Fat Tissue data

December 20, 2023

1. Filtering criteria:

```
subset(fatRES2, subset = nFeature_RNA>200 & nFeature_RNA < 2000 & percent.mt <10)
FindVariableFeatures(fatRES2, selection.method = "vst", nfeatures = 2000)

# Identify integration anchors
anchors <- FindIntegrationAnchors(object.list = list(fatRES2, fatCONTR2), dims = 1:20)
# Integrate data
seurat_combined <- IntegrateData(anchorset = anchors, dims = 1:20)</pre>
seurat_combined <- FindNeighbors(seurat_combined, dims = 1:15)
```

2. UMAP

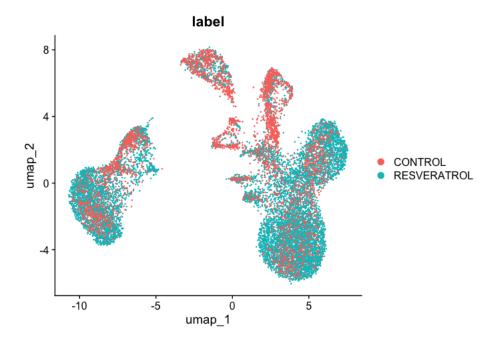


Figure 1: umap by groups

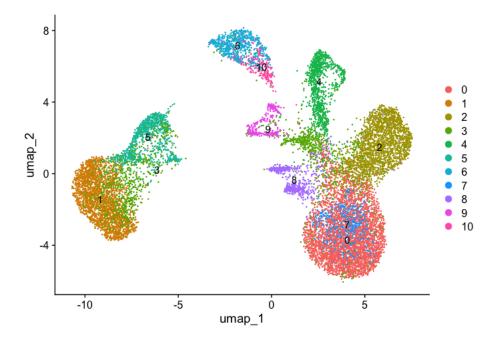


Figure 2: umap by clusters

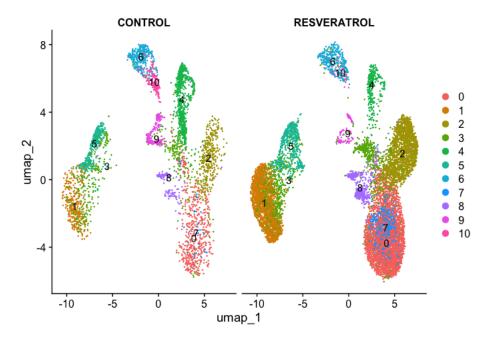


Figure 3: umap by clusters split by groups

3. TSNE

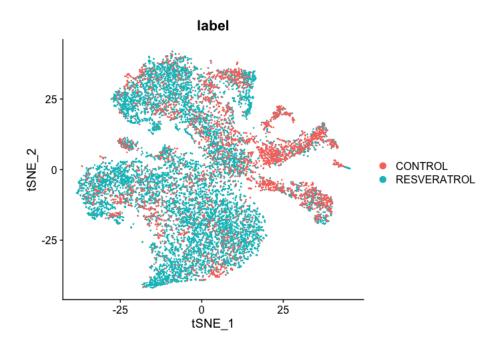


Figure 4: Tsne by groups

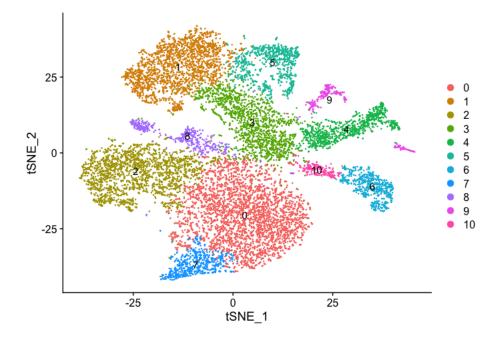


Figure 5: Tsne by clusters

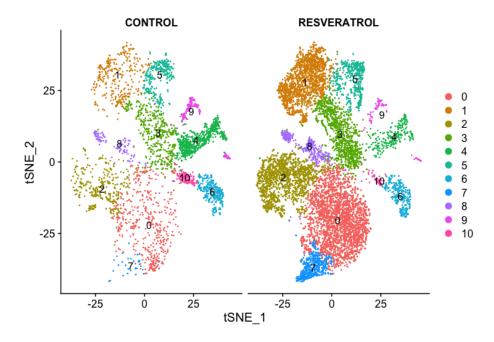


Figure 6: Tsne by clusters split by groups