

Multiome data (RNA+ATAC), Qinyu Zhang @ David Bryder lab

Meeting 2022-02-10

Focus on ATAC integration and cluster annotation

Agreed-upon focus on integrating the two samples' ATAC modalities, as well as annotating RNA clusters based on differentially expressed genes, with the help of BM genes and given list of 10 genes.

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What was accomplished was integration of ATAC modalities, as well as formalising what has been done this far, which means higher reproducibility and the data being ready for annotation efforts.

Naming

The two samples:

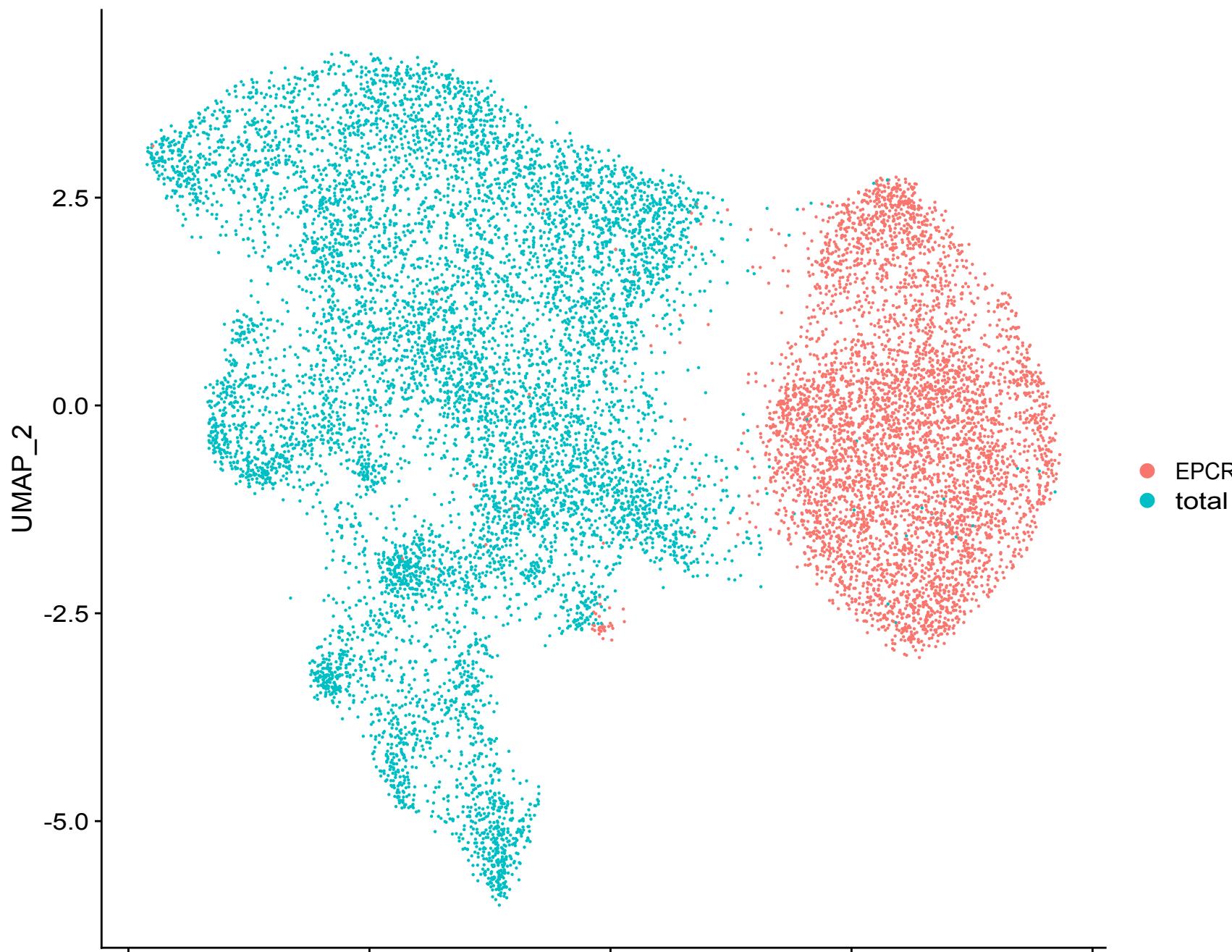
1. Immature (formerly EPCR)
2. Diverse (Formerly Total, formerly Viable_RNA)

Integration methods for ATAC tried

- Harmony
- Partial PCA
- Projection
 - k-Nearest Neighbours (Scarf)
 - Reciprocal LSI (Signac/Seurat), aka anchor-based approach

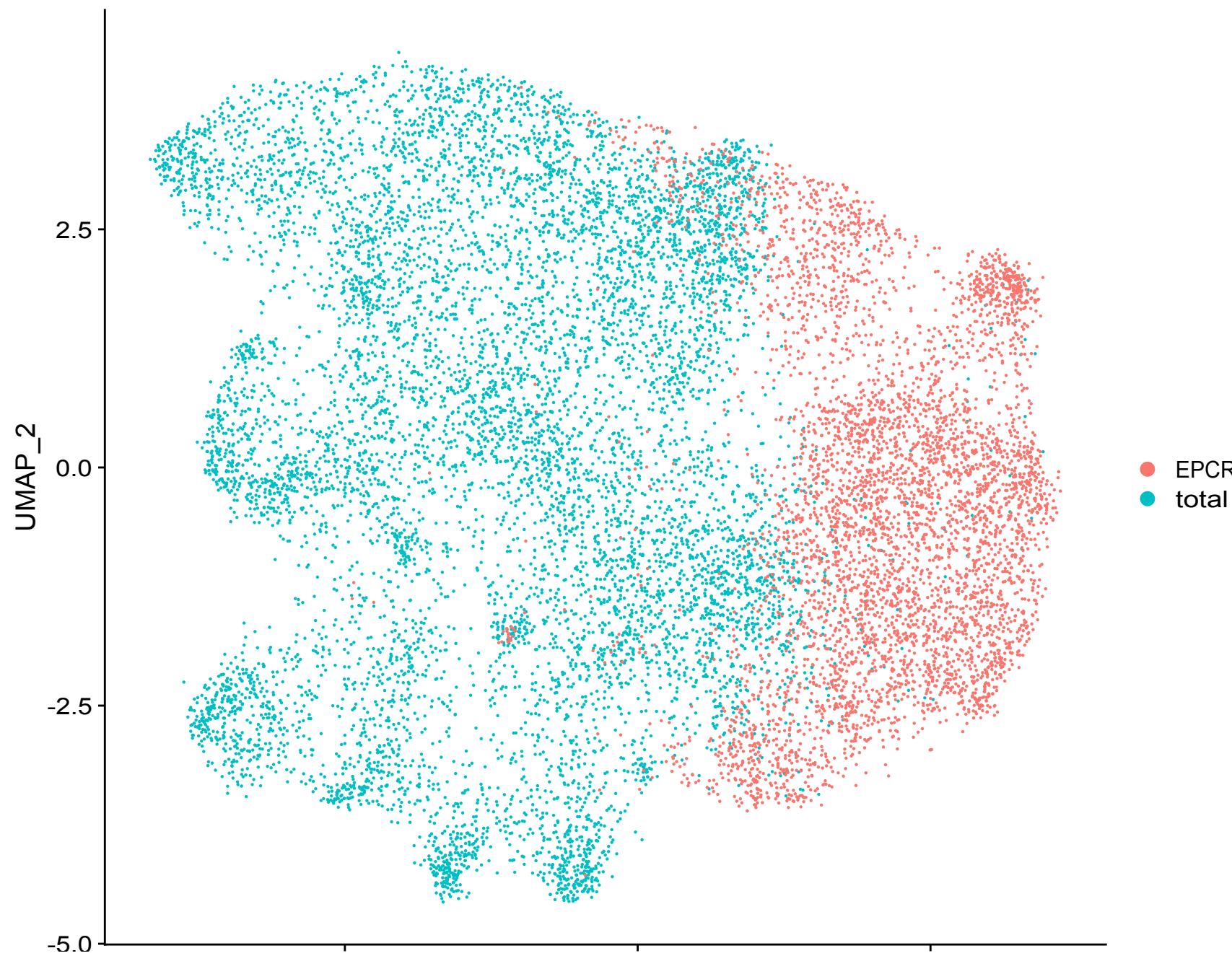
Not yet integrated (baseline/starting point)

origin



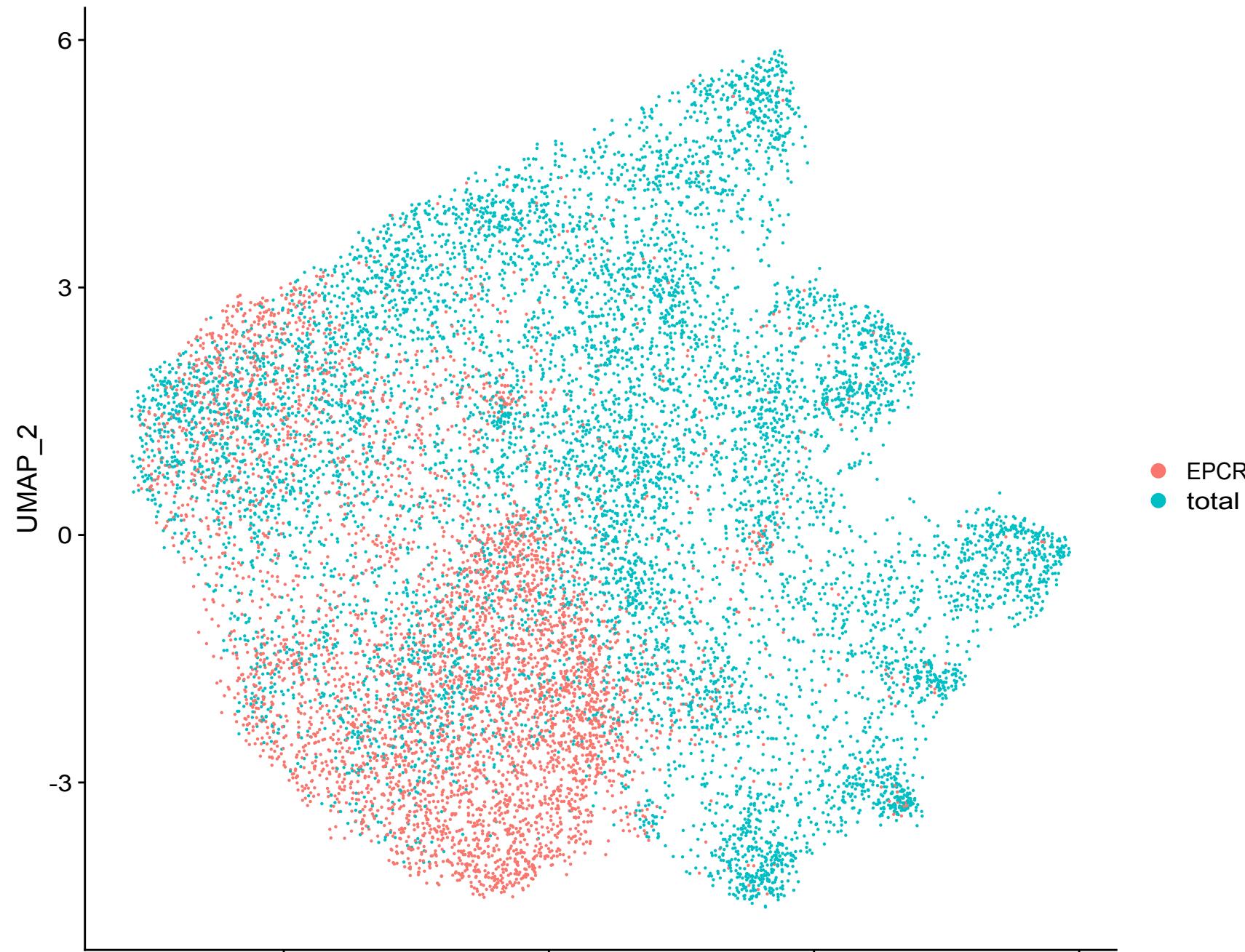
rLSI/anchor-based approach

origin

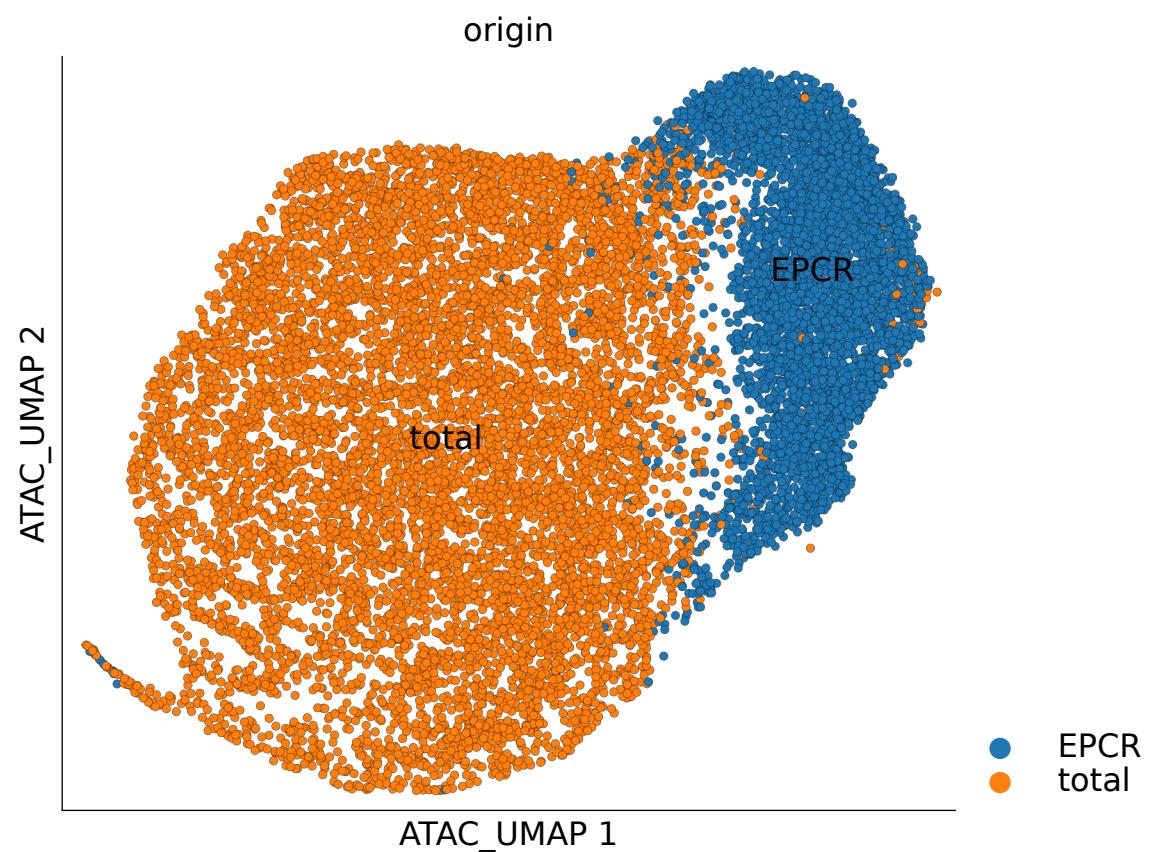


Harmony

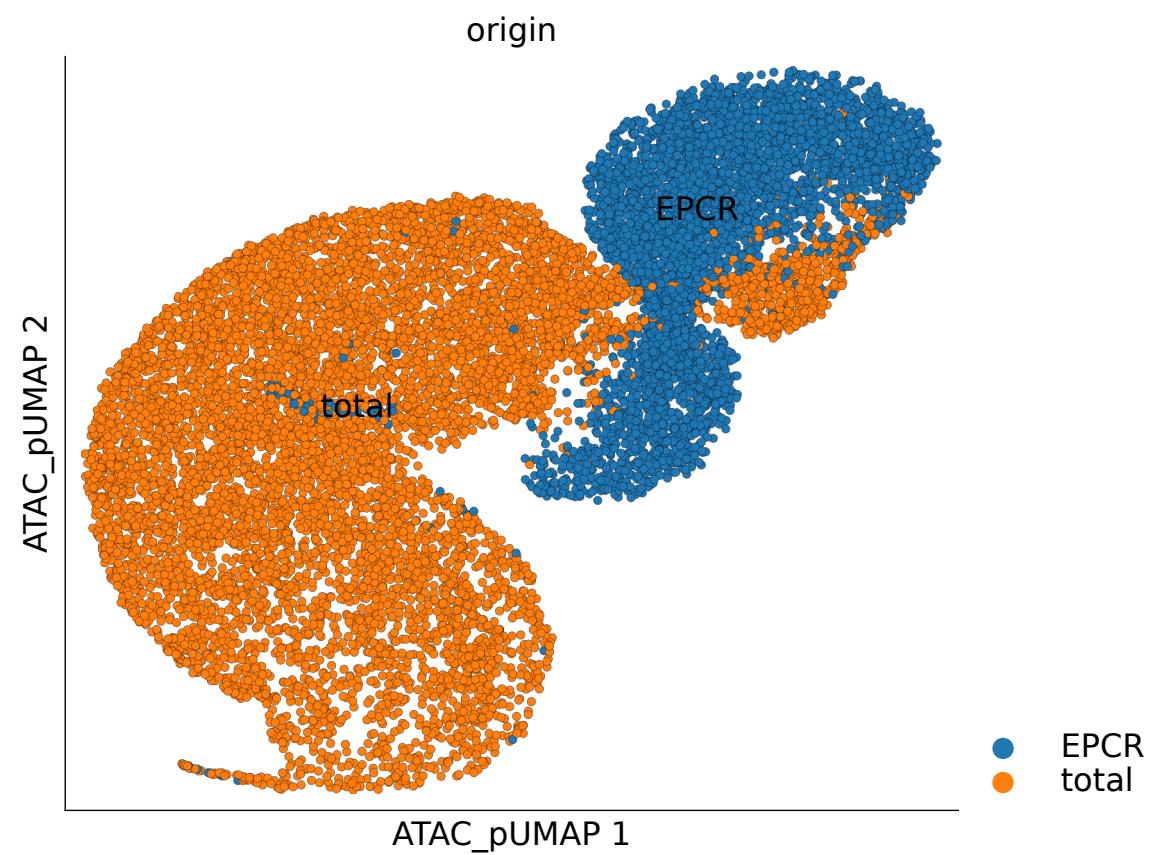
Harmony-integrated ATAC



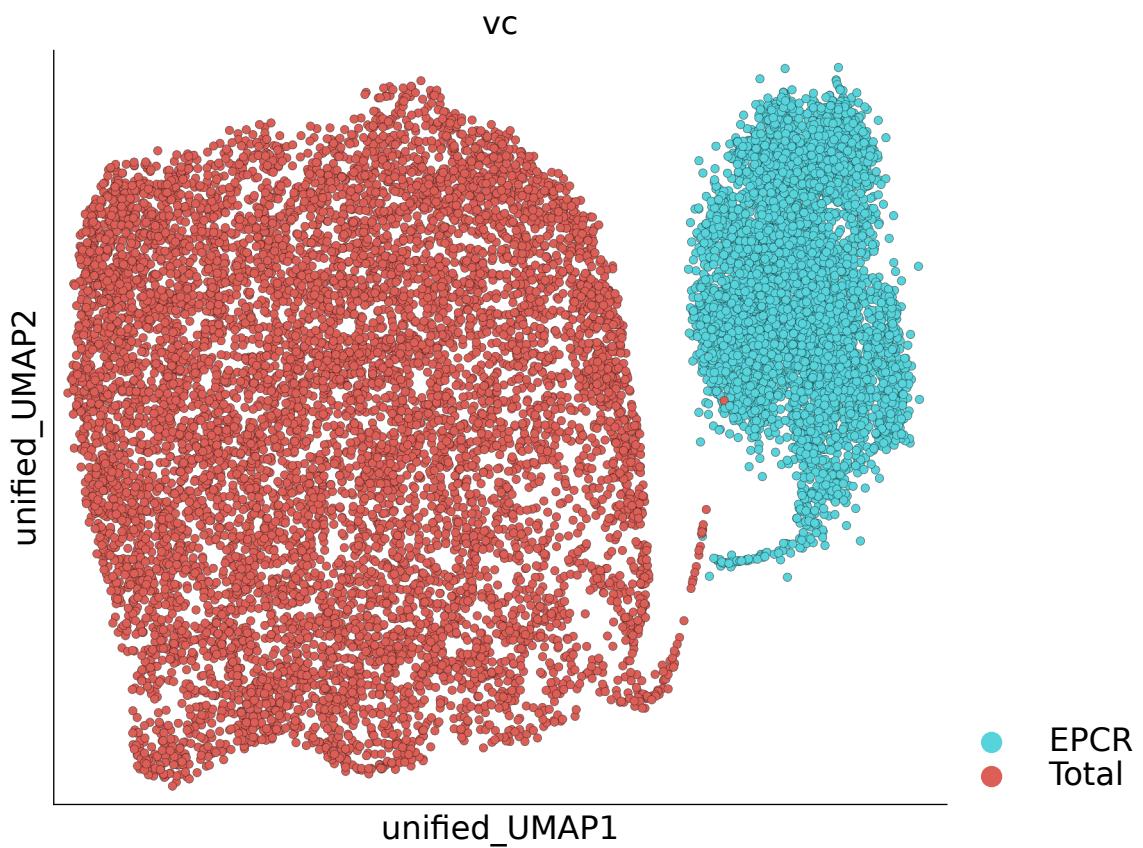
Unintegrated



Partial PCA



kNN-based Projection

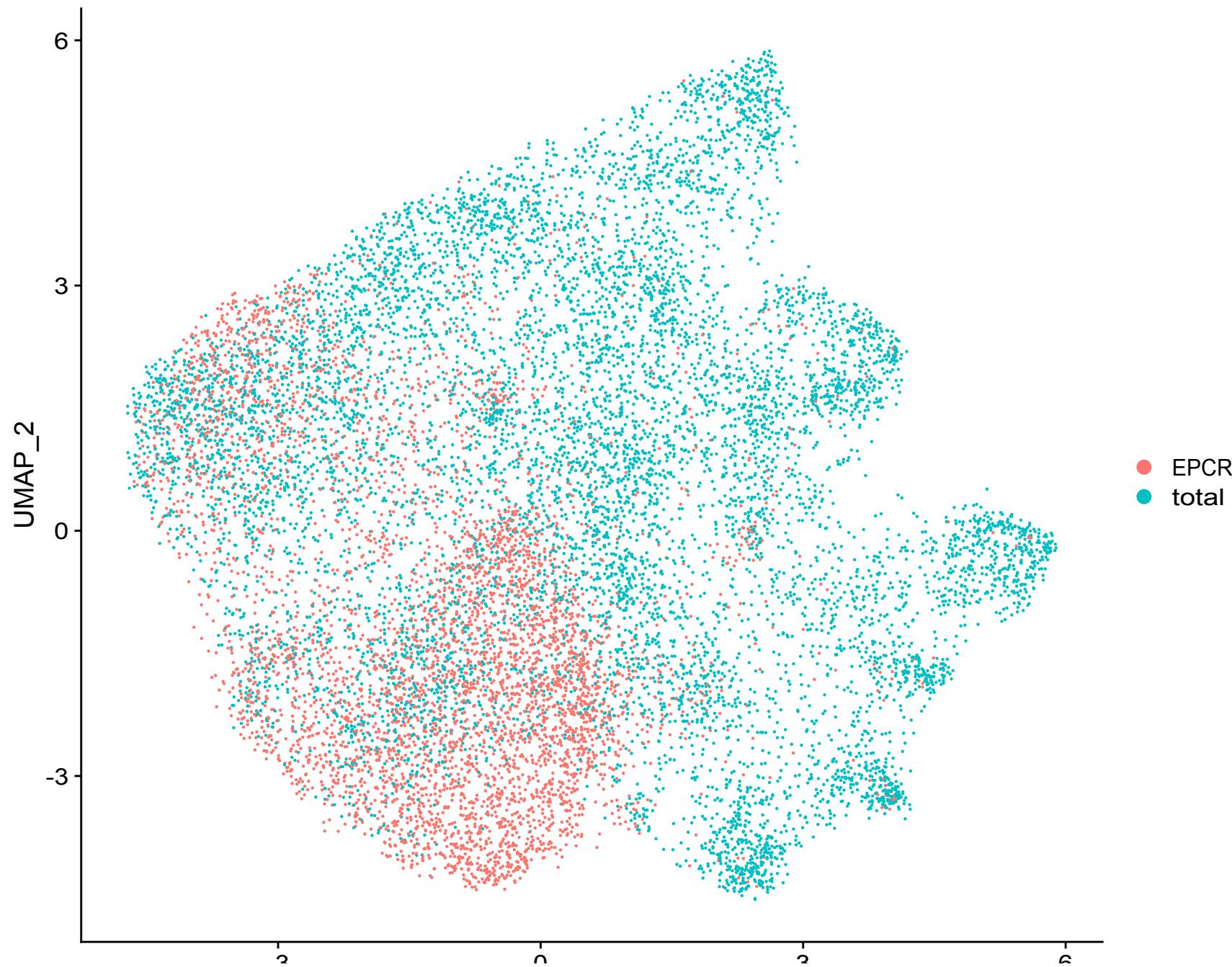


This looks not good at all, however not entirely improbable there is something I overlooked. Nevertheless, the Harmony results looks good enough that I think we should go forward with that.

Discussion

Similarly to for the RNA data, I think Harmony gave the best result, and is what we should move forward with.

Harmony-integrated ATAC



by Rasmus Olofzon