# pipeline\_seurat.py: summary report

Pancreatic endocrinogenesis (e15.5; scvelo example dataset)

Sansom group

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Sample: e15

Run specs: no. components: 30, cluster resolution: 0.7, cluster algorithm: leiden, de test: wilcox Code: https://github.com/sansomlab/tenx

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#### 1 Introduction

The core of the data analysis was performed using Seurat and scanpy:

- The construction of the nearest neighbor graph, clustering and UMAP computation were performed using scanpy (or scvelo for use of hnswlib).
- The differential expression analysis was performed using Seurat.
- The geneset analysis was performed using gsfisher
- Please see https://github/sansomlab/tenx for more details.

The key parameter choices used for this analysis were:

- The number of pca components: 30
- The number of nearest neighbors: 30
- The distance metric used for the nearest neighbor graph: euclidean
- The method used for construction of the nearest neighbor graph: hnsw
- The resolution of the clustering: 0.7
- The clustering algorithm: leiden
- The differential expression test: wilcox

#### 1.1 Optional tasks

This table summarises the status of the optional tasks. Tasks set to "True" were run.

task	run
explore_hvg_and_cell_cycle	True
$\operatorname{singleR}$	True
jackstraw	True
compare_clusters	True
characterise_markers	True
$top\_marker\_heatmap$	True
$extra\_cluster\_marker\_plots$	True
diffusionmap	True
phate	True
paga	True
velocity	True
knownmarkers	False
marker_report	True
exprsreport	False
genesets	True
cellbrowser	False

- 2 Data quality control
- 2.1 Quality assessment and removal of low-quality cells





Figure 2: QC: violin plots

The dataset was filtered to remove (1) cells expressing fewer than 500 genes per cell and (2) cells with a fraction of mitochondrial reads greater than 0.05. Genes expressed in less than 3 cells were removed from the analysis.

## 3 Removal of unwanted variation

#### 3.1 Removal of unwanted variation (data normalisation)

- The type of normalization applied was: log-normalization.
- A linear model was used to regress out the latent variables [percent.mito] before further analysis.
- The type of cell cycle regression applied was: none.

#### 3.2 Summary statistics

	х
no_cells	3696.00
$qc_min_gene_threshold$	500.00
$qc_min_percent_mito_threshold$	0.00
$qc_max_percent_mito_threshold$	0.05
no_cells_after_qc	3628.00

Table 1: Run statistics

	input	after_qc_filters
pancreas_e15	3696	3628

Table 2: Numbers of cells

## 4 Dimension reduction

4.1 Scree (elbow) plot



Figure 3: Scree plot showing proportion of variance explained by each PCA component

#### 4.2 Component heatmaps



Figure 4: Heatmaps of the top genes for each PCA component

#### 5 Exploration of cell cycle effects

5.1 Visualisation of cell cycle effects



Figure 5: PCA analysis of cells based on expression of cell cycle genes (without regression of cell-cyle effects)

#### 6 Highly variable gene identification

#### 6.1 Identification of variable genes

The selection method used to identify highly variable genes was: vst



Figure 6: Mean dispersion relationship



Figure 7: Seurat Jack Straw analysis of PCA components

## 7 Visualisation of clusters and factors of interest

7.1 umap.mindist\_0 plot colored by cluster\_id



Figure 8: umap.mindist\_0 plot colored by cluster\_id





Figure 9: umap.mindist\_0.1 plot colored by cluster\_id

## 7.3 umap.mindist\_0.3 plot colored by cluster\_id



Figure 10: umap.mindist\_0.3 plot colored by cluster\_id

## 7.4 umap.mindist\_0.5 plot colored by cluster\_id



Figure 11: umap.mindist\_0.5 plot colored by cluster\_id





Figure 12: umap.mindist\_0.7 plot colored by cluster\_id



Figure 13: umap plot colored by nCount\_RNA

## 7.7 umap plot colored by percent.mito



Figure 14: umap plot colored by percent.mito

## 8 singleR

See the singleR paper and bioconductor package for more information.

#### 8.1 ImmGenData



Figure 15: singleR predictions (ImmGenData)



Figure 16: pruned singleR predictions (ImmGenData)

#### 8.2 MouseRNAseqData



Figure 17: singleR predictions (MouseRNAseqData)



Figure 18: pruned singleR predictions (MouseRNAseqData)

# 9 Plots of summary statistics

Plots of summary statistics (e.g. cell number) by factor of interest (e.g. cluster)



#### 9.1 Cells by cluster

Figure 19: Cells by cluster



#### 9.2 Percent cells by cluster

Figure 20: Percent cells by cluster



## 9.3 Number of genes per cell per cluster

Figure 21: Number of genes per cell per cluster



## 9.4 Number of umi per cell per cluster

Figure 22: Number of umi per cell per cluster

# 10 Cluster dissimilarity

#### 10.1 Dissimilarity by gene expression

The distances between the clusters was assessed using the "BuildClusterTree" function in the Seurat package, which "constructs a phylogenetic tree relating the "average" cell from each identity class".



Figure 23: Visualisation of inter-cluster distances (cluster average, gene-based)

## 11 Cluster resolution analysis

The clustree algorithm is used to compare the different clustering resolutions.



Figure 24: The relationships between the clusters identified at different resolutions

# 12 Diffusion map

12.0.1 Diffusion map plots (first 3 dimensions, different rotations) colored by cluster



Figure 25: Diffusion map plots (first 3 dimensions, different rotations) colored by cluster

# 13 Phate maps

See: https://www.nature.com/articles/s41587-019-0336-3.



PHATE1

Figure 26: 2D Phate map



Figure 27: 3D Phate map

# 14 Partion-based graph abstraction (PAGA)

The original method is described here: **PAGA** 



Figure 28: PAGA graph





# UMAP1

Figure 29: PAGA initialised UMAP



Figure 30: Force atlas 2 (FA2) force directed graph




# 15 RNA velocity

The original method is described here: RNA velocity

We now use scyclo Generalizing RNA velocity to transient cell states through dynamical modeling

### 15.1 reduced dimension maps



Figure 32: Velocity plot on umap



Figure 33: Velocity stream plot on umap

cluster



Figure 34: Velocity grid plot on umap

## 15.2 PAGA initialised FA2 graphs



Figure 35: Velocity plot on PAGA initialised force atlas 2 graph



Figure 36: Velocity stream plot on PAGA initialised force atlas 2 graph

cluster



Figure 37: Velocity grid plot on PAGA intialised force atlas 2 graph



Figure 38: Velocity plot on PHATE graph





Figure 39: Velocity stream plot on PHATE graph

# cluster



Figure 40: Velocity grid plot on PHATE graph

## 16 Identification of cluster marker genes

Cluster marker genes were identified using the Seurat FindMarkers routine and the wilcox test. A summary table containing all of the significant markers for all of the clusters (based on BH adjusted p value) is available separately. Key parameters are:

- Differential expression methods: wilcox
- Testing limited to genes with a log fold change of > 0.25
- Testing limited to genes detected in a minimum fraction of 0.1 of cells
- Conservation factor applied: None

# 17 Top cluster marker genes



Figure 41: Heatmap of the top cluster-specific genes (based on differential expression analysis)

### 18 Marker genes by cluster

### 18.0.1 Summary of numbers of DE genes per-cluster



Figure 42: Numbers of differentially expressed genes (adjusted p-value < 0.05, fold change > 2) per cluster

#### 18.1 Cluster 0: summary plots



Figure 43: Differential expression summary plots for cluster 0



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 0



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 0



Figure 46: Differential expression summary plots for cluster 1



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 1



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 1



18.7 Cluster 2: summary plots

Figure 49: Differential expression summary plots for cluster 2





(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 2



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 2



Figure 52: Differential expression summary plots for cluster 3

#### 18.11 Cluster 3 violin plots: positive marker genes



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 3

#### 18.12 Cluster 3 violin plots: negative marker genes



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 3





Figure 55: Differential expression summary plots for cluster 4

#### 18.14 Cluster 4 violin plots: positive marker genes



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 4

#### 18.15 Cluster 4 violin plots: negative marker genes



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 4





Figure 58: Differential expression summary plots for cluster 5



#### 18.17 Cluster 5 violin plots: positive marker genes

(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 5

#### 18.18 Cluster 5 violin plots: negative marker genes



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 5



Figure 61: Differential expression summary plots for cluster 6

#### 18.20 Cluster 6 violin plots: positive marker genes



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 6



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 6





Figure 64: Differential expression summary plots for cluster 7



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 7

#### 18.24 Cluster 7 violin plots: negative marker genes



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 7




Figure 67: Differential expression summary plots for cluster 8

#### 18.26 Cluster 8 violin plots: positive marker genes



(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 8

### 18.27 Cluster 8 violin plots: negative marker genes



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 8





Figure 70: Differential expression summary plots for cluster 9





(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 9



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 9

#### 18.31 Cluster 10: summary plots



Figure 73: Differential expression summary plots for cluster 10





(b) Additional positive marker genes ordered by minimum fold-change vs all other clusters, cluster: 10



(b) Additional negative marker genes ordered by minimum fold-change vs all other clusters, cluster: 10

# 19 Geneset analysis

A hypergeometric test is used to test for the enrichment of GO, KEGG and msigdb genesets amongst the positive marker genes for each cluster. The full results are available as a separate xlsx document.

### 19.1 GO.BP



Figure 76: Heatmap of the top GO.BP genesets



Figure 77: Cluster 0 GO.BP genesets clustered by similarity between over-represented genes.



Figure 78: Cluster 1 GO.BP genesets clustered by similarity between over-represented genes.



Figure 79: Cluster 2 GO.BP genesets clustered by similarity between over-represented genes.



Figure 80: Cluster 3 GO.BP genesets clustered by similarity between over-represented genes.



Figure 81: Cluster 4 GO.BP genesets clustered by similarity between over-represented genes.



Figure 82: Cluster 5 GO.BP genesets clustered by similarity between over-represented genes.



Figure 83: Cluster 6 GO.BP genesets clustered by similarity between over-represented genes.



Figure 84: Cluster 7 GO.BP genesets clustered by similarity between over-represented genes.



Figure 85: Cluster 8 GO.BP genesets clustered by similarity between over-represented genes.



Figure 86: Cluster 9 GO.BP genesets clustered by similarity between over-represented genes.



Figure 87: Cluster 10 GO.BP genesets clustered by similarity between over-represented genes.

### 19.2 GO.MF



Figure 88: Heatmap of the top GO.MF genesets

94

### 19.3 GO.CC



Figure 89: Heatmap of the top GO.CC genesets

## 19.4 KEGG



Figure 90: Heatmap of the top KEGG genesets

![](_page_96_Figure_0.jpeg)

## 19.5 msigdb\_biocarta

Figure 91: Heatmap of the top msigdb\_biocarta genesets

![](_page_97_Figure_1.jpeg)

Figure 92: Heatmap of the top msigdb\_reactome genesets

### 19.7 msigdb\_canonical\_pathways

![](_page_98_Figure_1.jpeg)

Figure 93: Heatmap of the top msigdb\_canonical\_pathways genesets

### 19.8 msigdb\_tf\_motifs

![](_page_99_Figure_1.jpeg)

Figure 94: Heatmap of the top msigdb\_tf\_motifs genesets

### 19.9 msigdb\_immunological\_signatures

![](_page_100_Figure_1.jpeg)

Figure 95: Heatmap of the top msigdb\_immunological\_signatures genesets

## 19.10 Top genesets by cluster

The table lists the top (filtered by nominal p value) genesets by cluster.

cluster	type	description	p.val	p.adj	n_fg	odds.ratio	n.clust
0	GO.BP	hormone transport	2.16e-17	3.8e-14	41	6.44	6
0	GO.BP	hormone secretion	8.67e-17	1.38e-13	40	6.32	6
0	GO.BP	regulation of hormone secretion	9.15e-16	1.32e-12	35	6.82	5
0	GO.BP	peptide hormone secretion	1.95e-15	2.39e-12	35	6.62	5
0	GOBP	regulation of peptide hormone secretion	8 97e-15	8.37e-12	31	7 27	5
ů 0	COME	oligosaccharyl transferase activity	5 760 10	1 150 07	8	1/3	3
0	COME	delighted diphogphoeligoggagharide protein gly	5.76e-10	1.15e-07	0	140	2
0	GO.MF	donchyi-diphosphoongosaccharide-protein giy	5.76e-10	1.15e-07	0	145	3
0	GO.MF	hormone activity	9.4e-07	5.38e-05	9	12.4	3
0	GO.MF	peptide disulfide oxidoreductase activity	1.66e-05	0.000497	6	17.8	2
0	GO.MF	proton-exporting ATPase activity	3.61e-05	0.000872	7	10.4	2
0	GO.CC	oligosaccharyltransferase complex	5.76e-10	2.53e-08	8	143	3
0	GO.CC	endoplasmic reticulum chaperone complex	9.59e-09	3.31e-07	8	47.5	2
0	GO.CC	secretory granule	4.26e-08	1.45e-06	25	4.18	4
0	GO.CC	smooth endoplasmic reticulum	4.56e-07	1.2e-05	10	11.2	2
0	GO CC	endoplasmic reticulum lumen	$1.74e_{-}06$	4 1e-05	11	79	3
ů 0	KEGG	Protein processing in endoplasmic reticulum	1.050.15	4 530 13	35	6.62	3
0	KEGG	O that a har har har har	1.956-15	4.556-15	00	5.02	3
0	KEGG	Oxidative phosphorylation	4.41e-09	5.11e-07	23	5.22	1
0	KEGG	Protein export	2.21e-08	1.92e-06	11	14.1	1
0	KEGG	Parkinson disease	7.36e-08	5.39e-06	30	3.49	2
0	KEGG	Maturity onset diabetes of the young	5.83e-07	3.38e-05	9	13.4	4
0	msigdb_reactome	peptide hormone metabolism	7.32e-11	2.23e-09	16	12.1	4
0	msigdb_reactome	asparagine n linked glycosylation	5.18e-09	1.28e-07	33	3.7	1
0	msigdb_reactome	synthesis secretion and inactivation of gluco	9.59e-09	2.28e-07	8	47.5	3
0	msigdb reactome	incretin synthesis secretion and inactivation	1.33e-08	3.09e-07	9	26.8	4
0	msigdh reactome	gpcr ligand hinding	1.26e-07	2 42e-06	14	7 44	5
0	maigdb_reactonic	portido hormono motobolism	7 220 11	2.420-00	16	10.1	4
0	insigub_canonical_pathways	peptide normone metabolism	7.326-11	2.836-09	10	12.1	4
0	msigdb_canonical_pathways	asparagine n linked glycosylation	5.18e-09	1.64e-07	33	3.7	1
0	msigdb_canonical_pathways	synthesis secretion and inactivation of gluco	9.59e-09	2.9e-07	8	47.5	3
0	msigdb_canonical_pathways	incretin synthesis secretion and inactivation	1.33e-08	3.91e-07	9	26.8	4
0	msigdb_canonical_pathways	gpcr ligand binding	1.26e-07	3.11e-06	14	7.44	5
0	msigdb_immunological_signatures	gse29164 cd8 tcell vs cd8 tcell and il12 trea	2.6e-10	5.25e-08	23	6.22	2
0	msigdb_immunological_signatures	gse29617 ctrl vs day7 tiv flu vaccine pbmc 20	1.98e-09	3.58e-07	25	5.01	1
0	msigdb immunological signatures	gse12366 plasma cell vs naive bcell up	5.52e-08	7.67e-06	21	4.86	2
0	msigdb immunological signatures	gse18281 cortical vs medullary thymocyte up	5.55e-08	7.69e-06	19	5.41	2
0	msigdh immunological signatures	gse22886 naive bcell vs bm plasma cell dn	5 57e-08	7 7e-06	23	4 44	1
1	CO BB	geteplacmia translation	2 700 15	4.010.12	20	10.2	4
1	GO BD		1.45.00	4.016-12	20	10.2	4
1	GO.BP	extracellular structure organization	1.45e-09	3.55e-07	20	4.95	5
1	GO.BP	regulation of epithelial cell proliferation	2.29e-09	5.27e-07	31	4.08	4
1	GO.BP	exocrine system development	1.48e-08	2.83e-06	12	12.8	3
1	GO.BP	extracellular matrix organization	1.52e-08	2.83e-06	22	5.11	5
1	GO.MF	structural constituent of ribosome	1.2e-39	2.4e-36	63	13.9	5
1	GO.MF	rRNA binding	2.72e-11	7.78e-09	21	8.33	5
1	GO.MF	cell adhesion molecule binding	3.79e-07	2.79e-05	19	4.72	3
1	GO.MF	sulfur compound binding	4.48e-07	2.99e-05	20	4.43	3
- 1	GOME	extracellular matrix structural constituent	6.47e-07	4.05e-05	12	7 99	4
1	COCC	autocolia ribocomo	0.470-55	4.580.52	62	26.6	5
1		cytosofic ribosofie	2.37e-33	4.586-52	03	50.0	5
1	GO.CC	cytosolic large ribosomal subunit	1.17e-38	7.52e-36	40	52.5	5
1	GO.CC	cytosolic part	6.88e-38	3.33e-35	67	11.3	5
1	GO.CC	ribosomal subunit	2.61e-35	6.31e-33	64	10.7	5
1	GO.CC	large ribosomal subunit	4.16e-23	5.37e-21	41	10.4	5
1	KEGG	Ribosome	2.22e-50	3.08e-47	69	20.3	5
1	KEGG	Glutathione metabolism	3.65e-08	2.82e-06	14	8.64	4
1	KEGG	Drug metabolism - cytochrome P450	1.89e-07	1.32e-05	10	13.3	2
1	KEGG	Tight junction	7.4e-07	3,96e-05	22	3.92	2
-	KEGG	Cell adhesion molecules	1 250 06	6.01c.05	12	7 37	-
-	maindh repatome	oukomotia translation al	6 10- 41	7 946 99	12	40.2	- 5
1	msigdb_reactome	eukaryotic translation elongation	0.19e-41	7.34e-38	43	49.2	о -
1	msigdb_reactome	response of eit2ak4 gcn2 to amino acid defici	9.06e-36	7.17e-33	41	33.4	5
1	msigdb_reactome	selenoamino acid metabolism	5.94e-30	2.35e-27	40	20	5
1	msigdb_reactome	srp dependent cotranslational protein targeti	2.4e-29	8.15e-27	40	18.9	6
1	msigdb_reactome	nonsense mediated decay nmd	4.73e-29	1.4e-26	40	18.4	5
1	msigdb_canonical_pathways	eukaryotic translation elongation	6.19e-41	1.07e-37	43	49.2	5
1	msigdb canonical pathways	kegg ribosome	1.48e-37	1.69e-34	40	45.5	5
-	msight canonical pathways	response of eif2ak4 gcn2 to amino acid defici	9.066-36	7 79e-33	41	33.4	5
1	meigdb_canonical_pathways	selencemino acid metabolicm	5.04-20	2 56c 27	40	20	5
1	msigub_canonical_pathways	serenoammo aciu metabolismi	0.4.00	2.508-27	40	20	G
1	msigdb_canonical_pathways	srp dependent cotranslational protein targeti	2.4e-29	9.19e-27	40	18.9	0
1	msigdb_tf_motifs	psmb5 target genes	1.66e-07	2.86e-05	25	3.88	7
1	$msigdb\_tf\_motifs$	wggaatgy tefl q6	1.99e-06	0.000298	27	3.14	1
1	msigdb_tf_motifs	gtf2a2 target genes	6.03e-06	0.000828	34	2.56	5
1	msigdb_tf_motifs	supt16h target genes	4.91e-05	0.00561	17	3.45	1
_		1 11 01				0 51	_
1	msigdb_tf_motifs	hnfl 01	6.75e-05	0.007	16	3.51	1

1	msigdb_immunological_signatures	gse2405 0h vs 24h a phagocytophilum stim neut	2.94e-25	2.87e-22	48	9.4	5
1	msigdb immunological signatures	gse2405 0h vs 9h a phagocytophilum stim neutr.	9.12e-21	5.94e-18	44	7.73	5
1	msigdb_immunological_signatures	gse42088 uninf vs leishmania inf dc 2h dn	5 54e-17	2.36e-14	34	8 11	5
1	msigdb_immunological_signatures	gse22886 naive hcell vs neutrophil up	1.61e-14	5 23e-12	30	7 52	5
1	maigdb_immunological_signatures	gse22000 haive been vs heutrophin up	4.710.11	1.040.08	26	6	4
	do pp	gse22880 haive teen vs de up	4.716-11	1.04e-08	20	0	4
2	GO.BP	hormone transport	4.52e-09	9.83e-07	26	4.55	6
2	GO.BP	hormone secretion	1.57e-08	2.83e-06	25	4.39	6
2	GO.BP	regulation of hormone secretion	5.43e-07	5.98e-05	20	4.28	5
2	GO.BP	peptide hormone secretion	8.08e-07	8.17e-05	20	4.16	5
2	GO.BP	positive regulation of hormone secretion	8.9e-06	0.000591	13	5.13	4
2	GO.MF	hormone activity	7.88e-08	7.52e-06	9	17.6	3
2	GO.MF	G protein-coupled receptor binding	2.62e-06	0.000112	16	4.66	4
- 2	GOME	G-protein heta/gamma-subunit complex hinding	0.000113	0.00218	5	15.2	3
2	COME	amulaid beta binding	0.000116	0.00210	6	7.54	1
2	GO.MF		0.000430	0.0039	0	1.54	1
2	GO.MF	cell-cell adhesion mediator activity	0.000702	0.00789	4	14.2	3
2	GO.CC	secretory granule	7.34e-09	2.63e-07	24	4.78	4
2	GO.CC	secretory granule membrane	1.81e-05	0.000326	9	7.45	4
2	GO.CC	heterotrimeric G-protein complex	1.84e-05	0.000326	6	16	3
2	GO.CC	GTPase complex	1.84e-05	0.000326	6	16	3
2	GO.CC	perikaryon	0.00011	0.00134	10	5.01	5
2	KEGG	GABAergic synapse	4.48e-06	0.000152	9	9.23	3
2	KEGG	Neuroactive ligand-receptor interaction	6.07e-06	0.000188	9	8 81	3
- 2	KEGG	Circadian entrainment	2 320 05	0.000601	å	7 18	4
2	KEGG	Chanadan entrainment	2.526-05	0.000001	0	6.46	-1
2	KEGG	Giutamatergic synapse	4.62e-05	0.000974	9	6.46	3
2	KEGG	Lysosome	8.11e-05	0.00147	13	4.02	2
2	msigdb_biocarta	gcr pathway	0.0116	0.0423	3	7.95	1
2	msigdb_reactome	adora2b mediated anti inflammatory cytokines	5.74e-08	1.21e-06	10	14.4	3
2	msigdb_reactome	peptide hormone metabolism	8.06e-08	1.65e-06	12	9.66	4
2	msigdb_reactome	gpcr ligand binding	2.02e-07	3.71e-06	12	8.69	5
2	msigdb_reactome	anti inflammatory response favouring leishman.	4.2e-07	7.03e-06	11	9.16	3
2	msigdb reactome	regulation of insulin secretion	4.89e-06	6.21e-05	10	7.71	3
- 2	msigdh canonical pathways	adora2h mediated anti inflammatory cytokines	5 74e-08	1.53e-06	10	14.4	3
2	maigdb_canonical_pathways	natida hormona metabolism	8.060.08	2.10.06	10	0.66	4
2	insigub_canonical_pathways		8.00e-08	2.16-00	12	9.00	4
2	msigdb_canonical_pathways	gpcr ligand binding	2.02e-07	4.72e-06	12	8.69	5
2	msigdb_canonical_pathways	anti inflammatory response favouring leishman	4.2e-07	8.88e-06	11	9.16	3
2	msigdb_canonical_pathways	regulation of insulin secretion	4.89e-06	7.66e-05	10	7.71	3
2	msigdb_tf_motifs	oct q6	0.000264	0.0208	13	3.52	1
2	msigdb_tf_motifs	oct1 q5 01	0.000264	0.0208	13	3.52	1
2	msigdb_tf_motifs	tata 01	0.000645	0.0393	11	3.59	1
2	msigdb tf motifs	nrsf 01	0.000708	0.0394	6	6.75	2
				0.0411	10	3.28	1
2	msigdh tf motifs	oct c	0.000776	1111411	1.2		1
2	msigdb_tf_motifs	oct c	0.000776	0.0411	12	2.01	1
2 2	msigdb_tf_motifs msigdb_immunological_signatures	oct c gse22886 igg iga memory bcell vs bm plasma ce	0.000776 1.02e-05	0.000927	12 17	3.91	1
2 2 2	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn	0.000776 1.02e-05 3.62e-05	0.000927 0.00291	12 17 14	3.91 4.11	1 1
2 2 2 2	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up	0.000776 1.02e-05 3.62e-05 3.7e-05	$\begin{array}{c} 0.0411\\ 0.000927\\ 0.00291\\ 0.00296\end{array}$	12 17 14 9	3.91 4.11 6.68	1 1 2
2 2 2 2 2 2	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn	0.000776 1.02e-05 3.62e-05 3.7e-05 4.02e-05	$\begin{array}{c} 0.0411\\ 0.000927\\ 0.00291\\ 0.00296\\ 0.00316 \end{array}$	12 17 14 9 16	3.91 4.11 6.68 3.63	1 1 2 3
2 2 2 2 2 2 2	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up	$\begin{array}{c} 0.000776\\ 1.02e{-}05\\ 3.62e{-}05\\ 3.7e{-}05\\ 4.02e{-}05\\ 4.9e{-}05\\ \end{array}$	0.0411 0.000927 0.00291 0.00296 0.00316 0.00376	12 17 14 9 16 17	3.91 4.11 6.68 3.63 3.4	1 1 2 3 2
2 2 2 2 2 2 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion	$\begin{array}{c} 0.000776\\ 1.02e-05\\ 3.62e-05\\ 3.7e-05\\ 4.02e-05\\ 4.9e-05\\ \hline 2.27e-12 \end{array}$	0.0411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09	12 17 14 9 16 17 30	3.91 4.11 6.68 3.63 3.4 5.79	1 1 2 3 2 6
2 2 2 2 2 2 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport	0.000776 1.02e-05 3.62e-05 3.7e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12	0.0411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09	12 17 14 9 16 17 30 30	3.91 4.11 6.68 3.63 3.4 5.79 5.69	1 1 2 3 2 6 6
2 2 2 2 2 2 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion	0.000776 1.02e-05 3.62e-05 3.7e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11	0.0411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08	$12 \\ 17 \\ 14 \\ 9 \\ 16 \\ 17 \\ 30 \\ 30 \\ 25$	3.91 4.11 6.68 3.63 3.4 5.79 5.69 6	1 1 2 3 2 6 6 5
2 2 2 2 2 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion	0.000776 1.02e-05 3.62e-05 3.7e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10	0.0411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07	12 17 14 9 16 17 30 30 25 24	$\begin{array}{c} 3.91 \\ 4.11 \\ 6.68 \\ 3.63 \\ 3.4 \\ \hline 5.79 \\ 5.69 \\ 6 \\ 5.49 \end{array}$	1 1 2 3 2 6 6 5 5 5
2 2 2 2 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of neptide hormone secretion	0.000776 1.02e-05 3.62e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4 94e-07	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ \end{array} $	$\begin{array}{c} 5.25\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\end{array}$	1 1 2 3 2 6 6 5 5 5 5
2 2 2 2 2 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse20618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein coupled recenter binding	0.000776 1.02e-05 3.62e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.10e.07	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4.94e-07 2.89e.05	12 17 14 9 16 17 30 30 25 24 21	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ \end{array}$	1 1 2 3 2 6 6 6 5 5 5 5 4
2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding	0.000776 1.02e-05 3.62e-05 3.7e-05 4.02e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 2.12e-07	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4.94e-07 2.89e-05	$     \begin{array}{r}       12 \\       17 \\       14 \\       9 \\       16 \\       17 \\       30 \\       30 \\       25 \\       24 \\       21 \\       17 \\       6 \\       \hline       6       \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\end{array}$	$     \begin{array}{c}       1 \\       1 \\       2 \\       3 \\       2 \\       6 \\       6 \\       5 \\       5 \\       5 \\       5 \\       4 \\       2 \\       \end{array} $
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla	0.000776 1.02e-05 3.62e-05 3.7e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4.94e-07 2.89e-05 4.93e-05	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 40.8\\ 757\end{array}$	1 1 2 3 2 6 6 5 5 5 4 2 2
2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla	$\begin{array}{c} 0.000776\\ 1.02e-05\\ 3.62e-05\\ 3.7e-05\\ 4.02e-05\\ \hline \\ 2.27e-12\\ 3.33e-12\\ 7.09e-11\\ 7.46e-10\\ 2.12e-09\\ 4.19e-07\\ 8.13e-07\\ 5.54e-06\\ \end{array}$	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 0.000222	$     \begin{array}{r}       12 \\       17 \\       14 \\       9 \\       16 \\       17 \\       30 \\       30 \\       25 \\       24 \\       21 \\       17 \\       6 \\       11 \\     \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ \end{array}$	$ \begin{array}{c} 1 \\ 2 \\ 3 \\ 2 \\ 6 \\ 6 \\ 5 \\ 5 \\ 4 \\ 2 \\ 2 \\ 2 \\ \end{array} $
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla	$\begin{array}{c} 0.000776\\ 1.02e{-}05\\ 3.62e{-}05\\ 3.7e{-}05\\ 4.02e{-}05\\ 4.02e{-}05\\ \hline 2.27e{-}12\\ 3.33e{-}12\\ 7.09e{-}11\\ 7.46e{-}10\\ 2.12e{-}09\\ 4.19e{-}07\\ 8.13e{-}07\\ 5.54e{-}06\\ 1.56e{-}05\\ \end{array}$	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482	$     \begin{array}{r}       12 \\       17 \\       14 \\       9 \\       16 \\       17 \\       30 \\       30 \\       25 \\       24 \\       21 \\       17 \\       6 \\       11 \\       7 \\       \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ \end{array}$	1 1 2 3 2 6 6 5 5 5 5 4 2 2 2
2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures go.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding	$\begin{array}{c} 0.000776\\ 1.02e{-}05\\ 3.62e{-}05\\ 3.7e{-}05\\ 4.9e{-}05\\ 4.9e{-}05\\ \hline 2.27e{-}12\\ 3.33e{-}12\\ 7.09e{-}11\\ 7.46e{-}10\\ 2.12e{-}09\\ 4.19e{-}07\\ 8.13e{-}07\\ 8.13e{-}07\\ 5.54e{-}06\\ 1.56e{-}05\\ 4.89e{-}05\\ \end{array}$	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.00113	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ \end{array} $	$\begin{array}{c} 5.25\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ \end{array}$	1 1 2 3 2 6 6 5 5 5 4 2 2 2 2
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule	$\begin{array}{c} 0.000776\\ 1.02e{-}05\\ 3.62e{-}05\\ 3.7e{-}05\\ 4.9e{-}05\\ \hline 2.27e{-}12\\ 3.33e{-}12\\ 7.09e{-}11\\ 7.46e{-}10\\ 2.12e{-}09\\ 4.19e{-}07\\ 8.13e{-}07\\ 5.54e{-}06\\ 1.56e{-}05\\ 4.89e{-}05\\ 4.35e{-}10\\ \end{array}$	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4.94e-07 2.89e-05 0.000222 0.000482 0.00113 1.96e-08	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ \end{array}$	$ \begin{array}{c} 1 \\ 1 \\ 2 \\ 3 \\ 2 \\ 6 \\ 6 \\ 5 \\ 5 \\ 4 \\ 2 \\ 2 \\ 2 \\ 2 \\ 4 \\ \end{array} $
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle	0.000776 1.02e-05 3.62e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 8.13e-07 5.54e-06 1.56e-05 4.89e-05 4.35e-10 1.55e-05	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 0.000222 0.000482 0.00113 1.96e-08 0.000297	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ \end{array}$	1 1 2 3 2 6 6 5 5 5 4 2 2 2 2 4 3
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon	$\begin{array}{c} 0.000776\\ 1.02e-05\\ 3.62e-05\\ 3.7e-05\\ 4.02e-05\\ 4.9e-05\\ \hline 2.27e-12\\ 3.33e-12\\ 7.09e-11\\ 7.46e-10\\ 2.12e-09\\ 4.19e-07\\ 8.13e-07\\ 5.54e-06\\ 1.56e-05\\ 4.89e-05\\ 4.35e-10\\ 1.55e-05\\ 2.01e-05\\ \end{array}$	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.00113 1.96e-08 0.000297 0.000251	$ \begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ \end{array} $	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ \end{array}$	$     \begin{array}{c}       1 \\       2 \\       3 \\       2 \\       6 \\       6 \\       5 \\       5 \\       5 \\       4 \\       2 \\       2 \\       2 \\       2 \\       2 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\       5 \\       5 \\       4 \\       3 \\       5 \\     $
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2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane	0.000776 1.02e-05 3.62e-05 4.9e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.89e-05 4.35e-10 1.55e-05 2.01e-05 2.28e-05	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.00113 1.96e-08 0.000297 0.000374 0.000374	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 12\\ \end{array}$	$\begin{array}{c} 5.25\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 5.06\\ \end{array}$	1 1 2 3 2 6 5 5 5 4 2 2 2 2 4 3 5 2 2 2 2 2 2 2 2 2 2 2 2 2
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KFCC	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion g protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane Maturity opert diabates of the young	0.000776 1.02e-05 3.62e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.89e-05 4.35e-10 1.55e-05 2.01e-05 2.28e-05 2.28e-05 3.2e,09	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 4.94e-07 4.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.00113 1.96e-08 0.000297 0.000374 0.000374 0.000374	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ \end{array}$	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 5.06\\ 5.2 \\ 0\end{array}$	1 1 2 3 2 6 5 5 5 4 2 2 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 2 2 2 2 2 2 2 2 2 2 2 2 2
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2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle	0.000776 1.02e-05 3.62e-05 4.02e-05 4.02e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.39e-05 4.35e-10 1.55e-05 2.01e-05 2.28e-05 3.2e-09 1.55e-08	0.00411 0.000927 0.00291 0.00291 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000113 1.96e-08 0.000297 0.000351 0.000374 4.05e-07 1.44e-06 2.51.05	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 10\\ 12\\ 2\end{array}$	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 5.06\\ 22.9\\ 11.8\\ 10.6\\ \end{array}$	$ \begin{array}{c} 1 \\ 1 \\ 2 \\ 3 \\ 2 \\ 6 \\ 6 \\ 5 \\ 5 \\ 4 \\ 2 \\ 2 \\ 2 \\ 2 \\ 4 \\ 3 \\ 5 \\ 2 \\ 2 \\ 4 \\ 4 \\ 4 \\ 2 \\ 2 \\ 4 \\ 4 \\ 2 \\ 4 \\ 4 \\ 2 \\ 2 \\ 4 \\ 4 \\ 4 \\ 2 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4 \\ 4$
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2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion geptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway pgc1a pathway nos1 pathway	0.000776 1.02e-05 3.62e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.39e-05 4.35e-10 1.55e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.009 0.00718 0.0131 1.14e-07	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000155 0.000427 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000155 0.000427 0.000427 0.000427 0.000452 2.21e-06	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 9\\ 9\\ 9\\ 5\\ 3\\ 3\\ 8\\ \end{array}$	$\begin{array}{c} 3.20\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06$	$ \begin{array}{c} 1\\ 1\\ 2\\ 3\\ 2\\ 6\\ 6\\ 5\\ 5\\ 5\\ 4\\ 2\\ 2\\ 2\\ 2\\ 4\\ 3\\ 5\\ 2\\ 2\\ 4\\ 3\\ 5\\ 2\\ 4\\ 3\\ 4\\ 3\\ 4\\ 3\\ 2\\ 1\\ 4\\ 3\\ 4\\ 3\\ 2\\ 1\\ 4\\ 4\\ 3\\ 2\\ 1\\ 4\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\$
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway nos1 pathway regulation of gene expression in beta cells resultion of gene exploaded synaptic of beta cell downlarmate	0.000776 1.02e-05 3.62e-05 4.02e-05 4.02e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.35e-10 1.55e-05 2.01e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.0009 0.00718 0.0131 1.14e-07 4.72e-06	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.00113 1.96e-08 0.000297 0.000351 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000155 0.000155 0.000155 0.000155 0.000155 0.000155 0.000155 0.000427 0.00907 0.0316 0.0452 2.21e-06 1.2e-09	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 9\\ 9\\ 9\\ 5\\ 3\\ 3\\ 8\\ 9\end{array}$	$\begin{array}{c} 3.91\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 22.9\\ 11.8\\ 10.9\\ 9.24\\ 7.7\\ 8.47\\ 10.1\\ 7.58\\ 23.4\\ 0.24\\ \end{array}$	1 1 2 3 2 6 6 5 5 4 2 2 2 2 4 3 5 2 2 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 1 4 4 3 5 5 5 5 5 5 4 2 2 2 2 4 4 3 5 5 5 5 5 5 5 5 5 5 5 5 5
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway nos1 pathway regulation of gene expression in beta cells regulation of beta cell development	0.000776 1.02e-05 3.62e-05 4.02e-05 4.02e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.35e-10 1.55e-05 2.01e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.0009 0.00718 0.0131 1.14e-07 4.73e-06	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000482 0.000297 0.000351 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000155 0.000427 0.000316 0.00427 0.00035 0.000427 0.0005 0.000	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 9\\ 9\\ 9\\ 9\\ 5\\ 3\\ 3\\ 8\\ 9\\ 6\end{array}$	3.20 3.91 4.11 6.68 3.63 3.4 5.79 5.69 6 5.49 6 5.15 40.8 6.67 11.9 2.95 5.19 3.61 5.67 5.06 5.06 5.06 22.9 11.8 10.9 9.24 7.7 8.47 10.1 7.58 23.4 9.24 9.24	$     \begin{array}{c}       1 \\       2 \\       3 \\       2 \\       6 \\       6 \\       5 \\       5 \\       5 \\       4 \\       2 \\       2 \\       2 \\       2 \\       2 \\       2 \\       2 \\       4 \\       3 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       1 \\       1 \\       4 \\       5 \\       2 \\       2 \\       1 \\       1 \\       5 \\       2 \\       1 \\       1 \\       5 \\       2 \\       1 \\       1 \\       5 \\       2 \\       2 \\       1 \\       1 \\       5 \\       2 \\       1 \\       1 \\       1 \\       1 \\       2 \\       1 \\     $
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway nos1 pathway regulation of gene expression in beta cells regulation of beta cell development insulin receptor recycling	0.000776 1.02e-05 3.62e-05 4.02e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.89e-05 4.35e-10 1.55e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.0009 0.00718 0.0131 1.14e-07 4.73e-06 2.37e-05 2.5e-05 2.57e-05 2.58e-05 0.0009 0.00718 0.0131 1.14e-07 4.73e-06 2.37e-05 0.56e-05 0.56e-05 0.0009 0.00718 0.0131 1.14e-07 4.73e-06 2.37e-05 0.56e-05 0.56e-05 0.56e-05 0.009 0.00718 0.0131 0.01	0.00411 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000482 0.000297 0.000351 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000427 0.000452 0.000452 2.21e-06 6.1e-05 0.000231 0.000231 0.000231 0.000231 0.00452 2.21e-06 6.1e-05 0.000231 0.000232 0.000231 0.000232 0.000232 0.000231 0.000232 0.00023 0.0002	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 9\\ 9\\ 9\\ 5\\ 3\\ 3\\ 8\\ 9\\ 6\\ 2\end{array}$	3.20 3.91 4.11 6.68 3.63 3.4 5.79 5.69 6 5.49 6 5.49 6 5.15 40.8 6.67 11.9 2.95 5.19 3.61 5.67 5.06 5.06 5.06 22.9 11.8 10.9 9.24 7.7 8.47 10.1 7.58 23.4 9.24 15.3 15.5	1 1 2 3 2 6 5 5 5 4 2 2 2 2 2 2 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 4 3 2 1 1 4 3 2 1 1 4 3 2 1 1 4 3 2 2 1 1 4 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 3 2 2 1 1 4 5 3 3 2 3 3 3 3 3 3 3 3
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion gptide hormone secretion regulation of peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle cycle GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway pgcla pathway regulation of gene expression in beta cells regulation of beta cell development insulin receptor recycling ros and rns production in phagocytes	0.000776 1.02e-05 3.62e-05 4.9e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.89e-05 4.35e-10 1.55e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.000718 0.0131 1.14e-07 4.73e-06 2.37e-05	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000482 0.000297 0.000351 0.000274 4.05e-07 1.44e-06 7.51e-05 0.000427 0.000452 2.21e-06 6.1e-05 0.000231 0.0	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 12\\ 10\\ 12\\ 9\\ 9\\ 9\\ 5\\ 3\\ 3\\ 8\\ 9\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\ 6\\$	$\begin{array}{c} 3.91\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 5.06\\ 5.06\\ 5.06\\ 5.06\\ 22.9\\ 11.8\\ 10.9\\ 9.24\\ 7.7\\ 8.47\\ 10.1\\ 7.58\\ 23.4\\ 9.24\\ 15.3\\ 15$	1 1 2 3 2 6 5 5 4 2 2 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 5 2 2 4 4 3 2 2 4 4 3 2 1 1 4 5 2 2 4 4 3 2 1 1 4 5 3 2 1 1 4 5 3 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 1 1 4 5 3 2 2 3 2 1 1 4 5 3 2 3 2 3 2 3 3 2 3 3 2 3 3 2 3 3 3 2 3 3 2 3 3 2 3 3 3 3 3 3 2 3 3 3 3 3 3 3 3
2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	msigdb_tf_motifs msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG msigdb_biocarta msigdb_reactome msigdb_reactome msigdb_reactome	oct c gse22886 igg iga memory bcell vs bm plasma ce gse6269 e coli vs staph aureus inf pbmc dn gse22886 neutrophil vs dc up gse29618 bcell vs pdc dn gse40273 eos ko vs wt treg up hormone secretion hormone transport regulation of hormone secretion peptide hormone secretion G protein-coupled receptor binding proton-exporting ATPase activity, phosphoryla syntaxin binding proton-exporting ATPase activity tubulin binding secretory granule exocytic vesicle perikaryon synaptic vesicle membrane exocytic vesicle membrane exocytic vesicle membrane Maturity onset diabetes of the young Synaptic vesicle agent GABAergic synapse Circadian entrainment Glutamatergic synapse bad pathway pgc1a pathway regulation of gene expression in beta cells regulation of beta cell development insulin receptor recycling ros and rns production in phagocytes regulation of insulin secretion	0.000776 1.02e-05 3.62e-05 4.9e-05 2.27e-12 3.33e-12 7.09e-11 7.46e-10 2.12e-09 4.19e-07 8.13e-07 5.54e-06 1.56e-05 4.39e-05 2.28e-05 2.28e-05 3.2e-09 1.55e-08 1.67e-06 4.73e-06 1.54e-05 0.0009 0.00718 0.0131 1.14e-07 4.73e-06 2.37e-05 2.59e-05 3.2e-05 3.2e-05 3.2e-05 3.2e-05 3.2e-05 3.2e-05 3.2e-05 3.37e-05 3.37e-05 3.37e-05 3.39e-05 3.37e-05 3.39e-05 3.37e-05 3.39e-05 3.39e-05 3.37e-05 3.59e-	0.00111 0.000927 0.00291 0.00296 0.00316 0.00376 1.2e-09 1.65e-09 2.56e-08 1.94e-07 2.89e-05 4.94e-07 2.89e-05 4.93e-05 0.000222 0.000482 0.000113 1.96e-08 0.000297 0.000351 0.000374 4.05e-07 1.44e-06 7.51e-05 0.000155 0.000427 0.00907 0.0316 0.0452 2.21e-06 6.1e-05 0.000231 0.000231 0.000248	$\begin{array}{c} 12\\ 17\\ 14\\ 9\\ 16\\ 17\\ 30\\ 25\\ 24\\ 21\\ 17\\ 6\\ 11\\ 7\\ 21\\ 26\\ 18\\ 11\\ 12\\ 26\\ 18\\ 11\\ 12\\ 12\\ 9\\ 9\\ 9\\ 5\\ 3\\ 8\\ 9\\ 6\\ 6\\ 9\\ 9\end{array}$	$\begin{array}{c} 3.91\\ 3.91\\ 4.11\\ 6.68\\ 3.63\\ 3.4\\ \hline 5.79\\ 5.69\\ 6\\ 5.49\\ 6\\ 5.15\\ 40.8\\ 6.67\\ 11.9\\ 2.95\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.19\\ 3.61\\ 5.67\\ 5.06\\ 5.06\\ 22.9\\ 11.8\\ 10.9\\ 9.24\\ 7.7\\ 8.47\\ 10.1\\ 7.58\\ 23.4\\ 9.24\\ 15.3\\ 15.3\\ 7.11\\ \end{array}$	$     \begin{array}{c}       1 \\       2 \\       3 \\       2 \\       3 \\       2 \\       5 \\       5 \\       5 \\       5 \\       4 \\       2 \\       2 \\       2 \\       2 \\       2 \\       2 \\       2 \\       2 \\       4 \\       3 \\       5 \\       2 \\       2 \\       4 \\       3 \\       4 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       3 \\       2 \\       3 \\       2 \\       1 \\       1 \\       4 \\       5 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       2 \\       3 \\       3 \\       3 \\       3 \\       3 \\       2 \\       3 \\     $

3	msigdb_canonical_pathways	regulation of gene expression in beta cells	1.14e-07	2.84e-06	8	23.4	4
3	msigdb_canonical_pathways	regulation of beta cell development	4.73e-06	7.5e-05	9	9.24	5
3	msigdb canonical pathways	insulin receptor recycling	2.37e-05	0.000288	6	15.3	3
3	msigdb canonical pathways	ros and rns production in phagocytes	2.37e-05	0.000288	6	15.3	2
3	msigdb tf motifs	rytgenwtggnr unknown	1 25e-06	0.000191	12	7.09	1
3	msigdh tf motifs	taxcreb 01	3 72e-05	0.00431	13	4 41	1
3	msigdb_tf_motifs	migri target genes	5 630 05	0.00618	18	3.23	1
2	maigdb_tf_motifa	mein ol	6.150.05	0.00658	16	2.5	1
3	msigdb_ti_motils		0.15e-05	0.00058	10	3.0	1
3	msigdb_ti_motifs	erc qo	8.54e-05	0.00872	16	3.39	1
3	msigdb_immunological_signatures	gse43863 naive vs memory th cd4 tcell d150 l	3.86e-06	0.000383	14	5.19	1
3	msigdb_immunological_signatures	gse2405 heat killed lysate vs live a phagocyt	2.62e-05	0.00219	14	4.26	3
3	msigdb_immunological_signatures	gse13522 wt vs ifnar ko sking t cruzi y strai	2.71e-05	0.00224	12	4.95	2
3	msigdb_immunological_signatures	gse21063 wt vs nfatc1 ko 16h anti igm stim bc	0.000148	0.00938	9	5.43	1
3	msigdb_immunological_signatures	gse29618 monocyte vs mdc day7 flu vaccine up	0.000163	0.0102	13	3.73	2
4	GO.BP	endocrine system development	2.46e-07	3.26e-05	15	6.39	6
4	GO.BP	pancreas development	1.21e-05	0.000751	11	6.2	7
4	GO.BP	endocrine pancreas development	1.53e-05	0.000881	9	7.98	5
4	GO.BP	negative regulation of neurogenesis	7.33e-05	0.00289	21	2.87	3
4	GO.BP	negative regulation of nervous system develop	7.41e-05	0.0029	22	2.79	4
4	GO.MF	voltage-gated cation channel activity	1.1e-05	0.00038	8	10.3	2
4	GO.MF	serine-type endopeptidase inhibitor activity	1.64e-05	0.000497	8	9.61	6
4	GO.MF	endopeptidase regulator activity	0.000301	0.00461	10	4.43	5
4	GO.MF	voltage-gated ion channel activity	0.00051	0.00676	8	5.17	3
4	GOME	voltage-gated channel activity	0.00051	0.00676	8	5.17	3
4	GO CC	presupartic cytoskeleton	0.000184	0.00201	3	Inf	1
-± 1	G0.00	cortical cytoskeleton	0.000164	0.00201	11	2.64	1
4	CO.CC	contrar cytoskeleton	0.000697	0.00073	11	0.04 4 20	1
4	GO.CC	anchored component of membrane	0.000694	0.00594	9	4.32	6
4	GO.CC	calyx of Held	0.00104	0.00801	4	13.3	1
4	GO.CC	intermediate filament	0.00148	0.0105	7	4.89	3
4	KEGG	Maturity onset diabetes of the young	3.24e-07	2.14e-05	9	15.2	4
4	KEGG	Transcriptional misregulation in cancer	4.39e-05	0.000953	14	4.09	2
4	KEGG	Epstein-Barr virus infection	5.52e-05	0.00108	17	3.41	3
4	KEGG	Hepatocellular carcinoma	0.000116	0.00196	15	3.49	3
4	KEGG	Chronic myeloid leukemia	0.000301	0.00428	10	4.43	2
4	msigdb_biocarta	p53 pathway	0.000204	0.0032	5	13.9	5
4	msigdb_biocarta	bad pathway	0.00205	0.0159	5	6.96	2
4	msigdb biocarta	p53hypoxia pathway	0.0066	0.031	4	6.67	2
4	msigdb biocarta	raccvcd pathway	0.00842	0.036	5	4.64	1
4	msigdb_reactome	regulation of gene expression in endocrine co	5.89e-07	9.71e-06	5	Inf	4
4	msigdb_reactome	regulation of beta cell development	1.69e-06	2 48e-05	10	9.38	5
4	msigdb_reactome	regulation of gene expression in hete calls	4.51e.06	5 850 05	7	16.8	4
4	msigdb_reactome	tegulation of gene expression in beta cens	4.510-00	0.000574	6	6.21	4
4	insight_reactome	tp55 regulates transcription of cell cycle ge	0.00-03	0.000374	9	0.51	3
4	msigdb_reactome	toxo mediated transcription of cell cycle gen	0.000117	0.000918	5	16.7	1
4	msigdb_canonical_pathways	regulation of gene expression in endocrine co	5.89e-07	1.21e-05	5	Inf	4
4	msigdb_canonical_pathways	kegg maturity onset diabetes of the young	8.97e-07	1.8e-05	8	16.8	5
4	msigdb_canonical_pathways	regulation of beta cell development	1.69e-06	3.03e-05	10	9.38	5
4	msigdb_canonical_pathways	pid p53 downstream pathway	3.11e-06	5.1e-05	15	5.01	3
4	msigdb_canonical_pathways	regulation of gene expression in beta cells	4.51e-06	7.19e-05	7	16.8	4
4	msigdb_tf_motifs	sox9 b1	6.75e-08	1.23e-05	24	4.24	2
4	msigdb_tf_motifs	smad3 q6	2.03e-07	3.33e-05	18	5.23	2
4	msigdb_tf_motifs	cattgtyy sox9 b1	2.86e-07	4.48e-05	28	3.42	2
4	msigdb_tf_motifs	ap4 q5	1.49e-05	0.00183	18	3.66	1
4	msigdb_tf_motifs	pitx2 q2	0.000146	0.0134	14	3.59	1
4	msigdb_immunological_signatures	gse16450 ctrl vs ifna 6h stim mature neuron c	5.68e-05	0.00423	12	4.61	1
4	msigdb_immunological_signatures	gse26928 centr memory vs cxcr5 pos cd4 tcell	7.13e-05	0.00509	13	4.15	1
4	msigdb_immunological_signatures	gse18791 ctrl vs newcastle virus dc 16h dn	7.39e-05	0.00526	10	5.44	1
4	msigdb_immunological_signatures	gse29618 pdc vs mdc up	9.11e-05	0.00631	16	3.4	4
4	msigdb_immunological_signatures	gse2706 unstim vs 2h lps and r848 dc dn	9.22e-05	0.00637	10	5.27	1
5	GO.BP	chromosome segregation	4.21e-35	6.68e-31	77	8.08	2
5	GO.BP	mitotic nuclear division	6.46e-26	5.13e-22	62	6.89	2
5	GO.BP	nuclear chromosome segregation	1.83e-24	9.71e-21	57	7.08	1
5	GO.BP	mitotic sister chromatid segregation	1.73e-23	6.86e-20	47	8.78	2
5	GO.BP	sister chromatid segregation	6.01e-23	1.916-10	50	7 69	- 2
5	GOME	catalytic activity acting on DNA	2 90-10	7 26c 08	30	4.43	2
5	COME	single stranded DNA dependent ATP dependent D	1.200.00	9.15c.07	11	2.40	2
ວ F	COME	single stranded DNA dependent ATF-dependent D.	1.298-09	2.100-07	11	20.2	2
0 F	CO ME	ATD dependent DNA believe set it	1.29e-09	2.100-07	11	20.2	4
э ~	GO.MF	ATP has been builded and the second s	3.1e-09	3.89e-07	11	21.6	2
5	GO.MF	Al P-dependent helicase activity	3.1e-09	3.89e-07	11	21.6	2
5	GO.CC	chromosome, centromeric region	9.82e-31	2.11e-28	59	9.76	2
5	GO.CC	condensed chromosome	5.05e-26	7.52e-24	45	11.5	1
5	GO.CC	kinetochore	1.51e-22	1.82e-20	43	9.43	2
5	GO.CC	condensed chromosome, centromeric region	1.84e-18	1.62e-16	24	21.1	1
5	GO.CC	spindle	6.81e-16	5.27e-14	51	4.63	1
5	KEGG	DNA replication	3.95e-24	1.37e-21	26	45.9	2
		a	7 17 1F	1 49 10	9.4	6 70	0

5	KEGG	Mismatch repair	1.24e-12	1.91e-10	14	32.3	2
5	KEGG	Ribosome	3.25e-11	4.52e-09	33	4.76	5
5	KEGG	Nucleotide excision repair	7.11e-09	7.61e-07	15	9.43	2
5	msigdb_biocarta	mcm pathway	4.87 e-07	3.43e-05	9	15.4	2
5	msigdb_biocarta	cellcycle pathway	6.77e-06	0.000305	8	12.2	4
5	msigdb_biocarta	sm pathway	3.58e-05	0.00101	6	16.4	2
5	msigdb_biocarta	ranms pathway	7.2e-05	0.00169	5	22.7	1
5	msigdb_biocarta	efp pathway	0.000118	0.00238	6	11.7	2
5	msigdb_reactome	cell cycle mitotic	2.09e-49	4.95e-46	122	7.24	2
5	msigdb_reactome	cell cycle checkpoints	2.26e-28	5.35e-26	68	6.96	3
5	msigdb_reactome	mitotic prometaphase	2.56e-27	5.51e-25	58	8.19	2
5	msigdb_reactome	resolution of sister chromatid cohesion	4.28e-27	7.82e-25	46	12	2
5	msigdb_reactome	chromosome maintenance	1.61e-26	2.54e-24	35	21.8	2
5	msigdb canonical pathways	cell cycle mitotic	2.09e-49	7.19e-46	122	7.24	2
5	msigdb canonical pathways	cell cycle checkpoints	2.26e-28	6.47e-26	68	6.96	3
5	msigdb canonical pathways	mitotic prometaphase	2.56e-27	6.77e-25	58	8.19	2
5	msigdb canonical pathways	resolution of sister chromatid cohesion	4.28e-27	9.83e-25	46	12	2
5	msigdb canonical pathways	chromosome maintenance	1.61e-26	3.25e-24	35	21.8	2
5	msigdb tf motifs	e2f1dp1rb 01	2 76e-16	1.86e-12	42	5.86	2
5	msigdb_tf_motifs	e2f a3	8 12e-16	2 73e-12	40	5.98	2
5	msigdb_tf_motifs	e2f q6 01	9.09e-15	2.10c-12	40	5.46	2
5	msigdb_tf_motifs	e2f q6	5.13o.14	7 31o 11	40	5.11	2
5	msigdb_tf_motifs	$e^{2f} q^{3} 01$	6 32o 14	7.316.11	30	5.21	2
5	maigdb_ti_mmunclogical_signatures	ezi (5 01	0.32e-14	1.31e-11	09	0.21 07.2	2
5	maigdb_immunological_signatures	gse12547 etrl ve anti igm etim beell 12b up	3.99e-70	1.710-71	90	21.5	2
5 F	msigdb_immunological_signatures	gse15547 ctrl vs anti igin stim been 12n up	1.30e-73	1.58e-70	94	29.0	2
Э F	msigdb_immunological_signatures	gse15750 dayb vs day10 en cd8 tcell up	1.79e-69	2.57e-65	93	24	2
5	msigdb_immunological_signatures	goldrath en vs memory cd8 tcell up	4e-62	4.3e-58	82	24.7	2
5	msigdb_immunological_signatures	gse14415 natural treg vs tconv dn	3.01e-60	2.59e-56	79	25.1	2
6	GO.BP	DNA replication	2.48e-12	1.27e-09	38	4.57	2
6	GO.BP	protein-DNA complex assembly	1.45e-08	2.81e-06	23	4.88	2
6	GO.BP	ribosome biogenesis	1.63e-08	2.9e-06	37	3.24	4
6	GO.BP	DNA-dependent DNA replication	3.96e-08	6.55e-06	22	4.78	2
6	GO.BP	protein-DNA complex subunit organization	8.95e-08	1.37e-05	25	4.02	2
6	GO.MF	structural constituent of ribosome	5.25e-28	3.51e-25	52	9.87	5
6	GO.MF	rRNA binding	2.03e-11	6.77e-09	21	8.47	5
6	GO.MF	single-stranded DNA-dependent ATP-dependent D	6.53e-08	6.54e-06	9	20.8	2
6	GO.MF	single-stranded DNA-dependent ATPase activity	6.53e-08	6.54e-06	9	20.8	2
6	GO.MF	ATP-dependent DNA helicase activity	1.31e-07	1.07e-05	9	18.2	2
6	GO.CC	cytosolic ribosome	4e-37	1.29e-34	50	20.1	5
6	GO.CC	ribosomal subunit	1.02e-28	1.79e-26	57	8.91	5
6	GO.CC	cytosolic part	2.87e-26	4.64e-24	55	8.12	5
6	GO.CC	cytosolic large ribosomal subunit	4.37e-21	4.98e-19	28	18.9	5
6	GO.CC	cytosolic small ribosomal subunit	1.19e-18	1.1e-16	23	22.5	5
6	KEGG	Ribosome	8.12e-34	3.76e-31	55	12.9	5
6	KEGG	DNA replication	2.63e-14	4.58e-12	18	19.8	2
6	KEGG	Drug metabolism - other enzymes	4.87e-07	2.94e-05	13	7.29	3
6	KEGG	Glutathione metabolism	1.96e-06	8.27e-05	12	6.96	4
6	KEGG	Cell cycle	3.6e-06	0.000129	19	3.94	2
6	msigdb biocarta	mcm pathway	1.31e-07	1.85e-05	9	18.2	2
6	msigdb biocarta	sm pathway	0.000244	0.00344	5	13.4	2
6	msigdb biocarta	htg2 nathway	0.000368	0.00472	4	21.3	2
6	msigdb_biocarta	efp pathway	0.000616	0.00724	5	10	2
6	msigdb_biocarta	cellcycle pathway	0.0018	0.0149	5	7 29	4
6	msigdb_reactome	eukarvotic translation elongation	9 79e-25	1 296-22	32	20.9	5
6	msigdb_reactome	response of eif2ak4 gcn2 to amine acid defici	7 120-20	6.030-18	29	14.8	5
6	msigdb_reactome	selenoamino acid metabolism	2 796 17	1 840 15	20	10.8	5
6	msigdb_reactome	sen dependent cotranslational protein targeti	6 58c 17	1 220 15	23	10.0	6
6	msigdb_reactome	aukaryotic translation initiation	7.51c 17	4.600.15	29 30	0.79	5
6	maigub_reactome	euraryout translation initiation	0.70- 05	4.096-10	30	9.14	ວ F
U C	msigub_canonical_pathways	eukaryoud translation elongation	9.79e-25	1.09e-22	32	∠U.9 10.0	о г
0 6	msigdb_canonical_pathways	kegg ribosome	9.11e-22 7 10- 00	1.13e-19 7 40- 10	29	18.8	Э F
D C	msigdb_canonical_pathways	response of elizak4 gcn2 to amino acid defici	(.12e-20	7.42e-18	29	14.8	э -
0 C	msigdb_canonical_pathways	selenoamino acid metadolism	2.79e-17	2.34e-15	29	10.8	э С
0 C	msigdb_canonical_pathways	srp dependent cotranslational protein targeti.	0.58e-17	0.4e-15	29 20	10.4	0 C
6	msigdb_tt_motifs		5.17e-10	1.94e-07	30	4.52	2
6	msigdb_tt_motifs	sgcgssaaa e211dp2 01	1.82e-09	6.13e-07	24	5.3	2
6	msigdb_tf_motifs	e2t q3 01	3.06e-09	9.8e-07	28	4.4	2
6	msigdb_tf_motifs	psmb5 target genes	3.65e-09	1.12e-06	28	4.36	7
6	msigdb_tf_motifs	e2f q6	5.46e-09	1.6e-06	29	4.13	2
6	$msigdb\_immunological\_signatures$	gse2405 0h vs 9h a phagocytophilum stim neutr	2.32e-26	2.56e-23	50	9.45	5
6	$msigdb\_immunological\_signatures$	gse 13547 ctrl vs anti igm stim b cell 12h up $% f(x)=0$	6.05e-23	4.56e-20	44	9.08	2
6	$msigdb\_immunological\_signatures$	goldrath eff vs memory cd8 tcell up	1.86e-22	1.38e-19	43	9.07	2
6	$msigdb\_immunological\_signatures$	gse $24634$ teff vs tconv day7 in culture up	7.64e-21	5.05e-18	40	8.93	2
6	msigdb_immunological_signatures	gse15750 day6 vs day10 eff cd8 tcell up	1.44e-20	9e-18	41	8.4	2
7	GO.BP	cytoplasmic translation	3.33e-11	1.29e-08	19	9.03	4
7	GO.BP	ribosome assembly	1.55e-08	2.83e-06	14	8.8	4

	7	GO.BP	ribosomal small subunit biogenesis	8.08e-08	1.26e-05	13	8.36	4
	7	GO.BP	extracellular structure organization	7.32e-07	7.49e-05	18	4.6	5
	7	COBP	extracellular matrix organization	8 860 07	8 730 05	16	51	5
	7	GO.ME	extracential matrix organization	5.000-07	5.01.04	10	15 7	5
	(	GO.MF	structural constituent of ribosome	5.2e-37	5.21e-34	53	15.7	Э
	7	GO.MF	rRNA binding	3.04e-12	1.22e-09	19	10.7	5
	7	GO.MF	peptidase inhibitor activity	1.34e-07	1.07e-05	13	7.93	6
	7	GO.MF	serine-type endopeptidase inhibitor activity	3.91e-07	2.79e-05	9	13.2	6
	7	GO ME	endopentidase inhibitor activity	5 25e-07	3 39e-05	12	7 69	5
	-	GO.MI <sup>P</sup>	endopeptidase initiator activity	3.256-07	3.336-05	12	1.03	5
	7	GO.CC	cytosolic ribosome	1.9e-51	1.84e-48	54	38.2	5
	7	GO.CC	cytosolic part	2.01e-37	7.77e-35	57	13.9	5
	7	GO.CC	ribosomal subunit	2.77e-36	7.67e-34	56	13.5	5
	7	GO.CC	cytosolic large ribosomal subunit	3.5e-30	6.77e-28	31	37.4	5
	. 7	0.00	enterelie energl eiterenergl entereit	1 14- 92	1 57- 21	24	27.1	F
	1	60.00	cytosofic small ribosofial subunit	1.14e-25	1.57e-21	24	57.1	5
	7	KEGG	Ribosome	1.24e-47	8.62e-45	59	23	5
	7	KEGG	PI3K-Akt signaling pathway	0.000103	0.00177	16	3.31	2
	7	KEGG	Glutathione metabolism	0.000202	0.00303	8	5.86	4
	7	KEGG	Glioma	0.000242	0.00357	8	5.68	3
	7	KEGG		0.000242	0.00507	0	5.00	0
	(	KEGG	Small cell lung cancer	0.000473	0.00587	8	5.06	3
	7	msigdb_biocarta	p53 pathway	0.00113	0.0107	4	11.6	5
	7	msigdb_biocarta	cellcycle pathway	0.00214	0.0159	4	9.27	4
	7	msigdb biocarta	prion pathway	0.00503	0.0284	3	11.6	3
	7	maigdh biogarta	tal pathway	0.00606	0.0216	2	0.01	1
	-	hisigub_biocarta	tei patiiway	0.00090	0.0310	3	9.91	1
	7	msigdb_biocarta	chemical pathway	0.012	0.0423	3	7.71	1
	7	msigdb_reactome	eukaryotic translation elongation	2.99e-34	1.77e-31	35	39.1	5
	7	msigdb_reactome	response of eif2ak4 gcn2 to amino acid defici	3.84e-30	1.82e-27	33	30.1	5
	7	msigdb_reactome	nonsense mediated decay nmd	3.52e-27	6.95e-25	34	20.2	5
	7	msigdh_reactome	solonoamino acid metabolism	1 410 96	2 30- 24	99 99	20.5	E C
	1	insigdb_reactome	seienoamino acid metabolism	1.410-20	2.396-24	33	20.5	0
	7	msigdb_reactome	srp dependent cotranslational protein targeti	4.12e-26	6.12e-24	33	19.6	6
	7	msigdb_canonical_pathways	eukaryotic translation elongation	2.99e-34	2.06e-31	35	39.1	5
	7	msigdb canonical pathways	kegg ribosome	3.26e-32	1.87e-29	33	38.3	5
	7	meigdh canonical pathwave	response of aif2ak4 gen2 to amino acid defici	3 840 30	1 890 27	33	30.1	5
	-	insigub_canonicai_pathways	response of enzaka genz to annito acid denci	0.59-05	1.036-27	00	30.1	5
	7	msigdb_canonical_pathways	nonsense mediated decay nmd	3.52e-27	8.64e-25	34	20.2	5
	7	msigdb_canonical_pathways	selenoamino acid metabolism	1.41e-26	3.03e-24	33	20.5	5
	7	msigdb_tf_motifs	gtf2a2 target genes	3.83e-06	0.000561	27	2.99	5
	7	msigdb tf motifs	psmb5 target genes	5.33e-06	0.000747	18	3.92	7
	7	meigdh tf motife	ac118540 1 target genes	0.000330	0.0246	16	2.04	2
	-		ac110049 1 target genes	0.000333	0.0240	10	2.34	2
	7	msigdb_tf_motifs	gre c	0.000641	0.0393	8	4.8	1
	7	msigdb_immunological_signatures	gse2405 0h vs 24h a phagocytophilum stim neut	4.82e-18	2.25e-15	34	8.55	5
	7	msigdb_immunological_signatures	gse2405 0h vs 9h a phagocytophilum stim neutr	2.09e-17	9.45e-15	34	8.06	5
	7	msigdb immunological signatures	gse42088 uninf vs leishmania inf dc 2h dn	2.29e-10	4.65e-08	22	6.47	5
	7 7	msigdb_immunological_signatures	gse42088 uninf vs leishmania inf dc 2h dn	2.29e-10	4.65e-08	22 21	6.47	5
	7 7	msigdb_immunological_signatures msigdb_immunological_signatures	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up	2.29e-10 2.54e-10	4.65e-08 5.15e-08	22 21	6.47 6.81	5 4
_	7 7 7	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell	2.29e-10 2.54e-10 3.93e-09	4.65e-08 5.15e-08 6.81e-07	22 21 22	6.47 6.81 5.41	5 4 5
_	7 7 7 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest	2.29e-10 2.54e-10 3.93e-09 2.54e-06	4.65e-08 5.15e-08 6.81e-07 0.000218	22 21 22 5	6.47 6.81 5.41 88.8	5 4 5 3
_	7 7 7 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645	22 21 22 5 14	6.47 6.81 5.41 88.8 4.77	5 4 5 3 4
_	7 7 7 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000866	22 21 22 5 14 11	6.47 6.81 5.41 88.8 4.77 5.99	5 4 5 3 4 2
_	7 7 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e.05	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000866 0.00205	22 21 22 5 14 11	6.47 6.81 5.41 88.8 4.77 5.99 2.81	5 4 5 3 4 2 5
_	7 7 7 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000866 0.00205	22 21 22 5 14 11 15	6.47 6.81 5.41 88.8 4.77 5.99 3.81	5 4 5 3 4 2 5
_	7 7 7 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis	$\begin{array}{c} 2.29e{-}10\\ 2.54e{-}10\\ 3.93e{-}09\\ 2.54e{-}06\\ 9.83e{-}06\\ 1.48e{-}05\\ 4.64e{-}05\\ 4.93e{-}05\\ \end{array}$	$\begin{array}{c} 4.65 \text{e-}08 \\ 5.15 \text{e-}08 \\ 6.81 \text{e-}07 \\ \hline 0.000218 \\ 0.000645 \\ 0.000866 \\ 0.00205 \\ 0.00215 \end{array}$	22 21 22 5 14 11 15 20	6.47 6.81 5.41 88.8 4.77 5.99 3.81 3.05	5 4 5 3 4 2 5 4
_	7 7 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14	$\begin{array}{c} 4.65e{-}08\\ 5.15e{-}08\\ 6.81e{-}07\\ \hline 0.000218\\ 0.000645\\ 0.000866\\ 0.00205\\ 0.00215\\ 4.76e{-}11\\ \end{array}$	22 21 22 5 14 11 15 20 34	6.47 6.81 5.41 88.8 4.77 5.99 3.81 3.05 5.84	5 4 5 3 4 2 5 4 5 5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding	$\begin{array}{c} 2.29e{-}10\\ 2.54e{-}10\\ 3.93e{-}09\\ 2.54e{-}06\\ 9.83e{-}06\\ 1.48e{-}05\\ 4.64e{-}05\\ 4.93e{-}05\\ 9.5e{-}14\\ 2.07e{-}09\\ \end{array}$	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000205 0.00205 0.00215 4.76e-11 3.19e-07	22 21 22 5 14 11 15 20 34 18	$6.47 \\ 6.81 \\ 5.41 \\ 88.8 \\ 4.77 \\ 5.99 \\ 3.81 \\ 3.05 \\ 5.84 \\ 7.47 \\ $	5 4 5 3 4 2 5 4 5 5 5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopentidase inhibitor activity	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05	22 21 22 5 14 11 15 20 34 18 10	6.47 6.81 5.41 88.8 4.77 5.99 3.81 3.05 5.84 7.47 12.8	5 4 5 3 4 2 5 4 5 5 6
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_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000866 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05	22 21 22 5 14 11 15 20 34 18 10 6	$\begin{array}{c} 6.47 \\ 6.81 \\ \hline 5.41 \\ \hline 88.8 \\ 4.77 \\ 5.99 \\ 3.81 \\ 3.05 \\ 5.84 \\ 7.47 \\ 12.8 \\ 35.6 \\ c \end{array}$	5 4 5 3 4 2 5 4 5 5 6 4 4 5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ \end{array}$	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237	22 21 22 5 14 11 15 20 34 18 10 6 12	$\begin{array}{c} 6.47 \\ 6.81 \\ \hline 5.41 \\ \hline 88.8 \\ 4.77 \\ 5.99 \\ 3.81 \\ 3.05 \\ 5.84 \\ 7.47 \\ 12.8 \\ 35.6 \\ 6 \\ \end{array}$	5 4 5 3 4 2 5 4 5 5 6 4 6
-	7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18	$\begin{array}{c} 22\\ 21\\ 22\\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline \\ 5.41\\ \hline \\ 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ \end{array}$	5 4 5 4 2 5 4 5 5 6 4 6 5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.000265 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12	$\begin{array}{c} 22\\ 21\\ 22\\ \hline \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline \\ 5.41\\ \hline \\ 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ \end{array}$	5 $4$ $5$ $3$ $4$ $2$ $5$ $4$ $5$ $5$ $6$ $4$ $6$ $5$ $5$ $5$
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic large ribosomal subunit	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11	$\begin{array}{c} 4.65\text{e-}08\\ 5.15\text{e-}08\\ 6.81\text{e-}07\\ 0.000218\\ 0.000645\\ 0.000205\\ 0.00205\\ 0.00205\\ 4.76\text{e-}11\\ 3.19\text{e-}07\\ 1.41\text{e-}05\\ 8.23\text{e-}05\\ 0.000237\\ 4.32\text{e-}18\\ 2.53\text{e-}12\\ 6.84\text{e-}10\\ \end{array}$	22 21 22 5 14 11 15 20 34 18 10 6 12 34 38 19	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ \end{array}$	5 $4$ $5$ $3$ $4$ $2$ $5$ $4$ $5$ $5$ $6$ $4$ $6$ $5$ $5$ $5$ $5$
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_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12 6.84e-10 9.7e-10 2.65 - 52	$\begin{array}{c} 22\\ 21\\ 22\\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 22\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline \\ 5.41\\ \hline \\ 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ \hline \end{array}$	5 4 5 2 5 4 5 5 6 4 6 5 5 5 5 5 5
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	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic part cytosolic large ribosomal subunit ribosomal subunit Ribosome Hepatocellular carcinoma	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292	$\begin{array}{r} 4.65 \text{e-}08\\ 5.15 \text{e-}08\\ 6.81 \text{e-}07\\ 0.000218\\ 0.000866\\ 0.00205\\ 0.00215\\ 4.76 \text{e-}11\\ 3.19 \text{e-}07\\ 1.41 \text{e-}05\\ 8.23 \text{e-}05\\ 0.000237\\ 4.32 \text{e-}18\\ 2.53 \text{e-}12\\ 6.84 \text{e-}10\\ 9.7 \text{e-}10\\ 3.85 \text{e-}09\\ 5.49 \text{e-}17\\ 0.00419\\ \end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 16\\ 39\\ 14\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ \end{array}$	5 4 5 3 4 2 5 4 5 5 4 6 5 5 5 5 5 5 5 3
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic ribosome cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292 0.000348	$\begin{array}{r} 4.65\text{e-}08\\ 5.15\text{e-}08\\ 6.81\text{e-}07\\ 0.000218\\ 0.000645\\ 0.000265\\ 0.00215\\ 4.76\text{e-}11\\ 3.19\text{e-}07\\ 1.41\text{e-}05\\ 8.23\text{e-}05\\ 0.000237\\ 4.32\text{e-}18\\ 2.53\text{e-}12\\ 6.84\text{e-}10\\ 9.7\text{e-}10\\ 3.85\text{e-}09\\ 5.49\text{e-}17\\ 0.00419\\ 0.00472\\ \end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ \hline \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline \\ 5.41\\ \hline \\ 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ 5.49\\ \end{array}$	5 4 5 3 4 2 5 4 5 5 6 4 6 5 5 5 5 5 5 5 3 3
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_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit Ribosome Hepatocellular carcinoma Melanoma MicoRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway gl pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ 4.25e-20\\ 3.75e-14\\ 1.13e-11\\ 1.75e-11\\ 7.16e-11\\ 1.97e-19\\ 0.000292\\ 0.000348\\ 0.000348\\ 0.000349\\ 0.000344\\ 8.65e-06\\ 0.0054\\ 0.00901\\ 4.29e-16\\ 2.21e-13\\ \end{array}$	$\begin{array}{r} 4.65 \text{e-}08\\ 5.15 \text{e-}08\\ 6.81 \text{e-}07\\ 0.000218\\ 0.000645\\ 0.00205\\ 0.00215\\ 4.76 \text{e-}11\\ 3.19 \text{e-}07\\ 1.41 \text{e-}05\\ 8.23 \text{e-}05\\ 0.000237\\ 4.32 \text{e-}18\\ 2.53 \text{e-}12\\ 6.84 \text{e-}10\\ 9.7 \text{e-}10\\ 3.85 \text{e-}09\\ 5.49 \text{e-}17\\ 0.00419\\ 0.00472\\ 0.00472\\ 0.00504\\ 0.00305\\ 0.0284\\ 0.0362\\ 2.42 \text{e-}14\\ 9.91 \text{e-}12\end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 10\\ 6\\ 12\\ 34\\ 10\\ 6\\ 12\\ 34\\ 10\\ 6\\ 12\\ 34\\ 13\\ 9\\ 6\\ 4\\ 4\\ 24\\ 22\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \overline{5.41}\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ $	5     4     5     3     4     2     5     4     5     5     5     5     5     5     5     3     3     5     4     5     4     5     4     5     4     5
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	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway g1 pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation initiation	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292 0.000348 0.000349 0.000349 0.000344 8.65e-06 0.0054 0.00901 4.29e-16 2.21e-13 2.31e-12 3.28e-12	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12 6.84e-10 9.7e-10 3.85e-09 5.49e-17 0.00419 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00472 0.00504 0.00305 0.0284 0.0362 2.42e-14 9.91e-12 8.43e-11 1.14e-10	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 24\\ 22\\ 23\\ 24\\ \end{array}$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ 5.9\\ 13.1\\ 10.4\\ 8.34\\ 7.67\end{array}$	5     4     5     3     4     2     5     4     5     5     5     5     5     5     5     3     3     5     4     5     4     3     5
	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG msigdb_biocarta msigdb_biocarta msigdb_reactome msigdb_reactome msigdb_reactome	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic large ribosomal subunit ribosomal subunit cytosolic large ribosomal subunit Ribosome Hepatocellular carcinoma Melanoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway gl pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation initiation	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ 4.25e-20\\ 3.75e-14\\ 1.13e-11\\ 1.75e-11\\ 7.16e-11\\ 1.97e-19\\ 0.000292\\ 0.000348\\ 8.65e-06\\ 0.0054\\ 0.00901\\ 4.29e-16\\ 2.21e-13\\ 2.31e-12\\ 3.28e-12\\ 3.42e-11\\ \end{array}$	$\begin{array}{r} 4.65 e-08\\ 5.15 e-08\\ 6.81 e-07\\ \hline 0.000218\\ 0.000645\\ 0.000265\\ 0.00215\\ 4.76 e-11\\ 3.19 e-07\\ 1.41 e-05\\ 8.23 e-05\\ 0.000237\\ 4.32 e-18\\ 2.53 e-12\\ 6.84 e-10\\ 9.7 e-10\\ 3.85 e-09\\ 5.49 e-17\\ 0.00419\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00504\\ 0.000305\\ 0.0284\\ 0.00305\\ 0.0284\\ 0.0362\\ 2.42 e-14\\ 9.91 e-12\\ 8.43 e-11\\ 1.14 e-10\\ 11 e-00\\ \end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 10\\ 6\\ 12\\ 24\\ 22\\ 23\\ 24\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22$	6.47 6.81 5.41 88.8 4.77 5.99 3.81 3.05 5.84 7.47 12.8 35.6 6 10.8 5.36 10.2 4.67 12.1 8.14 3.32 5.49 3.44 4.73 21.3 7.08 5.9 13.11 10.4 8.34 7.51	5     4     5     3     4     2     5     4     5     5     5     5     5     5     5     3     3     5     4     3     5
	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic ribosome cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway g1 pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation al protein targeti	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-13 7.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292 0.000348 0.000349 0.000344 8.65e-06 0.0054 0.00901 4.29e-16 2.21e-13 2.31e-12 3.28e-12 3.28e-12	$\begin{array}{r} 4.65 e-08\\ 5.15 e-08\\ 6.81 e-07\\ 0.000218\\ 0.000645\\ 0.00205\\ 0.00215\\ 4.76 e-11\\ 3.19 e-07\\ 1.41 e-05\\ 8.23 e-05\\ 0.000237\\ 4.32 e-18\\ 2.53 e-12\\ 6.84 e-10\\ 9.7 e-10\\ 3.85 e-09\\ 5.49 e-17\\ 0.00419\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00504\\ 0.00305\\ 0.0284\\ 0.00305\\ 0.0284\\ 0.00305\\ 0.0284\\ 0.00305\\ 0.0284\\ 0.00305\\ 0.0284\\ 0.0362\\ 2.42 e-14\\ 9.91 e-12\\ 8.43 e-11\\ 1.14 e-10\\ 1.1 e-09\\ 2.5 t t t t t t t t t t t t t t t t t t t$	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24$	$\begin{array}{c} 6.47\\ 6.81\\ \hline \\5.41\\ \hline \\88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ 5.9\\ 13.1\\ 10.4\\ 8.34\\ 7.67\\ 7.51\\ 10.1\\ \hline \end{array}$	5     4     5     3     4     2     5     4     5     5     5     5     5     5     5     3     3     5     4     5     4     5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway gl pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation aprotein targeti eukaryotic translation elongation	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ 4.25e-20\\ 3.75e-14\\ 1.13e-11\\ 1.75e-11\\ 7.16e-11\\ 1.97e-19\\ 0.000292\\ 0.000348\\ 0.000348\\ 0.000348\\ 8.65e-06\\ 0.0054\\ 0.00901\\ 4.29e-16\\ 2.21e-13\\ 2.31e-12\\ 3.28e-12\\ 3.42e-11\\ 4.29e-16\\ \end{array}$	$\begin{array}{r} 4.65 e-08\\ 5.15 e-08\\ 6.81 e-07\\ \hline 0.000218\\ 0.000645\\ 0.00205\\ 0.00215\\ 4.76 e-11\\ 3.19 e-07\\ 1.41 e-05\\ 8.23 e-05\\ 0.000237\\ 4.32 e-18\\ 2.53 e-12\\ 6.84 e-10\\ 9.7 e-10\\ 3.85 e-09\\ 5.49 e-17\\ 0.00419\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00472\\ 0.00419\\ 0.00472\\ 0.00419\\ 0.00472\\ 0.00419\\ 0.00472\\ 0.00419\\ 0.00472\\ 0.00504\\ 0.00305\\ 0.0284\\ 0.0362\\ 2.42 e-14\\ 9.91 e-12\\ 8.43 e-11\\ 1.14 e-10\\ 1.1 e-09\\ 3.14 e-14\\ \end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 22\\ 23\\ 24\\ 22\\ 24\\ 22\\ 24\\ 24\\ 22\\ 24\\ 24\\ 22\\ 24\\ 24$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ 5.9\\ 13.1\\ 10.4\\ 8.34\\ 7.67\\ 7.51\\ 13.1\\ \end{array}$	5     4     5     3     4     2     5     4     5     5     5     5     5     5     5     3     3     5     4     3     5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway g1 pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation aprotein targeti eukaryotic translation elongation kegg ribosome	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ 4.25e-20\\ 3.75e-14\\ 1.73e-11\\ 1.75e-11\\ 7.16e-11\\ 1.97e-19\\ 0.000292\\ 0.000348\\ 0.000349\\ 0.000384\\ 8.65e-06\\ 0.0054\\ 0.00901\\ 4.29e-16\\ 2.21e-13\\ 2.31e-12\\ 3.28e-12\\ 3.42e-11\\ 4.29e-16\\ 1.76e-14\\ \end{array}$	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12 6.84e-10 9.7e-10 3.85e-09 5.49e-17 0.00419 0.00472 0.00472 0.00504 0.00305 0.0284 0.00305 0.0284 0.00305 0.0284 0.0362 2.42e-14 9.91e-12 8.43e-11 1.14e-10 1.1e-09 3.14e-14 1.16e-12	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 22\\ 23\\ 24\\ 22\\ 24\\ 24$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ 5.99\\ 3.81\\ 3.05\\ 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ 5.9\\ 13.1\\ 10.4\\ 8.34\\ 7.67\\ 7.51\\ 13.1\\ 12.3\\ \end{array}$	5     4     5     3     4     2     5     4     5
_	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic ribosome cytosolic large ribosomal subunit ribosomal subunit cytosolic large ribosomal subunit Ribosome Hepatocellular carcinoma Melanoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway g1 pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation alongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici	$\begin{array}{c} 2.29e-10\\ 2.54e-10\\ 3.93e-09\\ 2.54e-06\\ 9.83e-06\\ 1.48e-05\\ 4.64e-05\\ 4.64e-05\\ 4.93e-05\\ 9.5e-14\\ 2.07e-09\\ 1.83e-07\\ 1.73e-06\\ 6.03e-06\\ 4.25e-20\\ 3.75e-14\\ 1.13e-11\\ 1.75e-11\\ 7.16e-11\\ 1.97e-19\\ 0.000292\\ 0.000348\\ 0.000349\\ 0.000344\\ 8.65e-06\\ 0.0054\\ 0.00901\\ 4.29e-16\\ 2.21e-13\\ 2.31e-12\\ 3.28e-12\\ 3.42e-11\\ 4.29e-16\\ 1.76e-14\\ 2.21e-13\\ \end{array}$	$\begin{array}{r} 4.65e-08\\ 5.15e-08\\ 6.81e-07\\ \hline 0.000218\\ 0.000645\\ 0.00205\\ 0.00205\\ 0.00215\\ 4.76e-11\\ 3.19e-07\\ 1.41e-05\\ 8.23e-05\\ 0.000237\\ 4.32e-18\\ 2.53e-12\\ 6.84e-10\\ 9.7e-10\\ 3.85e-09\\ 5.49e-17\\ 0.00419\\ 0.00472\\ 0.00504\\ 0.00305\\ 0.0284\\ 0.0362\\ 2.42e-14\\ 9.91e-12\\ 8.43e-11\\ 1.14e-10\\ 1.1e-09\\ 3.14e-14\\ 1.6e-12\\ 1.23e-11\\ \end{array}$	$\begin{array}{c} 22\\ 21\\ 22\\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 10\\ 6\\ 4\\ 12\\ 23\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 22\\ 23\\ 24\\ 22\\ 24\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22\\ 22$	6.47 6.81 5.41 88.8 4.77 5.99 3.81 3.05 5.84 7.47 12.8 35.6 6 10.8 5.36 10.2 4.67 12.1 8.14 3.32 5.49 3.44 4.73 21.3 7.08 5.9 13.1 10.4 8.34 7.67 7.51 13.1 12.3 10.4	5     4     5     3     4     2     5     4     5
	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic ribosome cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma Melanoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway g1 pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation aprotein targeti eukaryotic translation elongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292 0.000348 0.000349 0.000348 0.000349 0.000348 8.65e-06 0.0054 0.00054 0.00054 0.00054 0.00054 0.00054 0.00054 0.00054 0.00054 0.00054 0.00054 0.221e-13 2.31e-12 3.231e-12	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12 6.84e-10 9.7e-10 3.85e-09 5.49e-17 0.00419 0.00472 0.00504 0.00305 0.0284 0.00305 0.0284 0.0362 2.42e-14 9.91e-12 8.43e-11 1.14e-10 1.1e-09 3.14e-14 1.16e-12 1.23e-11 1.07e-10	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 24\\ 22\\ 23\\ 23\\ 23\\ 22\\ 23\\ 23\\ 22\\ 23\\ 23$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ \hline 5.99\\ 3.81\\ 3.05\\ \hline 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ \hline 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ \hline 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ \hline 5.9\\ 13.1\\ 10.4\\ 8.34\\ \hline 7.67\\ 7.51\\ 13.1\\ 12.3\\ 10.4\\ 8.34\\ \end{array}$	5     4     5     3     4     2     5     4     5
	7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO	gse42088 uninf vs leishmania inf dc 2h dn gse22886 naive tcell vs dc up gse41978 klrg1 high vs low effector cd8 tcell mitotic cell cycle arrest cytoplasmic translation B cell differentiation extracellular matrix organization gliogenesis structural constituent of ribosome rRNA binding serine-type endopeptidase inhibitor activity large ribosomal subunit rRNA binding peptidase inhibitor activity cytosolic ribosome cytosolic part cytosolic large ribosomal subunit ribosomal subunit cytosolic small ribosomal subunit Ribosome Hepatocellular carcinoma MicroRNAs in cancer p53 signaling pathway p53 pathway cellcycle pathway gl pathway eukaryotic translation elongation response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation elongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation elongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation elongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation elongation kegg ribosome response of eif2ak4 gcn2 to amino acid defici selenoamino acid metabolism eukaryotic translation elongation	2.29e-10 2.54e-10 3.93e-09 2.54e-06 9.83e-06 1.48e-05 4.64e-05 4.64e-05 4.93e-05 9.5e-14 2.07e-09 1.83e-07 1.73e-06 6.03e-06 4.25e-20 3.75e-14 1.13e-11 1.75e-11 7.16e-11 1.97e-19 0.000292 0.000348 0.000349 0.000349 0.000344 8.65e-06 0.0054 0.00901 4.29e-16 2.21e-13 2.31e-12 3.28e-12 1.76e-14 2.21e-13 2.31e-12 3.28e-12	4.65e-08 5.15e-08 6.81e-07 0.000218 0.000645 0.00205 0.00215 4.76e-11 3.19e-07 1.41e-05 8.23e-05 0.000237 4.32e-18 2.53e-12 6.84e-10 9.7e-10 3.85e-09 5.49e-17 0.00419 0.00472 0.00472 0.00472 0.00472 0.00504 0.00305 0.0284 0.00305 0.0284 0.00305 0.0284 0.0362 2.42e-14 9.91e-12 8.43e-11 1.14e-10 1.1e-09 3.14e-14 1.16e-12 1.23e-11 1.07e-10 1.4e-10 1.	$\begin{array}{c} 22\\ 21\\ 22\\ \\ \\ 5\\ 14\\ 11\\ 15\\ 20\\ 34\\ 18\\ 10\\ 6\\ 12\\ 34\\ 38\\ 19\\ 34\\ 16\\ 39\\ 34\\ 16\\ 39\\ 14\\ 8\\ 13\\ 9\\ 6\\ 4\\ 4\\ 22\\ 23\\ 24\\ 22\\ 24\\ 22\\ 24\\ 22\\ 24\\ 22\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 24\\ 24\\ 22\\ 23\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24\\ 24$	$\begin{array}{c} 6.47\\ 6.81\\ \hline 5.41\\ \hline 88.8\\ 4.77\\ \hline 5.99\\ 3.81\\ 3.05\\ \hline 5.84\\ 7.47\\ 12.8\\ 35.6\\ 6\\ 10.8\\ \hline 5.36\\ 10.2\\ 4.67\\ 12.1\\ 8.14\\ 3.32\\ \hline 5.49\\ 3.44\\ 4.73\\ 21.3\\ 7.08\\ \hline 5.9\\ 13.1\\ 10.4\\ 8.34\\ 7.67\\ 7.51\\ 13.1\\ 12.3\\ 10.4\\ 8.34\\ 7.67\\ \end{array}$	5     4     5     3     4     2     5     4     5

8	msigdb_tf_motifs	psmb5 target genes	1.28e-05	0.00162	20	3.4	7
8	msigdb tf motifs	smad3 q6	1.38e-05	0.00172	15	4.3	2
8	msigdb_tf_motifs	lef1 q6	9 19e-05	0.00923	17	3 24	2
8	msigdb_tf_motifs	rota de	9.480.05	0.00038	11	4.7	-
0	msigdb_tf_metife		0.000267	0.00000	17	2.02	2
8			0.000207	0.0208	17	2.92	2
8	msigdb_immunological_signatures	gse2405 0h vs 24h a phagocytophilum stim neut	4.13e-10	8.11e-08	28	4.87	5
8	msigdb_immunological_signatures	gse2405 0h vs 9h a phagocytophilum stim neutr	1.41e-09	2.6e-07	28	4.56	5
8	msigdb_immunological_signatures	gse41978 klrg1 high vs low effector cd8 tcell	8.82e-08	1.17e-05	23	4.31	5
8	msigdb_immunological_signatures	gse26488 wt vs vp16 transgenic hdac7 ko doubl	4.28e-07	5.06e-05	18	4.89	2
8	$msigdb\_immunological\_signatures$	gse24634 treg vs tconv post day10 il4 convers	4.79e-07	5.59e-05	17	5.15	3
9	GO.BP	regulation of G protein-coupled receptor sign	6.93e-07	7.19e-05	11	8.29	4
9	GO.BP	peptide hormone processing	1.1e-05	0.000695	5	28.1	3
9	GO.BP	response to metal ion	3.56e-05	0.00169	14	4.07	2
9	GO BP	calcitonin family recentor signaling pathway	4 230 05	0.00103	3	Inf	-
9	GO BR	calcitonini ianniy receptor signaning pathway	4.23e-05	0.00193	2	T. f	1
9	GO.MF	amynn receptor signanng pathway	4.23e-05	0.00193	о С	10.6	1
9	GO.MF	monooxygenase activity	8.03e-05	0.00163	0	10.6	3
9	GO.MF	ketosteroid monooxygenase activity	0.000165	0.00278	3	83.3	3
9	GO.MF	hormone activity	0.000646	0.00789	5	8.77	3
9	GO.MF	oxidoreductase activity, acting on paired don	0.000948	0.00974	8	4.43	1
9	GO.MF	alditol:NADP+ 1-oxidoreductase activity	0.00208	0.0168	3	16.7	3
9	GO.CC	endoplasmic reticulum lumen	1.44e-07	4.49e-06	10	11.9	3
9	GO.CC	secretory granule	6.5e-07	1.66e-05	18	4.61	4
9	GO.CC	smooth endoplasmic reticulum	1.65e-05	0.00031	7	11	2
9	GO.CC	endoplasmic reticulum chaperone complex	0.000397	0.00377	4	16	2
a a	GO CC	nerikaryon	0.000665	0.00577	8	4 71	-
9	KEGG	Destain and and the indial	6 80 05	0.00377	15	94.71 9.6	
9	KEGG	Frotein processing in endoplasmic reticulum	0.82e-05	0.00128	10	3.0	3
9	KEGG	Neuroactive ligand-receptor interaction	0.000727	0.00839	6	6.49	3
9	KEGG	Circadian entrainment	0.000863	0.00968	6	6.25	4
9	KEGG	Oxytocin signaling pathway	0.000948	0.0105	8	4.43	2
9	KEGG	Various types of N-glycan biosynthesis	0.00181	0.017	5	6.68	2
9	msigdb_biocarta	prion pathway	0.00304	0.0214	3	13.9	3
9	msigdb_reactome	calcitonin like ligand receptors	4.23e-05	0.000383	3	Inf	1
9	msigdb reactome	gpcr ligand binding	8.43e-05	0.00071	8	6.66	5
9	msigdb reactome	g alpha i signalling events	0.000394	0.00276	10	4.12	4
<u>o</u>	msigdh_reactome	class a 1 rhodonsin like recentors	0.000813	0.00512	5	8.25	6
9	maigdb_reactome	poptide ligand binding receptors	0.00147	0.00854	4	10.2	4
9	insigub_reactome	peptide ligand binding receptors	0.00147	0.00834	4	10.2	4
9	msigdb_canonical_pathways	calcitonin like ligand receptors	4.23e-05	0.000474	3	Inf	1
9	msigdb_canonical_pathways	gpcr ligand binding	8.43e-05	0.000869	8	0.00	5
9	msigdb_canonical_pathways	g alpha i signalling events	0.000394	0.00331	10	4.12	4
9	msigdb_canonical_pathways	class a 1 rhodopsin like receptors	0.000813	0.00603	5	8.25	6
9	msigdb_canonical_pathways	peptide ligand binding receptors	0.00147	0.00985	4	10.2	3
9	msigdb_tf_motifs	gata6 01	3.11e-05	0.00367	12	4.77	1
9	msigdb_tf_motifs	gataagr gata c	6.26e-05	0.00658	12	4.4	1
9	msigdb_tf_motifs	lmo2com 02	0.000134	0.0127	11	4.36	1
9	msigdb tf motifs	pxr q2	0.000233	0.0194	12	3.77	1
9	msigdb tf motifs	atfb	0.000256	0.0207	12	3 73	2
9	msigdb_immunological_signatures	geo17074 ctrl vs act il4 and anti il12 72h cd	2 430 05	0.00203	12	4.91	-
9	msigdb_immunological_signatures	gsel1974 ctil vs act in and anti ili 2 72n cu.	2.436-05	0.00203	12	4.51	1
9	msigdb_immunological_signatures	gse12500 plasma cen vs naive bcen up	9.03e-03	11 11111220	1.2		2
9	mandb immunologiant argenturoa		0.000110	0.00505		4.18	-
9	hisigdb_inihidioiogicai_signatures	gse35543 in vivo ntreg vs converted ex itreg	0.000119	0.00787	8	4.18 6.29	2
	msigdb_immunological_signatures	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi	0.000119 0.000229	0.00787 0.0134	8 10	4.18 6.29 4.44	2 1
9	msigdb_immunological_signatures msigdb_immunological_signatures	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up	0.000119 0.000229 0.000294	0.00787 0.0134 0.0163	8 10 7	4.18 6.29 4.44 6.37	2 1 2
9 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation	0.000119 0.000229 0.000294 1.01e-05	0.00787 0.0134 0.0163 0.000657	8 10 7 12	4.18 6.29 4.44 6.37 5.68	2 1 2 2
9 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret	0.000119 0.000229 0.000294 1.01e-05 1.28e-05	0.00787 0.0134 0.0163 0.000657 0.000781	8 10 7 12 12	$ \begin{array}{r} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ \end{array} $	2 1 2 2 4
9 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866	8 10 7 12 12 11	$ \begin{array}{r} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ 6.03\\ \end{array} $	2 1 2 2 4 4
9 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976	8 10 7 12 12 11 22	$ \begin{array}{r} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ 6.03\\ 3.11\\ \end{array} $	2 1 2 2 4 4 6
9 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103	8 10 7 12 12 11 22 11	$ \begin{array}{r} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ \end{array} $	2 1 2 4 4 6 2
9 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of peptide hormone secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023	8 10 7 12 12 11 22 11 22 11 15	$\begin{array}{r} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ \end{array}$	2 1 2 4 4 6 2 4
9 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000543	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693	8 10 7 12 12 11 22 11 22 11 15 23	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32	2 1 2 4 4 4 6 2 4 2
9 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000594	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00722	8 10 7 12 11 22 11 22 11 15 23 4	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32 16.8	2 1 2 4 4 6 2 4 2 3
9 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00742	8 10 7 12 12 11 22 11 22 11 15 23 4 2	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32 16.8 50.2	2 1 2 4 4 6 2 4 2 3 3 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monocygenase activity	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000694	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00789 0.00789	8 10 7 12 12 11 22 11 22 11 15 23 4 3 22	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32 16.8 50.2 2.24	2 1 2 4 4 6 2 4 2 3 3 3 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00789 0.00886	8 10 7 12 11 22 11 15 23 4 3 23	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32 16.8 50.2 2.24 2.24	2 1 2 4 4 6 2 4 2 3 3 3 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.0023 0.00742 0.00789 0.00886 7.43e-08	8 10 7 12 11 22 11 15 23 4 3 23 11	4.18 6.29 4.44 6.37 5.68 5.52 6.03 3.11 5.85 3.46 2.32 16.8 50.2 2.24 20.8	2 1 2 4 4 6 2 4 2 3 3 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex	$\begin{array}{c} 0.000119\\ 0.000229\\ 0.000294\\ \hline 1.01e-05\\ 1.28e-05\\ 1.47e-05\\ 1.74e-05\\ 1.88e-05\\ 0.000124\\ 0.000543\\ 0.000594\\ 0.000693\\ 0.000836\\ 1.8e-09\\ 6.83e-09\\ \hline 6.83e-09\\ \hline \end{array}$	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00742 0.00742 0.00789 0.00886 7.43e-08 2.49e-07	8 10 7 12 11 22 11 22 11 15 23 4 3 23 11 11	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ \end{array}$	2 1 2 4 4 4 6 2 4 2 3 3 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex	$\begin{array}{c} 0.000119\\ 0.000229\\ 0.000294\\ \hline 1.01e-05\\ 1.28e-05\\ 1.74e-05\\ 1.74e-05\\ 1.88e-05\\ 0.000124\\ 0.000543\\ 0.000543\\ 0.000594\\ 0.000836\\ 1.8e-09\\ 6.83e-09\\ 1.34e-07\\ \hline \end{array}$	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06	$\begin{array}{c} 8 \\ 8 \\ 10 \\ 7 \\ 12 \\ 11 \\ 22 \\ 11 \\ 22 \\ 11 \\ 15 \\ 23 \\ 4 \\ 3 \\ 23 \\ 11 \\ 11 \\ 15 \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ \end{array}$	2 1 2 4 4 4 6 2 4 2 3 3 2 2 2 1
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07	$\begin{array}{c} 0.00787\\ 0.0134\\ 0.0163\\ 0.000657\\ 0.000781\\ 0.000866\\ 0.000976\\ 0.00103\\ 0.0023\\ 0.00693\\ 0.00742\\ 0.00789\\ 0.00886\\ 7.43e-08\\ 2.49e-07\\ 4.24e-06\\ 5.39e-06\\ \end{array}$	$\begin{array}{c} 8 \\ 8 \\ 10 \\ 7 \\ 12 \\ 11 \\ 22 \\ 11 \\ 15 \\ 23 \\ 4 \\ 3 \\ 23 \\ 11 \\ 11 \\ 15 \\ 15 \\ \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 2 1 1
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex endopeptidase complex myelin sheath	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000762 0.00103 0.0023 0.00693 0.00742 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05	$\begin{array}{c} 8\\ 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 11\\ 15\\ 15\\ 24\\ \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 1 1 6
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex endopeptidase complex endopeptidase complex myelin sheath Proteasome	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00742 0.00789 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06	$\begin{array}{c} 8\\ 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 11\\ 15\\ 15\\ 24\\ 14\\ \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 2 1 1 6 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000594 0.000594 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00742 0.00742 0.00789 0.00742 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06	$\begin{array}{c} 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 11\\ 15\\ 15\\ 24\\ 14\\ 20\\ \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ \end{array}$	2 1 2 4 4 4 6 2 4 2 3 3 2 2 2 2 1 1 6 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000694 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.77e-06	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.0023 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.001007	$\begin{array}{c} & & & \\$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 2 1 1 6 2 2 2 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Huntington disease	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000594 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08 2.77e-06 3.08e-05	$\begin{array}{c} 0.00787\\ 0.0134\\ 0.0163\\ 0.000657\\ 0.000781\\ 0.000866\\ 0.000976\\ 0.00103\\ 0.00976\\ 0.00103\\ 0.00742\\ 0.00789\\ 0.00693\\ 0.00742\\ 0.00789\\ 0.00886\\ 7.43e-08\\ 2.49e-07\\ 4.24e-06\\ 5.39e-06\\ 2.45e-05\\ 1.16e-06\\ 2.26e-06\\ 0.000107\\ 0.00764 \end{array}$	$\begin{array}{c} 8\\ 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 11\\ 15\\ 15\\ 24\\ 14\\ 20\\ 27\\ 28\end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 1 1 6 2 2 2 1 1 6 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monoxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex endopeptidase complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Huntington disease Baskingen disease	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08 2.77e-06 3.08e-05	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000781 0.000781 0.0023 0.00742 0.00789 0.00742 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.000107 0.000764	8 10 7 12 12 11 22 11 15 23 4 3 23 11 15 23 4 3 23 11 15 23 4 3 23 11 15 23 4 3 23 11 15 23 4 3 23 23 11 15 23 23 23 23 24 25 23 25 23 23 23 23 24 25 25 25 25 25 25 25 25 25 25	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ 2.68\end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 1 1 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome accessory complex endopeptidase complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Huntington disease	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08 2.77e-06 3.08e-05 4.48e-05 0.0055	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00742 0.00789 0.00789 0.00742 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.000107 0.000764 0.000958	$\begin{array}{c} 8\\ 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 15\\ 15\\ 24\\ 14\\ 20\\ 27\\ 28\\ 25\\ 4\end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ 2.68\\$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 2 1 1 6 2 2 2 2 2 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Huntington disease Parkinson disease nol pathway	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000693 0.000836 1.8e-09 6.83e-09 6.83e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08 2.77e-06 3.08e-05 4.48e-05 0.0035 0.0035	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00789 0.00789 0.00789 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.000107 0.000764 0.000958 0.0215	$\begin{array}{c} 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 11\\ 15\\ 15\\ 24\\ 14\\ 20\\ 27\\ 28\\ 25\\ 4\\ 25\\ 4\\ 4\end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ 2.68\\ 8.39\\ 2.68\\ 8.39\\ 3.71\end{array}$	2 1 2 4 4 4 6 2 4 2 3 3 2 2 2 2 1 1 6 2 2 2 2 2 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of insulin secretion hormone secretion negative regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Huntington disease no1 pathway p53hypoxia pathway	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.74e-05 1.88e-05 0.000124 0.000543 0.000594 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.77e-06 3.08e-05 4.48e-05 0.0035 0.00647	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00742 0.00789 0.00789 0.00789 0.00789 0.00789 0.00789 0.00789 0.00789 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.000107 0.000764 0.000958 0.0215 0.031		$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ 2.68\\ 8.39\\ 6.71\\ \hline \end{array}$	2 1 2 4 4 6 2 4 2 3 3 2 2 2 1 1 6 2 2 2 2 2 2 2 2 2 2 2 2 2
9 10 10 10 10 10 10 10 10 10 10	msigdb_immunological_signatures msigdb_immunological_signatures GO.BP GO.BP GO.BP GO.MF GO.MF GO.MF GO.MF GO.MF GO.MF GO.CC GO.CC GO.CC GO.CC GO.CC GO.CC KEGG KEGG KEGG KEGG KEGG KEGG KEGG KE	gse35543 in vivo ntreg vs converted ex itreg gse20151 ctrl vs fusobact nucleatum neutrophi gse22886 neutrophil vs dc up negative regulation of cell activation positive regulation of peptide hormone secret positive regulation of leukocyte activation G protein-coupled receptor binding GTP binding cell-cell adhesion mediator activity ketosteroid monooxygenase activity purine nucleoside binding proteasome regulatory particle proteasome accessory complex proteasome complex endopeptidase complex myelin sheath Proteasome Spinocerebellar ataxia Prion disease Parkinson disease nol pathway prion pathway	0.000119 0.000229 0.000294 1.01e-05 1.28e-05 1.47e-05 1.88e-05 0.000124 0.000543 0.000594 0.000836 1.8e-09 6.83e-09 1.34e-07 1.76e-07 1.01e-06 1.17e-08 2.76e-08 2.76e-08 2.77e-06 3.08e-05 4.48e-05 0.0035 0.00647 0.0118	0.00787 0.0134 0.0163 0.000657 0.000781 0.000866 0.000976 0.00103 0.0023 0.00693 0.00742 0.00789 0.00886 7.43e-08 2.49e-07 4.24e-06 5.39e-06 2.45e-05 1.16e-06 2.26e-06 0.000107 0.0000764 0.000958 0.0215 0.031 0.0423	$\begin{array}{c} 8\\ 8\\ 10\\ 7\\ 12\\ 12\\ 11\\ 22\\ 11\\ 15\\ 23\\ 4\\ 3\\ 23\\ 11\\ 15\\ 15\\ 24\\ 14\\ 20\\ 27\\ 28\\ 25\\ 4\\ 4\\ 3\\ \end{array}$	$\begin{array}{c} 4.18\\ 6.29\\ 4.44\\ 6.37\\ \hline \\ 5.68\\ 5.52\\ 6.03\\ 3.11\\ 5.85\\ 3.46\\ 2.32\\ 16.8\\ 50.2\\ 2.24\\ 20.8\\ 17\\ 6.77\\ 6.6\\ 3.56\\ 9.6\\ 5.41\\ 3.07\\ 2.58\\ 2.68\\ 8.39\\ 6.71\\ 8.37\\ \end{array}$	$ \begin{array}{c} 2\\ 1\\ 2\\ 4\\ 4\\ 6\\ 2\\ 4\\ 2\\ 3\\ 3\\ 2\\ 2\\ 2\\ 1\\ 1\\ 6\\ 2\\ 2\\ 2\\ 2\\ 1\\ 1\\ 2\\ 2\\ 2\\ 2\\ 1\\ 3\\ 3\\ 3\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 3\\ 3\\ 3\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 3\\ 3\\ 3\\ 2\\ 2\\ 2\\ 2\\ 2\\ 3\\ 3\\ 3\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 3\\ 3\\ 3\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\ 2\\$

10	msigdb_reactome	metabolism of polyamines	6.84 e-08	1.41e-06	14	8	1
10	msigdb_reactome	abc transporter disorders	1.01e-07	2e-06	15	6.96	1
10	msigdb_reactome	disorders of transmembrane transporters	1.21e-07	2.34e-06	19	5.13	1
10	msigdb_reactome	defective cftr causes cystic fibrosis	2.33e-07	4.22e-06	14	7.05	1
10	msigdb_canonical_pathways	the role of gtse1 in g2 m progression after g	4.37e-08	1.18e-06	16	6.88	2
10	msigdb_canonical_pathways	metabolism of polyamines	6.84e-08	1.8e-06	14	8	1
10	msigdb_canonical_pathways	abc transporter disorders	1.01e-07	2.56e-06	15	6.96	1
10	msigdb_canonical_pathways	disorders of transmembrane transporters	1.21e-07	3.01e-06	19	5.13	1
10	msigdb_canonical_pathways	defective cftr causes cystic fibrosis	2.33e-07	5.38e-06	14	7.05	1
10	msigdb_tf_motifs	rp58 01	5.69e-05	0.00618	13	4.26	1
10	msigdb_tf_motifs	argggttaa unknown	0.00074	0.0405	8	4.83	1
10	msigdb_tf_motifs	foxd3 01	0.000945	0.0474	12	3.23	1
10	msigdb_tf_motifs	hlf 01	0.00095	0.0474	14	2.9	1
10	$msigdb\_immunological\_signatures$	gse3982 dc vs nkcell up	1.72e-05	0.00149	17	3.79	3
10	$msigdb\_immunological\_signatures$	gse17721 ctrl vs gardiquimod 24h bmdc dn	5.78e-05	0.00431	18	3.25	1
10	$msigdb\_immunological\_signatures$	gse 44649 wt vs mir 155 ko naive cd 8 tcell d n $% \left( 1,1,2,2,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,3,$	6.56e-05	0.00476	16	3.51	1
10	$msigdb\_immunological\_signatures$	gse 5099 day 3 vs day 7 mcsf treated macrophage $\ldots$	8.28e-05	0.00578	15	3.61	1
10	$msigdb\_immunological\_signatures$	gse29618 bcell vs mdc day7 flu vaccine dn	9.5e-05	0.00649	15	3.56	3

Table 3: The top (lowest p-value) genesets found (uniquely) in each cluster