PRACTICAL

唐凯临

2021.6

REVIEW: DATA

Platforms (1) GPL26963 Agilent-085982 Arraystar human lncRNA V5 microarray

Samples (15)
Less...

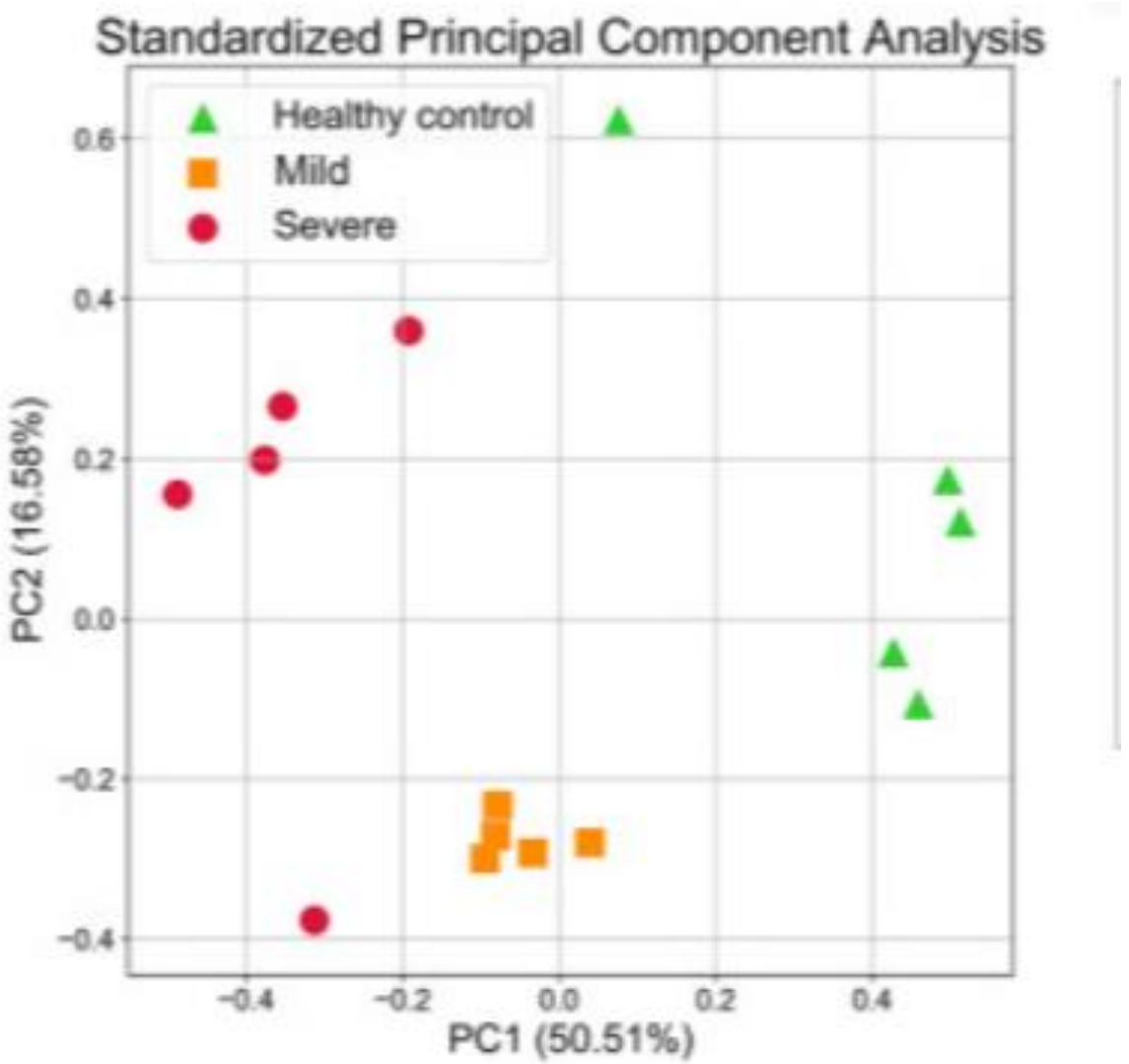
GSM5019817 PBMC_healthy_subject1
GSM5019818 PBMC_healthy_subject2
GSM5019819 PBMC_healthy_subject3
GSM5019820 PBMC_healthy_subject4
GSM5019821 PBMC_healthy_subject5
GSM5019822 PBMC_mild_patient_subject1
GSM5019823 PBMC_mild_patient_subject2
GSM5019824 PBMC_mild_patient_subject3
GSM5019825 PBMC_mild_patient_subject4
GSM5019826 PBMC_mild_patient_subject5
GSM5019827 PBMC_severe patient_subject1
GSM5019828 PBMC_severe patient_subject2
GSM5019829 PBMC_severe patient_subject3
GSM5019830 PBMC_severe patient_subject4
GSM5019831 PBMC_severe patient_subject5

Data table header descriptions

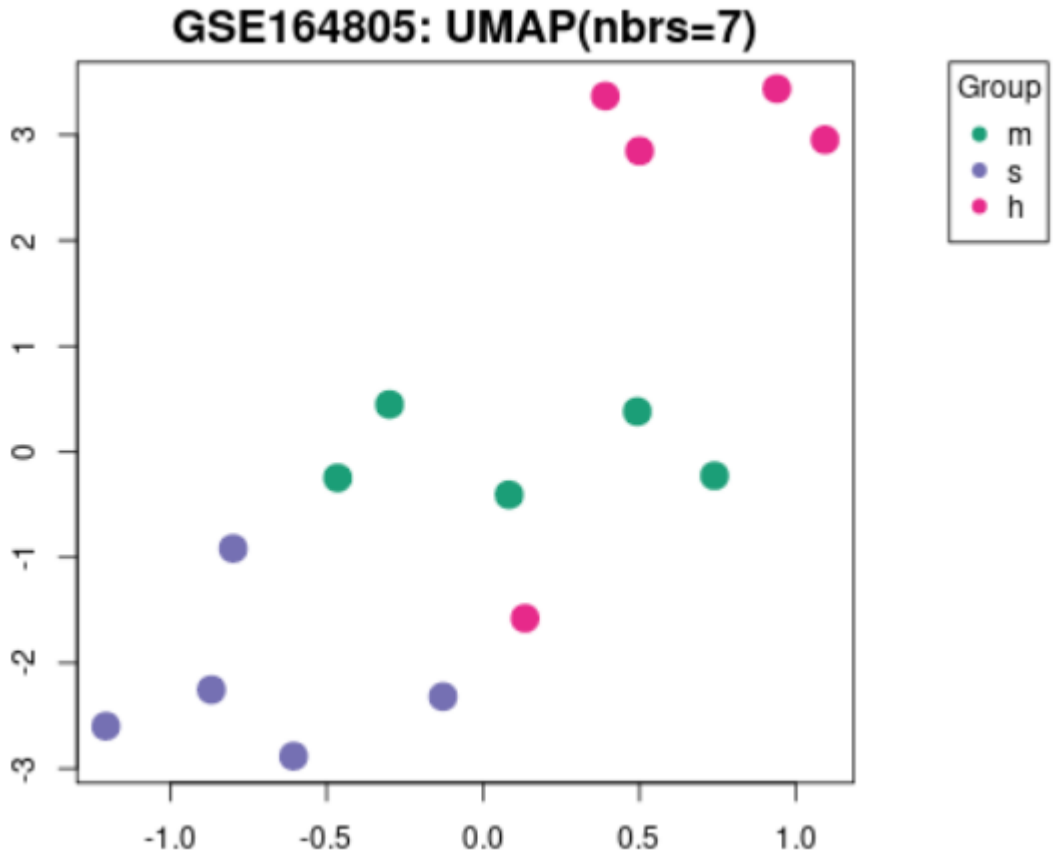
ID	
TRANSCRIPT_TYPE	protein_coding or noncoding or smallRNA
ACC	Accession number of spotted sequence
ORF	
SOURCE	source database
BUILD	Genome Version

REVIEW

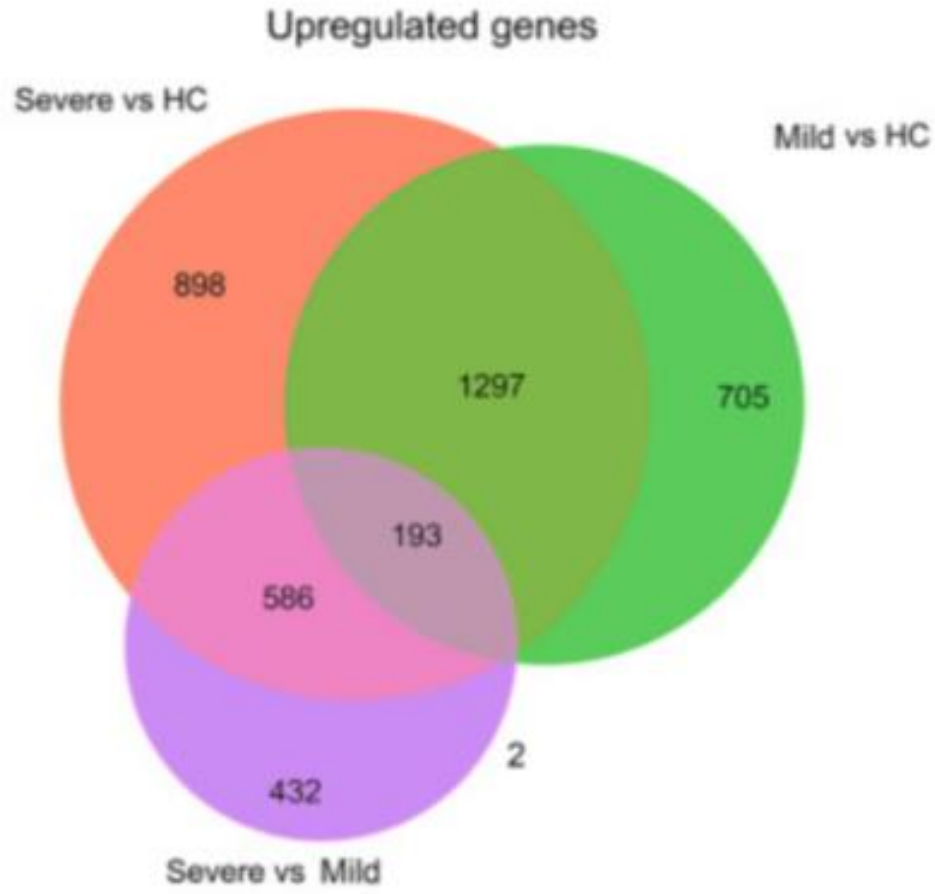
- Normalization

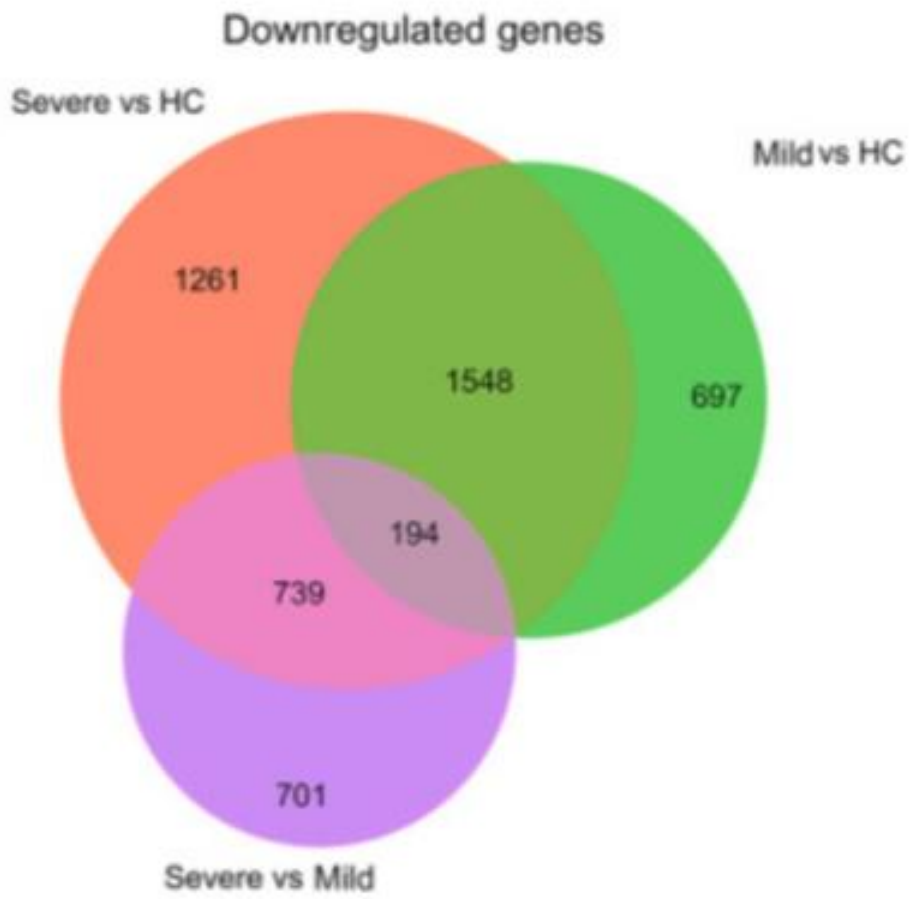


GEO2R

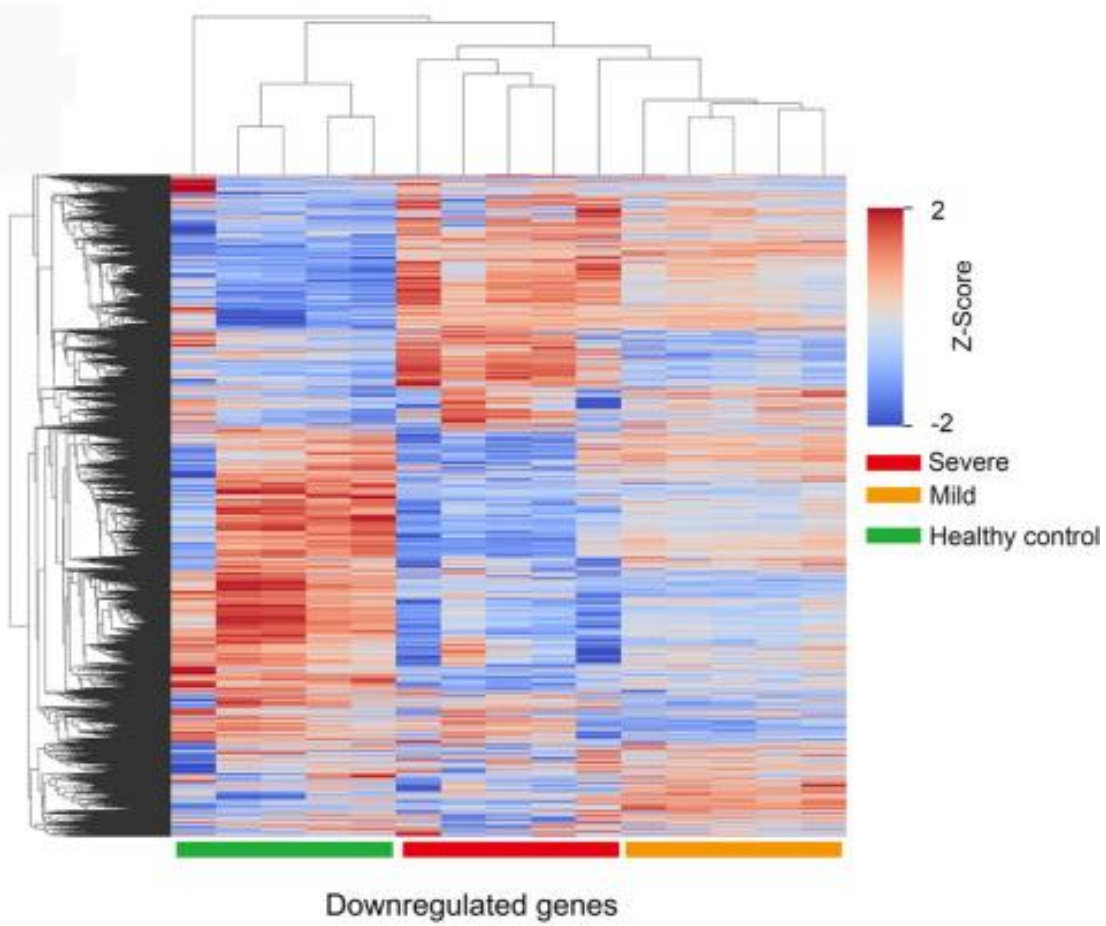


DEGs

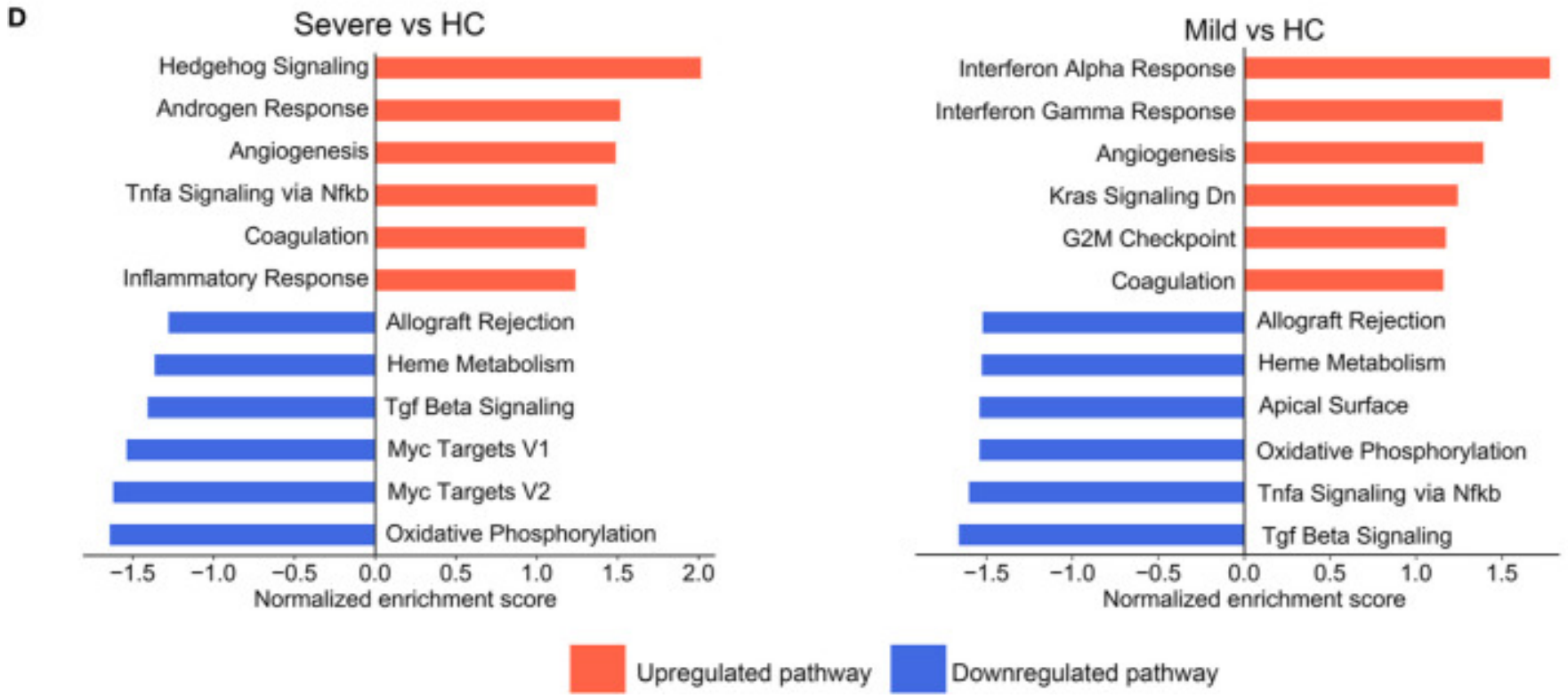

Upregulated genes
Severe vs HC
Mild vs HC
898
1297
705
193
586
2
432
Severe vs Mild


Downregulated genes
Severe vs HC
Mild vs HC
1261
1548
697
194
739
701
Severe vs Mild

Only DEG is not enough



Only DEG is not enough



常用工具

- 热图绘制
- 功能富集
- 网络构建

Data format

UNIQID	d1-1	d1-2	d1-3	d1-4	d2-1	d2-2	d2-3	d2-4	d2-5	d3-1	d3-2	d3-3	d3-4
GPNMB	6.07	5.18	6.74	6.75	6.61	6.49	6.93	6.71	6.88	6.65	6.98	7.37	6.84
ANKRD36BP2		8.32	8.11	9.13	8.92	7.37	7.3	7.25	7.29	7.26	7.52	7.93	7.96
KRT19	11	11.18	9.89	10.61	11.18	10.83	10.79	10.58	11.26	8.64	9.1	9.27	9.13
SLC6A1	5.42	4.18	3.59	4.27	4.68	4.7	4.87	4.71	4.6	4.99	4.49	4.35	4.33
GNMT	4.68	4.2	4.11	4.38	4.76	3.99	4.39	4.72	4.49	5.99	5.15	4.37	5.4
IGLV1-40///IGLV1-44			8.9	8.99	9.7	9.65	9.6	9.91	9.54	9.33	9.55	9.24	9.53
KRT23	8.1	8.39	8.45	8.67	9.2	9.62	9.14	9.45	9.54	7.78	7.87	7.68	7.96
KCNN2	4.43	4	4.15	4.27	4.22	4.72	4.83	4.99	4.45	4.22	4.15	4.05	4.09
SLCO4C1	4.84	4.36	4.47	4.7	4.08	4.16	4.27	4.35	4.22	4.48	4.33	4.59	4.36
FCRL5	7.46	7.92	8.43	7.99	7.1	6.51	6.63	6.33	6.45	7.39	7.65	7.46	7.44
PPP1R1A	4.31	4.42	4.26	4.43	4.21	4.31	3.88	3.99	4.51	4.98	4.57	4.18	4.59
ACSM2A	3.48	3.41	3.65	3.56	4.73	4.63	4.17	4.67	4.16	5.97	5.56	5.43	6.1

Heatmap

- http://www.heatmapper.ca/expression/

UNIQID	NAME	1	1	1	2	2	2
Hs.9305	angiotensin receptor-like 1	0.533865724	2.667389535	1.98516763	4.832817262	3.590801314	3.309607441
Hs.181307	H3 histone, family 3A	-0.942951315	-0.500171526	-0.705453196	-0.32191231	-0.14030858	-0.427467964
Hs.83484	SRY (sex determining region Y)-box 4	-3.418094026	-3.181358856	-3.276305367	-2.392780506	-1.740889988	-2.248737455

Data Format

Select Data File.

- (•) Example File
- ( ) Upload File
- ( ) Upload Multiple Files

Select Example File

Example 1

Scale Type Row

Colour Brightness -50 0 50

-50 -40 -30 -20 -10 0 10 20 30 40 50

Number of Shades 3 50 100

3 13 23 33 43 53 63 73 83 93 100

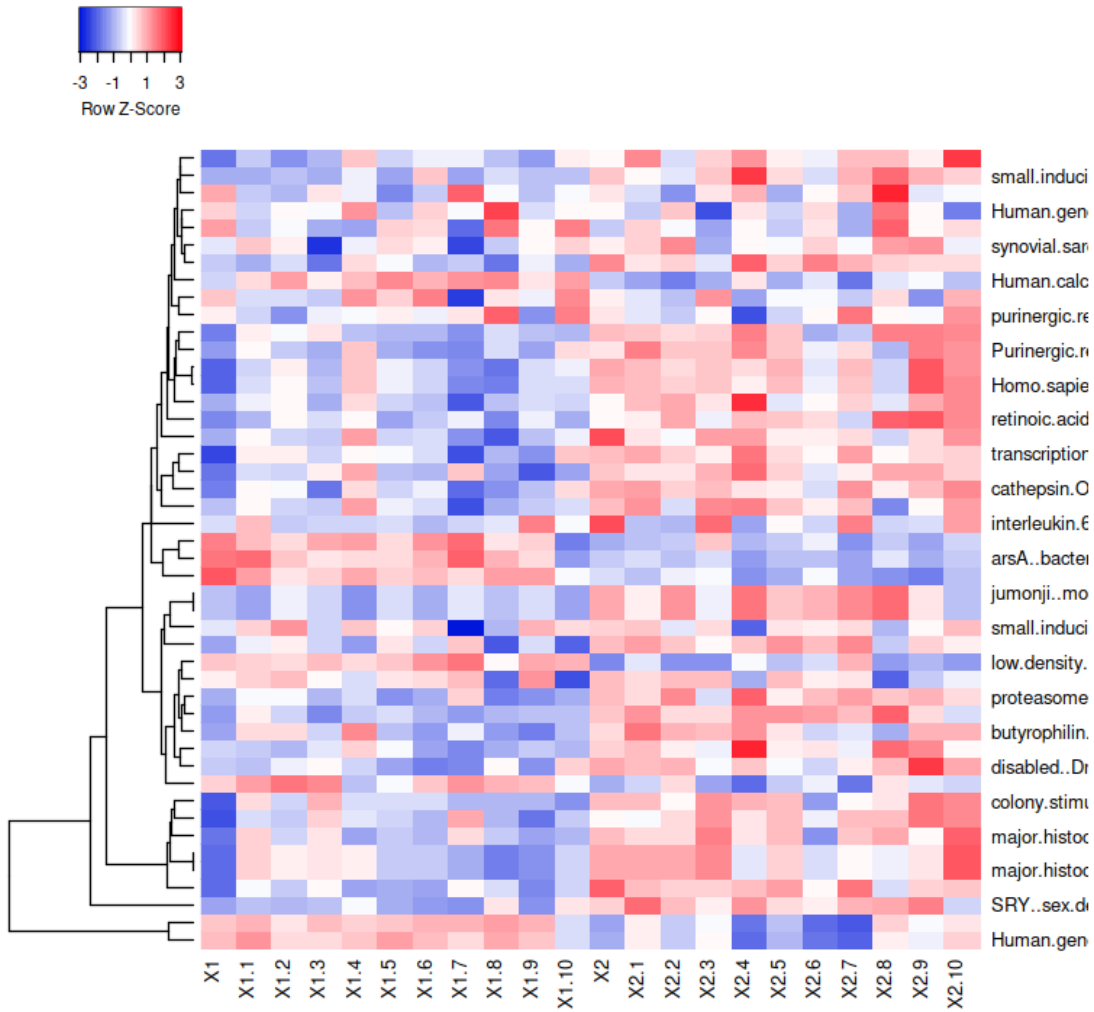
Colour Scheme Custom

Low Colour	Middle Colour	High Colour
#0016DB	#FFFFFF	#FF0516

Missing Data Colour #000000

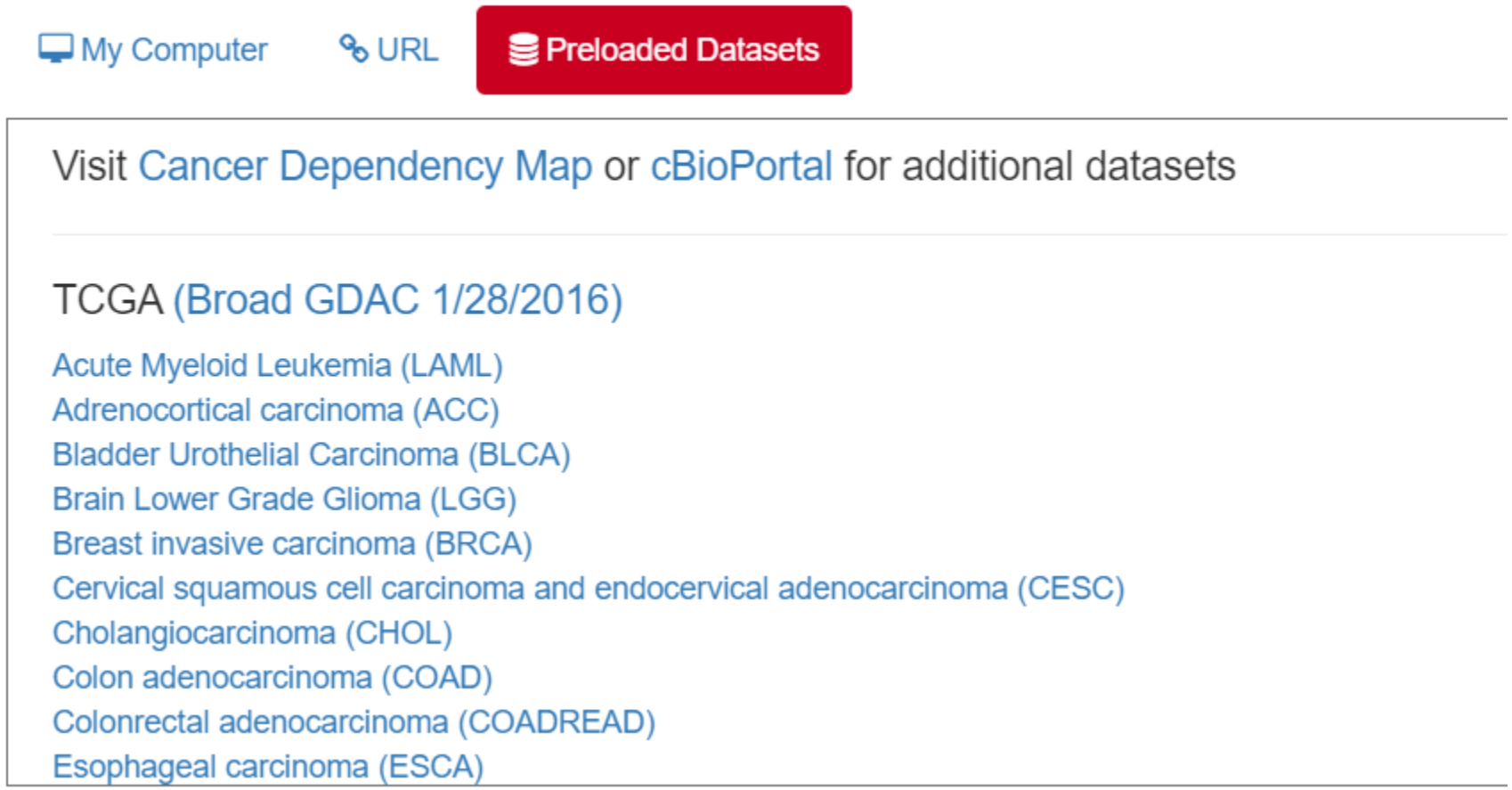
Clustering Method

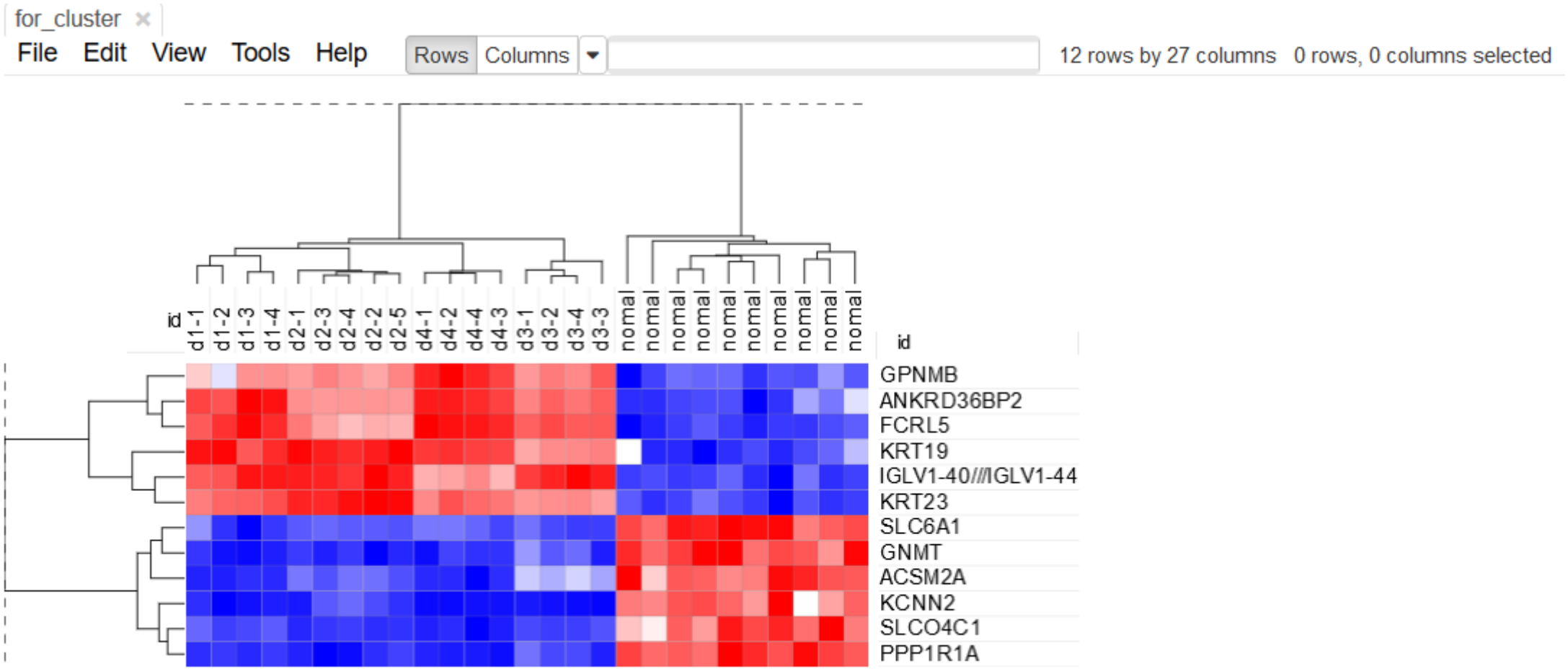
Plot | Interactive | Row Dendrogram | Column Dendrogram | Table



Heatmap

- Open




for_cluster
File
Edit
View
Tools
Help
Rows
Columns
12 rows by 27 columns
0 rows, 0 columns selected
id
d1-1
d1-2
d1-3
d1-4
d2-1
d2-3
d2-4
d2-2
d2-5
d4-1
d4-2
d4-4
d4-3
d3-1
d3-2
d3-4
d3-3
nomal
nomal
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nomal
nomal
nomal
nomal
id
GPNMB
ANKRD36BP2
FCRL5
KRT19
IGLV1-40///IGLV1-44
KRT23
SLC6A1
GNMT
ACSM2A
KCNN2
SLCO4C1
PPP1R1A

Function annotation method

- Step1:

  cluster genes on the basis of similarity measures

  Select up-regulated or down-regulated genes
- Step2:

  Select a reference function frame
- Step3:

  Determine the statistical significance of the mapping between cluster (differential genes group) and a functional category.

功能富集

工具名称	工具分类	网址
DAVID	在线工具	https://david.ncifcrf.gov/
PANTHER	在线工具	http://www.pantherdb.org/
GenMAPP	在线工具	http://www.genmapp.org/
GoMiner	在线工具	https://discover.nci.nih.gov/gominer/index.jsp
GSEA	Java软件、R语言包	http://software.broadinstitute.org/gsea
Goplot	R语言包	https://CRAN.R-project.org/package=Goplot
topGO	R语言包	http://www.bioconductor.org/packages/release/bioc/html/topGO.html
Sigpathway	R语言包	http://www.bioconductor.org/packages/release/bioc/html/sigPathway.html
ClueGO	Cytoscape插件	http://apps.cytoscape.org/apps/cluego
CluePedia	Cytoscape插件	http://apps.cytoscape.org/apps/cluepedia
BiNGO	Cytoscape插件	http://apps.cytoscape.org/apps/bingo

DAVID

Shortcut to DAVID Tools

Functional Annotation

Gene-annotation enrichment analysis, functional annotation clustering , BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and more

Gene Functional Classification

Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. More

Gene ID Conversion

Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically. More

Gene Name Batch Viewer

Display gene names for a given gene list; Search functionally related genes within your list or not in your list; Deep links to enriched detailed information. More

Hot Links

Call for papers

Submit papers for a Special Issue:"DNA or RNA-Mediated Innate Immune Response" of the International Journal of Molecular Sciences

DAVID Forum

Forum for DAVID users to ask questions, suggest a new functions for DAVID and help other users by answering their questions.

FAQ

Frequently Asked Questions

LHRI Publications

Publications of the Laboratory of Human Retrovirology and Immunoinformatics, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research

DAVID Publications

Publications for DAVID

Recommending: A paper published in ***Nature Protocols*** describes step-by-step procedure to use DAVID!

Welcome to DAVID 6.8

2003 - 2020

The **D**atabase for **A**nnotation, **V**isualization and **I**ntegrated **D**iscovery (**DAVID**) v6.8 comprises a full Knowledgebase update to the sixth version of our original web-accessible programs. DAVID now provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:

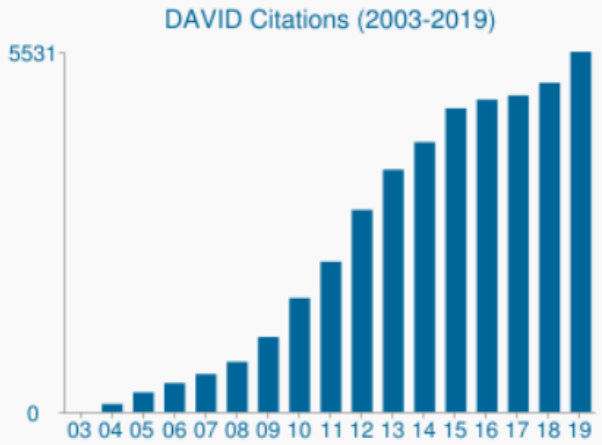
- Identify enriched biological themes, particularly GO terms
- Discover enriched functional-related gene groups
- Cluster redundant annotation terms
- Visualize genes on BioCarta & KEGG pathway maps
- Display related many-genes-to-many-terms on 2-D view.
- Search for other functionally related genes not in the list
- List interacting proteins
- Explore gene names in batch
- Link gene-disease associations
- Highlight protein functional domains and motifs

Search

What's Important in DAVID?

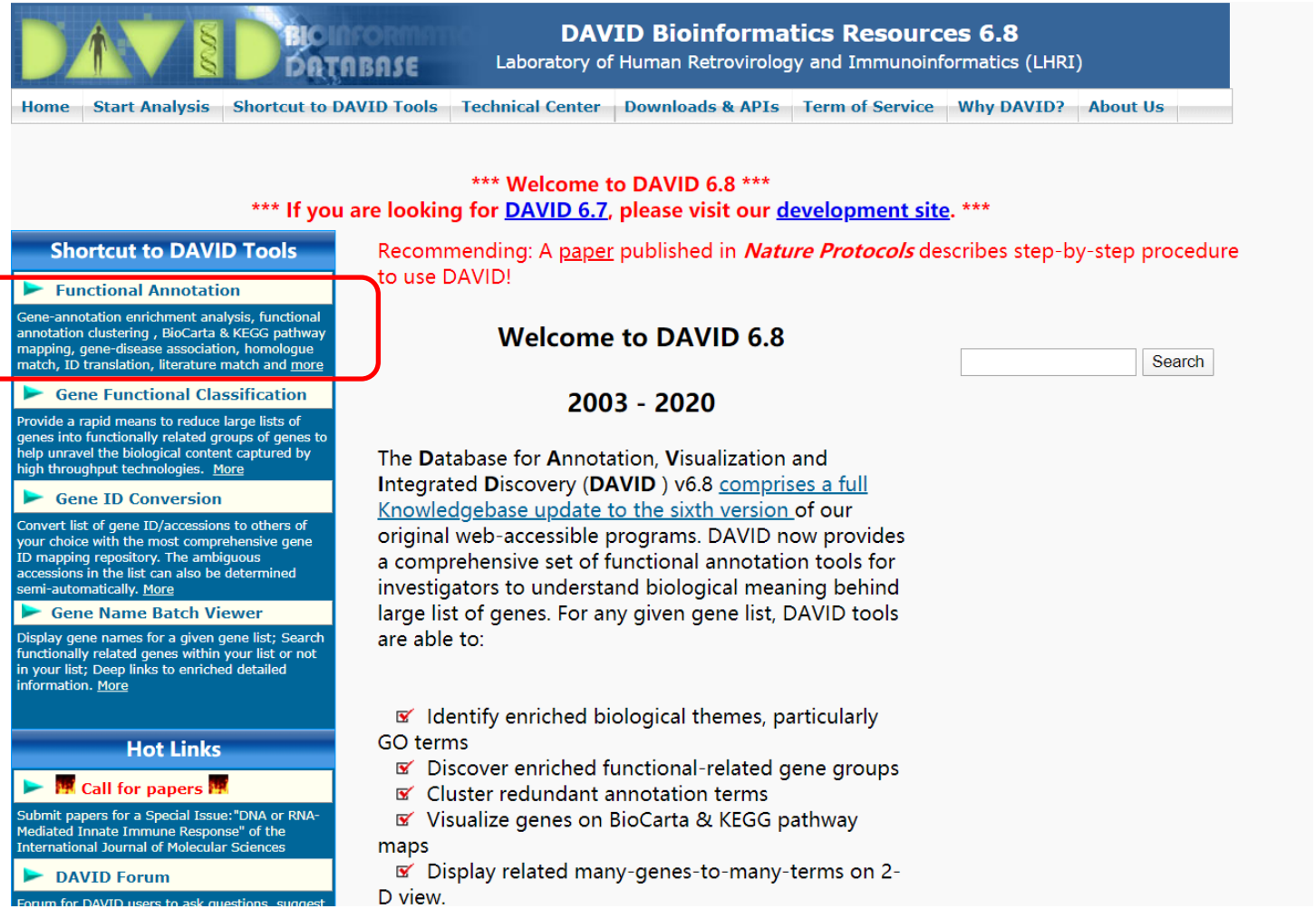
- Cite DAVID
- IDs of Affy Exon and Gene arrays supported
- Novel Classification Algorithms
- Pre-built Affymetrix and Illumina backgrounds
- User's customized gene background
- Enhanced calculating speed

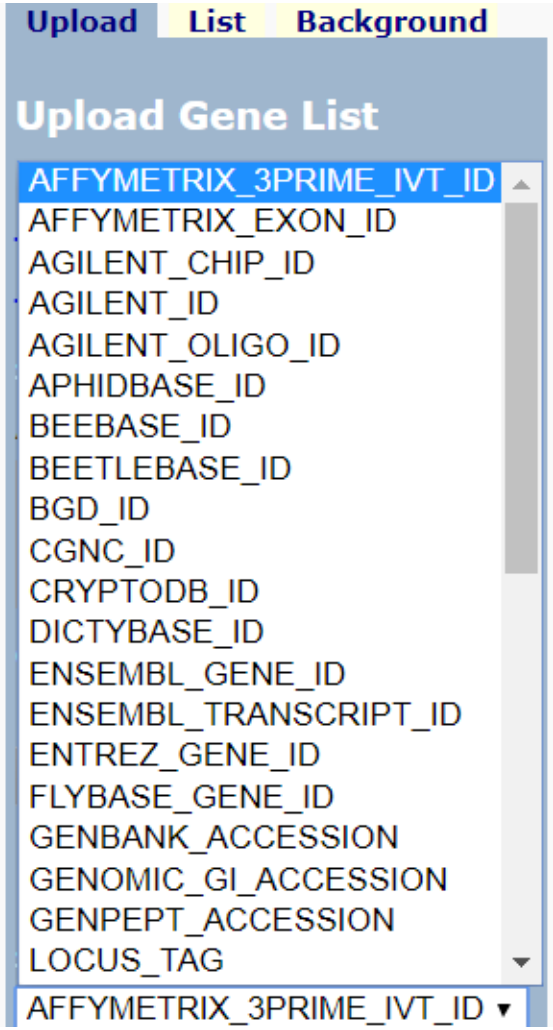
Statistics of DAVID



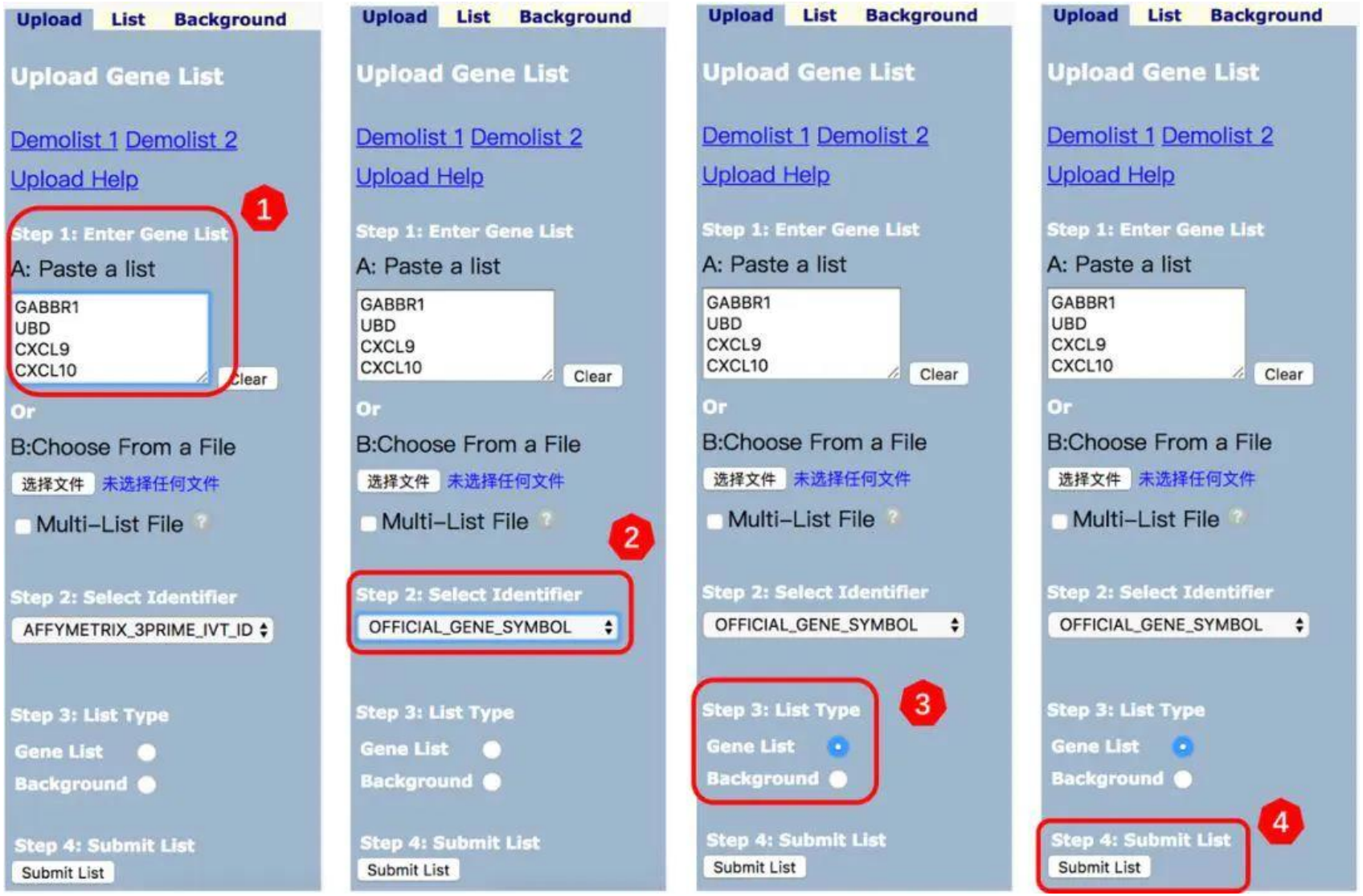
- > 38,000 Citations
- Average Daily Usage: ~2,700 gene lists/sublists from ~900 unique researchers.

Functional Annotation





FUNCTIONAL ANNOTATION



*** Welcome to DAVID 6.8 ***

*** If you are looking for DAVID 6.7, please visit our development site. ***

Upload | List | Background

Gene List Manager

Select to limit annotations by one or more species

Help

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager Help

demolist1
demolist1

Select List to:

Use | Rename | Remove | Combine | Show Gene List

Annotation Summary Results

Help and Tool Manual

Current Gene List: demolist1 — **145 DAVID IDs**

Current Background: Homo sapiens — **Check Defaults** ☑ Clear All

- ⊞ Disease (1 selected)
- ⊞ Functional_Categories (3 selected)
- ⊞ Gene_Ontology (3 selected)
- ⊞ General_Annotations (0 selected)
- ⊞ Literature (0 selected)
- ⊞ Main_Accessions (0 selected)
- ⊞ Pathways (3 selected)
- ⊞ Protein_Domains (3 selected)
- ⊞ Protein_Interactions (0 selected)
- ⊞ Tissue_Expression (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

Functional Annotation Clustering

Functional Annotation Chart

GO

Gene_Ontology (3 selected)

☐	GOTERM_BP_1	91.7%	133	Chart
☐	GOTERM_BP_2	91.7%	133	Chart
☐	GOTERM_BP_3	91.7%	133	Chart
☐	GOTERM_BP_4	91.7%	133	Chart
☐	GOTERM_BP_5	89.0%	129	Chart
☐	GOTERM_BP_ALL	91.7%	133	Chart
☑	GOTERM_BP_DIRECT	91.7%	133	Chart
☐	GOTERM_BP_FAT	91.7%	133	Chart
☐	GOTERM_CC_1	92.4%	134	Chart
☐	GOTERM_CC_2	91.0%	132	Chart
☐	GOTERM_CC_3	91.0%	132	Chart
☐	GOTERM_CC_4	86.9%	126	Chart
☐	GOTERM_CC_5	82.8%	120	Chart
☐	GOTERM_CC_ALL	92.4%	134	Chart
☑	GOTERM_CC_DIRECT	92.4%	134	Chart
☐	GOTERM_CC_FAT	86.9%	126	Chart
☐	GOTERM_MF_1	87.6%	127	Chart
☐	GOTERM_MF_2	86.9%	126	Chart
☐	GOTERM_MF_3	83.4%	121	Chart
☐	GOTERM_MF_4	79.3%	115	Chart
☐	GOTERM_MF_5	70.3%	102	Chart
☐	GOTERM_MF_ALL	87.6%	127	Chart
☑	GOTERM_MF_DIRECT	87.6%	127	Chart
☐	GOTERM_MF_FAT	85.5%	124	Chart

Functional Annotation Chart

Help and Manual

Current Gene List: demolist1
Current Background: Homo sapiens
145 DAVID IDs

Options

Thresholds: Count 2 EASE 0.05

Display: Fold Enrichment Bonferroni Benjamini FDR Fisher Exact LT,PH,PT # of Records 1000

Percentage 5/149=3.4%

Rerun Using Options

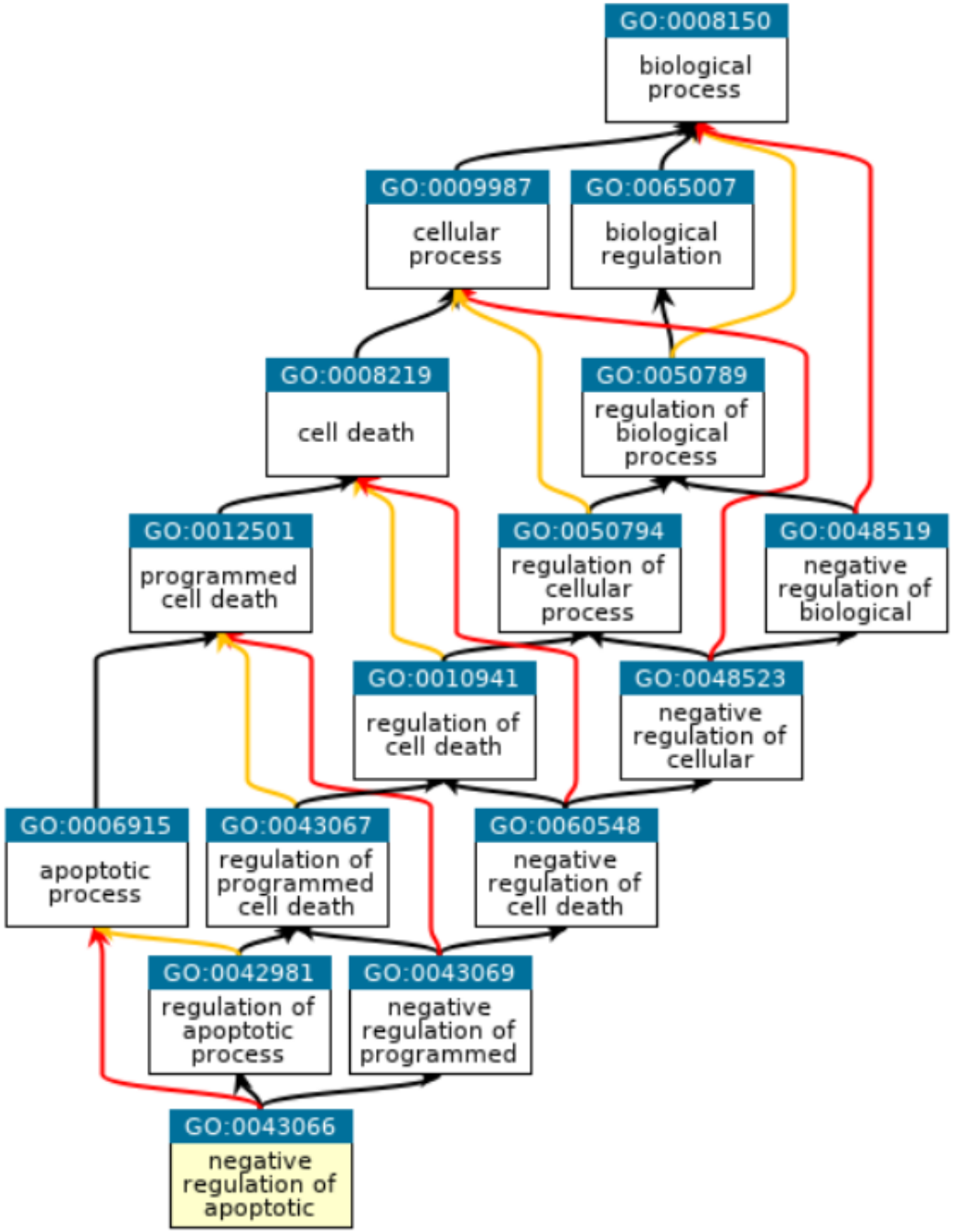
GO term

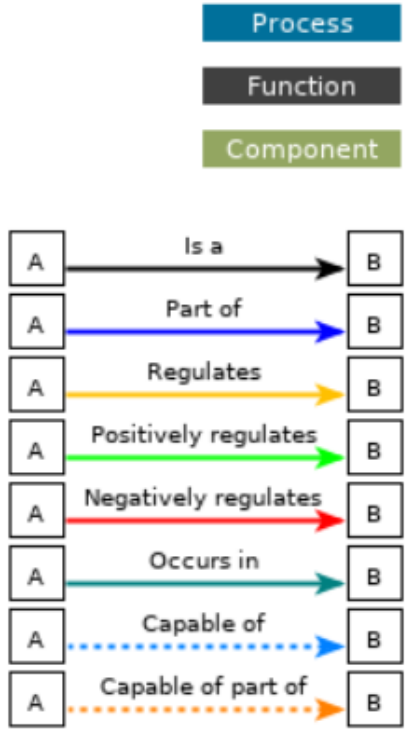
52 chart records

Download File

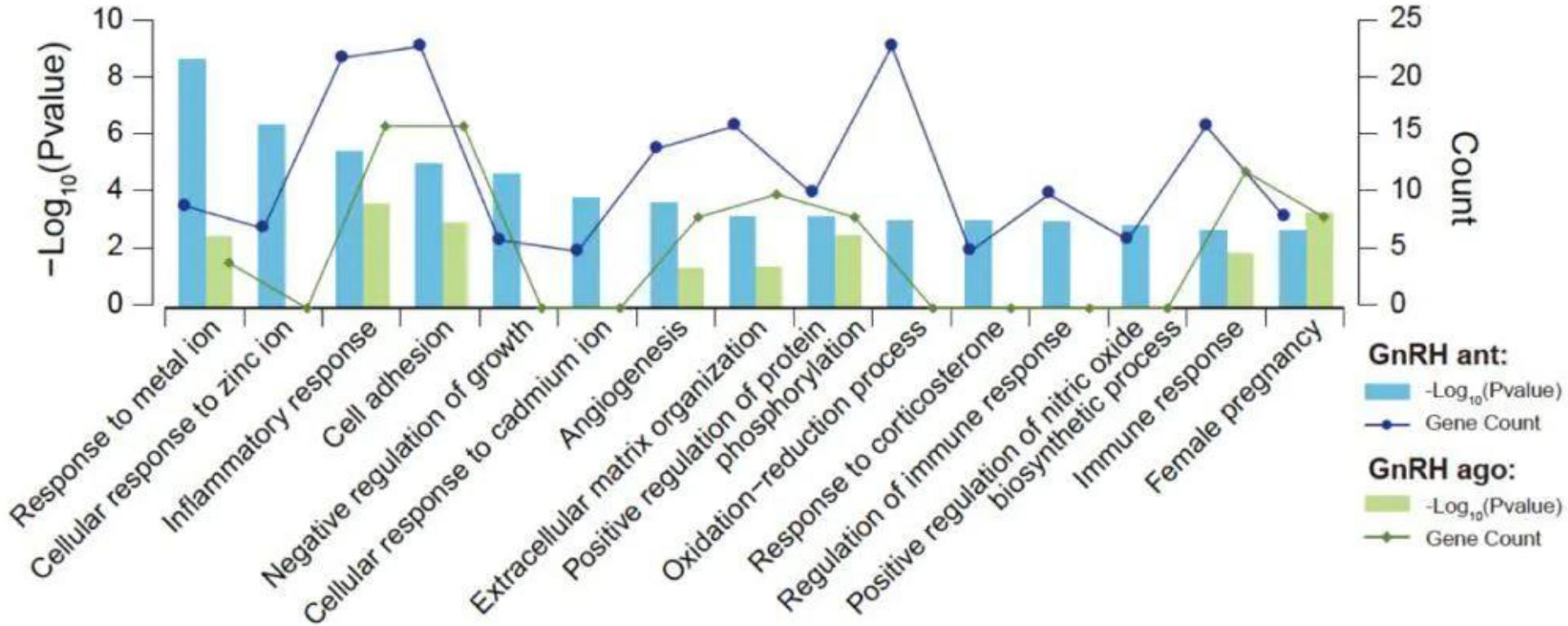
Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	GOTERM_BP_DIRECT	defense response to fungus	RT		5	3.4	5.6E-	5.6E-2
	GOTERM_BP_DIRECT	antibacterial humoral response	RT		5		3.9E-4	1.8E-1
	GOTERM_BP_DIRECT	negative regulation of apoptotic process	RT		1	3	9.4E-4	2.8E-1
	GOTERM_BP_DIRECT	positive regulation of gene expression					1.1E-	2.5E-1
	GOTERM_BP_DIRECT	positive regulation of GTPase activity					1.7E-	2.9E-1
	GOTERM_BP_DIRECT	cell chemotaxis	RT		5	3.4	1.7E-3	2.6E-1
	GOTERM_BP_DIRECT	eosinophil chemotaxis	RT		3	2.1	2.1E-3	2.7E-1
	GOTERM_BP_DIRECT	chemotaxis	RT		6	4.1	2.8E-3	3.0E-1
	GOTERM_BP_DIRECT	chondrocyte differentiation	RT		4	2.8	3.5E-3	3.4E-1
	GOTERM_BP_DIRECT	cell-cell signaling	RT		8	5.5	4.0E-3	3.4E-1
	GOTERM_BP_DIRECT	monocyte chemotaxis	RT		4	2.8	4.4E-3	3.4E-1

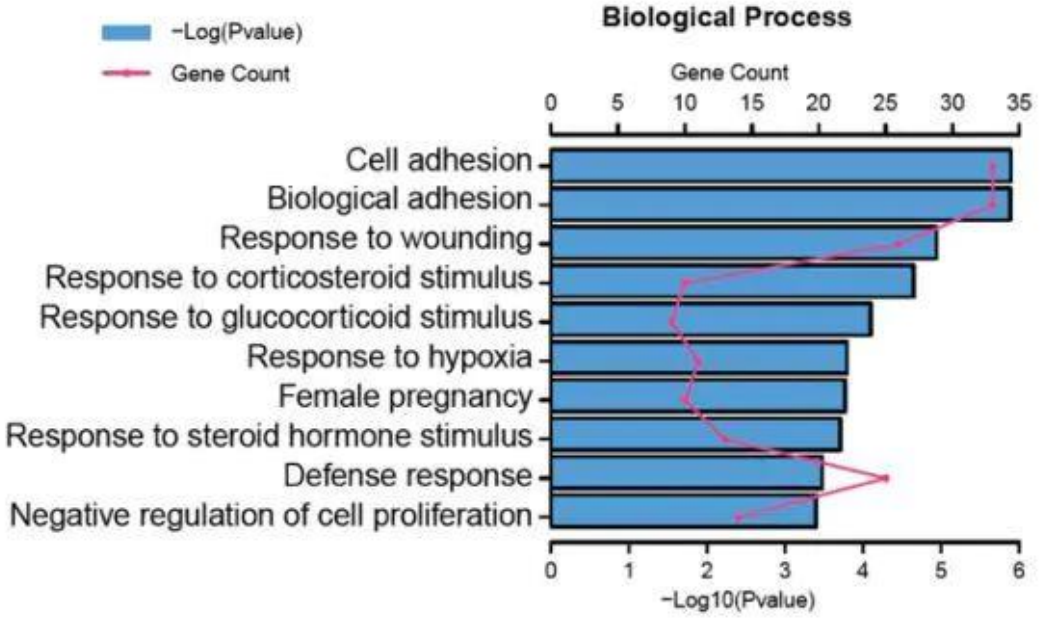
Fisher exact test p-value

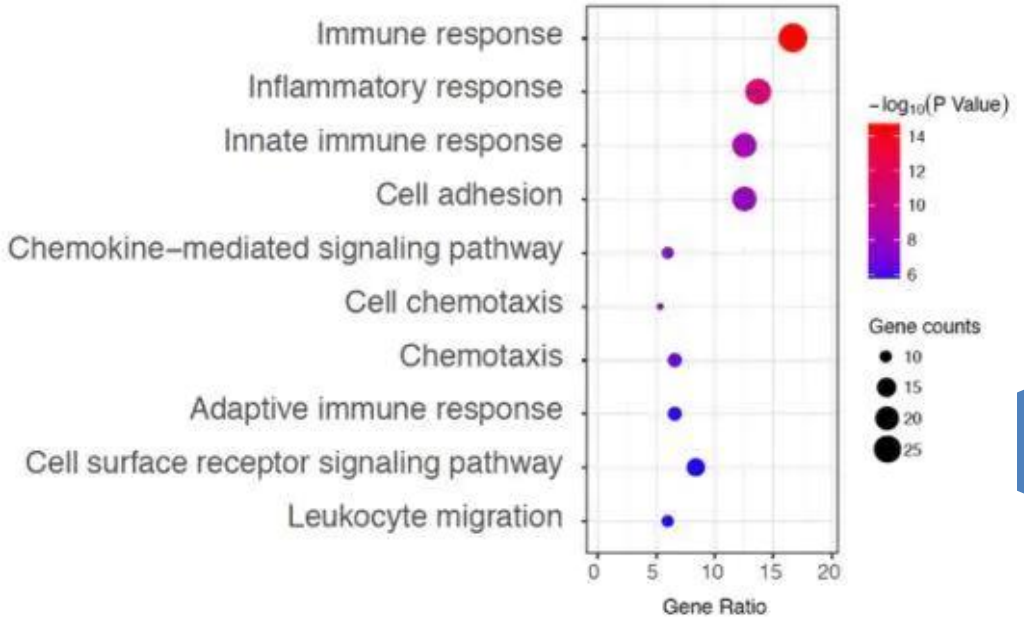




QuickGO - https://www.ebi.ac.uk/QuickGO


−Log10(Pvalue)
Count
Response to metal ion
Cellular response to zinc ion
Inflammatory response
Cell adhesion
Negative regulation of growth
Cellular response to cadmium ion
Angiogenesis
Extracellular matrix organization
Positive regulation of protein phosphorylation
Oxidation−reduction process
Response to corticosterone
Regulation of immune response
Positive regulation of nitric oxide biosynthetic process
Immune response
Female pregnancy
GnRH ant:
-Log10(Pvalue)
Gene Count
GnRH ago:
-Log10(Pvalue)
Gene Count


−Log(Pvalue)
Gene Count
Biological Process
Gene Count
Cell adhesion
Biological adhesion
Response to wounding
Response to corticosteroid stimulus
Response to glucocorticoid stimulus
Response to hypoxia
Female pregnancy
Response to steroid hormone stimulus
Defense response
Negative regulation of cell proliferation
−Log10(Pvalue)


Immune response
Inflammatory response
Innate immune response
Cell adhesion
Chemokine−mediated signaling pathway
Cell chemotaxis
Chemotaxis
Adaptive immune response
Cell surface receptor signaling pathway
Leukocyte migration
Gene Ratio
−log10(P Value)
Gene counts

⊟ Pathways (3 selected)

☑	BBID	4.8%	7	Chart
☑	BIOCARTA	17.9%	26	Chart
☐	EC_NUMBER	24.1%	35	Chart
☑	KEGG_PATHWAY	45.5%	66	Chart
☐	REACTOME_PATHWAY	61.4%	89	Chart

⊞ Protein_Domains (3 selected)

⊞ Protein_Interactions (0 selected)

⊞ Tissue_Expression (0 selected)

Functional Annotation Chart

Help and Manual

Current Gene List: List_4
Current Background: Homo sapiens
1140 DAVID IDs

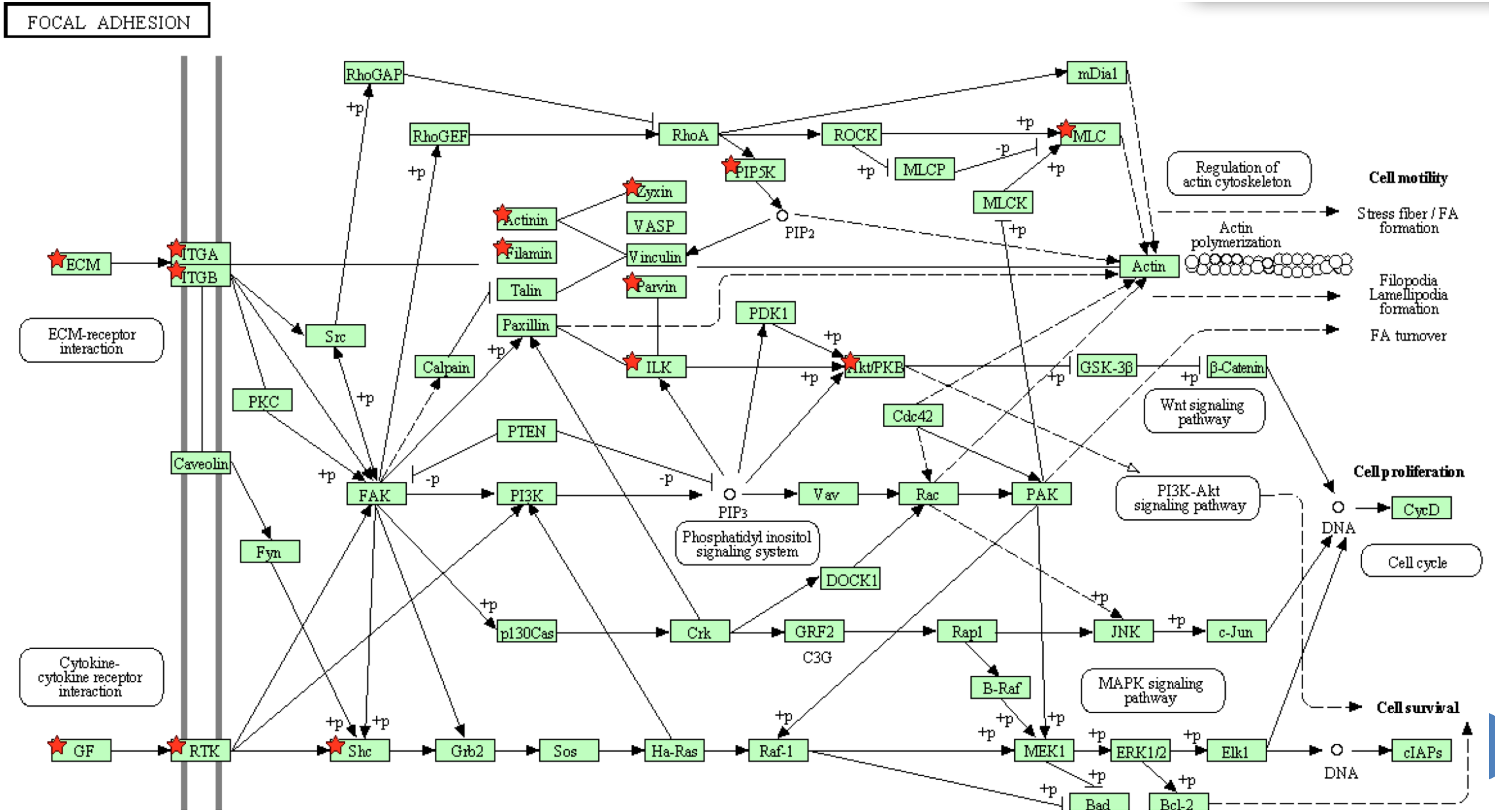
⊞ **Options**

Rerun Using Options | Create Sublist

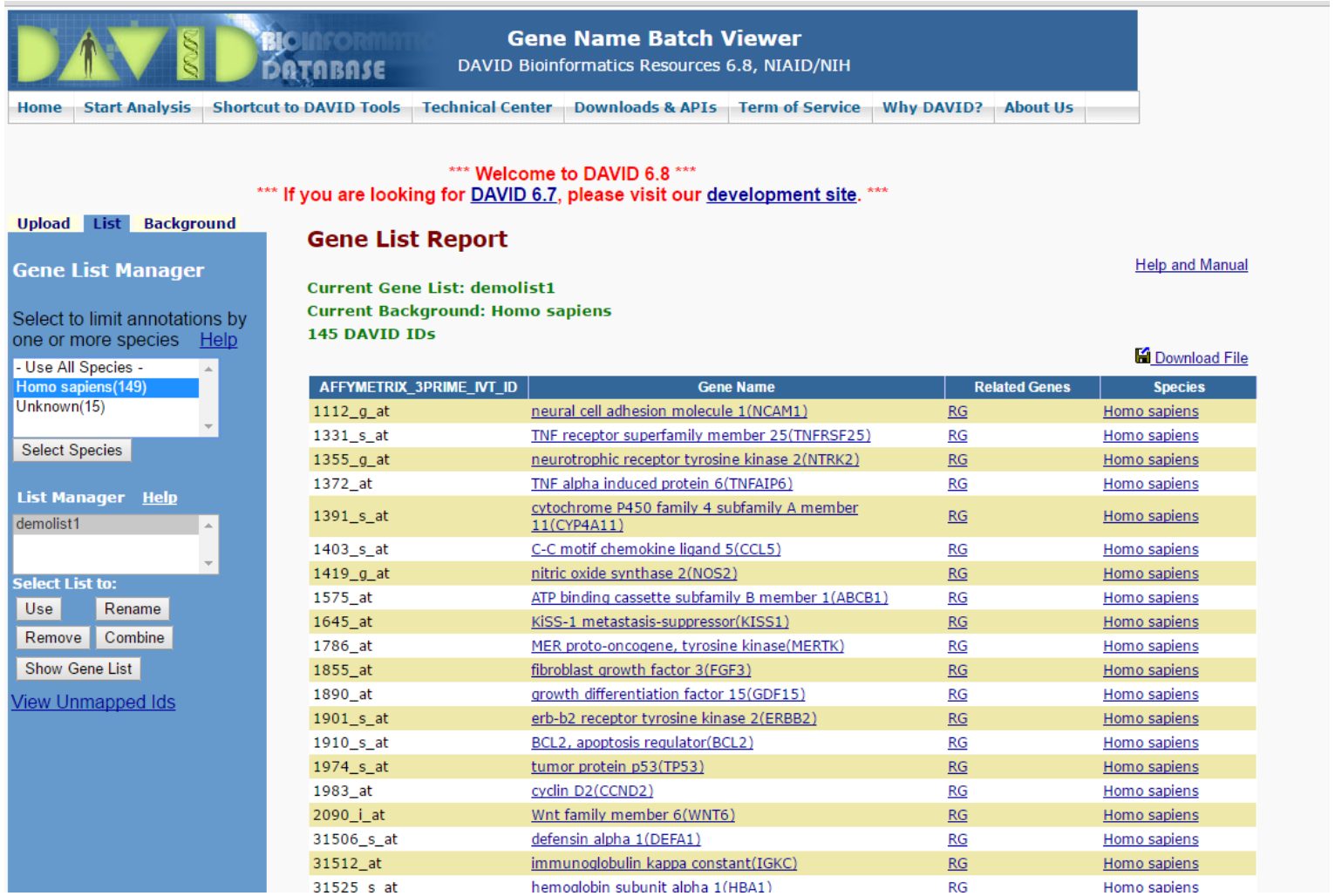
24 chart records

Download File

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	ECM-receptor interaction	RT		37	3.2	1.8E-21	2.8E-19
	KEGG_PATHWAY	Focal adhesion	RT		49	4.3	6.2E-16	5.1E-14
	KEGG_PATHWAY	TGF-beta signaling pathway	RT		18	1.6	3.9E-5	2.0E-3
	KEGG_PATHWAY	Pathways in cancer	RT		40	3.5	1.7E-4	6.5E-3
	KEGG_PATHWAY	Complement and coagulation cascades	RT		14	1.2	4.6E-4	1.4E-2
	KEGG_PATHWAY	Basal cell carcinoma	RT		12	1.1	7.5E-4	1.9E-2
	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT		28	2.5	7.7E-4	1.7E-2
	KEGG_PATHWAY	Cell adhesion molecules (CAMs)	RT		19	1.7	2.3E-3	4.3E-2
	KEGG_PATHWAY	Chondroitin sulfate biosynthesis	RT		7	0.6	2.4E-3	3.9E-2
	KEGG_PATHWAY	Hedgehog signaling pathway	RT		11	1.0	3.1E-3	4.7E-2
	KEGG_PATHWAY	Hematopoietic cell lineage	RT		14	1.2	3.8E-3	5.1E-2
	KEGG_PATHWAY	Gap junction	RT		13	1.1	1.3E-2	1.5E-1
	KEGG_PATHWAY	Vascular smooth muscle contraction	RT		15	1.3	1.5E-2	1.6E-1


FOCAL ADHESION
RhoGAP
RhoGEF
RhoA
ROCK
MLCP
MLC
MLCK
PIP5K
PIP2
mDia1
Regulation of actin cytoskeleton
Cell motility
Stress fiber / FA formation
Actin polymerization
Actin
Filopodia Lamellipodia formation
FA turnover
Cyxin
VASP
Vinculin
Parvin
Actinin
Filamin
Talin
Paxillin
ECM
ITGA
ITGB
ECM-receptor interaction
Src
Calpain
PKC
PDK1
ILK
Akt/PKB
GSK-3β
β-Catenin
Wnt signaling pathway
Cdc42
PTEN
Caveolin
FAK
PI3K
PIP3
Vav
Rac
PAK
PI3K-Akt signaling pathway
Cell proliferation
CycD
DNA
Phosphatidyl inositol signaling system
Fyn
DOCK1
Cell cycle
p130Cas
Crk
GRF2
C3G
Rap1
JNK
c-Jun
Cytokine-cytokine receptor interaction
B-Raf
MAPK signaling pathway
Cell survival
GF
RTK
Shc
Grb2
Sos
Ha-Ras
Raf-1
MEK1
ERK1/2
Elk1
DNA
cIAPs
Bad
Bcl-2
+p
-p

GENE NAME BATCH VIEWER



Gene Name Batch Viewer
DAVID Bioinformatics Resources 6.8, NIAID/NIH

Home | Start Analysis | Shortcut to DAVID Tools | Technical Center | Downloads & APIs | Term of Service | Why DAVID? | About Us

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Upload | List | Background

Gene List Manager

Select to limit annotations by one or more species Help

- Use All Species -
Homo sapiens(149)
Unknown(15)

Select Species

List Manager Help

demolist1

Select List to:

Use | Rename | Remove | Combine | Show Gene List

View Unmapped Ids

Gene List Report

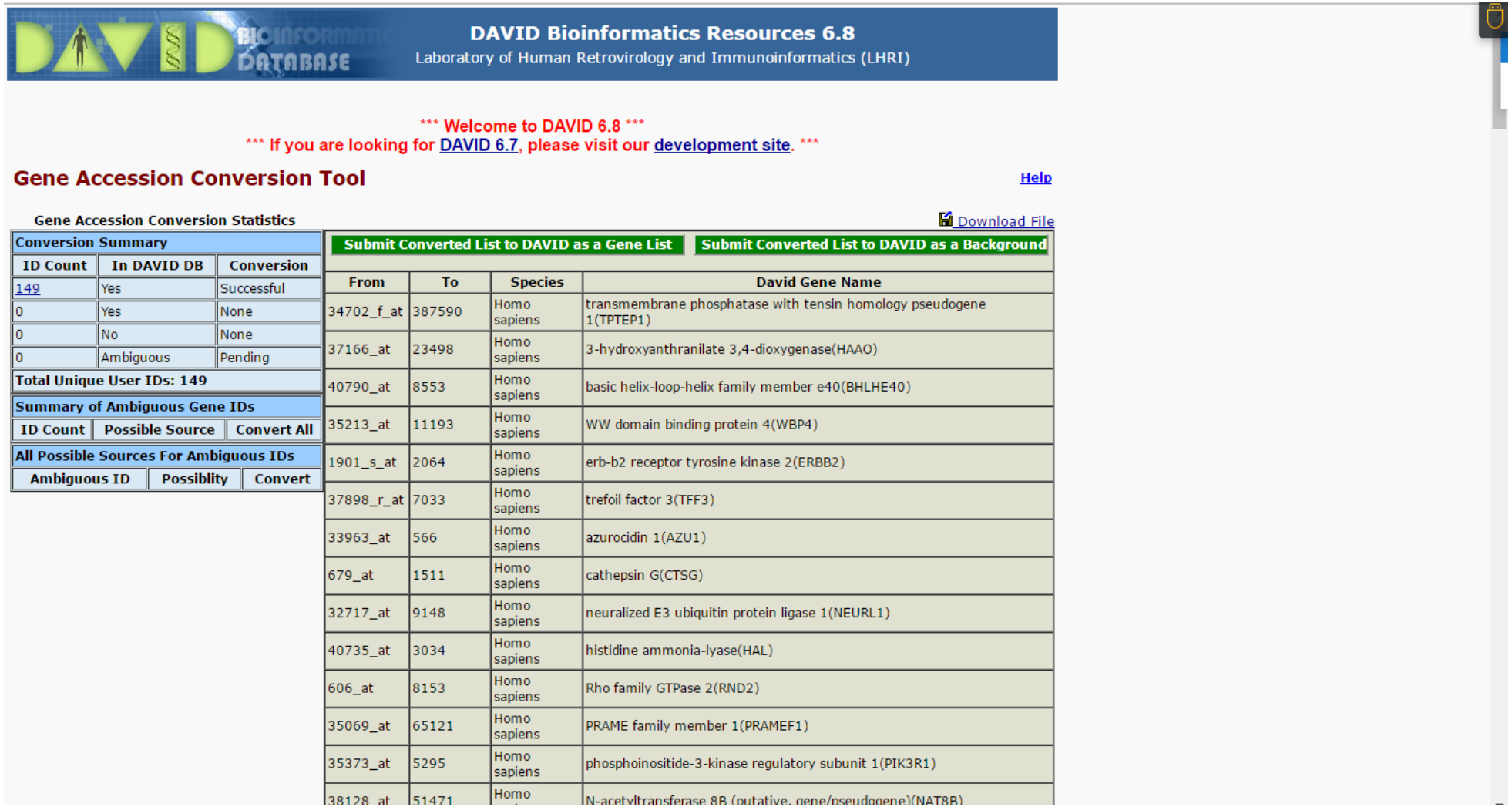
Help and Manual

Current Gene List: demolist1
Current Background: Homo sapiens
145 DAVID IDs

Download File

AFFYMETRIX_3PRIME_IVT_ID	Gene Name	Related Genes	Species
1112_g_at	neural cell adhesion molecule 1(NCAM1)	RG	Homo sapiens
1331_s_at	TNF receptor superfamily member 25(TNFRSF25)	RG	Homo sapiens
1355_g_at	neurotrophic receptor tyrosine kinase 2(NTRK2)	RG	Homo sapiens
1372_at	TNF alpha induced protein 6(TNFAIP6)	RG	Homo sapiens
1391_s_at	cytochrome P450 family 4 subfamily A member 11(CYP4A11)	RG	Homo sapiens
1403_s_at	C-C motif chemokine ligand 5(CCL5)	RG	Homo sapiens
1419_g_at	nitric oxide synthase 2(NOS2)	RG	Homo sapiens
1575_at	ATP binding cassette subfamily B member 1(ABCB1)	RG	Homo sapiens
1645_at	KiSS-1 metastasis-suppressor(KISS1)	RG	Homo sapiens
1786_at	MER proto-oncogene, tyrosine kinase(MERTK)	RG	Homo sapiens
1855_at	fibroblast growth factor 3(FGF3)	RG	Homo sapiens
1890_at	growth differentiation factor 15(GDF15)	RG	Homo sapiens
1901_s_at	erb-b2 receptor tyrosine kinase 2(ERBB2)	RG	Homo sapiens
1910_s_at	BCL2, apoptosis regulator(BCL2)	RG	Homo sapiens
1974_s_at	tumor protein p53(TP53)	RG	Homo sapiens
1983_at	cyclin D2(CCND2)	RG	Homo sapiens
2090_i_at	Wnt family member 6(WNT6)	RG	Homo sapiens
31506_s_at	defensin alpha 1(DEFA1)	RG	Homo sapiens
31512_at	immunoglobulin kappa constant(IGKC)	RG	Homo sapiens
31525_s_at	hemoglobin subunit alpha 1(HBA1)	RG	Homo sapiens

ID CONVERSION



DAVID Bioinformatics Resources 6.8
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

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*** If you are looking for DAVID 6.7, please visit our development site. ***

Gene Accession Conversion Tool

Help

Gene Accession Conversion Statistics

Download File

Conversion Summary		
ID Count	In DAVID DB	Conversion
149	Yes	Successful
0	Yes	None
0	No	None
0	Ambiguous	Pending
Total Unique User IDs: 149		

Summary of Ambiguous Gene IDs		
ID Count	Possible Source	Convert All

All Possible Sources For Ambiguous IDs		
Ambiguous ID	Possiblity	Convert

Submit Converted List to DAVID as a Gene List | Submit Converted List to DAVID as a Background

From	To	Species	David Gene Name
34702_f_at	387590	Homo sapiens	transmembrane phosphatase with tensin homology pseudogene 1(TPTEP1)
37166_at	23498	Homo sapiens	3-hydroxyanthranilate 3,4-dioxygenase(HAAO)
40790_at	8553	Homo sapiens	basic helix-loop-helix family member e40(BHLHE40)
35213_at	11193	Homo sapiens	WW domain binding protein 4(WBP4)
1901_s_at	2064	Homo sapiens	erb-b2 receptor tyrosine kinase 2(ERBB2)
37898_r_at	7033	Homo sapiens	trefoil factor 3(TFF3)
33963_at	566	Homo sapiens	azurocidin 1(AZU1)
679_at	1511	Homo sapiens	cathepsin G(CTSG)
32717_at	9148	Homo sapiens	neuralized E3 ubiquitin protein ligase 1(NEURL1)
40735_at	3034	Homo sapiens	histidine ammonia-lyase(HAL)
606_at	8153	Homo sapiens	Rho family GTPase 2(RND2)
35069_at	65121	Homo sapiens	PRAME family member 1(PRAMEF1)
35373_at	5295	Homo sapiens	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)
38128_at	51471	Homo	N-acetyltransferase 8B (putative, gene/pseudogene)(NAT8B)

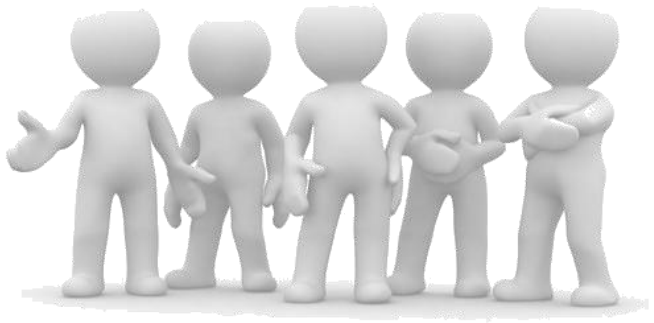
Network visulazation

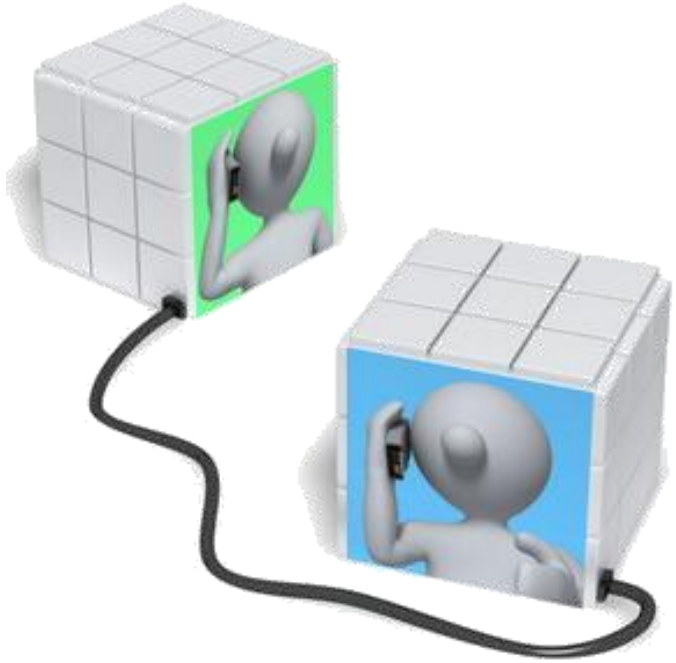
Graph Theory

SMALL WORLD

- Six degrees of separation

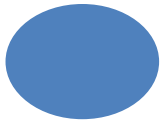
Steps ≤ 6





常用网络参数

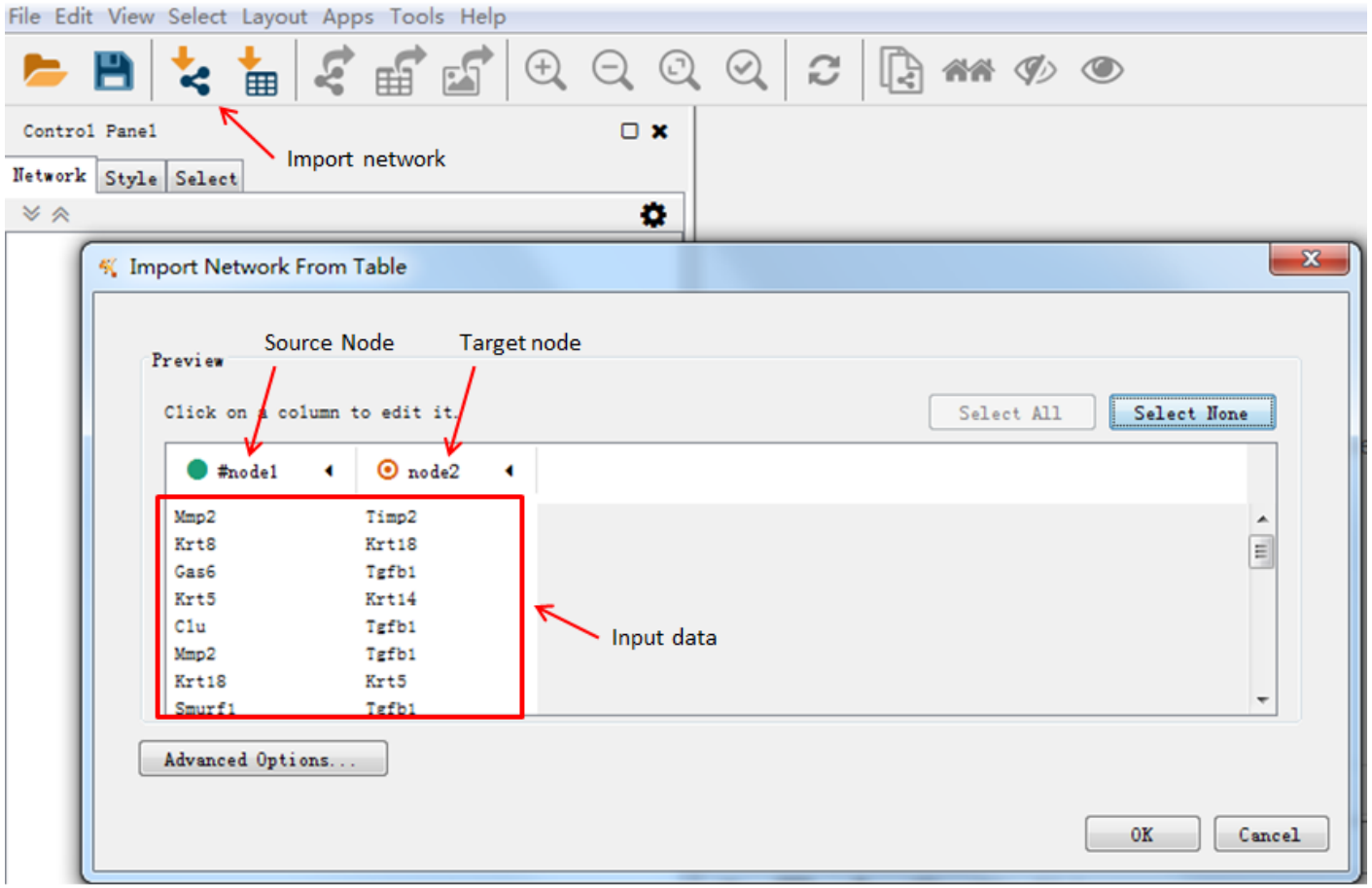
Degree	How many links a node has to other node. Find hubs.
Betweenness centrality(BC)	Find important node as bottlenecks in a network.
The edge BC	Reflect edges role instead of nodes.
The closeness centrality(CC)	Indicate which node is close to the topological center of the network.

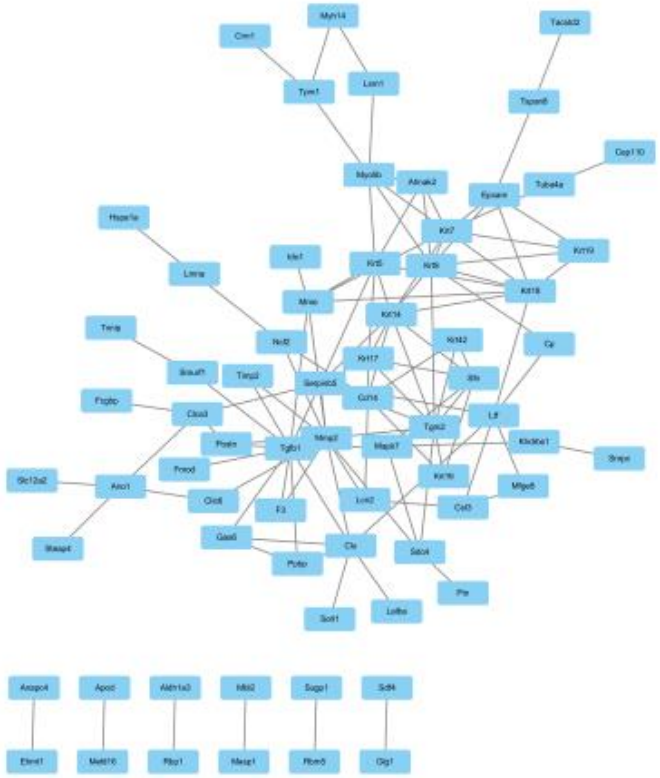


CYTOSCAPE?

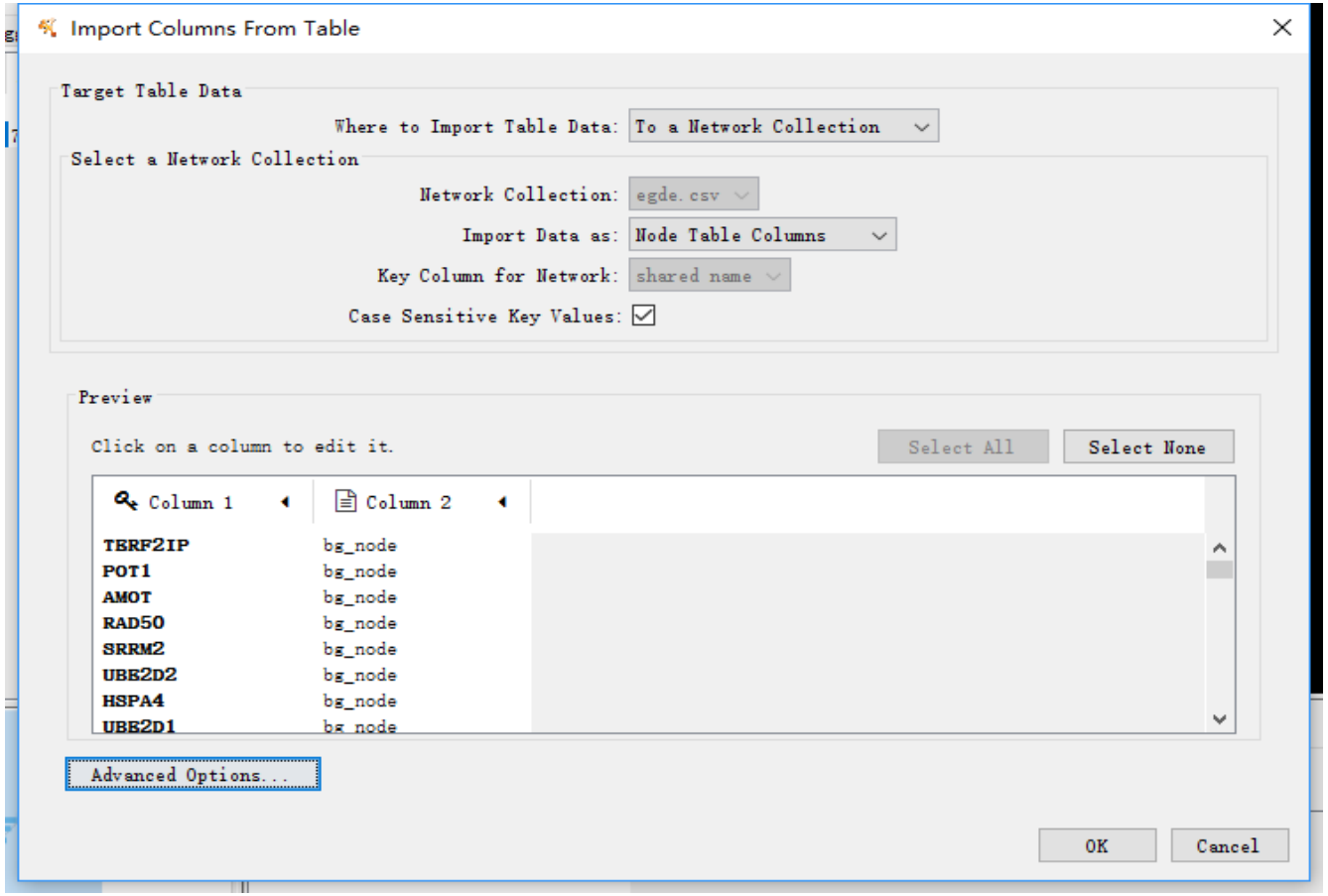
- http://www.cytoscape.org/

File -> Import -> Network

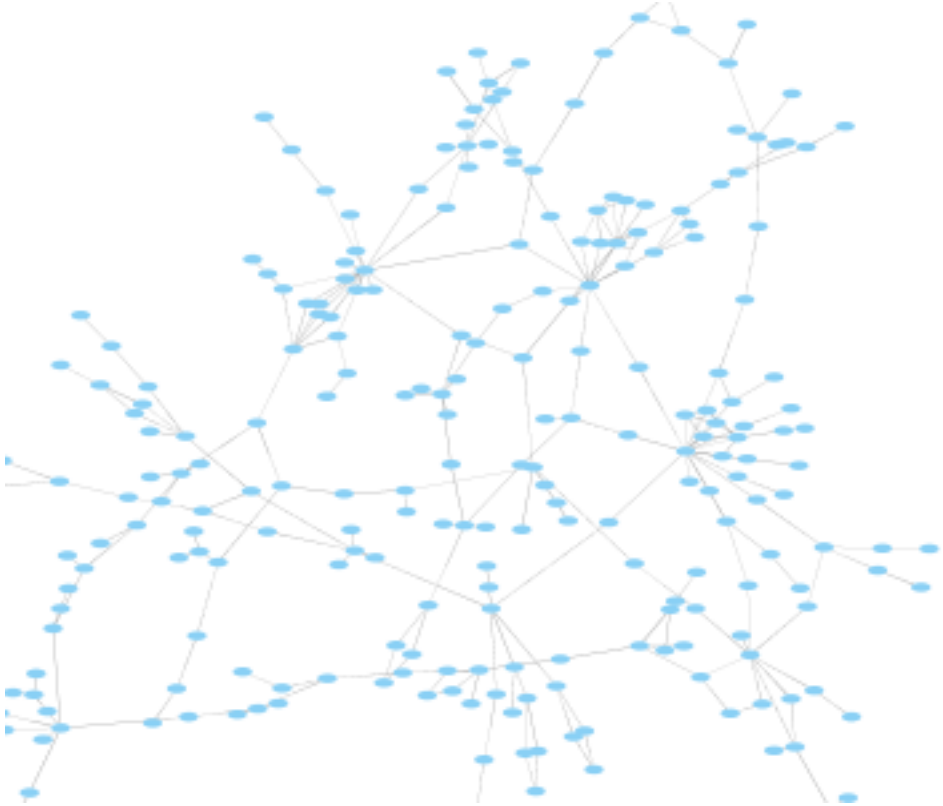


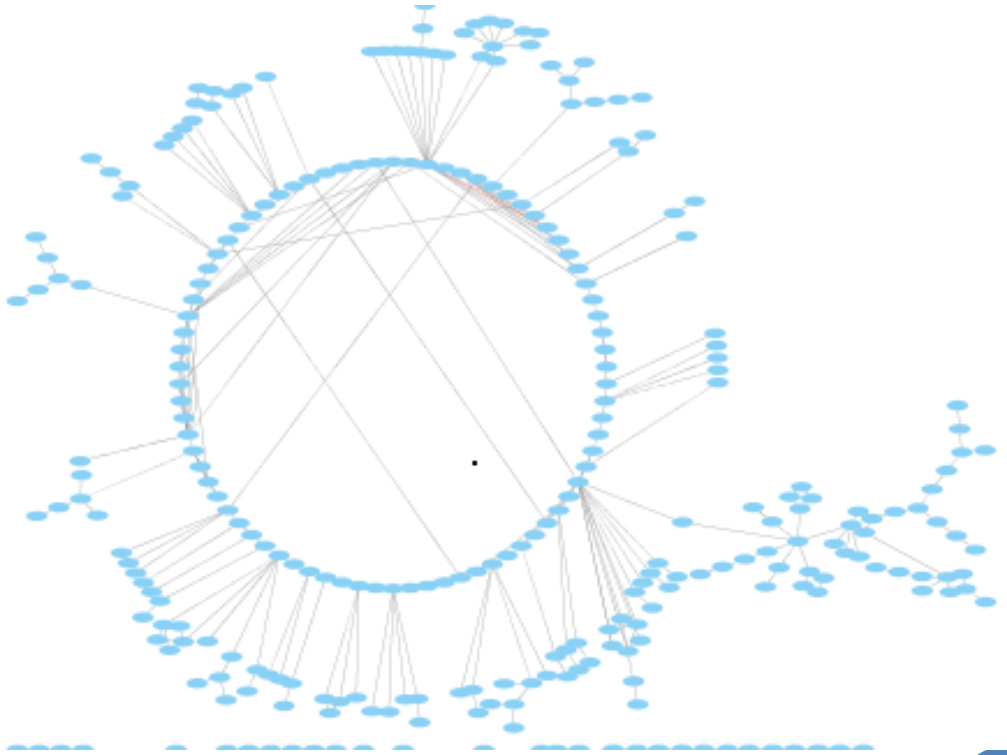


FILE>IMPORT>TABLE>FILE

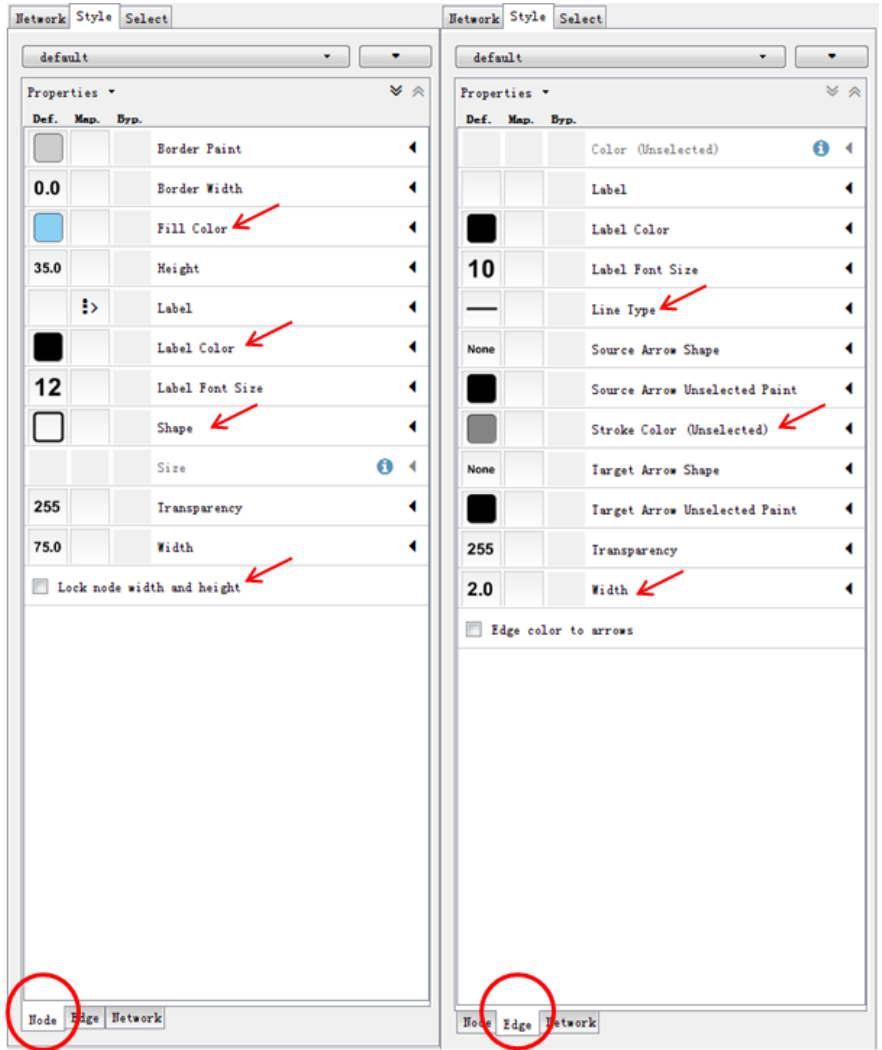


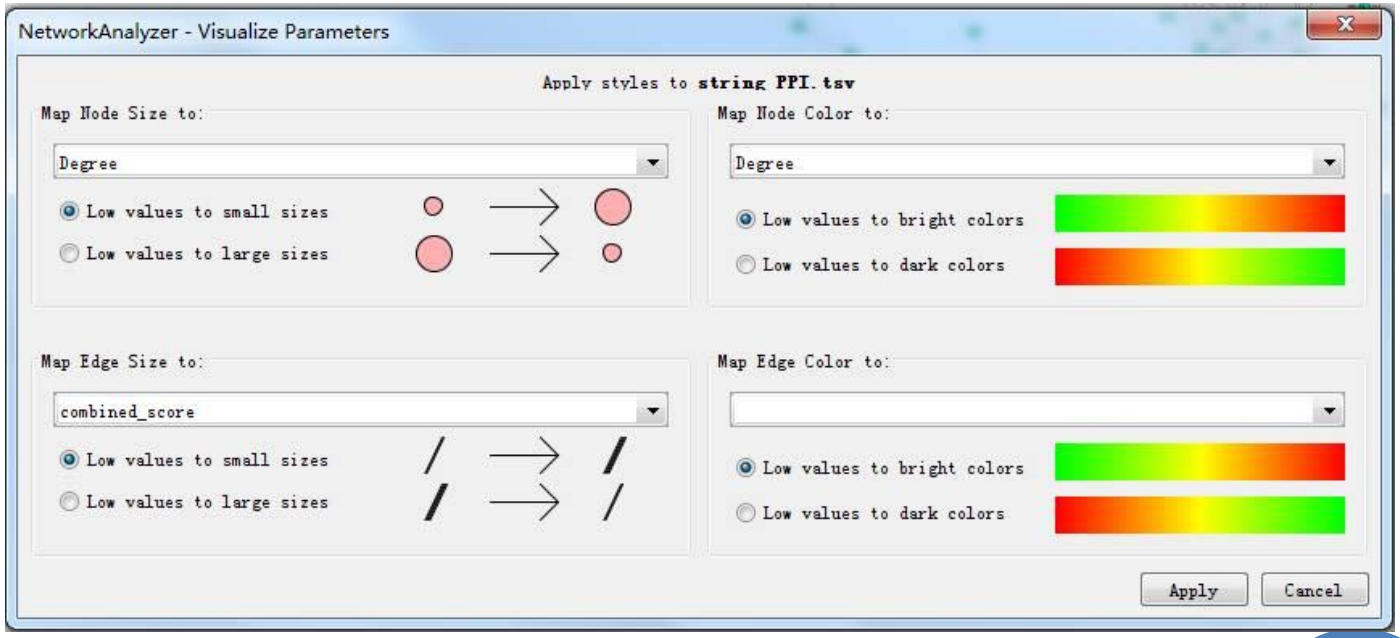
Layout > yFiles layouts > organic > circular



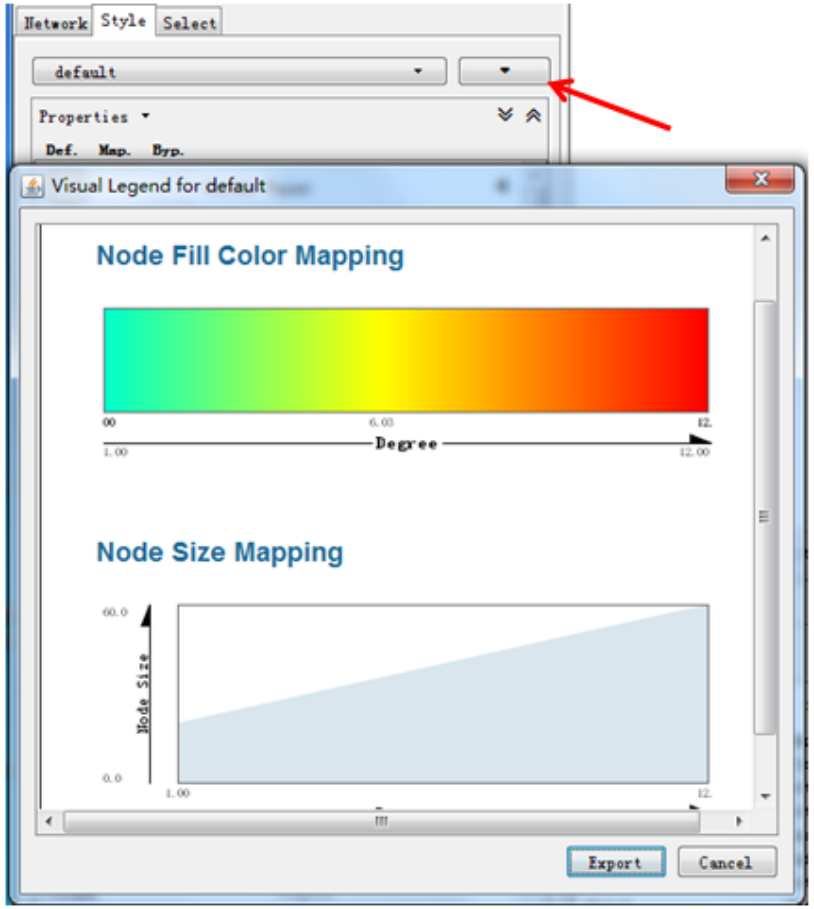


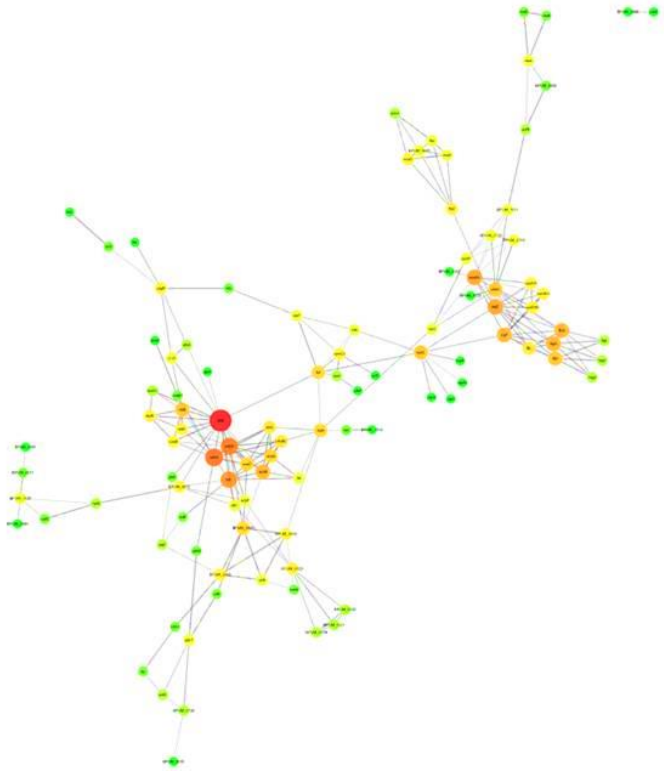
Tools -> NetworkAnlyzer -> Network Anlysis
Tools -> NetworkAnlyzer -> Generate style from statistics



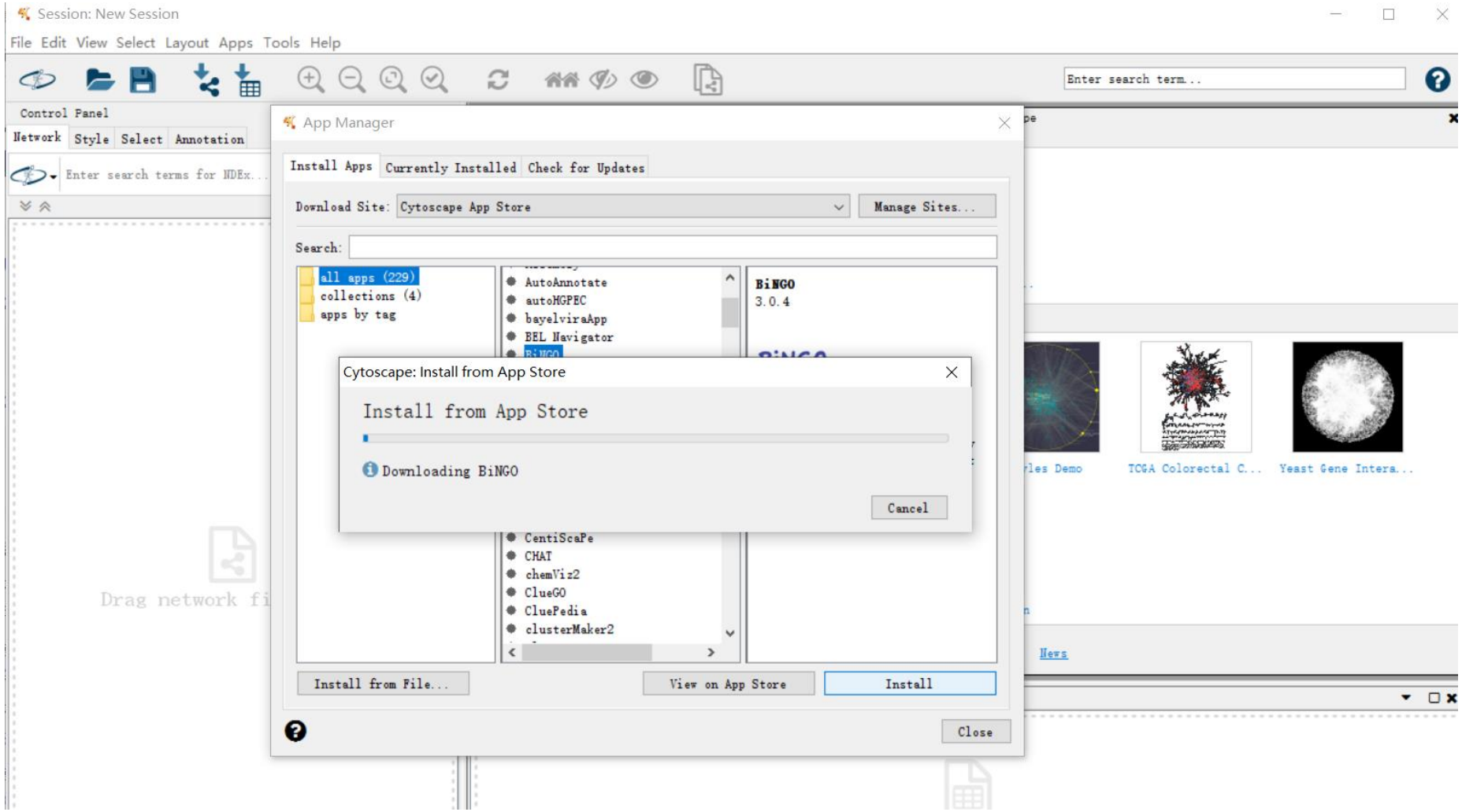


-> CREAT LEGEND





PLUG-INS

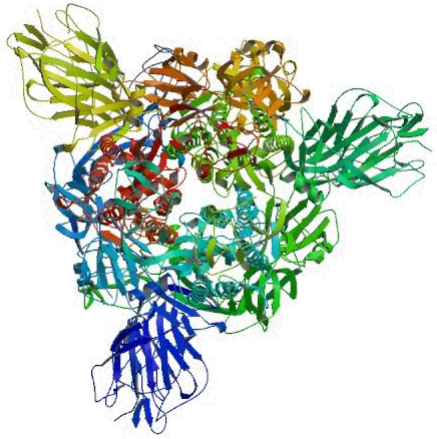

Session: New Session
File Edit View Select Layout Apps Tools Help
Enter search term...
Control Panel
Network Style Select Annotation
App Manager
Install Apps
Currently Installed
Check for Updates
Download Site: Cytoscape App Store
Manage Sites...
Search:
all apps (229)
collections (4)
apps by tag
AutoAnnotate
autoHGPEC
bayelviraApp
BEL Navigator
BiNGO
3.0.4
Cytoscape: Install from App Store
Install from App Store
Downloading BiNGO
Cancel
CentiScaPe
CHAT
chemViz2
ClueGO
CluePedia
clusterMaker2
Install from File...
View on App Store
Install
Close
Drag network fi
TCGA Colorectal C...
Yeast Gene Intera...
News

SUMMARY

- Database

序列分析的内容

- 蛋白质家族分析
- 相似序列搜索
- 系统发育分析
- 蛋白质理化性质
- 序列模式、结构域、基序搜索
- 翻译后修饰预测
- 二级结构、三级结构预测
- 定位、跨膜预测
- 功能、生化途径

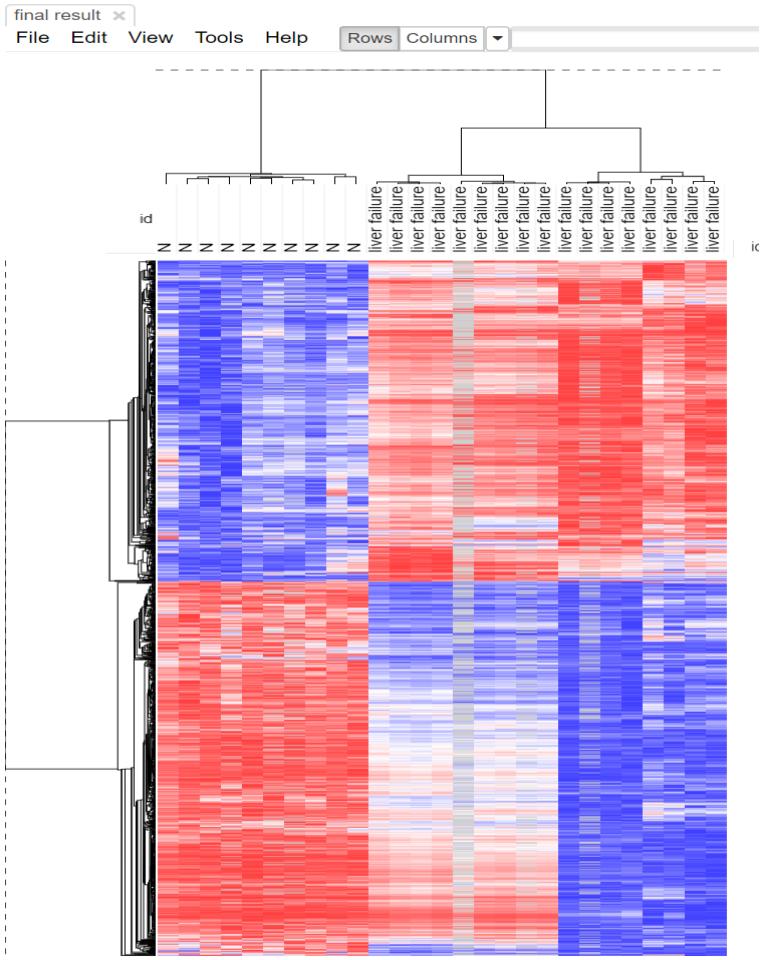


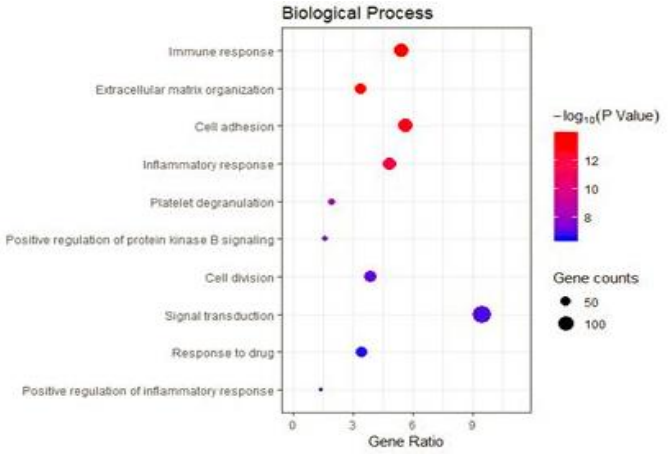
- Who
- What
- Where
- How

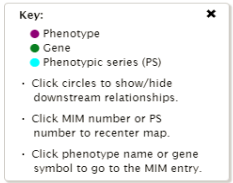
序列比对，进化

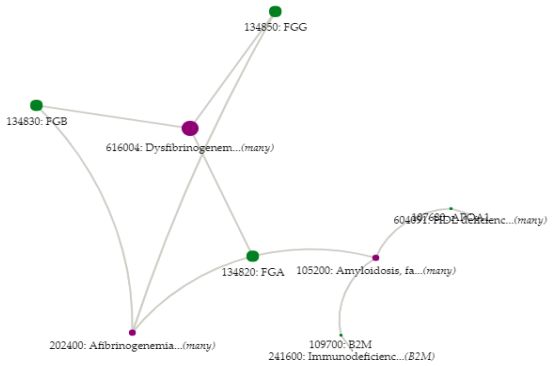
- Blast
- MSA
- tree

OMICS


final result
File Edit View Tools Help
Rows Columns
id
liver failure


Biological Process
Immune response
Extracellular matrix organization
Cell adhesion
Inflammatory response
Platelet degranulation
Positive regulation of protein kinase B signaling
Cell division
Signal transduction
Response to drug
Positive regulation of inflammatory response
0
3
6
9
Gene Ratio
−log10(P Value)
12
10
8
Gene counts
50
100


Key:
Phenotype
Gene
Phenotypic series (PS)
Click circles to show/hide downstream relationships.
Click MIM number or PS number to recenter map.
Click phenotype name or gene symbol to go to the MIM entry.


134850: FGG
134830: FGB
616004: Dysfibrinogenem...(many)
134820: FGA
105200: Amyloidosis, fa...(many)
202400: Afibrinogenemia...(many)
109700: B2M
241600: Immunodeficienc...(B2M)