Loupe Browser Introduction

ScRNAseq in the Cloud

MDIBL Comparative Genomics and Data Science Core

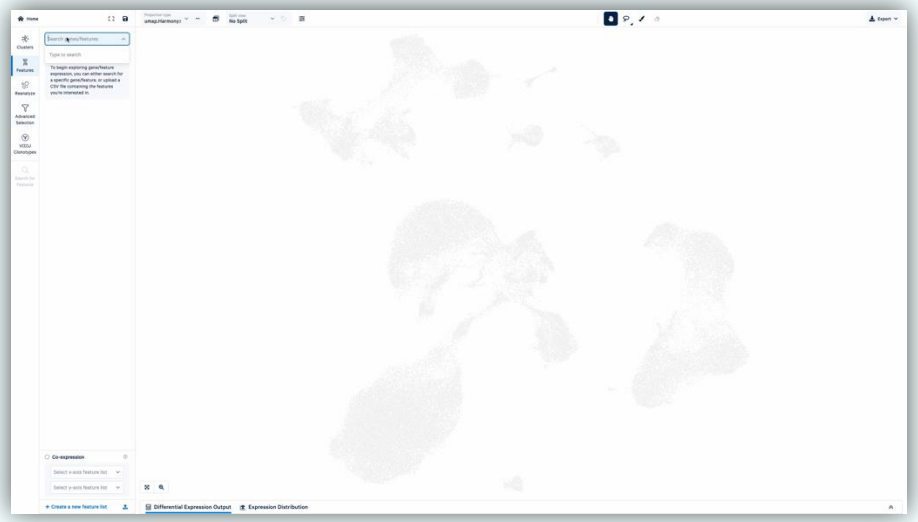
MDI Biological Laboratory

WHY

```
# ┌──────────────────────┐
# ├─ Plot Integrated UMAP (if run) ─┤
# └──────────────────────┘
pdf(paste0(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))+1, features = "nFeature_RNA", order = T) + scale_color_viridis(limits =c(min(MergedSO@nFeature_RNA),max(MergedSO@nFeature_RNA)), direction = -1)
    p3 <- FeaturePlot(MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedSO@orig.ident))+1, features = "nCount_RNA", order = T) + scale_color_viridis(limits =c(min(MergedSO@nCount_RNA),max(MergedSO@nCount_RNA)), direction = -1)
    p4 <- FeaturePlot(MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size = (-0.00001837*length(MergedSO@orig.ident))+1, features = "percent.mt", order = T) + scale_color_viridis(limits =c(min(MergedSO@percent.mt),max(MergedSO@percent.mt)), direction = -1)

    print(p1 + p2 + p3 + p4 + plot_layout(design = Pagellayout))
    try(expr = (print(DimPlot(object = MergedSO, reduction = paste0("umap.",params.IntegrationMethod), pt.size =(-0.00007653*length(MergedSO@orig.ident))+4, label = T, group.by = "CIscCATCH"))))
    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



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INTERFACE

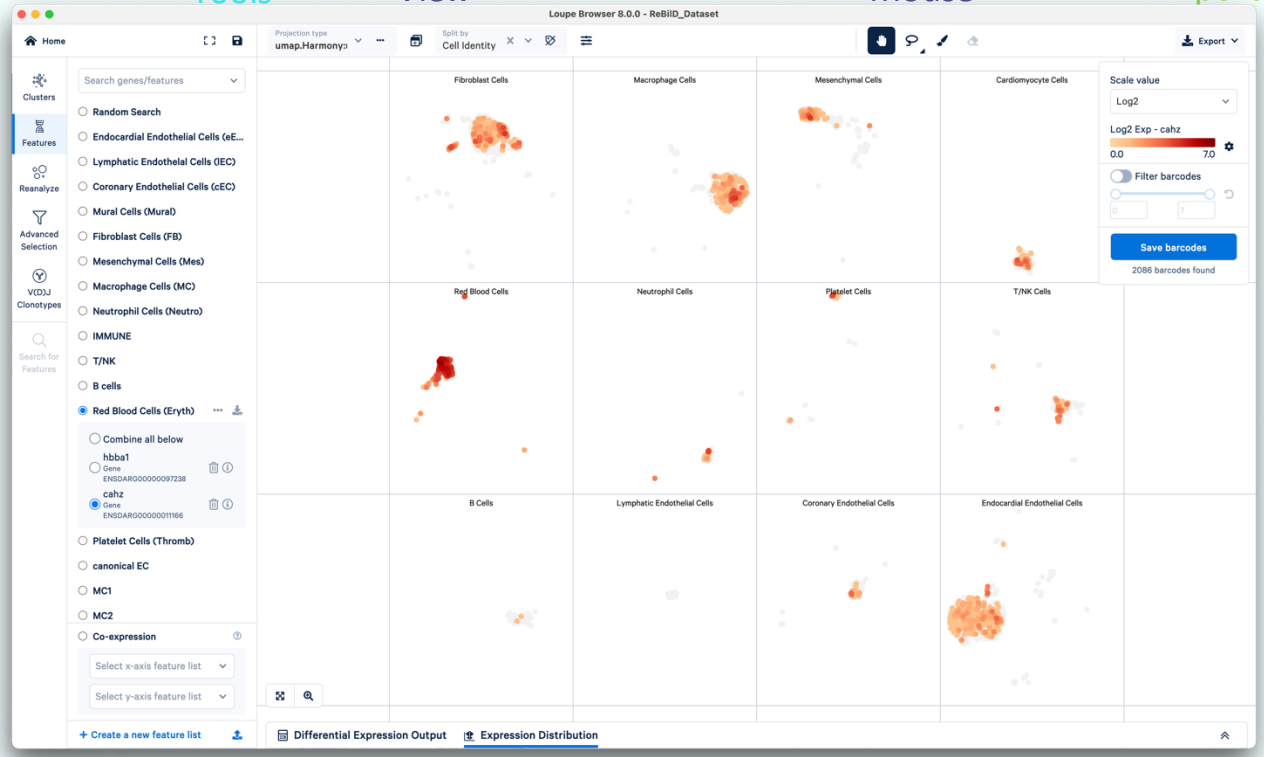
Tools

View

Mouse

Export

Modes



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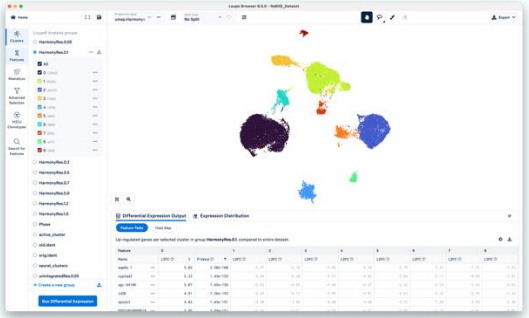
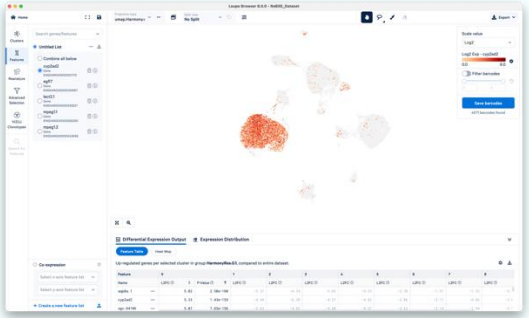
MODES

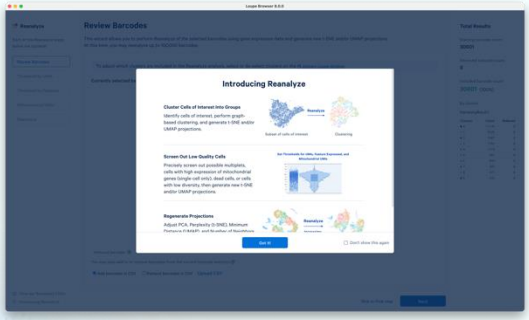
Clusters



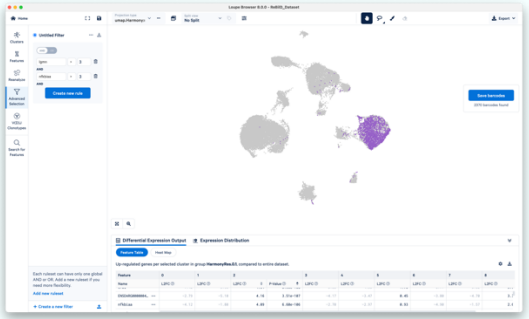
Features



Reanalyze



Advanced Selection



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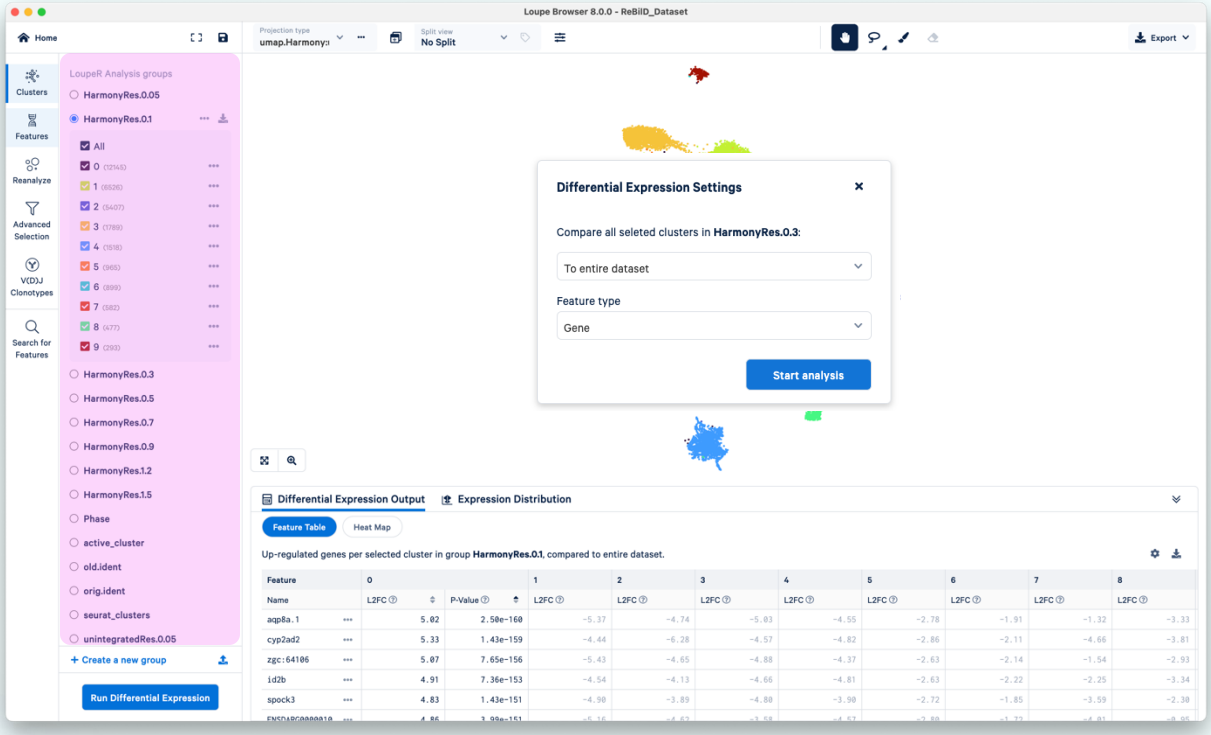
CLUSTERS



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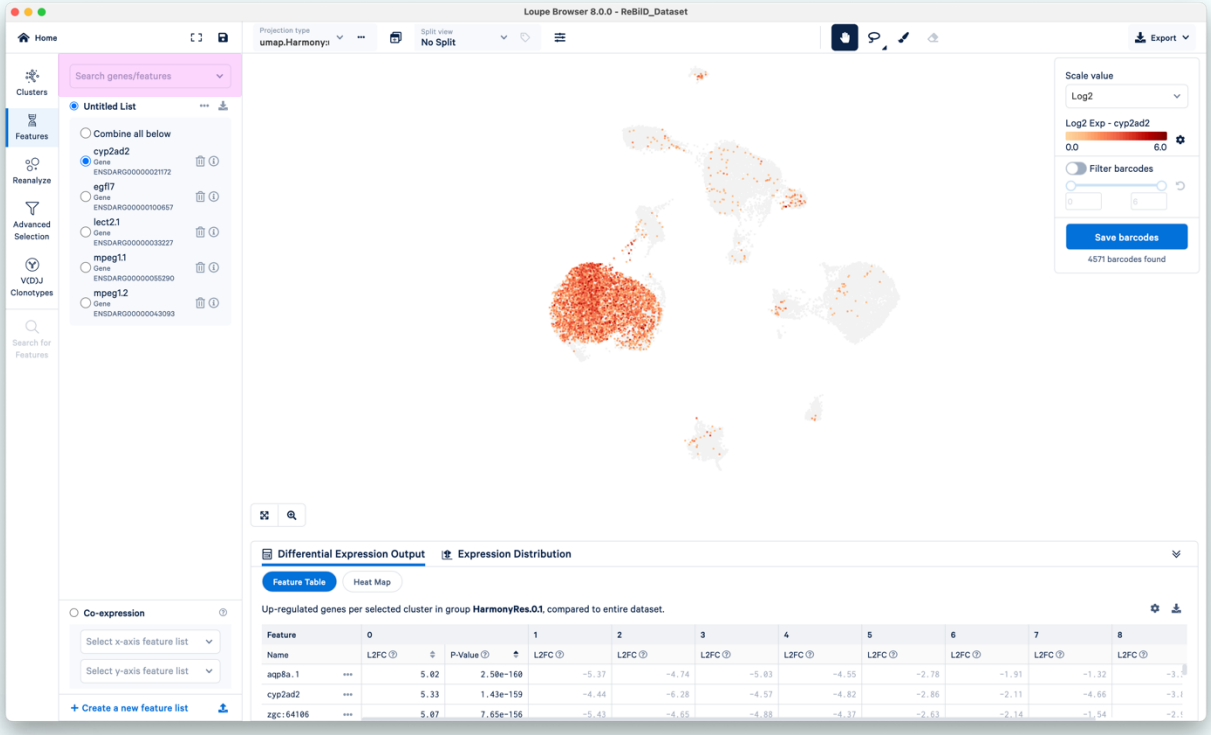
FEATURES



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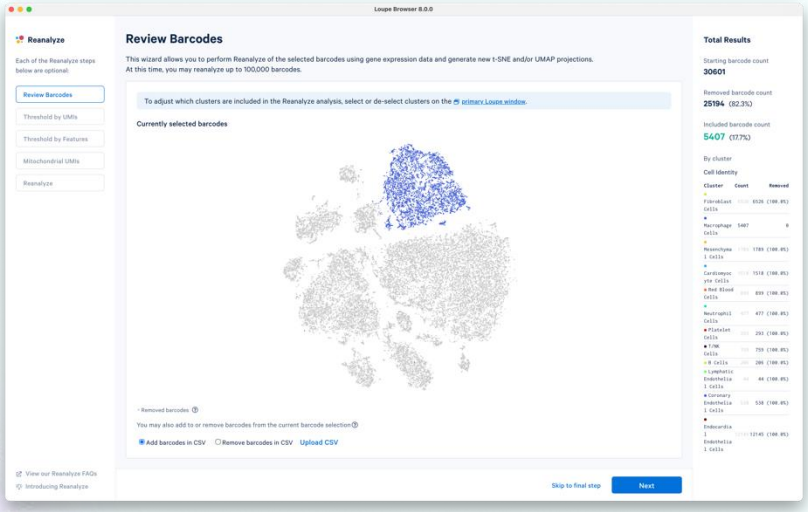
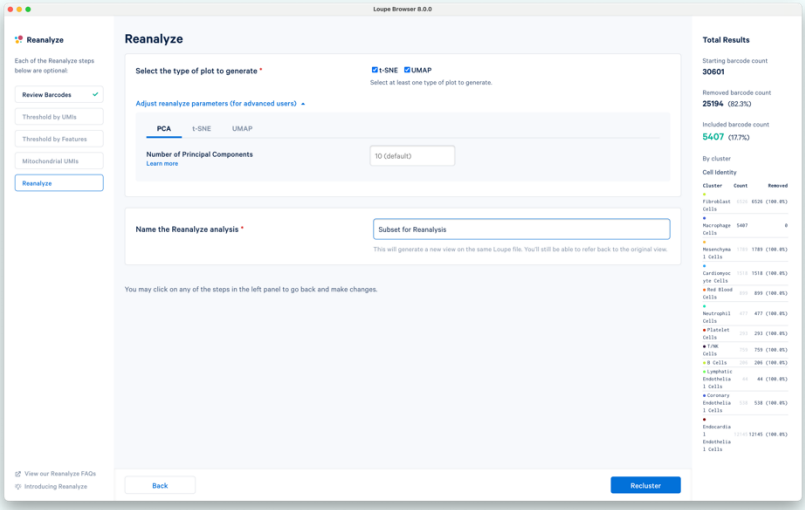
REANALYZE





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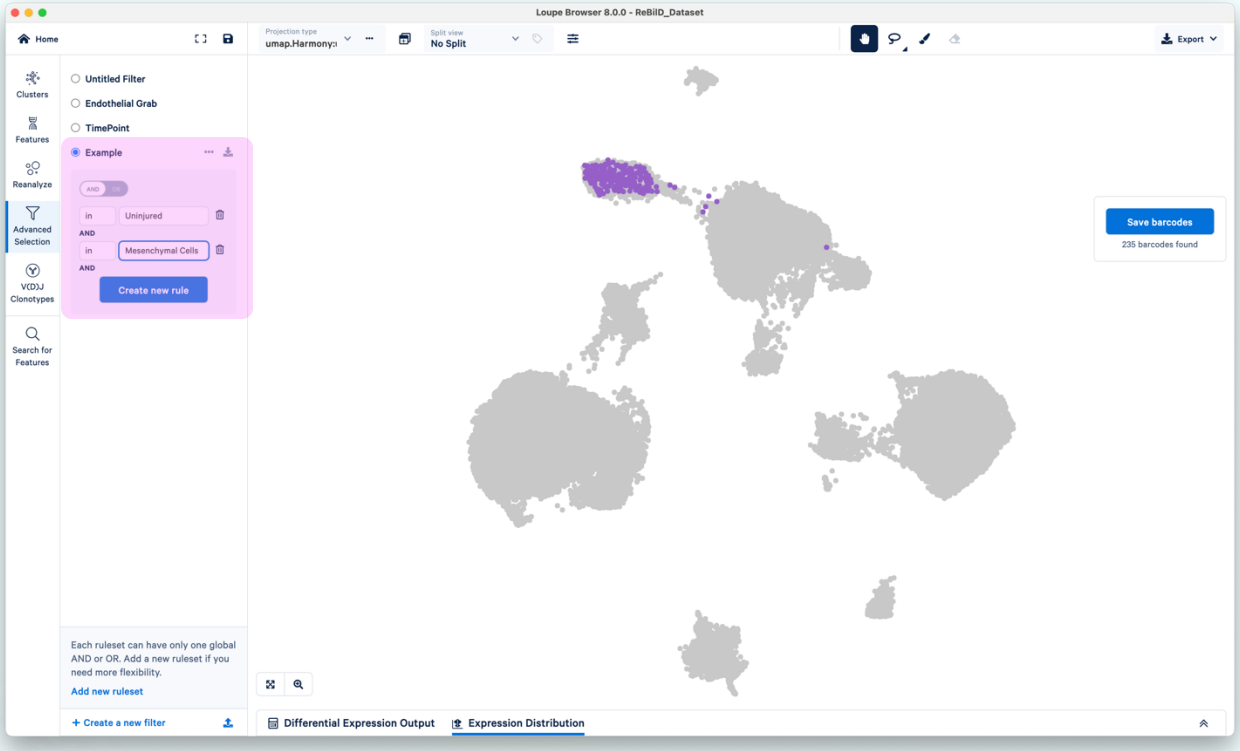
ADVANCED SELECTION



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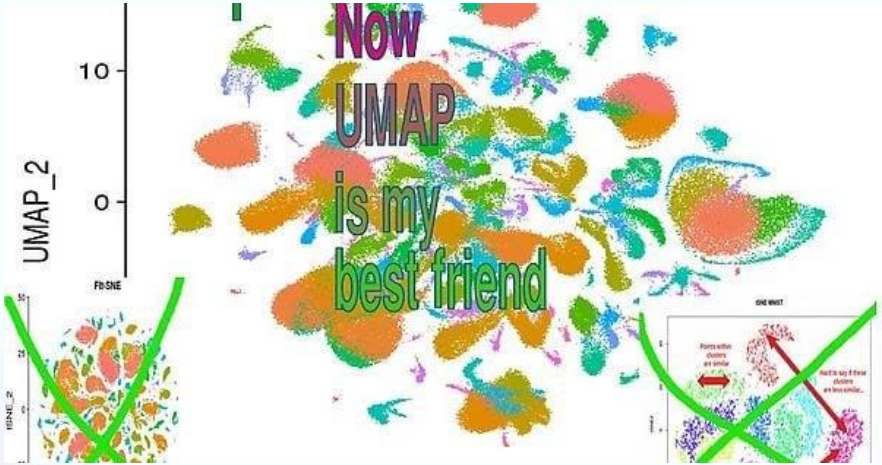
Questions?



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