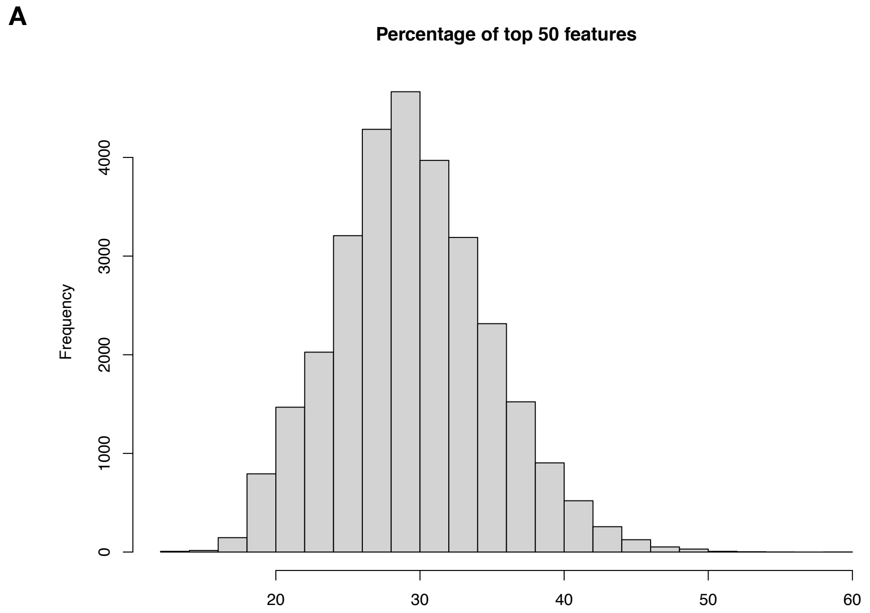

Fig. S2 Percentage of top 50 features.

Fig. S3

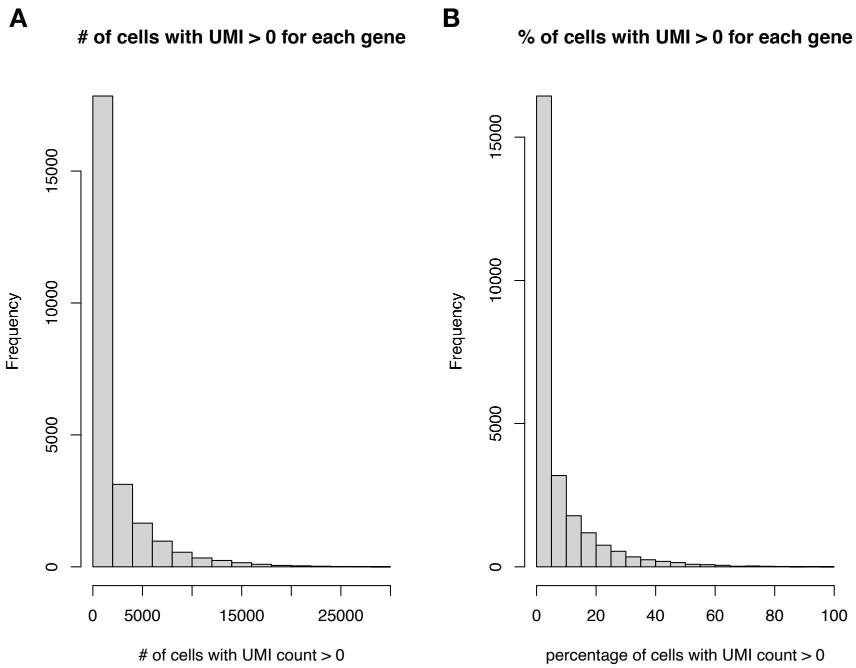

Fig. S3 Number of cells with UMI > 0 for each gene (left) and the percentage of cells with UMI > 0 for each gene (right).