

Pathway & Go term analysis

20190828

Zheng et al. 2017 , T cell scRNAseq of Liver cancer. C4-CD8-LAYN cluster

20180905

Pathway analysis – Scheme (20180828)

Table S2
Zheng et al.,
2017

List of signature
genes in each
cluster
(C4-CD8-LAYN)

Extract EntrezID (274 genes)

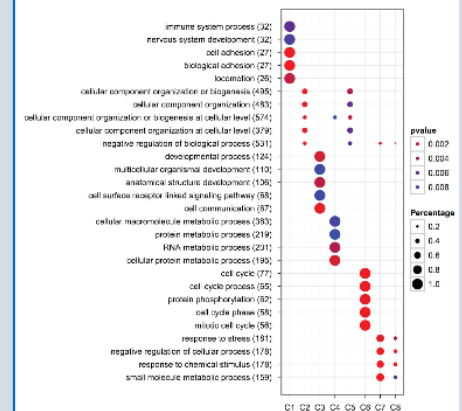
```
> head(test)
[1] 5996 84868 5133 1493 10663 201633
> test
      5996 84868 5133 1493 10663 201633 3604 22822
[1] 4647 939 678655 1846 143903 3122
[9] 4643 5552 9495 4929 84632 1435 23406
[17] 1130 1757 2115 100287534 728558 3458 3805 55423
[25] 114614 9882 9452 10563 64759 116449 339789 79895
[33] 1390 64092 952 25861 3399 29851 51676 84969
[41] 406947 5740 3108 5997 2597 7412 8302 64231
[49] 60489 4345 639 116841 3560 7453 3682 54
[57] 3398 7133 3902 9901 26191 8638 7462 84159
[65] 27333 160365 27115 7292 2530 2731 51429 54602
[73] 55501 1509 285025 27350 4664 92906 3732 100528031
[81] 7128 1251 54438 5066 2280 677 3892 81
[89] 868 4046 356 1890 80727 100616438 25897 200316
[97] 3516 5763 3162 10018 924 7227 5873 64333
[105] 64218 79890 4689 164118 94240 7188 6310 10447
[113] 22876 6503 3428 894 10797 29988 8611 160851
[121] 79413 4739 5778 22806 970 967 2820 130589
[129] 5900 23231 27334 8832 140564 83982 79713 84959
[137] 7167 2537 8565 23062 10538 9260 9619 57162
[145] 57205 100506190 10950 54806 9246 26031 5445 9585
[153] 684 9746 3987 5781 2650 8536 4061 100130093
[161] 54625 57157 23710 4522 403 54434 7979 5583
[169] 11315 3984 65094 5359 100506755 10791 7037 10906
[177] 10421 1495 115361 5496 3430 7867 7633 6709
[185] 23741 80219 134429 836 23517 9766 8027 57414
[193] 5315 2762 6774 79718 9997 25824 10589 2590
[201] 808 55320 81671 5573 4940 9144 5721 50615
[209] 4599 308 9051 55500 10982 10459 2969 10725
[217] 3660 2182 10379 2633 57835 29110 5606 405
[225] 1499 399 219285 9158 5214 2625 2634 11243
[233] 5993 29959 54790 55601 11262 55072 100527963 4170
[241] 79415 57819 9446 9049 5686 3939 2130 10956
[249] 10095 847 3385 55608 9205 830 8775 9784
[257] 11164 6717 132160 1508 10241 282991 80344 4678
[265] 1460 58496
```

Over-representation test (e.g. 250 genes – depending on geneset)

```
# over-representation test
#
#...@organism Homo sapiens
#...@ontology DisGeNET
#...@keytype ENTREZID
#...@gene chr [1:274] "5996" "84868" "5133" "1493" "10663" "201633" "3604" "22822" "4647"
"6348" ...
#...pvalues adjusted by 'BH' with cutoff <0.05
#...171 enriched terms found
'data.frame': 171 obs. of 9 variables:
 $ ID : chr "umls:c0021400" "umls:c0024138" "umls:c0026896" "umls:c0409974" ...
 $ Description: chr "Influenza" "Lupus Erythematosus, Discoid" "Myasthenia Gravis" "Lupus Erythe
matorius" ...
 $ GeneRatio : chr "28/250" "21/250" "16/250" "22/250" ...
 $ BgRatio : chr "494/17381" "316/17381" "181/17381" "356/17381" ...
 $ pvalue : num 6.47e-10 6.39e-09 8.06e-09 1.04e-08 2.08e-08 ...
 $ p.adjust : num 1.40e-06 5.62e-06 5.62e-06 5.62e-06 8.99e-06 ...
 $ qvalue : num 1.07e-06 4.31e-06 4.31e-06 4.31e-06 6.90e-06 ...
 $ geneID : chr "1493/3604/6348/939/1757/3458/1390/2597/3682/8638/7292/25897/3162/2537/9246/
5781/4061/5359/3430/836/9997/4940/45" | _truncated_ "5133/1493/939/1435/3458/3805/10563/1390/298
51/639/7453/7133/26191/356/3428/970/84959/10950/6774/50615/2625" "5133/1493/939/1435/3458/10563/
29851/406947/3560/26191/7128/5066/25897/9260/7979/836" "5133/1493/939/1435/3458/3805/10563/1390/9
52/29851/3108/639/7133/26191/356/3428/970/84959/10950/6774/50615/2625" ...
 $ Count : int 28 21 16 22 20 21 24 13 24 10 ...
#...Citation
Guangchun Yu, Li-Gen Wang, Yanyan Han and Qing-Yu He.
ClusterProfiler: an R package for comparing biological themes among
gene clusters. OMICS: A Journal of Integrative Biology
2012, 16(5):284-287
```

DOSE – DisGeNET, DO
clusterProfiler – GO, KEGG

Visualization



enrichPlot
ggplot2

Limitation of the whole approach: ALL gene set analysis is knowledge-based. Novel genes and known genes with novel function will not be considered in the pathway analysis

Pathway analysis: over-representation analysis (ORA)

Over-representation analysis (ORA) - completed

- DisGenNET – Disease
- DO ontology - Disease
- KEGG - Pathway
- GO ontology – Cellular Component, Molecular Function, Biological Process

Limitations: ORA treats each gene equally! (No fold change or significance are considered for representation)

Analysis requires fold-changes or p-values as input (FCS)

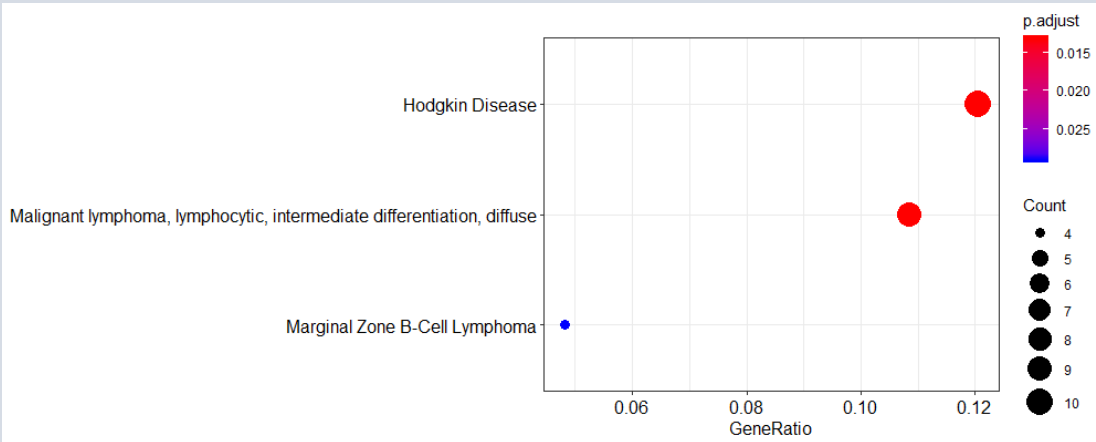
- **GSEA** and others

Comment: It does not require an arbitrary threshold for dividing expression data into significant and non-significant pool, but require whole gene expression dataset

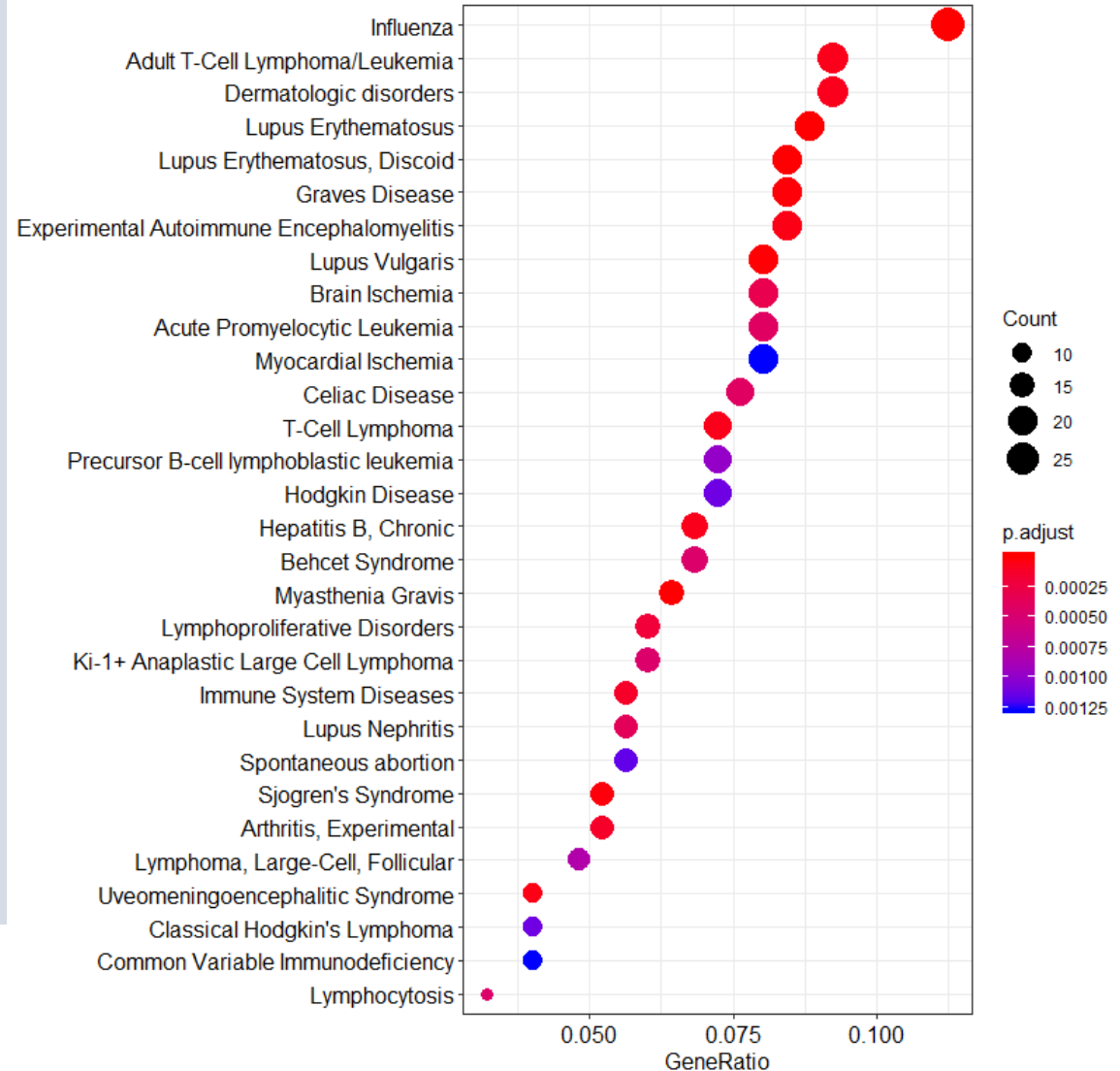
Analysis: Over-representation test

DisGeNET Ontology

C1-CD8-LEF1 (Input: 101 genes)

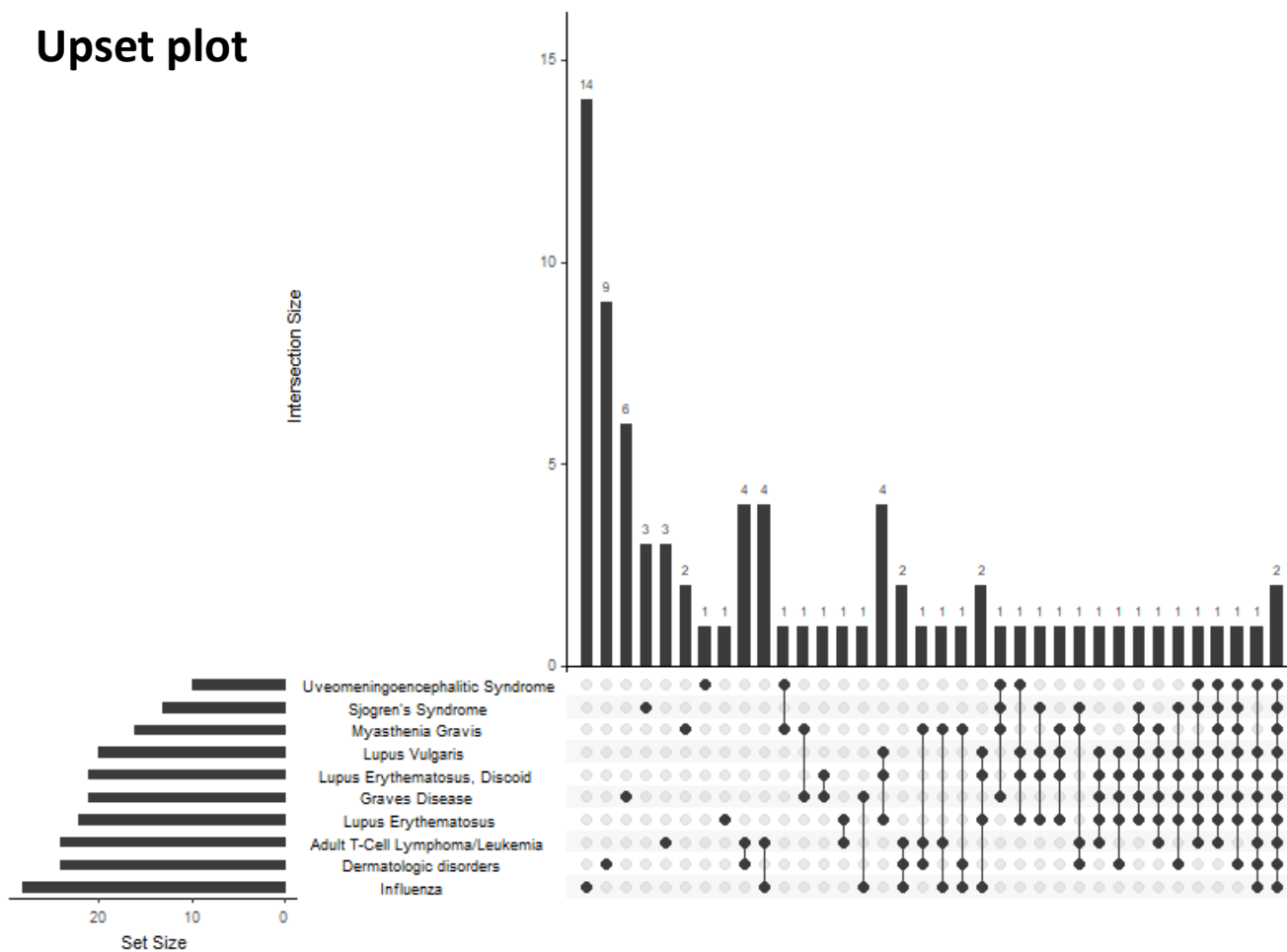


C4-CD8-LAYN (Input: 274 genes)

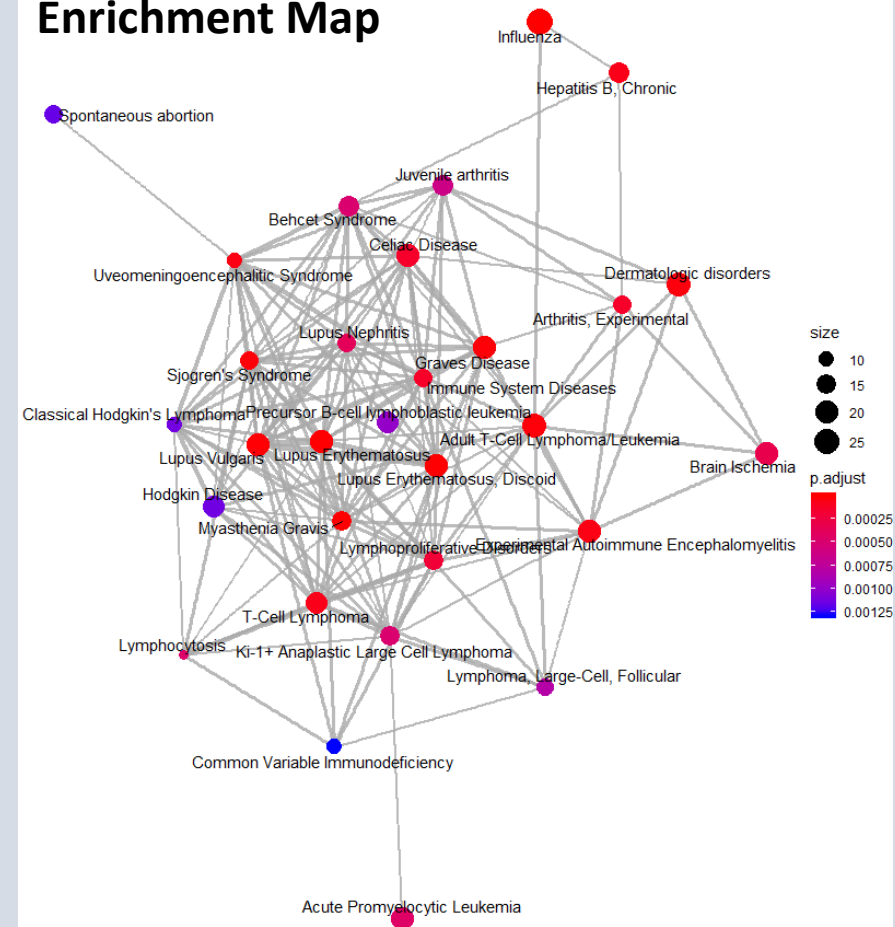


Analysis: Visualization

Upset plot



Enrichment Map



Analysis: Top Gene List (DisGeNet)

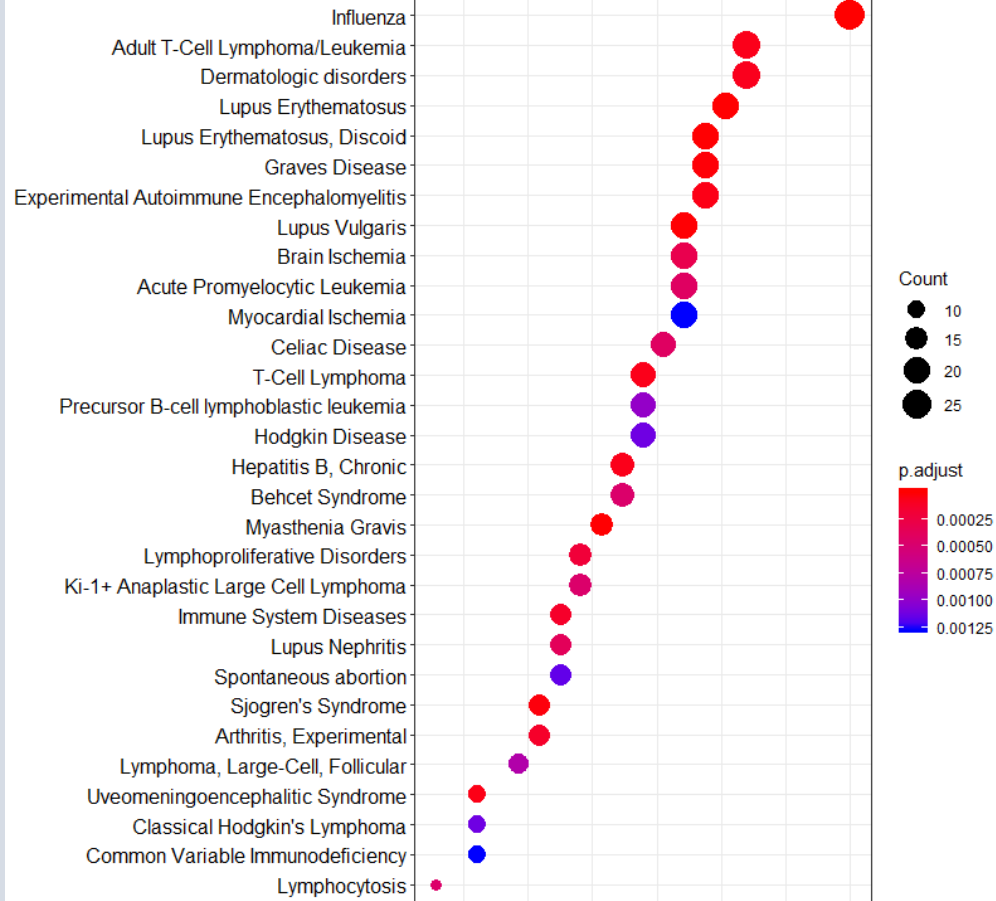
Description	GeneRatio	pvalue	geneID
Influenza	28/250	6.47E-10	CTLA4/TNFRSF9/CCL3/CD27/SARDH/IFNG/CREM/GAPDH/ITGAE/OASL/TNFSF4/RNF19A/HMOX1/IFI6/UBE2L6/PTPN11/LY6E/PLSCR1/IFI35/CASP3/SCO2/OAS3/MX1/IRF9/GBP1/GATA3/DDX60/CAT
Lupus Erythematosus, Discoid	21/250	6.39E-09	PDCD1/CTLA4/CD27/CSF1/IFNG/KIR2DL4/CXCL13/CREM/ICOS/PRDM1/WARS/TNFRSF1B/PTPN22/FASLG/IFI16/CD70/UBASH3B/BTG3/STAT3/IL21R/GATA3
Myasthenia Gravis	16/250	8.06E-09	PDCD1/CTLA4/HLA-DRA/CSF1/IFNG/CXCL13/ICOS/MIR155/IL2RB/PTPN22/TNFAIP3/PAM/RNF19A/PDLIM7/SEM1/CASP3
Lupus Erythematosus	22/250	1.04E-08	PDCD1/CTLA4/CD27/CSF1/IFNG/KIR2DL4/CXCL13/CREM/CD38/ICOS/HLA-DMA/PRDM1/TNFRSF1B/PTPN22/FASLG/IFI16/CD70/UBASH3B/BTG3/STAT3/IL21R/GATA3
Lupus Vulgaris	20/250	2.08E-08	PDCD1/CTLA4/CD27/CSF1/IFNG/KIR2DL4/CXCL13/CREM/ICOS/PRDM1/TNFRSF1B/PTPN22/FASLG/IFI16/CD70/UBASH3B/BTG3/STAT3/IL21R/GATA3
Graves Disease	21/250	4.83E-08	PDCD1/CTLA4/CXCR6/IFNG/ITM2A/CXCL13/ICOS/WARS/ITGAE/TNFRSF1B/PTPN22/ARID5B/TNFAIP3/CBLB/FASLG/SEM1/STAT3/PRDX5/IL21R/RHOH/GATA3
Adult T-Cell Lymphoma/Leukemia	24/250	8.09E-08	RGS1/PDCD1/CTLA4/CCL3/TOX/IFNG/CD38/ICOS/MIR155/VCAM1/IL2RB/TNFSF4/HMOX1/AHI1/CASP3/STAT3/OAS3/IL21R/IRF9/GATA3/MCL1/GSTO1/CAT/CSNK2B
Sjogren's Syndrome	13/250	8.33E-08	PDCD1/CTLA4/IFNG/CXCL13/ID3/MIR155/PRDM1/PTPN22/TNFAIP3/FASLG/SPTAN1/STAT3/GTF2I
Dermatologic disorders	24/250	1.20E-07	RGS1/CTLA4/CCL3/NR4A2/TOX/IFNG/MIR155/VCAM1/IL2RB/ID2/TNFRSF1B/PTPN22/FKBP1A/FASLG/RNF19A/HMOX1/IGFLR1/PELI1/PON2/MTHFD1/LIMK1/IRF2/GATA3/GSTO1
Uveomeningoencephalitic Syndrome	10/250	2.16E-07	PDCD1/CTLA4/HLA-DRA/IFNG/KIR2DL4/PTPN22/TNFAIP3/TRAFF5/STAT3/GATA3
Experimental Autoimmune Encephalomyelitis	21/250	2.25E-07	HAVCR2/CTLA4/TNFRSF9/CCL3/ENTPD1/NR4A2/IFNG/CXCL13/MIR155/VCAM1/IL2RB/TNFRSF1B/CBLB/RNF19A/SEMA4A/CASP3/STAT3/PRDX5/GATA3/GSTO1/CAT
Hepatitis B, Chronic	17/250	3.41E-07	HAVCR2/PDCD1/CTLA4/TNFRSF9/IFNG/KIR2DL4/KLR4/APOBEC3G/WARS/ACP5/OASL/FASLG/OAS3/MX1/IRF2/IRF9/CAT
T-Cell Lymphoma	18/250	3.68E-07	PDCD1/CTLA4/CD27/IFNG/CXCL13/ID3/MIR155/PRDM1/IL2RB/ID2/BCL2L11/CCND2/CD70/PDLIM7/STAT3/CTNNA1/GATA3/TET2
Immune System Diseases	14/250	8.60E-07	HAVCR2/PDCD1/CTLA4/ENTPD1/IFNG/ICOS/PTPN22/TNFAIP3/RAB27A/IKZF3/BATF/STAT3/GATA3/TET2
Arthritis, Experimental	13/250	9.07E-07	HAVCR2/CTLA4/CCL3/NR4A2/IFNG/TNFRSF1B/PAM/CBLB/FASLG/STAT3/ACSL4/CAT/CTSB
Celiac Disease	20/250	9.88E-07	RGS1/PDCD1/CTLA4/TNFRSF9/HLA-DRA/IFNG/KIR2DL4/CD38/ICOS/IL2RB/PTPN22/TNFSF4/TNFAIP3/ZFP36L1/FASLG/PON2/PARK7/TFRC/GATA3/CTSB
Lymphoproliferative Disorders	15/250	1.56E-06	CTLA4/CD27/IFNG/CXCL13/CD38/MIR155/PRDM1/IL2RB/TNFRSF1B/TNFAIP3/CBLB/FASLG/BCL2L11/PDLIM7/STAT3
Brain Ischemia	20/250	2.56E-06	CTLA4/CCL3/TOX/PTGIS/VCAM1/ITGAE/TNFRSF1B/FASLG/HMOX1/PON2/MTHFD1/PRKCH/LIMK1/CASP3/STAT3/GALNT2/GSTO1/CAT/CTSB/LY6G5B
Lupus Nephritis	14/250	3.25E-06	PDCD1/CSF1/IFNG/CXCL13/VCAM1/TNFSF4/TNFAIP3/FASLG/UBASH3B/LY6E/CASP3/STAT3/MX1/GATA3
Acute Promyelocytic Leukemia	20/250	4.08E-06	SRGN/CSF1/IFNG/CD38/ASB2/ID2/FASLG/ATXN1/UBE2L6/PLSCR1/TFRC/CASP3/STAT3/TBL1XR1/PRDX5/PRKAR1A/IRF9/TET2/SP140/MCL1
Lymphocytosis	8/250	4.58E-06	CTLA4/CD27/IFNG/CD38/MIR155/ITGAE/FASLG/PDLIM7
Behcet Syndrome	17/250	5.05E-06	PDCD1/CTLA4/IFNG/KIR2DL4/KLR4/TNFRSF1B/PTPN22/TNFAIP3/HMOX1/TRAFF5/IFI16/UBASH3B/PHTF2/STAT3/PSTPIP1/GATA3/CAT
Ki-14 Anaplastic Large Cell Lymphoma	15/250	5.10E-06	IFNG/MIR155/PRDM1/ID3/TNFRSF1B/FASLG/BCL2L11/PDLIM7/PTPN11/CACD2/STAT3/CALM2/IL21R/GATA3/MCL1

Caution 1 : Only “upregulated genes” were defined as signature genes to start with, but loss of function mutation etc could define select gene as “geneset”

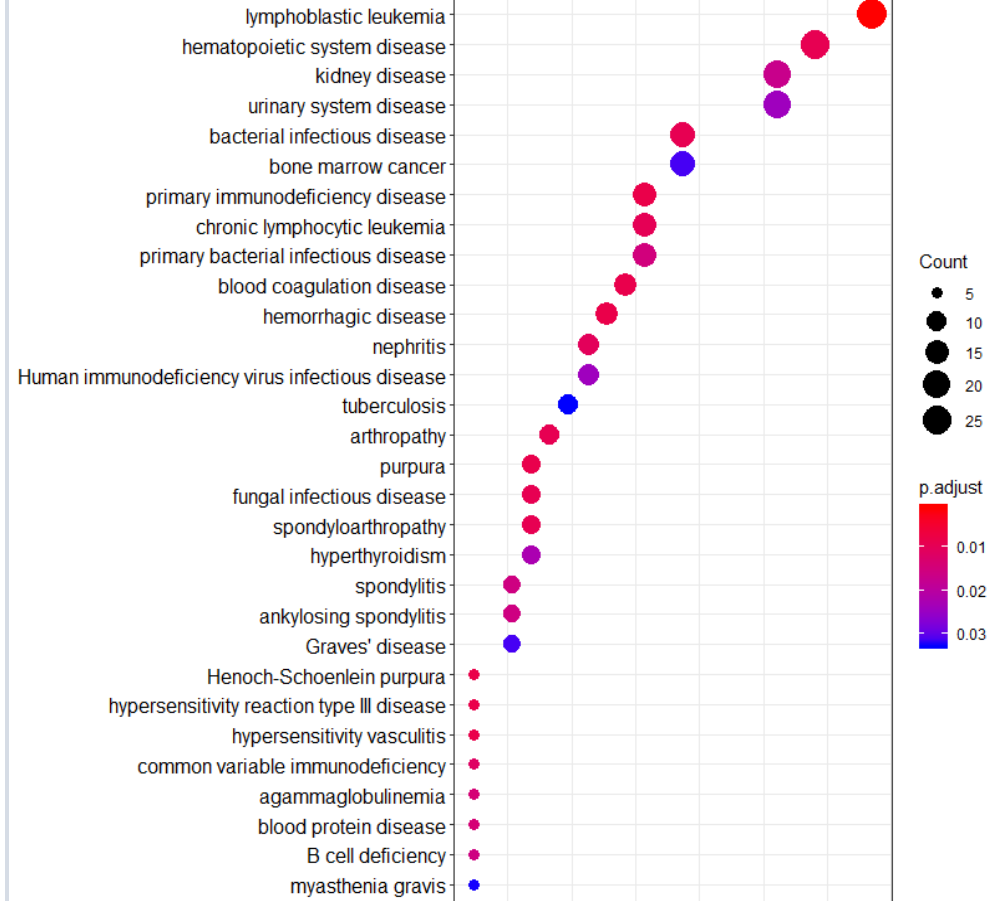
Caution 2 : Each pathway was treated independently – a gene can function in multiple pathway so identified pathways were frequently overlapped → Obscure true source of signals

Analysis: DO term analysis

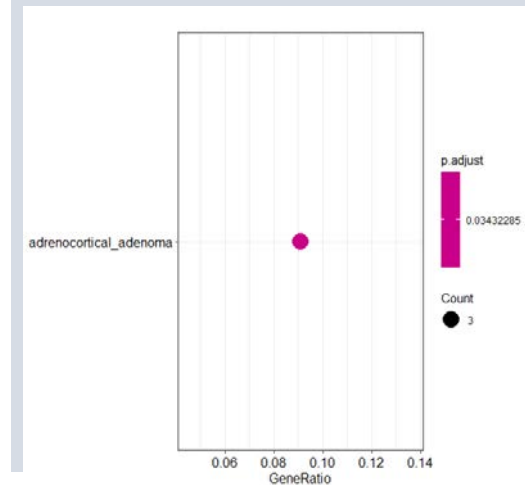
DisGeNET



DO Term



Network of Cancer Gene (NCG) Database
– top 30 pathway, only one as significant



Commonly Enriched Genesets:

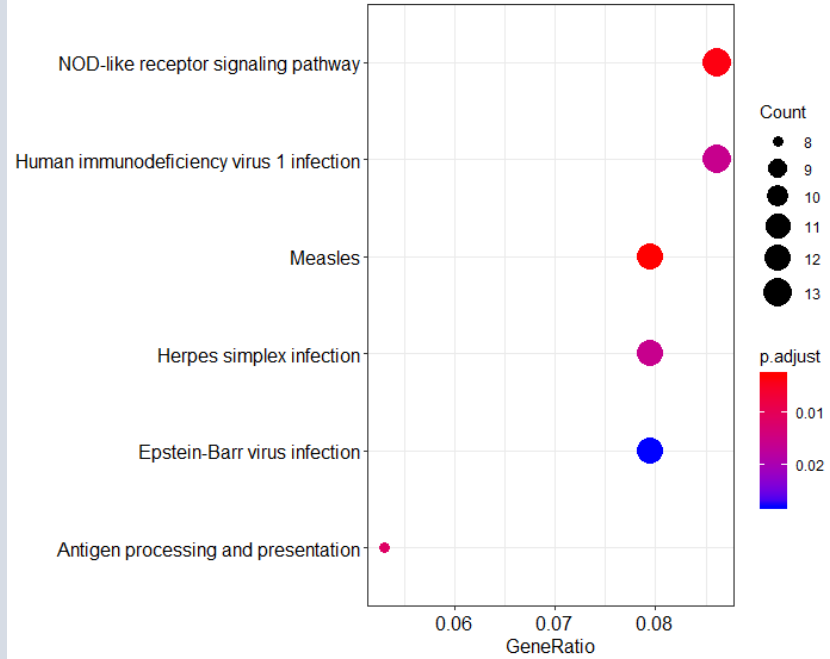
Infectious disease, Leukemia/Lymphoma, Autoimmune disease, Graves Disease/hyperthyroidism, Blood Vessle (Ischemia \leftrightarrow Purpura/hemorrhagic/Behcet Syndrome)

Analysis: Top Gene List (DO term)

ID	Description	GeneRatio	p.adjust	geneID
DOID:1037	lymphoblastic leukemia	26/169	0.001016	CCL3/IFNG/CXCL13/CD38/IL2RB/LAT2/ARID5B/CLECL1/PDE7B/TNFAIP3/ZFP36L1/FASLG/BCL2L11/CCND2/IKZF3/CD70/PTPN11/TFRC/PKM/TBL1XR1/IL21R/ARNT/RHOH/MCL1/LDHA/CSNK2B
DOID:612	primary immunodeficiency disease	14/169	0.008202	PDCD1/CTLA4/IFNG/ICOS/APOBEC3G/TNFRSF1B/FASLG/APOBEC3F/NCF4/CD70/CD63/BST2/PRKAR1A/NFAT5
DOID:11123	Henoch-Schoenlein purpura	5/169	0.008202	CTLA4/PTPN22/TNFSF4/HMOX1/CAT
DOID:1557	hypersensitivity reaction type III disease	5/169	0.008202	CTLA4/PTPN22/TNFSF4/HMOX1/CAT
DOID:9809	hypersensitivity vasculitis	5/169	0.008202	CTLA4/PTPN22/TNFSF4/HMOX1/CAT
DOID:2213	hemorrhagic disease	12/169	0.008202	CTLA4/HLA-DRA/IFNG/PTPN22/TNFSF4/FASLG/HMOX1/CASP3/CTNNB1/TET2/LDHA/CAT
DOID:1247	blood coagulation disease	13/169	0.008473	CTLA4/HLA-DRA/IFNG/PTPN22/TNFSF4/FASLG/HMOX1/PTPN11/CASP3/CTNNB1/TET2/LDHA/CAT
DOID:3326	purpura	8/169	0.008473	CTLA4/IFNG/PTPN22/TNFSF4/FASLG/HMOX1/CASP3/CAT
DOID:74	hematopoietic system disease	23/169	0.009264	CTLA4/HLA-DRA/IFNG/CD38/ICOS/VCAM1/TNFRSF1B/PTPN22/TNFSF4/FASLG/HMOX1/CD70/PTPN11/TFRC/SPTAN1/CASP3/PRKAR1A/NFAT5/CTNNB1/GATA3/TET2/LDHA/CAT
DOID:104	bacterial infectious disease	16/169	0.009264	PDCD1/CTLA4/CXCR6/CCL3/CD27/IFNG/CD38/ICOS/PRDM1/TNFRSF1B/PTPN22/CBLB/FASLG/BCL2L11/STAT3/MCL1
DOID:1564	fungal infectious disease	8/169	0.009264	PDCD1/CTLA4/CXCR6/IFNG/TNFRSF1B/PTPN22/STAT3/ICAM3
DOID:381	arthropathy	9/169	0.009264	RGS1/PDCD1/CTLA4/CSF1/IFNG/ICOS/PTGIS/TNFRSF1B/STAT3
DOID:1123	spondyloarthropathy	8/169	0.009264	RGS1/PDCD1/CTLA4/IFNG/ICOS/PTGIS/TNFRSF1B/STAT3
DOID:1040	chronic lymphocytic leukemia	14/169	0.00968	CCL3/IFNG/CXCL13/CD38/PDE7B/TNFAIP3/ZFP36L1/FASLG/BCL2L11/TFRC/IL21R/RHOH/MCL1/CSNK2B
DOID:10952	nephritis	11/169	0.010447	PDCD1/MYO1E/CSF1/IFNG/CXCL13/VCAM1/TNFSF4/ACTN4/FASLG/CASP3/GATA3
DOID:12177	common variable immunodeficiency	5/169	0.011504	CTLA4/ICOS/TNFRSF1B/CD70/PRKAR1A
DOID:2583	agammaglobulinemia	5/169	0.01414	CTLA4/ICOS/TNFRSF1B/CD70/PRKAR1A
DOID:620	blood protein disease	5/169	0.01414	CTLA4/ICOS/TNFRSF1B/CD70/PRKAR1A
DOID:0050338	primary bacterial infectious disease	14/169	0.015208	PDCD1/CTLA4/CCL3/CD27/IFNG/CD38/ICOS/PRDM1/TNFRSF1B/PTPN22/CBLB/FASLG/BCL2L11/MCL1
DOID:6590	spondylitis	7/169	0.015915	RGS1/PDCD1/CTLA4/IFNG/PTGIS/TNFRSF1B/STAT3
DOID:2115	B cell deficiency	5/169	0.015915	CTLA4/ICOS/TNFRSF1B/CD70/PRKAR1A
DOID:7147	ankylosing spondylitis	7/169	0.015915	RGS1/PDCD1/CTLA4/IFNG/PTGIS/TNFRSF1B/STAT3
DOID:557	kidney disease	21/169	0.017219	PDCD1/MYO1E/CSF1/IFNG/CXCL13/RGS2/VCAM1/ACP5/TNFRSF1B/TNFSF4/ACTN4/FASLG/RBPJ/HMOX1/AHI1/LIMS1/TFRC/CASP3/STAT3/GATA3/ICAM3
DOID:7998	hyperthyroidism	8/169	0.022529	CTLA4/CXCR6/TNFRSF9/IFNG/TNFRSF1B/PTPN22/FASLG/PRDX5
DOID:526	Human immunodeficiency virus infection	11/169	0.024254	PDCD1/CXCR6/CCL3/CD27/CSF1/IFNG/CXCL13/VCAM1/APOBEC3G/IL2RB/FASLG
DOID:18	urinary system disease	21/169	0.024254	PDCD1/MYO1E/CSF1/IFNG/CXCL13/RGS2/VCAM1/ACP5/TNFRSF1B/TNFSF4/ACTN4/FASLG/RBPJ/HMOX1/AHI1/LIMS1/TFRC/CASP3/STAT3/GATA3/ICAM3
DOID:12361	Graves' disease	7/169	0.031455	CTLA4/CXCR6/TNFRSF9/TNFRSF1B/PTPN22/FASLG/PRDX5
DOID:4960	bone marrow cancer	16/169	0.031469	CCL3/SRGN/IFNG/VCAM1/PRDM1/ACP5/LAG3/FASLG/BCL2L11/CCND2/PTPN11/STAT3/CTNNB1/TET2/MCL1/LDHA
DOID:437	myasthenia gravis	5/169	0.032656	PDCD1/CTLA4/HLA-DRA/CXCL13/PTPN22

Analysis: KEGG analysis

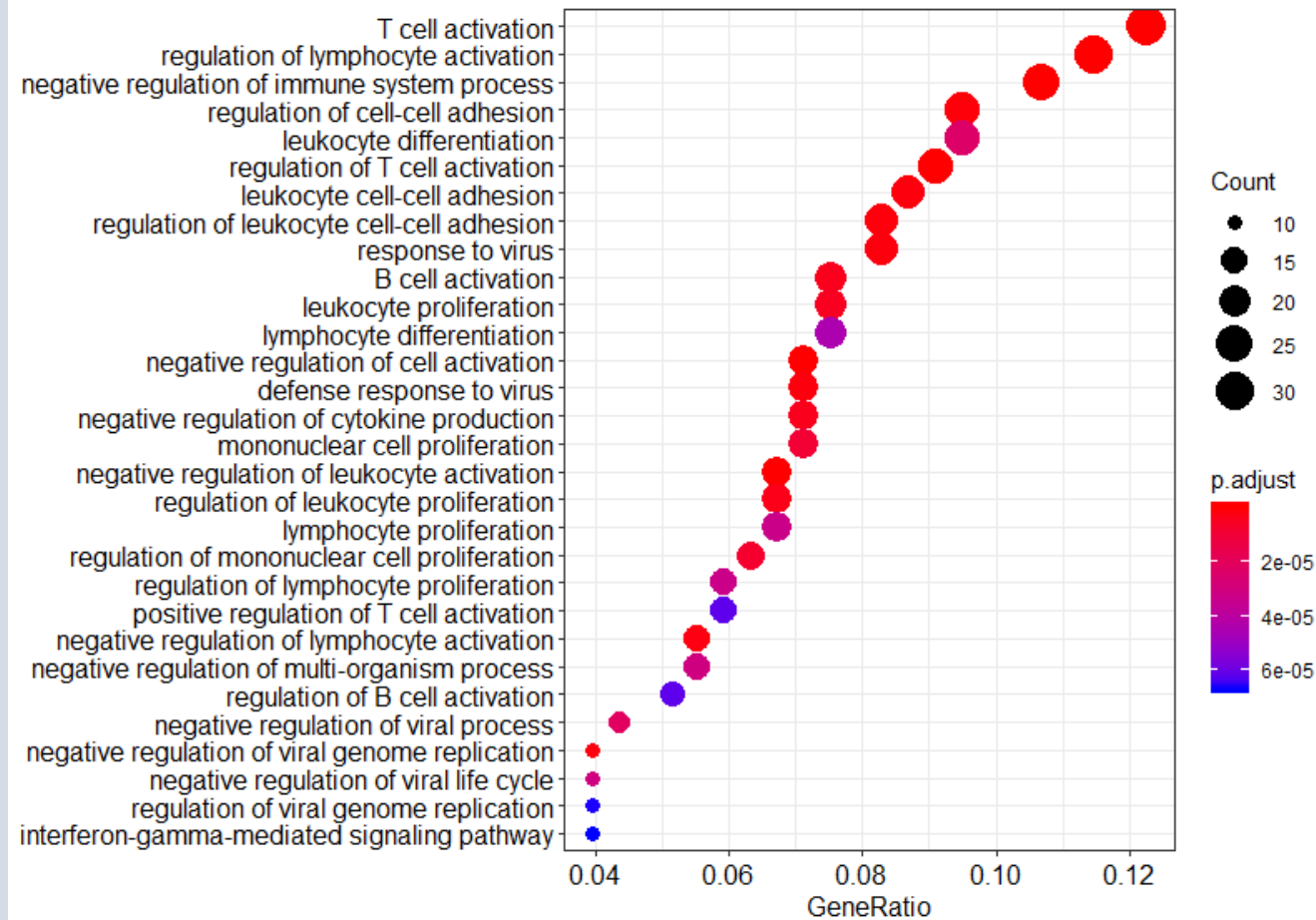
KEGG



ID	Description	GeneRatio	p.adjust	qvalue	geneID	Count
hsa05162	Measles	12/151	0.003005	0.002636	IFNG/IL2RB/TNFAIP3/CBLB/FASLG/CCND2/STAT3/OAS3/MX1/IRF9/TBK1/CSNK2B	12
hsa04621	NOD-like receptor signaling pathway	13/151	0.003707	0.003251	TNFAIP3/TRA5/IFI16/GABARAPL1/GBP4/OAS3/PSTPIP1/IRF9/GBP1/TBK1/GBP2/RNF31/CTSB	13
hsa04612	Antigen processing and presentation	8/151	0.011375	0.009978	HLA-DRA/IFNG/KIR2DL4/HLA-DMA/KLRC4/PSME2/RFX5/CTSB	8
hsa05170	Human immunodeficiency virus 1 infection	13/151	0.015951	0.013992	APOBEC3G/TNFRSF1B/APOBEC3C/FASLG/APOBEC3F/TRA5/APOBEC3D/BST2/LIMK1/CASP3/CALM3/TBK1/MAP2K3	13
hsa05168	Herpes simplex infection	12/151	0.015951	0.013992	HLA-DRA/IFNG/HLA-DMA/FASLG/TRA5/PTPN11/CASP3/OAS3/GTF2I/IRF9/TBK1/CSNK2B	12
hsa05169	Epstein-Barr virus infection	12/151	0.028047	0.024603	ENTPD1/HLA-DRA/IFNG/CD38/TNFAIP3/RBPJ/TRA5/SEM1/STAT3/TBK1/MAP2K3/CSNK2B	12

C4-CD8-LAYN (Input: 274 genes)

Analysis: GO – Biological Process



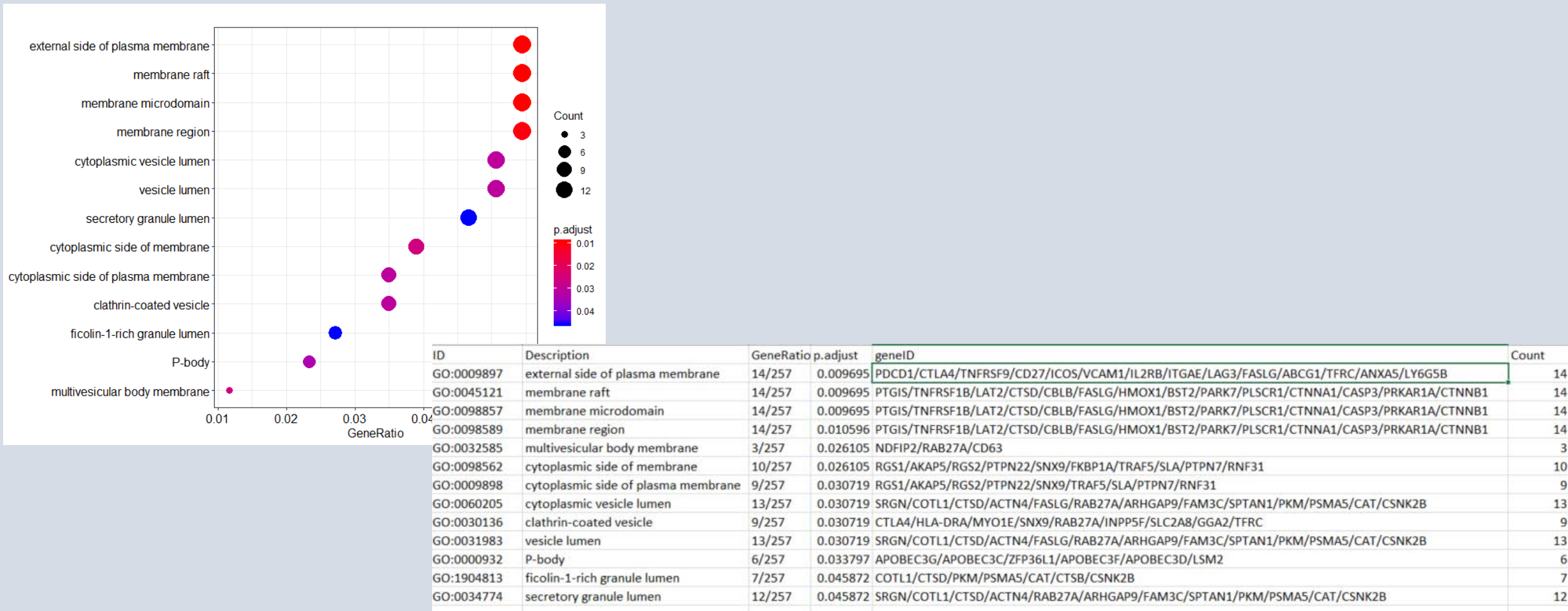
C4-CD8-LAYN (Input: 274 genes)

Analysis: GO – Biological Process

ID	Description	GeneRatio	p.adjust	geneID
GO:0042110	T cell activation	31/253	3.49E-09	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/ICOS/MIR155/VCAM1/PRDM1/LAG3/PTPN22/CLECL1/TNFSF4/FKBP1A/ZFP36L1/CD7/RAB27A/SEMA4A/BATF/PELI1/PTPN11/TFRC/CASP3/STAT3/PRKAR1A/CTNNB1/RHOH/GATA3
GO:0051249	regulation of lymphocyte activation	29/253	3.69E-08	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/SAMSN1/CD38/ICOS/MIR155/VCAM1/PRDM1/ID2/LAG3/PTPN22/CLECL1/TNFSF4/TNFAIP3/ZFP36L1/IKZF3/PELI1/PTPN11/TFRC/CASP3/PRKAR1A/CTNNB1/GATA3
GO:0050866	negative regulation of cell activation	18/253	7.36E-08	HAVCR2/CTLA4/TIGIT/SAMSN1/MIR155/CD200/PRDM1/ID2/LAG3/PTPN22/TNFSF4/TNFAIP3/HMOX1/CD84/UBASH3B/PELI1/CASP3/PRKAR1A
GO:0002695	negative regulation of leukocyte activation	17/253	7.45E-08	HAVCR2/CTLA4/TIGIT/SAMSN1/MIR155/CD200/PRDM1/ID2/LAG3/PTPN22/TNFSF4/TNFAIP3/HMOX1/CD84/PELI1/CASP3/PRKAR1A
GO:0002683	negative regulation of immune system process	27/253	7.87E-08	HAVCR2/PDCD1/CTLA4/TIGIT/CCL3/SAMSN1/MIR155/CD200/PRDM1/ID2/LAG3/PTPN22/TNFSF4/TNFAIP3/ZFP36L1/HMOX1/IFI16/CD84/UBASH3B/PELI1/BST2/PARP14/TRAFF1/CASP3/PRKAR1A/GBP1/CTNNB1
GO:0050863	regulation of T cell activation	23/253	1.57E-07	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/ICOS/MIR155/VCAM1/PRDM1/LAG3/PTPN22/CLECL1/TNFSF4/PELI1/PTPN11/TFRC/CASP3/PRKAR1A/CTNNB1/GATA3
GO:0022407	regulation of cell-cell adhesion	24/253	1.06E-06	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/CXCL13/ICOS/MIR155/VCAM1/LAG3/PTPN22/CLECL1/TNFSF4/UBASH3B/PELI1/PTPN11/TFRC/CASP3/PRKAR1A/MAD2L2/GATA3
GO:1903037	regulation of leukocyte cell-cell adhesion	21/253	1.26E-06	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/ICOS/MIR155/VCAM1/LAG3/PTPN22/CLECL1/TNFSF4/PELI1/PTPN11/TFRC/CASP3/PRKAR1A/GATA3
GO:0007159	leukocyte cell-cell adhesion	22/253	1.33E-06	HAVCR2/PDCD1/CTLA4/TIGIT/CD27/HLA-DRA/IFNG/SIRPG/ICOS/MIR155/VCAM1/LAG3/PTPN22/CLECL1/TNFSF4/PELI1/PTPN11/GCNT1/TFRC/CASP3/PRKAR1A/GATA3
GO:0051607	defense response to virus	18/253	1.46E-06	LYST/IFNG/APOBEC3G/OASL/APOBEC3C/TNFAIP3/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1/IRF2/IRF9/GBP1/TBK1/DDX60
GO:0009615	response to virus	21/253	1.46E-06	LYST/IFNG/APOBEC3G/OASL/TNFSF4/APOBEC3C/TNFAIP3/APOBEC3F/BCL2L11/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1/IRF2/IRF9/GBP1/TBK1/GATA3/DDX60
GO:0045071	negative regulation of viral genome replication	10/253	1.58E-06	APOBEC3G/OASL/APOBEC3C/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1
GO:0051250	negative regulation of lymphocyte activation	14/253	1.88E-06	HAVCR2/CTLA4/TIGIT/SAMSN1/MIR155/PRDM1/ID2/LAG3/PTPN22/TNFSF4/TNFAIP3/PELI1/CASP3/PRKAR1A
GO:0070663	regulation of leukocyte proliferation	17/253	3.01E-06	HAVCR2/CTLA4/CSF1/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/TNFAIP3/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/CTNNB1
GO:0042113	B cell activation	19/253	3.81E-06	CTLA4/CD27/ITM2A/SAMSN1/CD38/VCAM1/PRDM1/ID2/LAT2/TNFSF4/TNFAIP3/ZFP36L1/RBP1/IKZF3/BATF/PELI1/BST2/TFRC/CASP3
GO:0001818	negative regulation of cytokine production	18/253	3.81E-06	HAVCR2/TIGIT/TNFRSF9/SRGN/IFNG/MIR155/ACPD5/LAG3/PTPN22/TNFSF4/TNFAIP3/HMOX1/CD84/UBE2L6/BST2/GBP1/TBK1/GATA3
GO:0070661	leukocyte proliferation	19/253	4.59E-06	HAVCR2/CTLA4/CSF1/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/TNFAIP3/FKBP1A/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/TBK1/CTNNB1
GO:0032944	regulation of mononuclear cell proliferation	16/253	7.60E-06	HAVCR2/CTLA4/CSF1/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/CTNNB1
GO:0032943	mononuclear cell proliferation	18/253	9.03E-06	HAVCR2/CTLA4/CSF1/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/FKBP1A/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/TBK1/CTNNB1
GO:0048525	negative regulation of viral process	11/253	2.12E-05	CCL3/APOBEC3G/OASL/APOBEC3C/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1
GO:0002521	leukocyte differentiation	24/253	2.33E-05	CTLA4/CCL3/CD27/CSF1/IFNG/ITM2A/MIR155/VCAM1/PRDM1/ID2/PTPN22/TNFSF4/ZFP36L1/RBP1/SEMA4A/IFI16/IKZF3/UBASH3B/BATF/TFRC/STAT3/CTNNB1/RHOH/GATA3
GO:1903901	negative regulation of viral life cycle	10/253	3.08E-05	APOBEC3G/OASL/APOBEC3C/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1
GO:0043901	negative regulation of multi-organism process	14/253	3.08E-05	HAVCR2/CCL3/APOBEC3G/PRDM1/OASL/APOBEC3C/TNFAIP3/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1
GO:0050670	regulation of lymphocyte proliferation	15/253	3.33E-05	HAVCR2/CTLA4/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/CTNNB1
GO:0046651	lymphocyte proliferation	17/253	3.33E-05	HAVCR2/CTLA4/CD38/MIR155/VCAM1/PRDM1/PTPN22/CLECL1/TNFSF4/FKBP1A/IKZF3/PELI1/TFRC/CASP3/PRKAR1A/TBK1/CTNNB1
GO:0030098	lymphocyte differentiation	19/253	4.45E-05	CTLA4/CD27/IFNG/ITM2A/MIR155/VCAM1/PRDM1/ID2/PTPN22/TNFSF4/ZFP36L1/RBP1/SEMA4A/IKZF3/BATF/STAT3/CTNNB1/RHOH/GATA3
GO:0050870	positive regulation of T cell activation	15/253	6.17E-05	HAVCR2/PDCD1/CTLA4/CD27/HLA-DRA/IFNG/SIRPG/ICOS/MIR155/VCAM1/CLECL1/TNFSF4/PTPN11/TFRC/GATA3
GO:0050864	regulation of B cell activation	13/253	6.17E-05	CTLA4/CD27/SAMSN1/CD38/PRDM1/ID2/TNFSF4/TNFAIP3/ZFP36L1/IKZF3/PELI1/TFRC/CASP3
GO:0045069	regulation of viral genome replication	10/253	6.66E-05	APOBEC3G/OASL/APOBEC3C/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1
GO:0060333	interferon-gamma-mediated signaling pathway	10/253	6.71E-05	HLA-DRA/IFNG/VCAM1/OASL/PARP14/OAS3/IRF2/IRF9/GBP1/GBP2
GO:0060337	type I interferon signaling pathway	10/253	6.71E-05	OASL/IFI6/BST2/PTPN11/IFI35/OAS3/MX1/IRF2/IRF9/GBP2
GO:0071357	cellular response to type I interferon	10/253	6.71E-05	OASL/IFI6/BST2/PTPN11/IFI35/OAS3/MX1/IRF2/IRF9/GBP2
GO:0034341	response to interferon-gamma	14/253	7.74E-05	CCL3/HLA-DRA/IFNG/GAPDH/VCAM1/OASL/BST2/PARP14/OAS3/IRF2/IRF9/GBP1/GBP2/CALCOCO2
GO:0051251	positive regulation of lymphocyte activation	18/253	7.84E-05	HAVCR2/PDCD1/CTLA4/CD27/HLA-DRA/IFNG/SIRPG/CD38/ICOS/MIR155/VCAM1/PRDM1/CLECL1/TNFSF4/PELI1/PTPN11/TFRC/GATA3
GO:0019079	viral genome replication	11/253	8.59E-05	CXCR6/APOBEC3G/OASL/APOBEC3C/APOBEC3F/IFI16/APOBEC3D/BST2/PLSCR1/OAS3/MX1

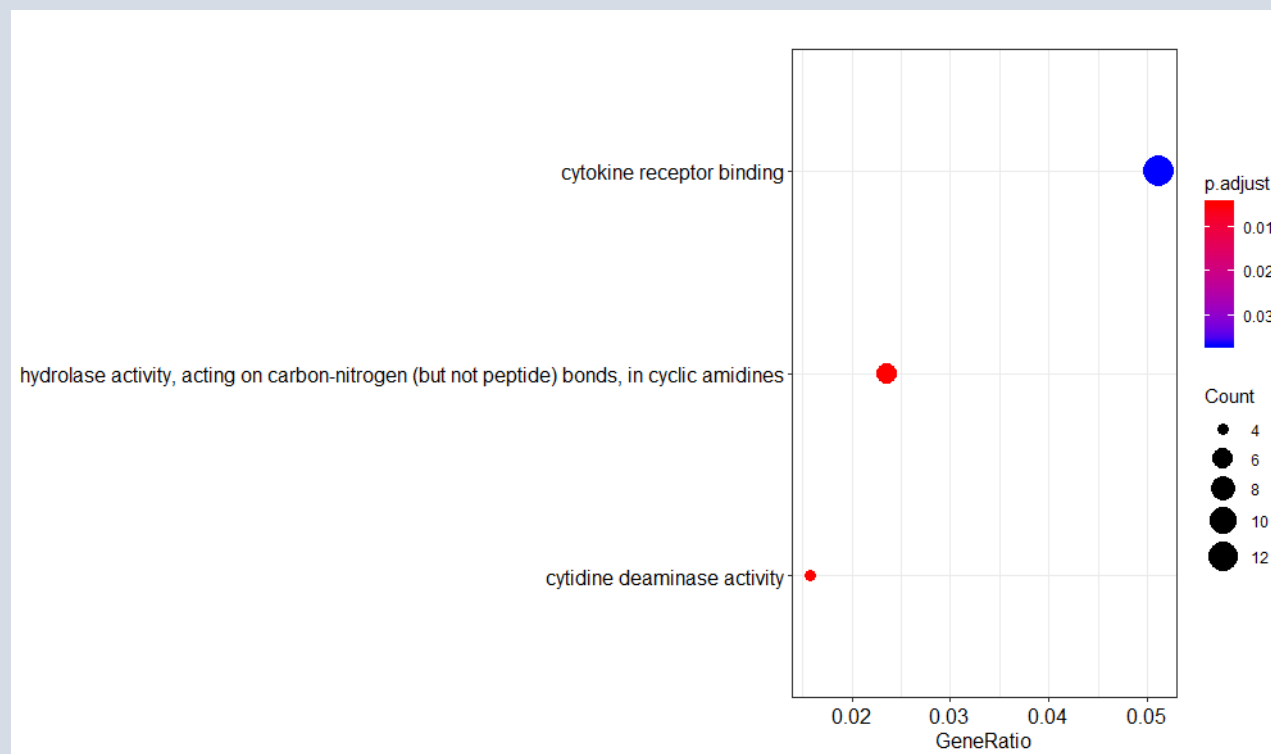
C4-CD8-LAYN (Input: 274 genes)

Analysis: GO – Cellular component



C4-CD8-LAYN (Input: 274 genes)

Analysis: GO – molecular function



ID	Description	GeneRatio	p.adjust	geneID
GO:0016814	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	6/254	0.00492	APOBEC3G/APOBEC3C/APOBEC3F/MTHFD2/APOBEC3D/MTHFD1
GO:0004126	cytidine deaminase activity	4/254	0.00492	APOBEC3G/APOBEC3C/APOBEC3F/APOBEC3D
GO:0005126	cytokine receptor binding	13/254	0.036655	CCL3/CSF1/IFNG/CXCL13/TNFSF4/FKBP1A/FASLG/TRAFF5/CD70/YARS/CASP3/STAT3/GATA3

C4-CD8-LAYN (Input: 274 genes)

Ongoing pathway Analysis (Future plan)

- Advanced analysis with fold changes & p-values inclusion
- Modified GSEA analysis using partial list of gene set might be doable
 - Without triplicate input? – Maybe I can manually add calculated statistics.
 - I have only partial list of gene expression – How rank is determined?
- Sorting genes expressed on cell surfaces
- Came up with potential target to follow