# F2F Meeting

06-06-25

Goals

- Analyse Adult dataset ✅
    - Create UMAPs for each dataset (x6)
    - Plot gene expression on UMAPS (Feature plots)
    - Recreate Aaliya's dotplots for 4 genes of interest
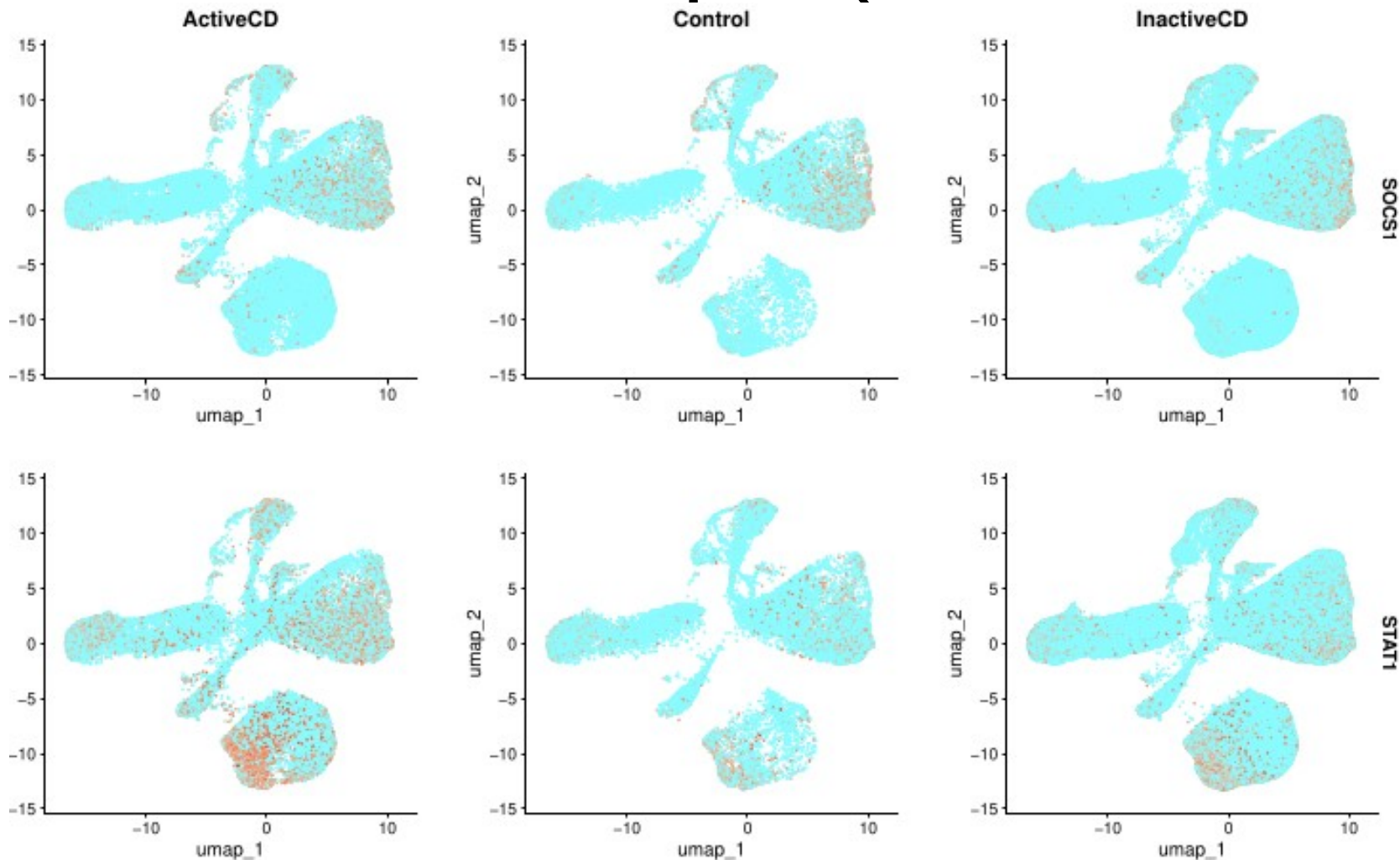- Analyse third dataset ✅

New pipeline (for UMAPs)

- Originally, UMAPs were created in python (as Scanpy programme was being used)

- New pipeline was made for UMAPs as we are now using Seurat/R.

- New pipeline creates UMAPs, feature plots, and dot plots.

- Couple tweaks needed to improve the appearance of the plots

UMAP Example (Colon Immune)
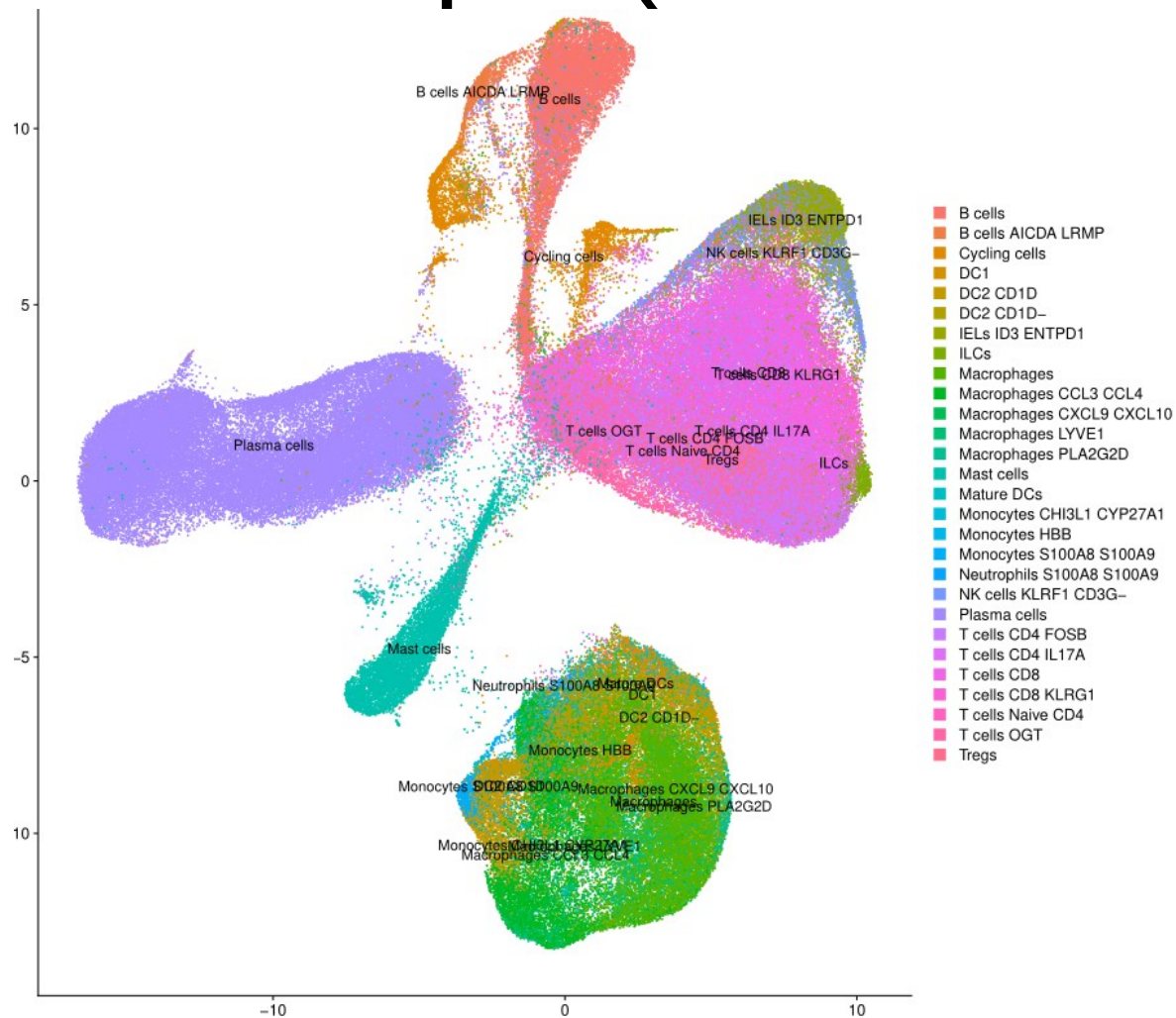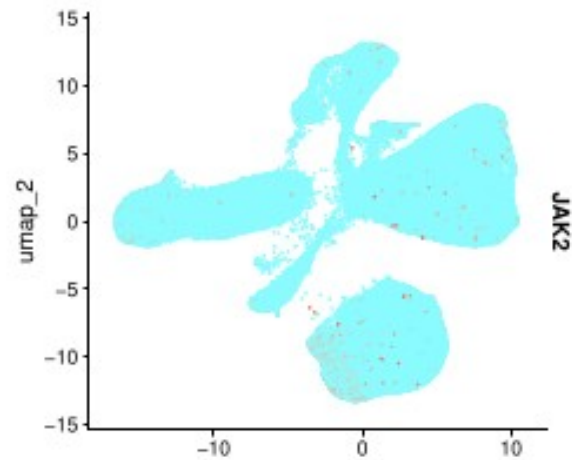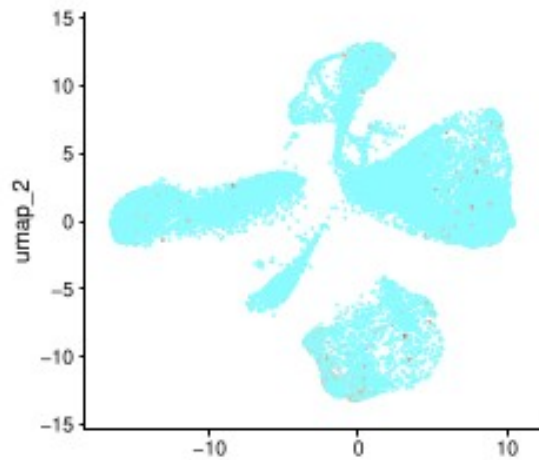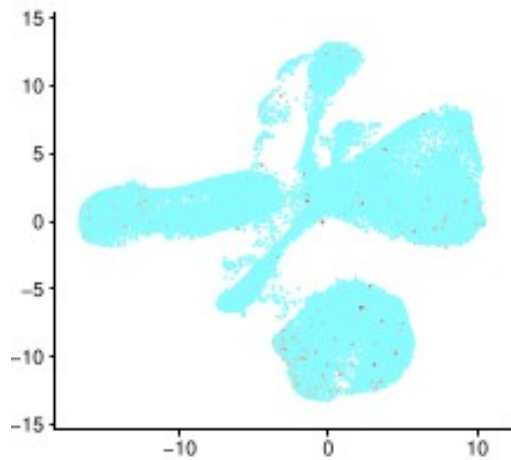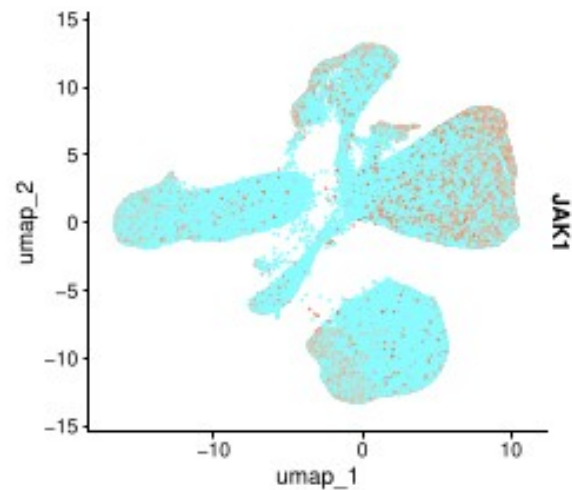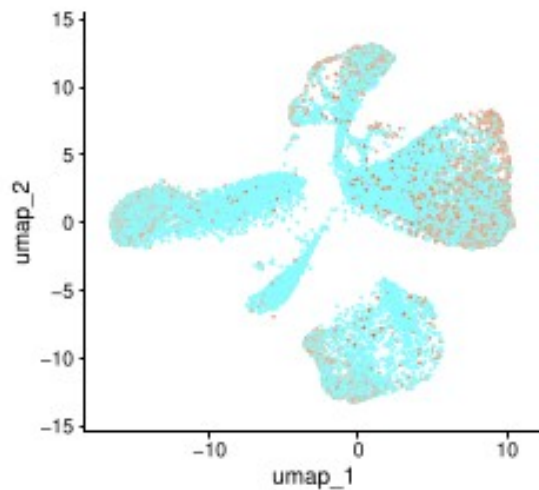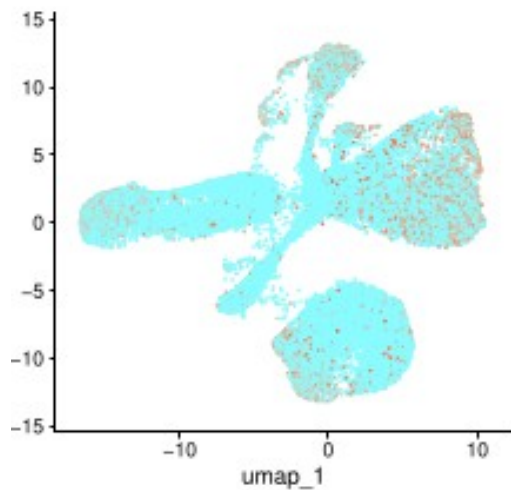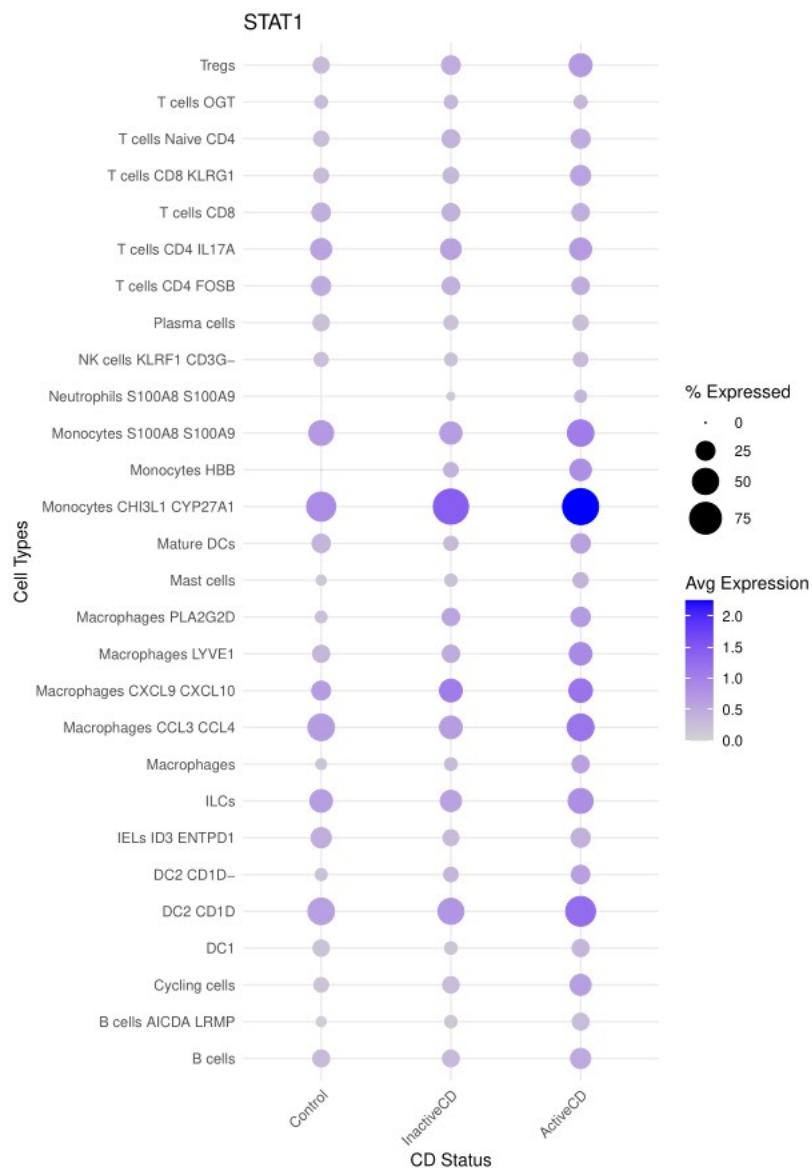
Feature Plot example (Colon Immune)

# Feature Plot example (Colon Immune)

Dot Plot Example (Colon Immune)

- One Dot plot per gene (to avoid visual clutter)

- Significance asterisks & p-values to be included (from DGE results)

Included *Jak1, Stat1, Stat2, Socs1* in DGE csv file

	A	B	C	D	J	K	L	M	N	O	P	Q	R
1	cell_type	upregulated	downregulated	total_significant		JAK1_padj	JAK1_log2FC	STAT1_padj	STAT1_log2FC	STAT2_padj	STAT2_log2FC	SOCS1_padj	SOCS1_log2FC
2	Plasma cells	3908	657	4565		2.25290497874595E-05	**0.989**	0.00992917237868876	**1.702**	7.43740291225169E-07	**1.812**	0.341129585602629	-0.406
3	T cells CD4 FOSB	2169	261	2430		2.77613867145576E-06	**1.339**	0.00741617490712994	**1.612**	0.0128471285003095	**1.303**	0.0695356986876922	-0.719
4	DC2 CD1D	1488	362	1850		0.125820100954405	0.748	0.00336013208702107	**2.89**	0.00194594742695254	**2.023**	0.111845853127754	1.145
5	T cells Naive CD4	1486	286	1772		7.34230631846201E-05	**1.292**	0.0329735024170518	**1.439**	0.0320254109437845	**1.232**	0.187792472261485	-0.578
6	Tregs	1331	171	1502		9.09833398598906-06	**1.569**	0.0995619763133104	1.072	0.0854727938769556	1.537	0.157930587133532	-0.603
7	Monocytes S100A8 S100A9	1371	54	1425		0.00159532213398155	**2.013**	0.0048582993441414	**2.919**	8.81908166227904E-05	**2.42**	0.796761763725462	0.29
8	Immune Cycling cells	1144	228	1372		4.03596627962978E-05	**1.622**	0.0675322702459475	1.899	0.189986711012316	1.514	0.434810776696763	0.57
9	T cells CD8 KLRG1	1144	171	1315		8.0941291083437E-07	**1.538**	0.0377253003652039	**1.569**	NA	NA	0.0765544945586292	-0.728
10	T cells CD4 IL17A	970	178	1148		6.00338875388425E-05	**1.489**	0.0531809427569985	1.617	NA	NA	0.341553693324453	-0.511
11	NK-like cells ID3 ENTPD1	891	141	1032		0.0032198325725069	**1.04**	0.278442294260055	1.21	NA	NA	0.200744023333729	-0.634
12	Macrophages CCL3 CCL4	802	103	905		0.00899523960897116	**1.827**	0.0486755163113977	**2.767**	0.0311832441147658	**1.762**	0.243925417500781	1.36
13	Macrophages LYVE1	763	57	820		0.00230732516547685	**1.911**	0.0146574941323032	**2.806**	0.00327425815775474	**2.317**	0.732014418864134	-0.456
14	B cells	649	30	679		0.0107460392785188	**1.083**	0.0136063028553174	**2.54**	0.0677565501971811	2.032	0.374676348997838	0.678
15	T cells CD8	440	90	530		0.00868557387520194	**0.918**	0.303723131899009	0.956	NA	NA	0.0431904369712111	**-0.761**
16	Mast cells	424	25	449		0.0094268025459603	**1.78**	0.0047293178997853	**2.259**	0.0184396605520743	**2.445**	0.185764427635783	1.079
17	Macrophages Metallothionein	340	7	347		0.03677884915875	**1.956**	0.21110377257358	2.313	0.104212919383224	1.937	NA	NA
18	NK cells KLRF1 CD3G-	202	39	241		0.00949384990718605	**1.191**	0.23099377695141	1.299	NA	NA	0.175863963049232	-0.642
19	DC1	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
20	DC2 CD1D-	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
21	ILCs	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
22	Macrophages	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
23	Mature DCs	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
24	T cells OGT	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
25	B cells AICDA LRMP	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
26	Monocytes CHI3L1 CYP27A1	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA

Colon Immune

GO Enricment Example (Colon Immune Macrophage)
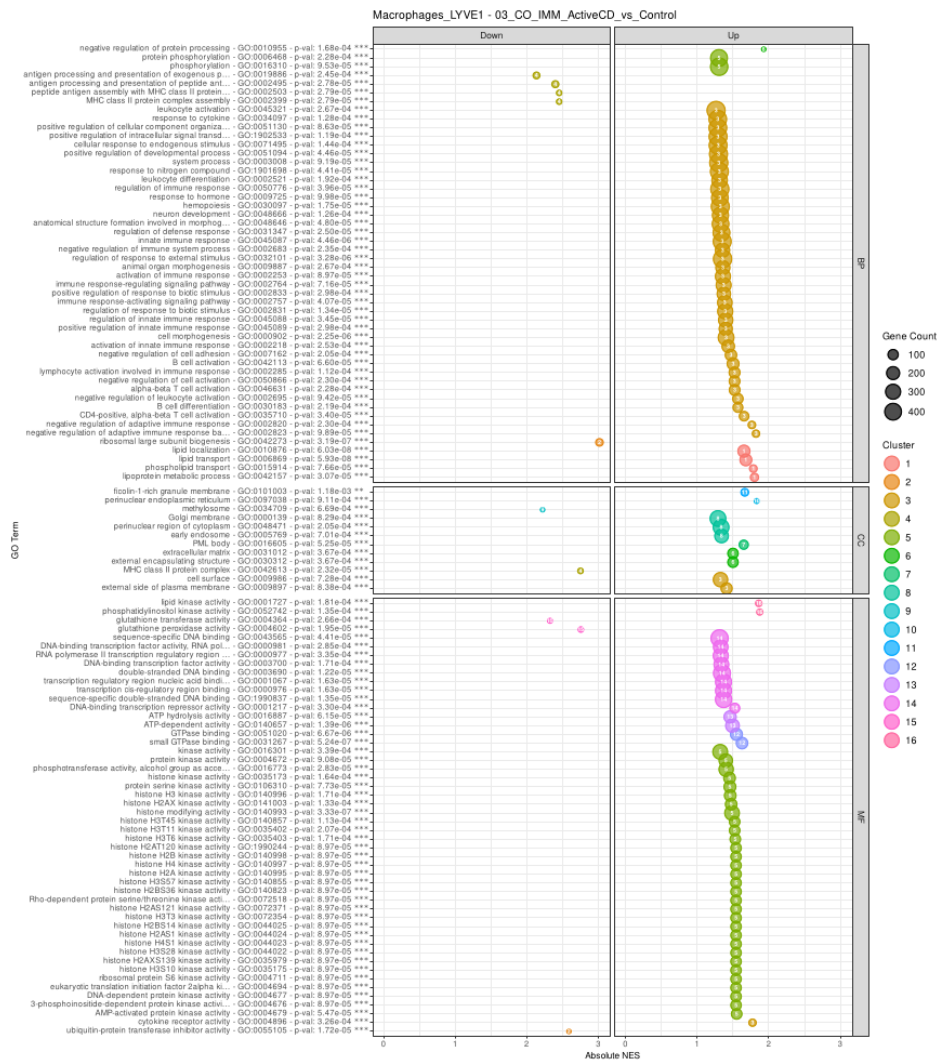
- Same as before

- One plot per cell type per dataset (2 tissue types x 3 cell type groups)

Next Goals

- Add p-values to dot plots

- Begin KEGG pathway analysis

- Create some clear research questions/hypotheses that we can test

- Explore if it is possible correlate data from different studies (Meta-analysis?)