

Loupe Browser Introduction

ScRNAseq in the Cloud

MDIBL Comparative Genomics and Data Science Core

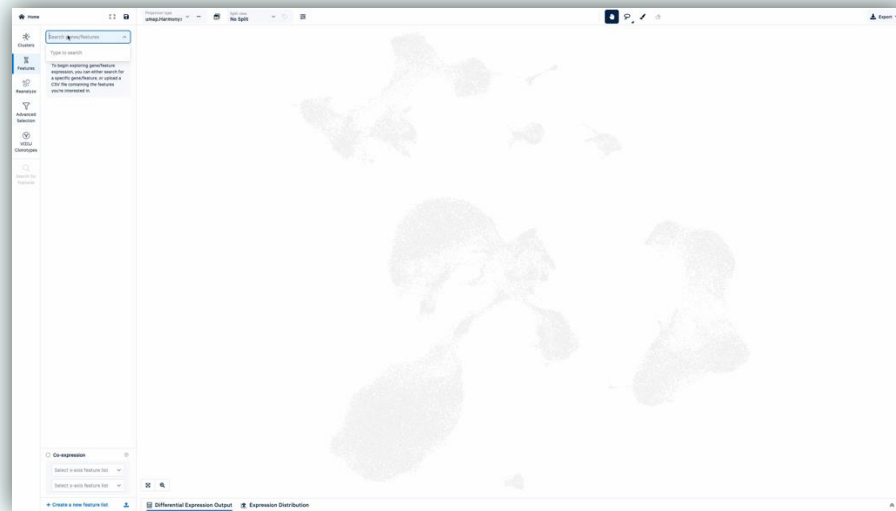


WHY

```
#
# Plot Integrated UNAP (if run) ->
#
pdf(paste0(params.ProjectName,params.IntegrationMethod,"IntegratedUNAP.pdf"),width = 20, height = 15)
if (params.IntegrationMethod != "NULL"){
  p1 <- DimPlot(object = MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00007653*length(MergedS0$orig.ident))+4, label = T, group.by = "orig.ident", shuffle = T)
  p2 <- FeaturePlot(MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedS0$orig.ident))+1, features = "nFeature_RNA", order = T) + scale_color_viridis(limits = c(min(MergedS0$nFeature_RNA),max(MergedS0$nFeature_RNA)), direction = -1)
  p3 <- FeaturePlot(MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedS0$orig.ident))+1, features = "nCount_RNA", order = T) + scale_color_viridis(limits = c(min(MergedS0$nCount_RNA),max(MergedS0$nCount_RNA)), direction = -1)
  p4 <- FeaturePlot(MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedS0$orig.ident))+1, features = "percent_mt", order = T) + scale_color_viridis(limits = c(min(MergedS0$percent_mt),max(MergedS0$percent_mt)), direction = -1)

  print(p1 + p2 + p3 + p4 + plot_layout(design = PageLayout))
  try(expr = (print(DimPlot(object = MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00007653*length(MergedS0$orig.ident))+4, label = T, group.by = "CiscCATCH"))))
  for (i in params.Resolutions){
    print(DimPlot(object = MergedS0, reduction = paste0("unap.",params.IntegrationMethod), pt.size = (-0.00007653*length(MergedS0$orig.ident))+4, label = T, group.by = paste0(params.IntegrationMethod,"Res.",i)))
  }
}
dev.off()
```

VS



LOUPE

INTERFACE

Tools

View

Mouse

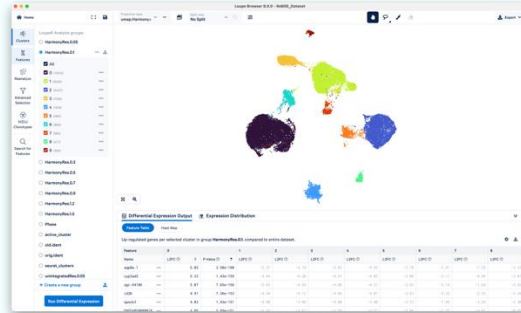
Export

Modes

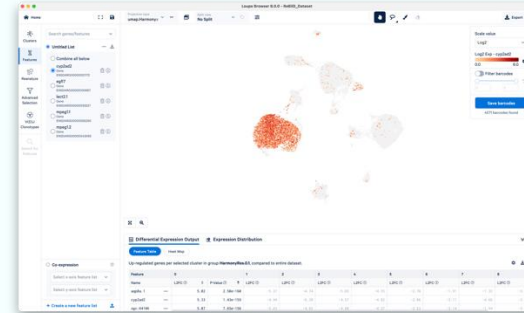


MODES

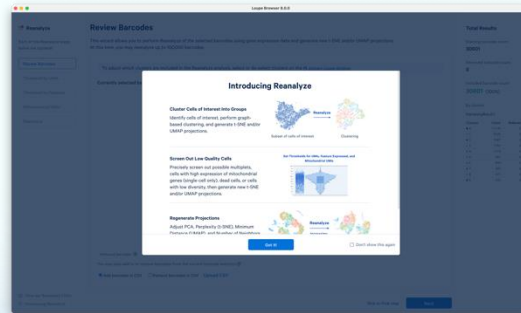
Clusters



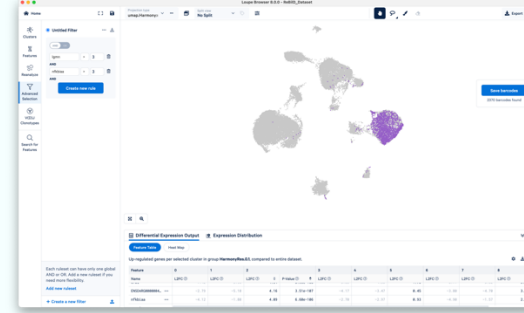
Features



Reanalyze



Advanced Selection



LOUPE

CLUSTERS

Loupe Browser 8.0.0 - ReBILD_Dataset

Projection type: umap, Harmony; Split view: No Split

Home

Clusters

LoupeR Analysis groups

- HarmonyRes.0.05
- HarmonyRes.0.1**
- HarmonyRes.0.3
- HarmonyRes.0.5
- HarmonyRes.0.7
- HarmonyRes.0.9
- HarmonyRes.1.2
- HarmonyRes.1.5
- Phase
- active_cluster
- old.ident
- orig.ident
- seurat_clusters
- unintegratedRes.0.05

Features

Reanalyze

Advanced Selection

VDJ Clonotypes

Search for Features

Differential Expression Settings

Compare all selected clusters in HarmonyRes.0.3:

To entire dataset

Feature type

Gene

Start analysis

Differential Expression Output

Feature Table

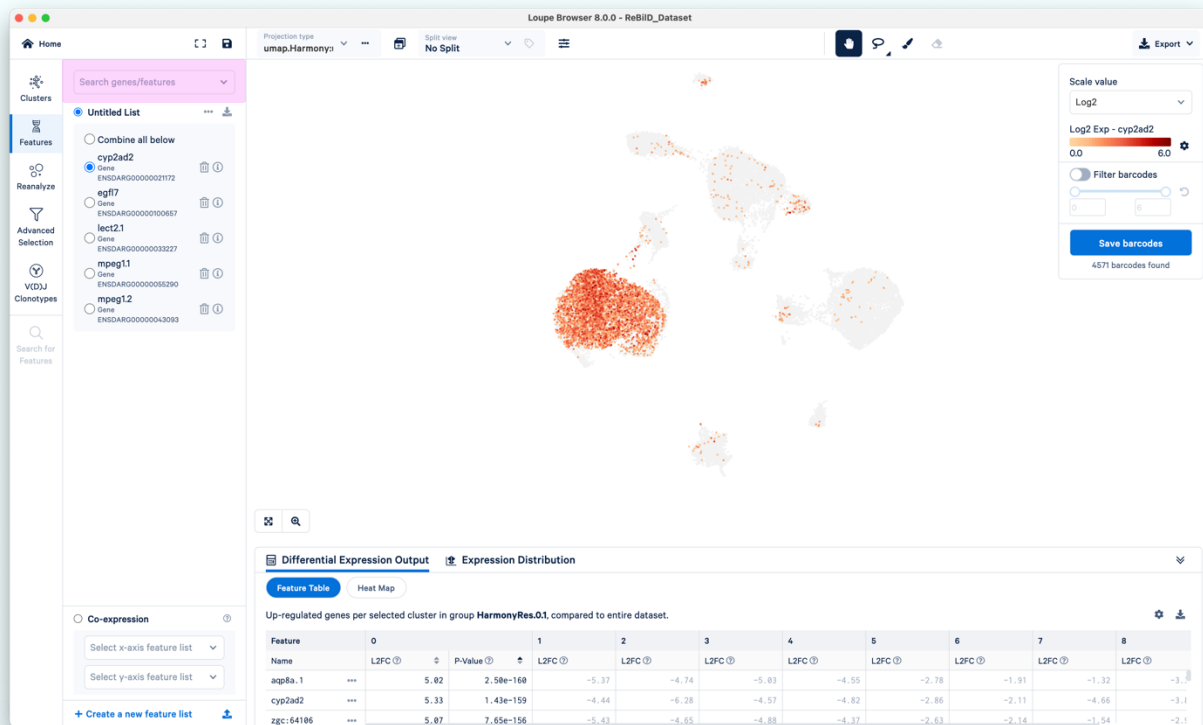
Heat Map

Up-regulated genes per selected cluster in group HarmonyRes.0.1 compared to entire dataset.

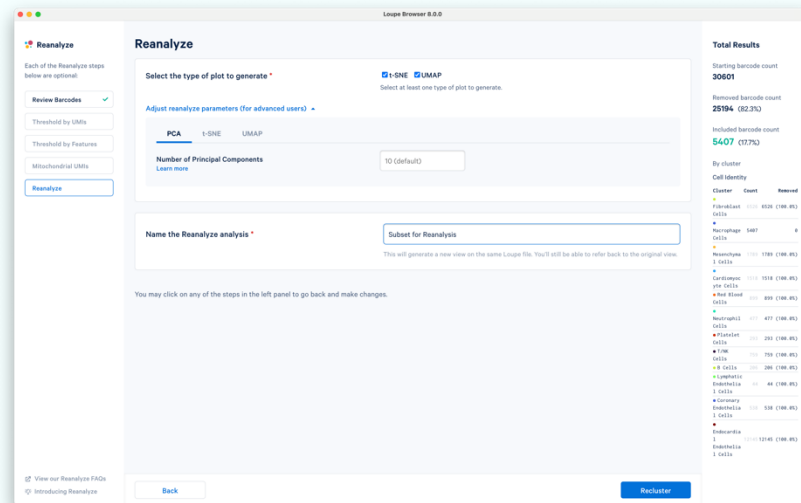
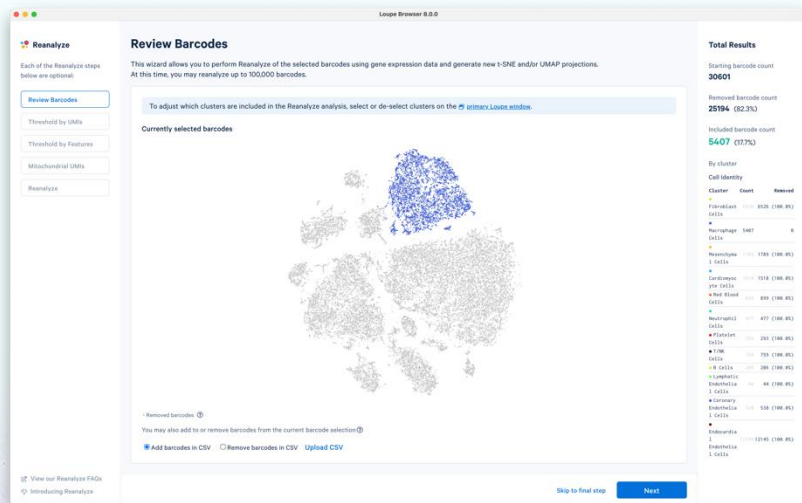
Feature	0	1	2	3	4	5	6	7	8
Name	L2FC	L2FC	L2FC	L2FC	L2FC	L2FC	L2FC	L2FC	L2FC
apb.1	5.02	2.58e-168	-5.37	-4.74	-5.03	-4.55	-2.78	-1.91	-1.32
cyp2a2	5.33	1.43e-159	-4.44	-6.28	-4.57	-4.82	-2.86	-2.11	-4.66
zgc:64106	5.07	7.65e-156	-5.43	-4.65	-4.88	-4.37	-2.63	-2.14	-1.54
ld2b	4.91	7.36e-153	-4.54	-4.13	-4.66	-4.81	-2.63	-2.22	-2.25
spock3	4.83	1.43e-151	-4.90	-3.89	-4.80	-3.90	-2.72	-1.85	-3.59
ENSO18C000001A	4.86	3.99e-151	-5.16	-4.63	-3.48	-4.57	-2.80	-2.33	-4.91



FEATURES



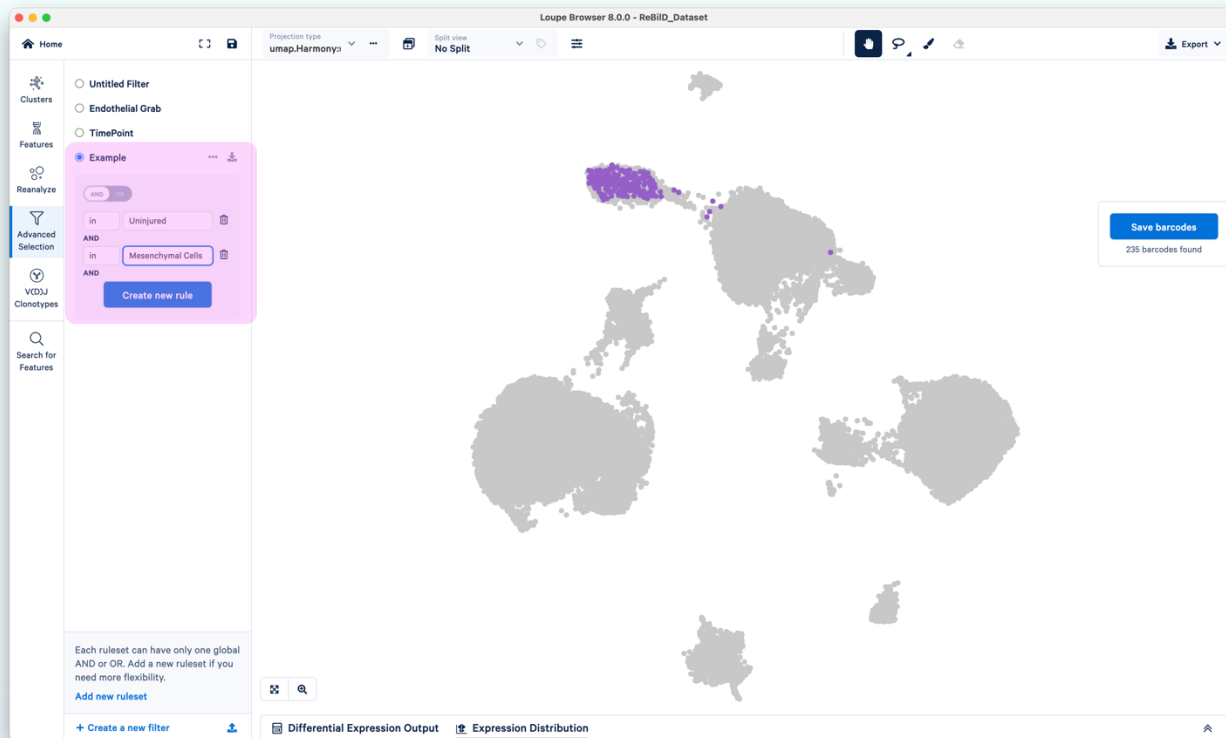
REANALYZE



LOUPE

MDI Biological Laboratory

ADVANCED SELECTION



Questions?

