nature methods

Article https://doi.org/10.1038/s41592-023-01933-9

Significance analysis for clustering with single-cell RNA-sequencing data

Supplementary Figures

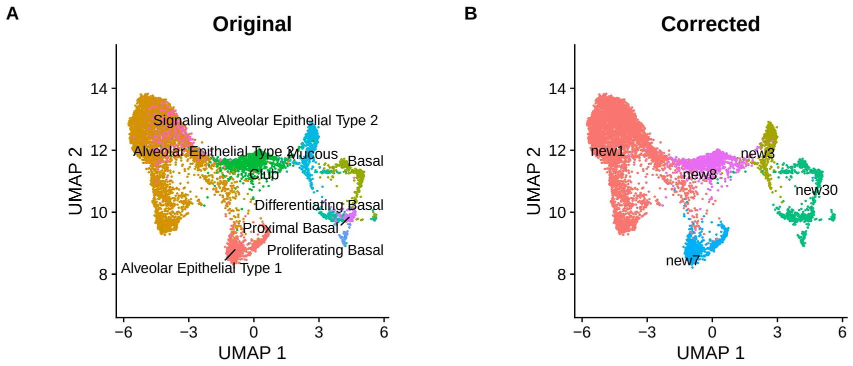

Figure 1: Zoomed-in UMAPs summarizing clustering results from the original Human Lung Cell Atlas annotations and after applying significance analysis, for an example set of clusters. (A) Original clusters. (B) Clusters after significance analysis.

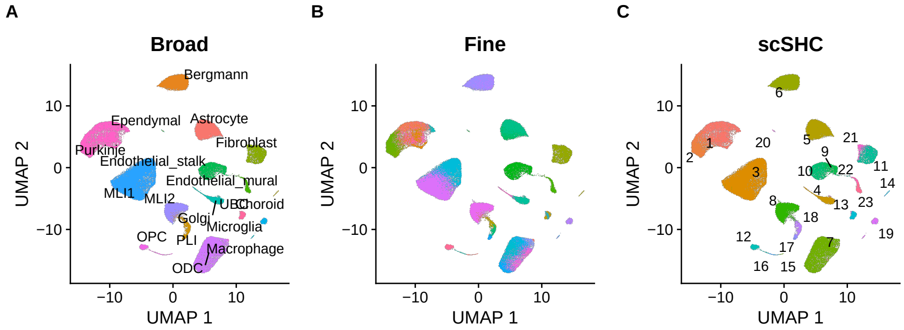

Figure 2: UMAPs summarizing clustering results from the original mouse cerebellum atlas and after applying our clustering pipeline. (A) Original clusters at the broadest level. (B) Original clusters at the fine-grained level. (C) Clusters after applying our pipeline.