

Loupe Browser Introduction

ScRNASeq in the Cloud

MDIBL Comparative Genomics and Data Science Core

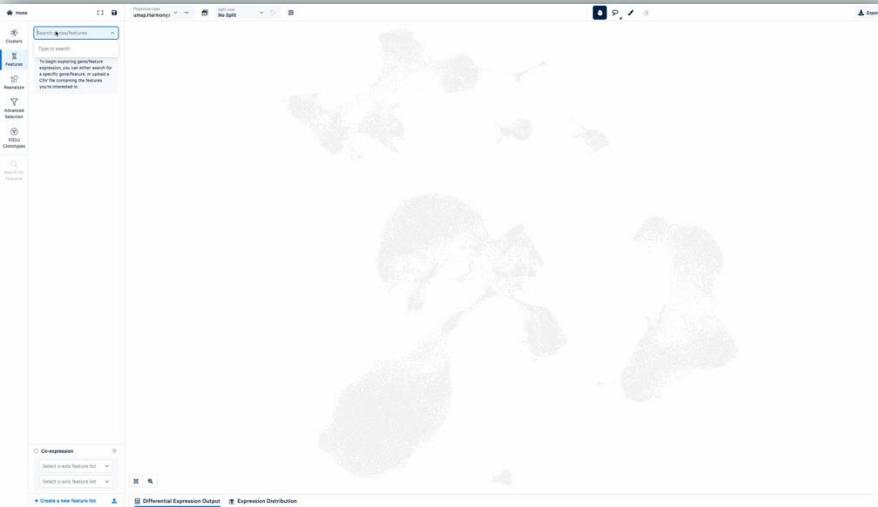


WHY

```
# [-- Plot Integrated UMAP (if run) --]
# [--]
# pdf:paste@params.ProjectName,params.IntegrationMethod,"IntegratedUMAP.pdf"),width = 20, height = 15)
if (params.IntegrationMethod == "NULL"){
  p1 <- DimPlot(object = MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00007653*length(MergedSO$orig.ident))+4, label = T, group.by = "orig.Ident", shuffle = T)
  p2 <- FeaturePlot(MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedSO$orig.ident))+4, features = "nFeature_RNA", order = T) + scale_color_viridis(limits =c(min(MergedSO$inFeature_RNA),max(MergedSO$inFeature_RNA)), direction = -1)
  p3 <- FeaturePlot(MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedSO$orig.ident))+4, features = "nCount_RNA", order = T) + scale_color_viridis(limits =c(min(MergedSO$inCount_RNA),max(MergedSO$inCount_RNA)), direction = -1)
  p4 <- FeaturePlot(MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedSO$orig.ident))+4, features = "percent_nt", order = T) + scale_color_viridis(limits =c(min(MergedSO$percent_nt),max(MergedSO$percent_nt)), direction = -1)

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

VS



INTERFACE



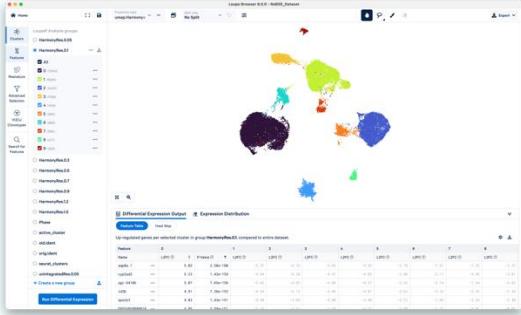
Modes

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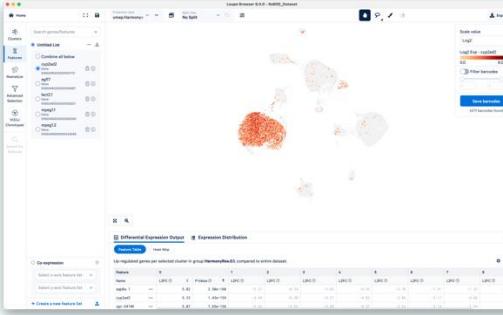


MODES

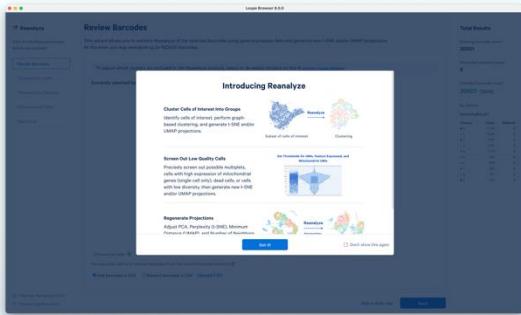
Clusters



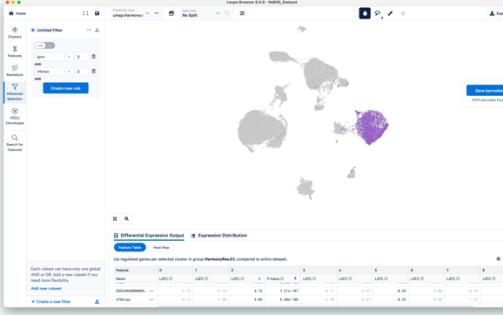
Features



Reanalyze



Advanced Selection



CLUSTERS

Loupe Browser 8.0.0 - ReBiID_Dataset

Home    

Clusters      

LoupeR Analysis groups

- HarmonyRes.0.05
- HarmonyRes.0.1

Projection type: umap.Harmony3   

Clusters      

0 (3245)          

1 (6520)          

2 (5407)          

3 (1788)          

4 (1318)          

5 (985)          

6 (6990)          

7 (3882)          

8 (4777)          

9 (2930)          

Differential Expression Settings

Compare all selected clusters in **HarmonyRes.0.3**:

To entire dataset

Feature type: Gene

Start analysis

Differential Expression Output 

Feature Table 

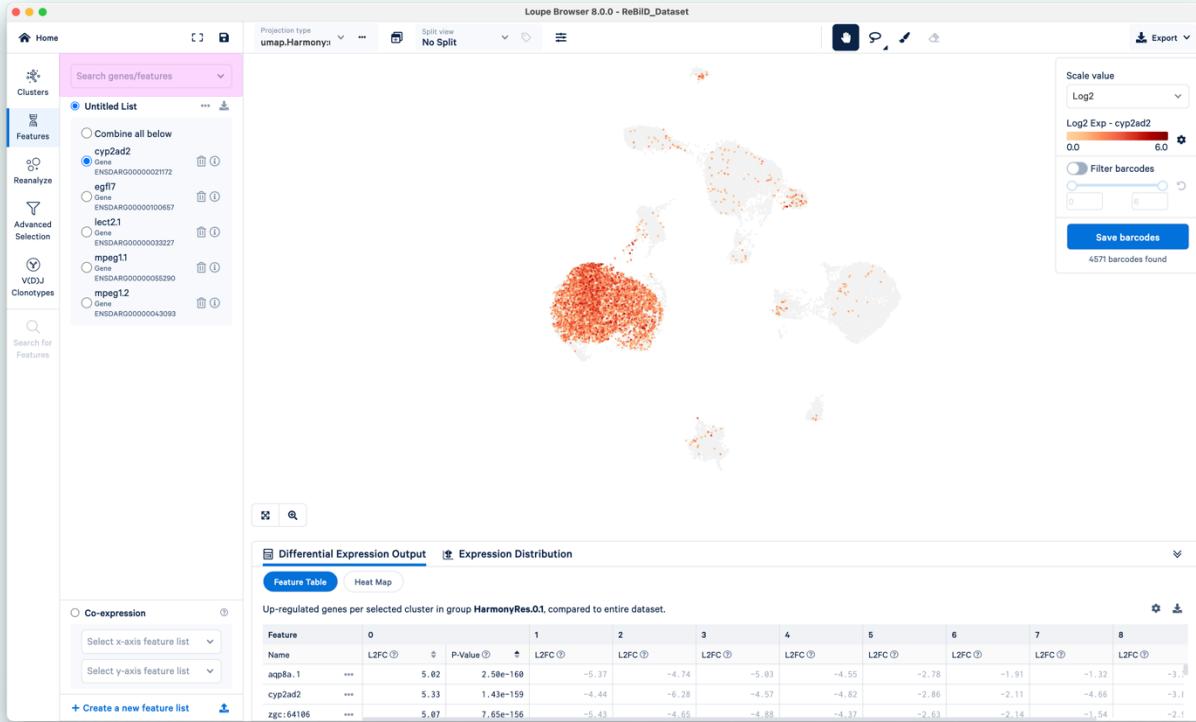
Up-regulated genes per selected cluster in group **HarmonyRes.0.1**, compared to entire dataset.

Feature	0	1	2	3	4	5	6	7	8
Name	L2FC 	P-Value 	L2FC 	L2FC 	L2FC 	L2FC 	L2FC 	L2FC 	L2FC 
agpB_1	***	5.02 2.50e-160	-5.37 -4.74	-5.03 -4.55	-4.55 -2.78	-1.91 -1.32	-1.32 -3.33		
cyp2ad2	***	5.33 1.43e-159	-6.44 -6.28	-6.57 -4.82	-4.82 -2.86	-2.11 -4.66	-4.66 -3.81		
zgc:64106	***	5.07 7.65e-156	-5.43 -4.65	-4.88 -4.37	-4.37 -2.63	-2.14 -1.54	-1.54 -2.93		
id2b	***	4.91 7.36e-153	-6.54 -4.13	-6.66 -4.81	-4.81 -2.63	-2.22 -1.85	-2.25 -3.59	-3.34 -2.38	
spock3	***	4.83 1.43e-151	-6.98 -3.89	-6.88 -3.98	-3.98 -2.72	-1.85 -1.85	-3.59 -2.38		
ENSDARG000000019	***	4.86 3.99e-151	-6.16 -4.65	-5.48 -4.67	-4.67 -2.80	-1.77 -1.77	-4.01 -2.05		



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FEATURES



LOUPE

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REANALYZE

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Review Barcodes

This wizard allows you to perform Reanalyze of the selected barcodes using gene expression data and generate new t-SNE and/or UMAP projections. At this time, you may reanalyze up to 100,000 barcodes.

Each of the Reanalyze steps below are optional:

- Review Barcodes**
- Threshold by UMTs
- Threshold by Features
- Mitochondrial UMTs
- Reanalyze

To adjust which clusters are included in the Reanalyze analysis, select or de-select clusters on the primary Loupe window.

Currently selected barcodes

Starting barcode count **30601**
Removed barcode count **25194** (82.3%)
Included barcode count **5407** (17.7%)

By cluster

Cluster	Count	Removed
Endothelial	926 (100.0%)	0
Macrophage	907 (100.0%)	0
Neutrophil	1781 (100.0%)	0
CD4 T cell	1518 (100.0%)	0
CD8 T cell	839 (100.0%)	0
Monocyte	477 (100.0%)	0
Neutrophil	477 (100.0%)	0
Monocyte	293 (100.0%)	0
CD4 T cell	750 (100.0%)	0
CD8 T cell	286 (100.0%)	0
Neutrophil	44 (100.0%)	0
Monocyte	1 (100.0%)	0
Granular	538 (100.0%)	0
Endothelial	1 (100.0%)	0
CD4 T cell	12140 (100.0%)	0
CD8 T cell	1 (100.0%)	0

- Removed barcodes

You may also add to or remove barcodes from the current barcode selection

Add barcodes in CSV Remove barcodes in CSV [Upload CSV](#)

[Skip to final step](#) [Next](#)

[View our Reanalyze FAQs](#) [Introducing Reanalyze](#)

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Reanalyze

Select the type of plot to generate *

t-SNE UMAP

Select at least one type of plot to generate.

Each of the Reanalyze steps below are optional:

- Review Barcodes**
- Threshold by UMTs
- Threshold by Features
- Mitochondrial UMTs
- Reanalyze

Number of Principal Components [Learn more](#)

Name the Reanalyze analysis *

Subset for Reanalyze

This will generate a new view on the same Loupe file. You'll still be able to refer back to the original view.

You may click on any of the steps in the left panel to go back and make changes.

[Back](#) [Reanalyze](#)

Results

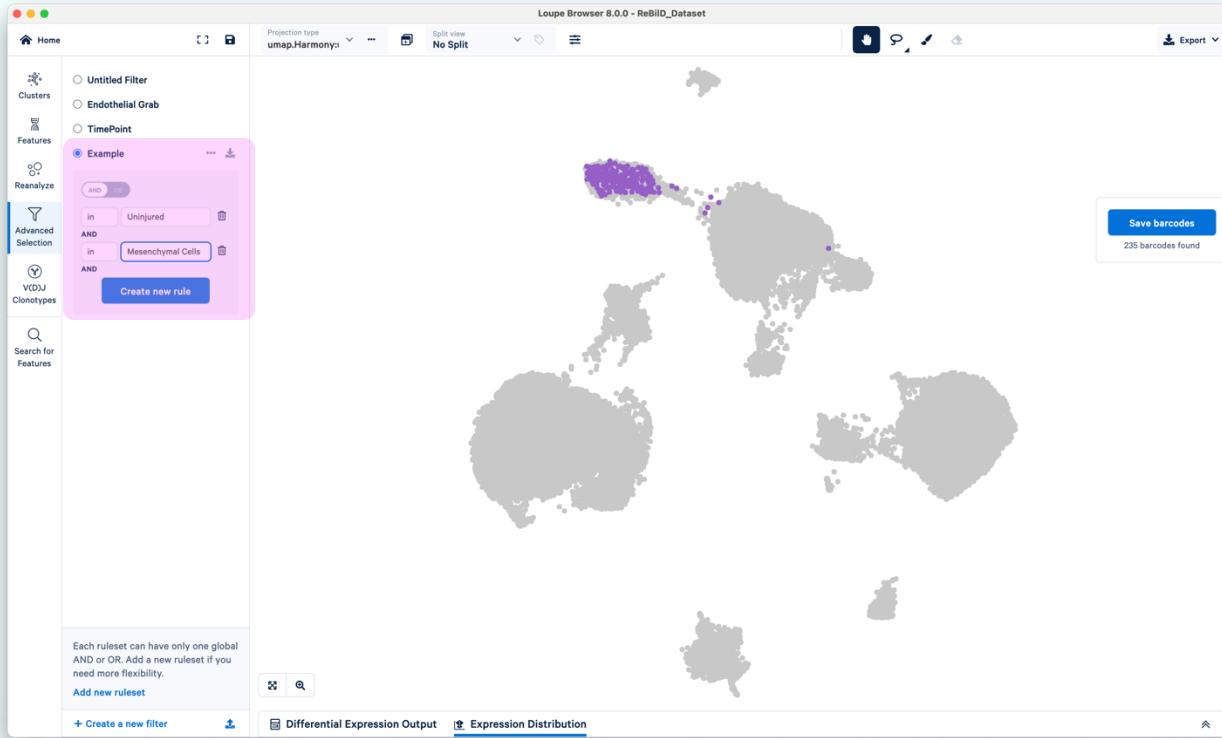
Starting barcode count **30601**
Removed barcode count **25194** (82.3%)
Included barcode count **5407** (17.7%)

By cluster

Cluster	Count	Removed
Endothelial	4520 (100.0%)	0
Macrophage	1781 (100.0%)	0
CD4 T cell	1518 (100.0%)	0
CD8 T cell	839 (100.0%)	0
Monocyte	293 (100.0%)	0
Neutrophil	477 (100.0%)	0
Monocyte	293 (100.0%)	0
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Neutrophil	44 (100.0%)	0
Monocyte	1 (100.0%)	0
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Endothelial	1 (100.0%)	0
CD4 T cell	12140 (100.0%)	0
CD8 T cell	1 (100.0%)	0



ADVANCED SELECTION



Questions?

