

Categorical Gene Set Practical Results


Panther

Analysis Summary: Please report in publication [?](#)

Analysis Type: PANTHER Overrepresentation Test (Released 20171205)

Annotation Version and Release Date: PANTHER version 13.1 Released 2018-02-03

Analyzed List: Client Text Box Input (Homo sapiens)

 There are duplicate IDs in the file. The unique set of IDs will be used.

[Change](#)

Reference List: Homo sapiens (all genes in database)

[Change](#)

Annotation Data Set: PANTHER GO-Slim Biological Process ▼

Test Type: Fisher's Exact with FDR multiple test correction Binomial

Results [?](#)

	Reference list	Client Text Box Input
Mapped IDs:	21042 out of 21042	1346 out of 1392
Unmapped IDs:	0	81
Multiple mapping information:	0	76

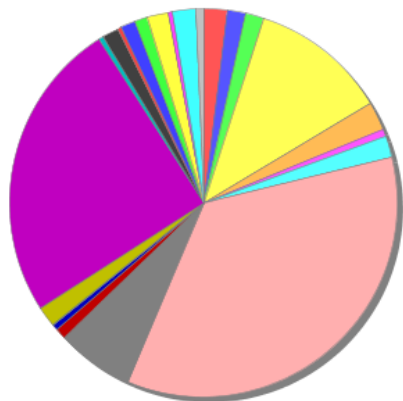
Panther

	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)					
PANTHER GO-Slim Biological Process	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
gluconeogenesis	23	7	1.52	4.60	+	2.01E-03	2.72E-02
↳ metabolic process	5878	441	388.85	1.13	+	2.84E-03	3.30E-02
segment specification	78	15	5.16	2.91	+	5.80E-04	9.43E-03
↳ developmental process	1501	167	99.30	1.68	+	5.03E-10	1.23E-07
transmembrane receptor protein tyrosine kinase signaling pathway	151	26	9.99	2.60	+	4.86E-05	1.08E-03
↳ cell communication	2686	226	177.69	1.27	+	2.86E-04	5.81E-03
↳ cellular process	8247	631	545.57	1.16	+	6.70E-06	3.27E-04
sulfur compound metabolic process	82	14	5.42	2.58	+	2.36E-03	3.02E-02
ectoderm development	212	34	14.02	2.42	+	1.22E-05	4.26E-04
embryo development	106	17	7.01	2.42	+	1.93E-03	2.77E-02
cell-cell adhesion	141	21	9.33	2.25	+	1.44E-03	2.20E-02
↳ cell adhesion	356	47	23.55	2.00	+	3.71E-05	1.01E-03
↳ biological adhesion	356	47	23.55	2.00	+	3.71E-05	9.06E-04
nervous system development	314	39	20.77	1.88	+	4.88E-04	8.51E-03
↳ system development	452	48	29.90	1.61	+	2.59E-03	3.16E-02
cell differentiation	548	65	36.25	1.79	+	2.67E-05	8.14E-04
cellular component morphogenesis	423	49	27.98	1.75	+	4.59E-04	8.61E-03
lipid metabolic process	394	42	26.06	1.61	+	4.75E-03	5.04E-02
Unclassified	10206	561	675.16	.83	-	2.89E-09	3.53E-07
G-protein coupled receptor signaling pathway	456	15	30.17	.50	-	4.83E-03	4.92E-02
sensory perception of smell	240	0	15.88	< 0.01	-	4.73E-07	2.88E-05
↳ sensory perception of chemical stimulus	282	1	18.66	.05	-	3.71E-07	3.02E-05
↳ sensory perception	424	7	28.05	.25	-	6.76E-06	2.75E-04
mitochondrion organization	92	0	6.09	< 0.01	-	4.28E-03	4.75E-02

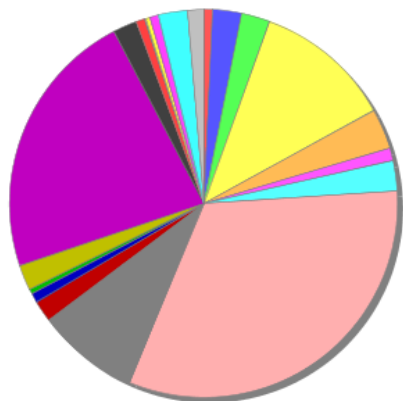
Panther

	Homo sapiens (REF)	Client Text Box Input (▼ Hierarchy NEW! ?)					
GO biological process complete	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
antigen processing and presentation of endogenous peptide antigen via MHC class I	10	6	.66	9.07	+	2.63E-04	1.36E-02
↳ immune system process	2575	216	170.35	1.27	+	4.92E-04	2.23E-02
↳ antigen processing and presentation of endogenous peptide antigen	11	6	.73	8.25	+	3.86E-04	1.87E-02
↳ antigen processing and presentation of endogenous antigen	14	6	.93	6.48	+	1.03E-03	3.96E-02
cellular response to forskolin	11	6	.73	8.25	+	3.86E-04	1.87E-02
↳ response to ketone	185	29	12.24	2.37	+	7.83E-05	5.02E-03
↳ response to oxygen-containing compound	1445	151	95.59	1.58	+	1.51E-07	2.45E-05
↳ response to chemical	4164	347	275.46	1.26	+	5.95E-06	5.80E-04
↳ response to stimulus	8142	654	538.62	1.21	+	1.23E-09	3.81E-07
↳ response to organic substance	2765	254	182.91	1.39	+	1.96E-07	2.95E-05
↳ cellular response to oxygen-containing compound	905	98	59.87	1.64	+	8.64E-06	7.98E-04
↳ cellular response to chemical stimulus	2624	234	173.59	1.35	+	5.79E-06	5.75E-04
↳ cellular response to stimulus	6423	506	424.90	1.19	+	6.90E-06	6.61E-04
↳ cellular process	15084	1120	997.86	1.12	+	3.21E-13	2.16E-10
↳ response to lipid	834	93	55.17	1.69	+	3.98E-06	4.23E-04
↳ cellular response to organic substance	2150	191	142.23	1.34	+	6.56E-05	4.43E-03
↳ cellular response to organic cyclic compound	503	55	33.28	1.65	+	6.83E-04	2.88E-02
↳ response to organic cyclic compound	879	102	58.15	1.75	+	3.05E-07	4.39E-05
↳ response to forskolin	11	6	.73	8.25	+	3.86E-04	1.86E-02
↳ response to platelet aggregation inhibitor	11	6	.73	8.25	+	3.86E-04	1.86E-02
↳ response to drug	911	101	60.27	1.68	+	1.93E-06	2.34E-04

Panther Plots

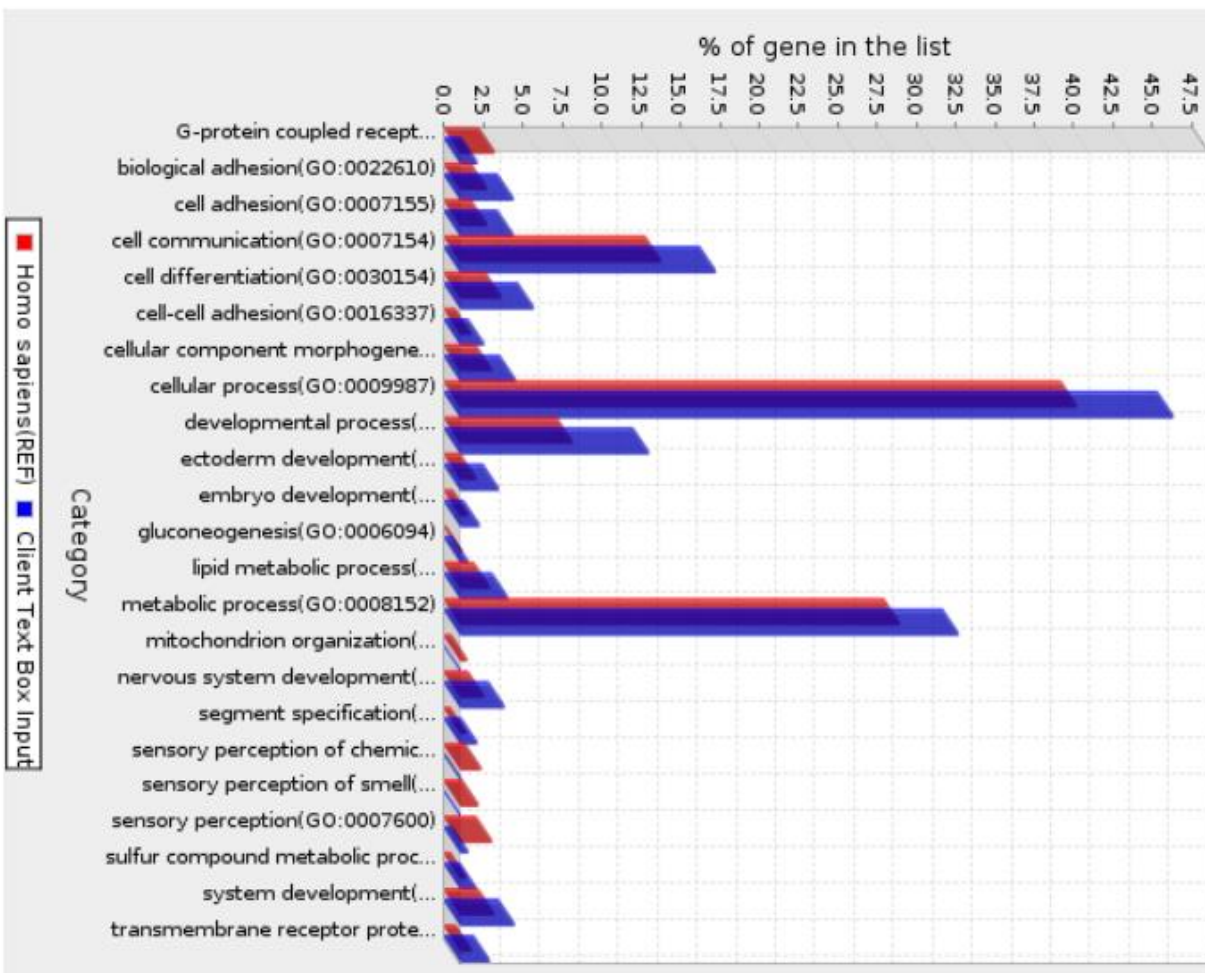


Homo sapiens(REF)



Client Text Box Input

- G-protein coupled receptor signaling pathway(GO:0007186)
- biological adhesion(GO:0022610)
- cell adhesion(GO:0007155)
- cell communication(GO:0007154)
- cell differen
- cell-cell adh
- cellular corr
- cellular pro
- developmer
- ectoderm d
- embryo dev
- gluconeoge
- lipid metab
- metabolic p
- mitochondri
- nervous sys
- segment sp
- sensory per
- sensory per
- sensory per
- sulfur comp
- system dev
- transmemb



Panther Export

Analysis Type:	PANTHER Overrepresentation Test (Released 20171205)						
Annotation Version and Release Date:	PANTHER version 13.1 Released 2018-02-03						
Analyzed List:	Client Text There are duplicate IDs in the file. The unique set of IDs will be use						
Reference List:	Homo sapiens (all genes in database)						
Test Type:	FISHER						
PANTHER GO-Slim Biological Process	Homo sapiens	Client Text	Client Text	Client Text	Client Text	Client Text	Client Text
gluconeogenesis (GO:0006094)	23	7	1.52	+	4.6	2.01E-03	2.72E-02
segment specification (GO:0007379)	78	15	5.16	+	2.91	5.80E-04	9.43E-03
transmembrane receptor protein tyros	151	26	9.99	+	2.6	4.86E-05	1.08E-03
sulfur compound metabolic process (G	82	14	5.42	+	2.58	2.36E-03	3.02E-02
ectoderm development (GO:0007398)	212	34	14.02	+	2.42	1.22E-05	4.26E-04
embryo development (GO:0009790)	106	17	7.01	+	2.42	1.93E-03	2.77E-02
cell-cell adhesion (GO:0016337)	141	21	9.33	+	2.25	1.44E-03	2.20E-02
cell adhesion (GO:0007155)	356	47	23.55	+	2	3.71E-05	1.01E-03
biological adhesion (GO:0022610)	356	47	23.55	+	2	3.71E-05	9.06E-04
nervous system development (GO:000	314	39	20.77	+	1.88	4.88E-04	8.51E-03
cell differentiation (GO:0030154)	548	65	36.25	+	1.79	2.67E-05	8.14E-04
cellular component morphogenesis (G	423	49	27.98	+	1.75	4.59E-04	8.61E-03
developmental process (GO:0032502)	1501	167	99.3	+	1.68	5.03E-10	1.23E-07
lipid metabolic process (GO:0006629)	394	42	26.06	+	1.61	4.75E-03	5.04E-02
system development (GO:0048731)	452	48	29.9	+	1.61	2.59E-03	3.16E-02
cell communication (GO:0007154)	2686	226	177.69	+	1.27	2.86E-04	5.81E-03
cellular process (GO:0009987)	8247	631	545.57	+	1.16	6.70E-06	3.27E-04
metabolic process (GO:0008152)	5878	441	388.85	+	1.13	2.84E-03	3.30E-02
Unclassified (UNCLASSIFIED)	10206	561	675.16	-	0.83	2.89E-09	3.53E-07
G-protein coupled receptor signaling p	456	15	30.17	-	0.5	4.83E-03	4.92E-02

Panther Gene Lists

<input type="button" value="clr"/> <input type="button" value="all"/>		Gene ID	Mapped IDs	Gene Name Gene Symbol Ortholog	PANTHER Family/Subfamily	PANTHER Protein Class	Species
<input type="checkbox"/>	1.	HUMAN HGNC=32418 UniProtKB=Q99666	RGPD6 RGPD5	RANBP2-like and GRIP domain-containing protein 5/6 RGPD5 ortholog	E3 SUMO-PROTEIN LIGASE RANBP2-RELATED (PTHR23138:SF124)	G-protein modulator	Homo sapiens
<input type="checkbox"/>	2.	HUMAN HGNC=12009 UniProtKB=P60174	TPI1	Triosephosphate isomerase TPI1 ortholog	TRIOSEPHOSPHATE ISOMERASE (PTHR21139:SF15)	isomerase	Homo sapiens
<input type="checkbox"/>	3.	HUMAN HGNC=6936 UniProtKB=Q96RQ3	MCCC1	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial MCCC1 ortholog	METHYLCROTONOYL-COA CARBOXYLASE SUBUNIT ALPHA, MITOCHONDRIAL (PTHR18866:SF33)	ligase	Homo sapiens
<input type="checkbox"/>	4.	HUMAN HGNC=9849 UniProtKB=O14715	RGPD8	RANBP2-like and GRIP domain-containing protein 8 RGPD8 ortholog	E3 SUMO-PROTEIN LIGASE RANBP2-RELATED (PTHR23138:SF124)	G-protein modulator	Homo sapiens
<input type="checkbox"/>	5.	HUMAN HGNC=3606 UniProtKB=P09467	FBP1	Fructose-1,6-bisphosphatase 1 FBP1 ortholog	FRUCTOSE-1,6-BISPHOSPHATASE 1 (PTHR11556:SF11)	carbohydrate phosphatase	Homo sapiens
<input type="checkbox"/>	6.	HUMAN HGNC=26353 UniProtKB=Q86VV4	RANBP3L	Ran-binding protein 3-like RANBP3L ortholog	RAN-BINDING PROTEIN 3-LIKE (PTHR23138:SF88)	G-protein modulator	Homo sapiens
<input type="checkbox"/>	7.	HUMAN HGNC=4458 UniProtKB=P06744	GPI	Glucose-6-phosphate isomerase GPI ortholog	GLUCOSE-6-PHOSPHATE ISOMERASE (PTHR11469:SF4)	isomerase	Homo sapiens

DAVID

Please note that multiple species have been detected in your gene list. You may select a specific specie(s) with the List Manager on the left side of the page by highlighting the specific specie(s) and pressing the "Select" button. As a default, all species in your list will be used for analysis. Also note that you may need to select an appropriate background under the "BACKGROUNDS" tab in the manager to the left. By default, the background corresponding to the first species in the list will be selected if an uploaded or Affymetrix background is not in use.

OK

Upload **List** **Background**

Gene List Manager

Select to limit annotations by one or more species [Help](#)

- Use All Species -
Homo sapiens(1303)
Pan troglodytes(1247)
Bos taurus(1222)

Select Species

List Manager [Help](#)

List_1

Annotation Summary Results

Current Gene List: List_1

1303 DAVID IDs

Current Background: Homo sapiens

Check Defaults

- 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)**

DAVID

Options










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

Rerun Using Options

Create Sublist

984 chart records



























[Download File](#)

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Fold Enrichment	Benjamin
<input type="checkbox"/>	GOTERM_CC_DIRECT	extracellular exosome	RT 		305	23.4	2.1E-19	1.6	1.2E-16
<input type="checkbox"/>	UP_KEYWORDS	Phosphoprotein	RT 		666	51.1	5.8E-18	1.3	2.9E-15
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 3	RT 		15	1.2	2.7E-16	15.5	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 5	RT 		15	1.2	2.7E-16	15.5	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 4	RT 		15	1.2	2.7E-16	15.5	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 2	RT 		15	1.2	2.7E-16	15.5	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 1	RT 		15	1.2	2.7E-16	15.5	7.5E-13
<input type="checkbox"/>	UP_KEYWORDS	Alternative splicing	RT 		795	61.0	1.0E-13	1.2	2.5E-11
<input type="checkbox"/>	UP_KEYWORDS	Calcium	RT 		114	8.7	1.8E-13	2.1	3.0E-11

DAVID

199 Cluster(s)

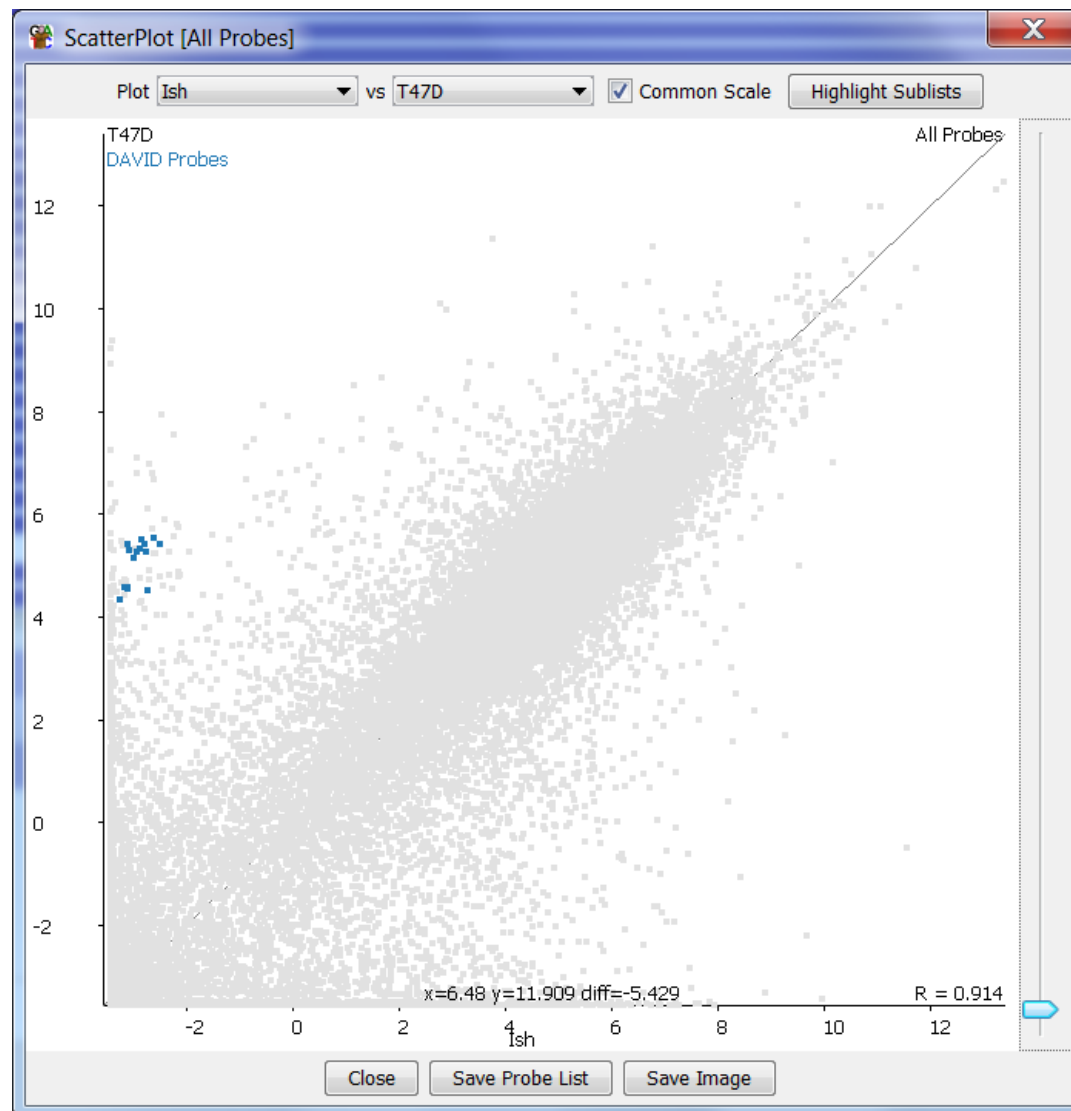
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Annotation Cluster 1		Enrichment Score: 9.56			Count	P_Value	Fold Change	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 1	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 12C/D/E	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 4	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 3	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 2A/2B	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 12F/G/I	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 8	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 7	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 6	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	chain:G antigen 5	RT		13	1.6E-10	1.1E1	1.3E-7
<input type="checkbox"/>	SMART	SM01379	RT		17	5.8E-10	6.6E0	2.1E-7
<input type="checkbox"/>	INTERPRO	GAGE	RT		14	3.4E-8	6.7E0	1.2E-5
Annotation Cluster 2		Enrichment Score: 8.58			Count	P_Value	Fold Change	Benjamini
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 1	RT		15	2.7E-16	1.6E1	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 2	RT		15	2.7E-16	1.6E1	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 3	RT		15	2.7E-16	1.6E1	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 4	RT		15	2.7E-16	1.6E1	7.5E-13
<input type="checkbox"/>	UP_SEQ_FEATURE	repeat:PXXP 5	RT		15	2.7E-16	1.6E1	7.5E-13
<input type="checkbox"/>	UP_KEYWORDS	Cell adhesion	RT		72	1.3E-11	2.4E0	8.9E-10
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 5	RT		29	6.3E-11	4.3E0	1.1E-7
<input type="checkbox"/>	INTERPRO	Cadherin conserved site	RT		30	2.0E-10	4.0E0	3.7E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 4	RT		29	3.3E-10	4.0E0	2.2E-7
<input type="checkbox"/>	UP_SEQ_FEATURE	domain:Cadherin 3	RT		29	3.3E-10	4.0E0	2.2E-7

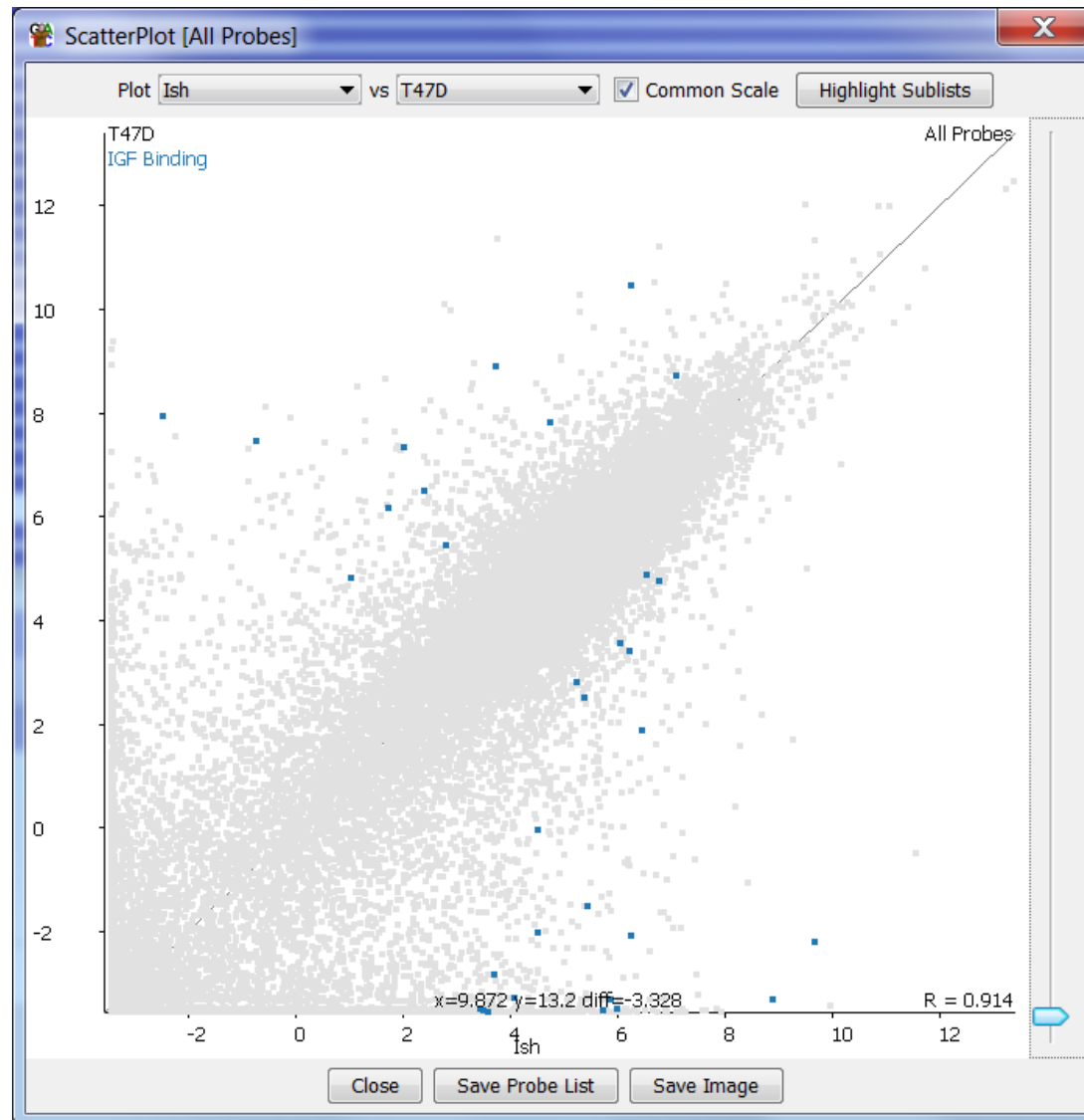
DAVID

Annotation Enrichment Score: 9.563105487061616												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferron	Benjamini	FDR
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
UP_SEQ_F	chain:G an	13	0.997698	1.57E-10	GAGE2A, GAGE2D, GAG	1291	19	20063	10.63309	5.32E-07	1.33E-07	2.86E-07
SMART	SM01379:!	17	1.304682	5.76E-10	GAGE2A, GAGE12H, GA	760	34	10057	6.616447	2.12E-07	2.12E-07	7.93E-07
INTERPRO	IPR008625	14	1.074444	3.36E-08	GAGE2A, GAGE12H, GA	1243	31	18559	6.742948	6.12E-05	1.22E-05	5.71E-05
Annotation Enrichment Score: 8.576455400771039												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferron	Benjamini	FDR
UP_SEQ_F	repeat:PX)	15	1.15119	2.71E-16	PCDHA6, PCDHA7, PCD	1291	15	20063	15.54067	7.52E-13	7.52E-13	4.11E-13
UP_SEQ_F	repeat:PX)	15	1.15119	2.71E-16	PCDHA6, PCDHA7, PCD	1291	15	20063	15.54067	7.52E-13	7.52E-13	4.11E-13
UP_SEQ_F	repeat:PX)	15	1.15119	2.71E-16	PCDHA6, PCDHA7, PCD	1291	15	20063	15.54067	7.52E-13	7.52E-13	4.11E-13
UP_SEQ_F	repeat:PX)	15	1.15119	2.71E-16	PCDHA6, PCDHA7, PCD	1291	15	20063	15.54067	7.52E-13	7.52E-13	4.11E-13
UP_SEQ_F	repeat:PX)	15	1.15119	2.71E-16	PCDHA6, PCDHA7, PCD	1291	15	20063	15.54067	7.52E-13	7.52E-13	4.11E-13
UP_KEYW	Cell adhesi	72	5.52571	1.26E-11	PCDHA6, PCDHA7, PCD	1296	479	20581	2.387033	6.24E-09	8.92E-10	1.81E-08
UP_SEQ_F	domain:Ca	29	2.225633	6.34E-11	PCDHA6, PCDHA7, PCD	1291	105	20063	4.292184	2.15E-07	1.07E-07	1.16E-07
INTERPRO	IPR020894	30	2.302379	2.03E-10	PCDHA6, ME1, PCDHA7	1243	113	18559	3.963933	3.71E-07	3.71E-07	3.46E-07
UP_SEQ_F	domain:Ca	29	2.225633	3.27E-10	PCDHA6, PCDHA7, PCD	1291	112	20063	4.023922	1.11E-06	2.22E-07	5.98E-07
UP_SEQ_F	domain:Ca	29	2.225633	3.27E-10	PCDHA6, PCDHA7, PCD	1291	112	20063	4.023922	1.11E-06	2.22E-07	5.98E-07

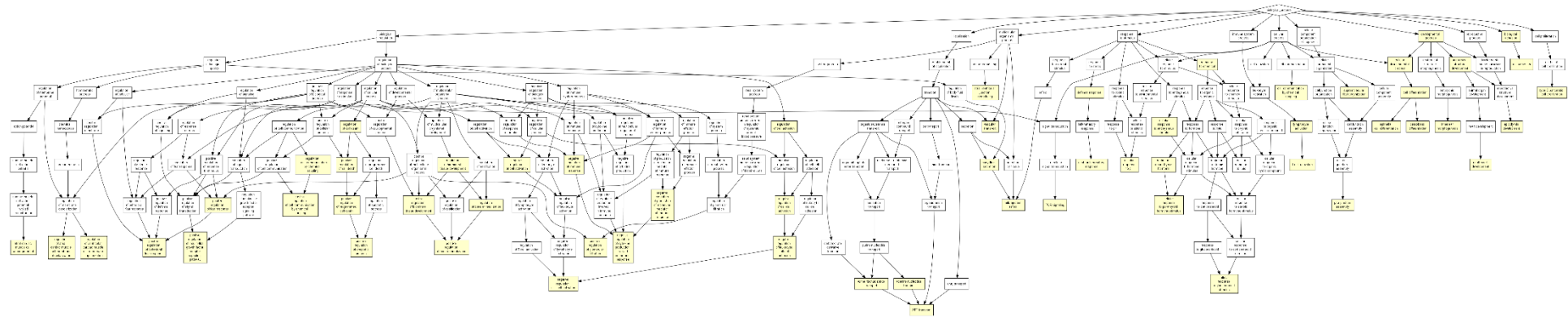
DAVID Validation



DAVID Validation



GOrilla



GOrilla

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
GO:0022408	negative regulation of cell-cell adhesion	8.68E-5	6.78E-1	3.23 (1313,18,294,13)	[-] Show genes
GO:0030154	cell differentiation	9.38E-5	3.66E-1	2.33 (1313,213,74,28)	[-] Show genes
GO:0048869	cellular developmental process	1.49E-4	3.89E-1	2.03 (1313,290,76,34)	[-] Show genes
GO:0050868	negative regulation of T cell activation	1.61E-4	3.14E-1	4.57 (1313,10,230,8)	[-] Show genes
GO:0010942	positive regulation of cell death	1.79E-4	2.8E-1	2.04 (1313,63,317,31)	[-] Show genes
GO:0030855	epithelial cell differentiation	3.13E-4	4.07E-1	3.60 (1313,37,128,13)	[-] Show genes
GO:0050777	negative regulation of immune response	3.13E-4	3.49E-1	4.24 (1313,14,199,9)	[-] Show genes
GO:0071385	cellular response to glucocorticoid stimulus	3.24E-4	3.17E-1	9.45 (1313,4,139,4)	[-] Show genes
GO:0031929	TOR signaling	3.27E-4	2.84E-1	17.51 (1313,3,75,3)	[-] Show genes
GO:0042472	inner ear morphogenesis	3.29E-4	2.57E-1	9.22 (1313,8,89,5)	[-] Show genes
GO:0042110	T cell activation	3.73E-4	2.65E-1	11.91 (1313,19,29,5)	[-] Show genes
GO:0030155	regulation of cell adhesion	3.79E-4	2.47E-1	1.87 (1313,77,329,36)	[-] Show genes
GO:0030500	regulation of bone mineralization	3.96E-4	2.38E-1	8.82 (1313,8,93,5)	[-] Show genes
GO:0070167	regulation of biomineral tissue development	3.96E-4	2.21E-1	8.82 (1313,8,93,5)	[-] Show genes
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	4.14E-4	2.16E-1	21.88 (1313,4,45,3)	[-] Show genes
GO:0044342	type B pancreatic cell proliferation	4.14E-4	2.02E-1	21.88 (1313,4,45,3)	[-] Show genes
GO:0046649	lymphocyte activation	5.12E-4	2.35E-1	8.76 (1313,31,29,6)	[-] Show genes

Genes

[\[-\] Hide genes](#)

MBP - myelin basic protein

FOXP1 - forkhead box j1

VTCN1 - v-set domain containing t cell activation inhibitor 1

PELI1 - pellino e3 ubiquitin protein ligase 1

BCL6 - b-cell cl/lymphoma 6

ABAT - 4-aminobutyrate aminotransferase

PODXL - podocalyxin-like

JAG1 - jagged 1

UBASH3B - ubiquitin associated and sh3 domain containing b

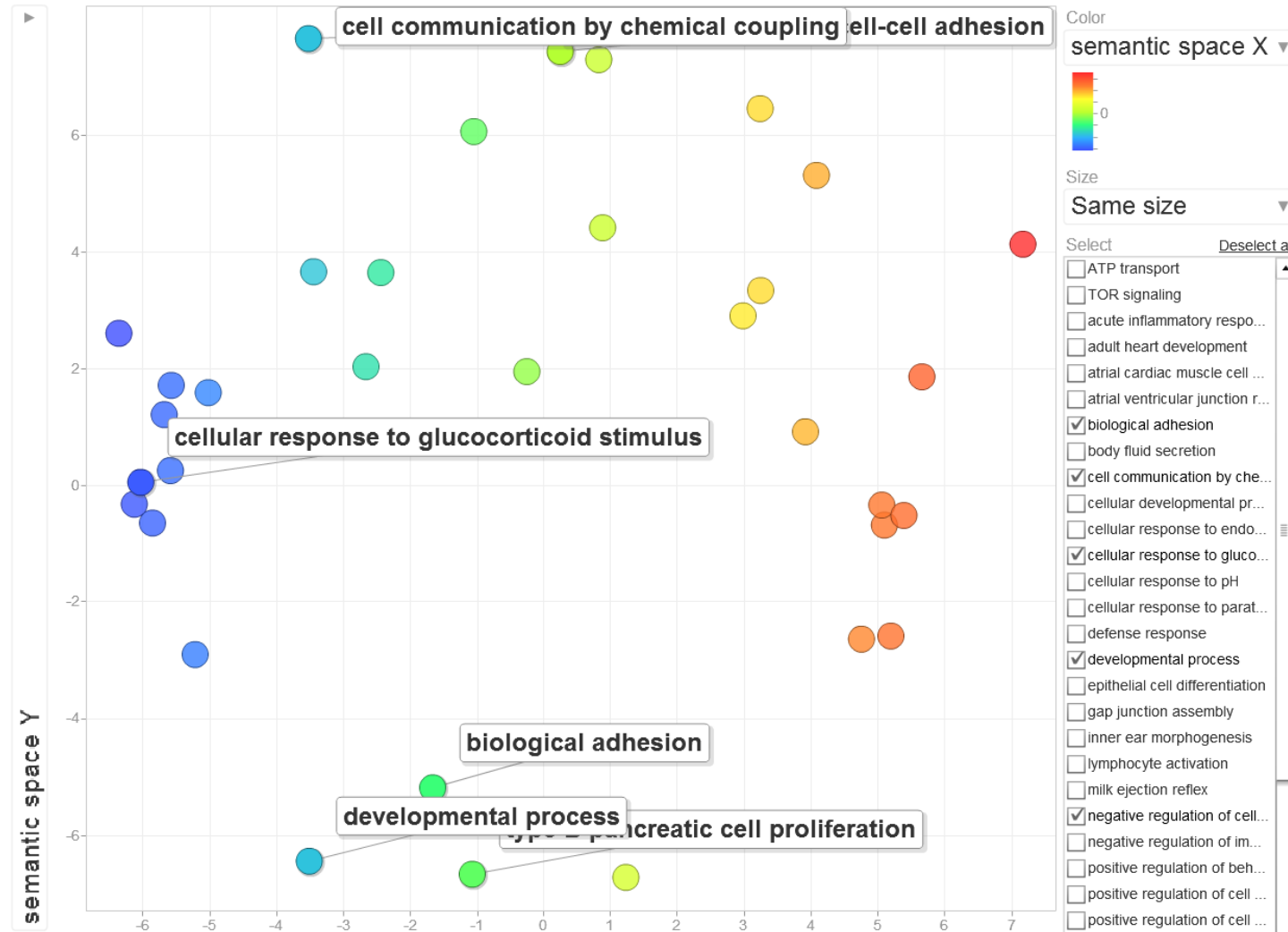
HFE - hemochromatosis

ANXA1 - annexin a1

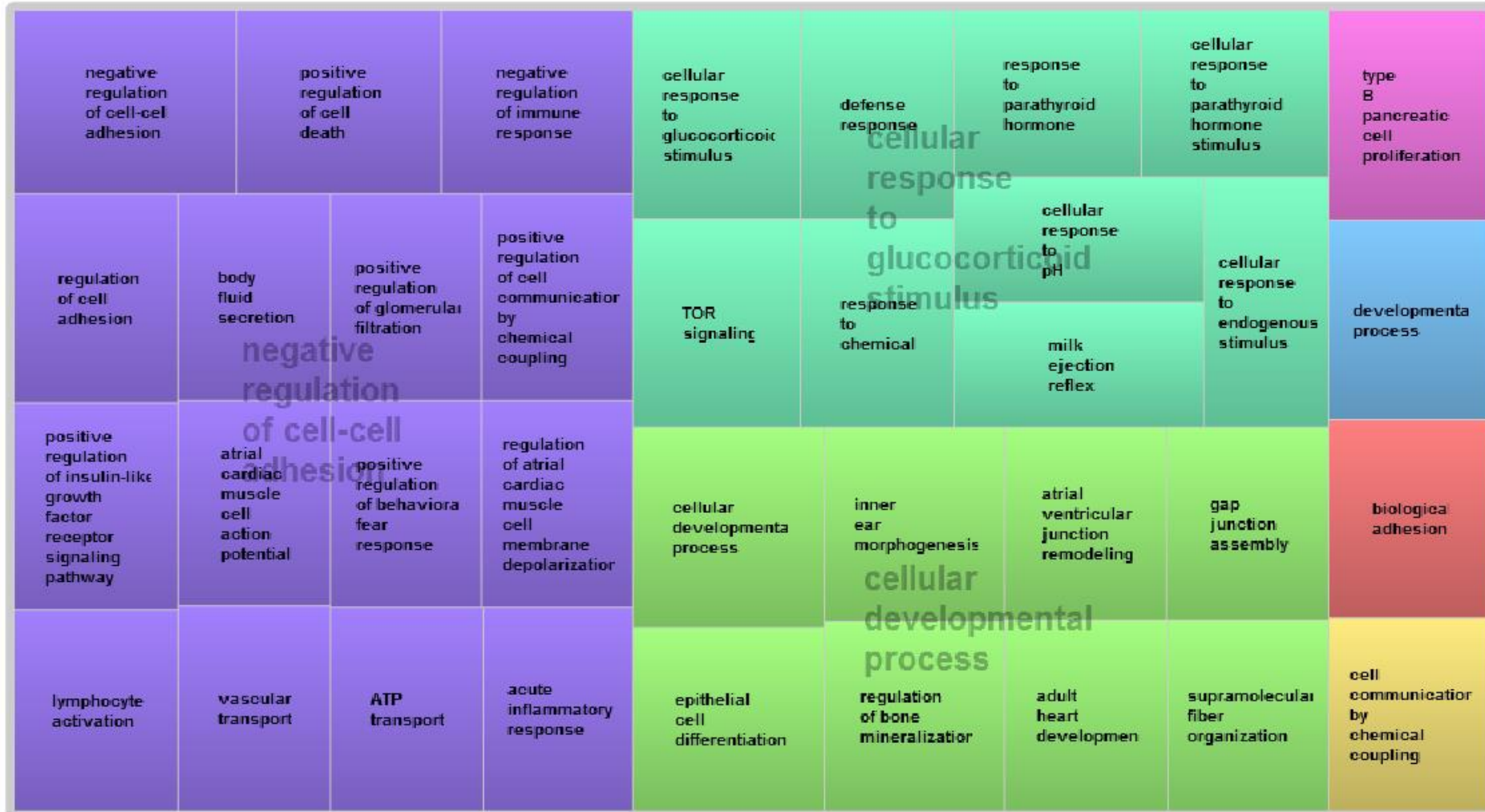
LGALS3 - lectin, galactoside-binding, soluble, 3

GPNMB - glycoprotein (transmembrane) nmb

GOrilla - REViGO



GOrilla - REViGO



REVIGO

Biological Process (25)

Tag Clouds

Scatterplot & Table

Interactive Graph




TreeMap

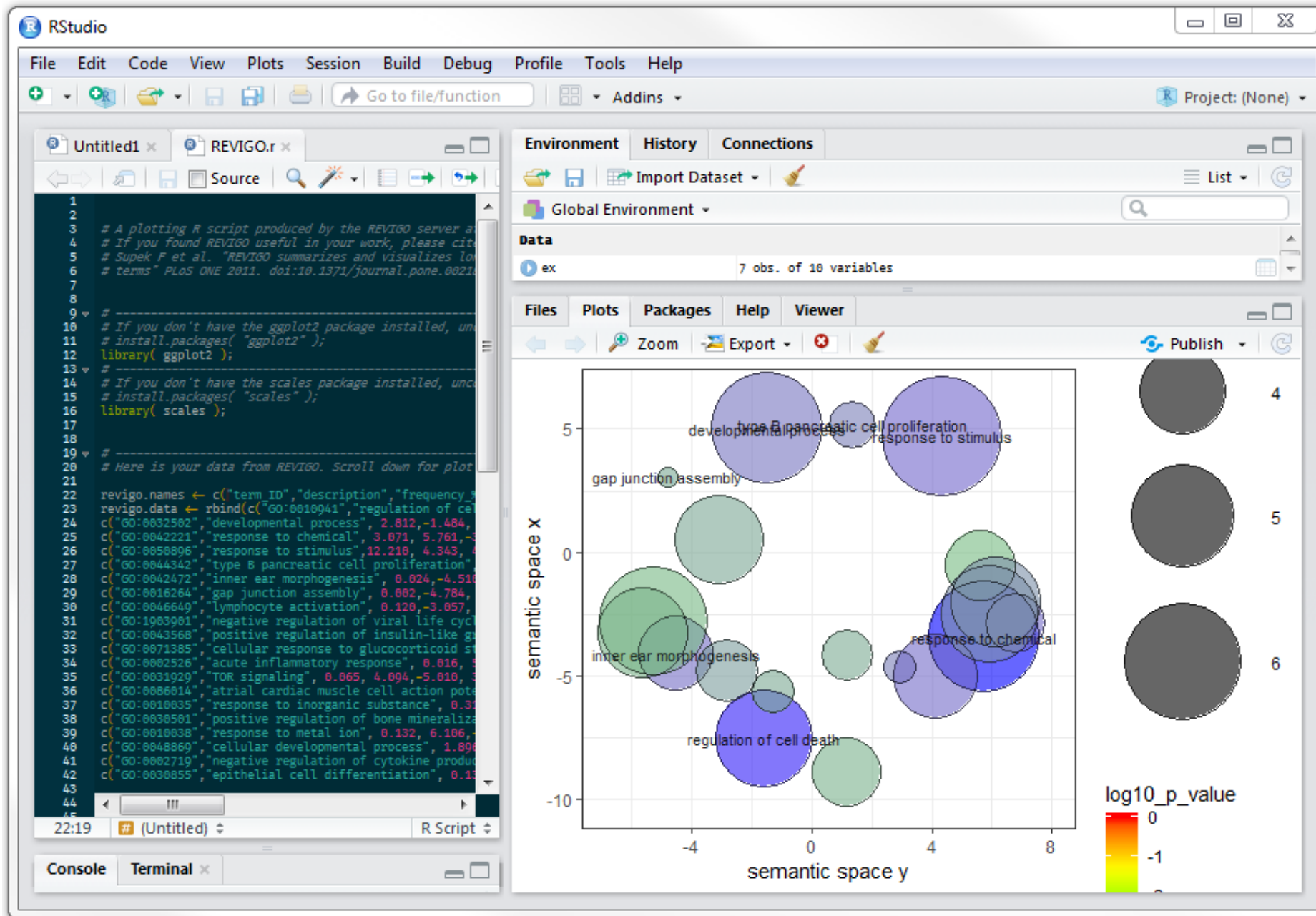
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 [Hide/show dispensable GO terms](#)

 [Export results to text table \(CSV\)](#)  [Make R script for plotting](#)

term ID	description	frequency	pin?	log10 p-value	uniqueness	dispensability
GO:0010941	regulation of cell death	0.344 %		-3.8477	0.62	0.00
GO:0010942	positive regulation of cell death	0.114 %		-3.0615	0.57	0.86
GO:0043067	regulation of programmed cell death	0.322 %		-3.2890	0.62	0.94
GO:0032502	developmental process	2.812 %		-3.4283	0.92	0.00
GO:0042221	response to chemical	3.071 %		-3.8996	0.75	0.00
GO:0050896	response to stimulus	12.210 %		-3.5114	0.93	0.00
GO:0044342	type B pancreatic cell proliferation	0.003 %		-3.3747	0.86	0.05
GO:0042472	inner ear morphogenesis	0.024 %		-3.4685	0.66	0.06
GO:0016264	gap junction assembly	0.002 %		-3.1198	0.83	0.11
GO:0046649	lymphocyte activation	0.120 %		-3.1314	0.66	0.15
GO:0042110	T cell activation	0.081 %		-3.2299	0.67	0.94
GO:1903901	negative regulation of viral life cycle	0.015 %		-3.0788	0.75	0.19
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	0.002 %		-3.3747	0.61	0.26



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g:GOST

Functional profiling

g:Convert

Gene ID conversion

g:Orth

Orthology search

g:SNPense

SNP id to gene name

Query

Upload query

Upload bed file

Input is whitespace-separated list of genes

Run query

random

example

Options

Organism:

Homo sapiens (Human)

Ordered query

Run as multiquery

Advanced options

All results

Measure underrepresentation

Statistical domain scope

Only annotated genes

Significance threshold

g:SCS threshold

User threshold

0.05

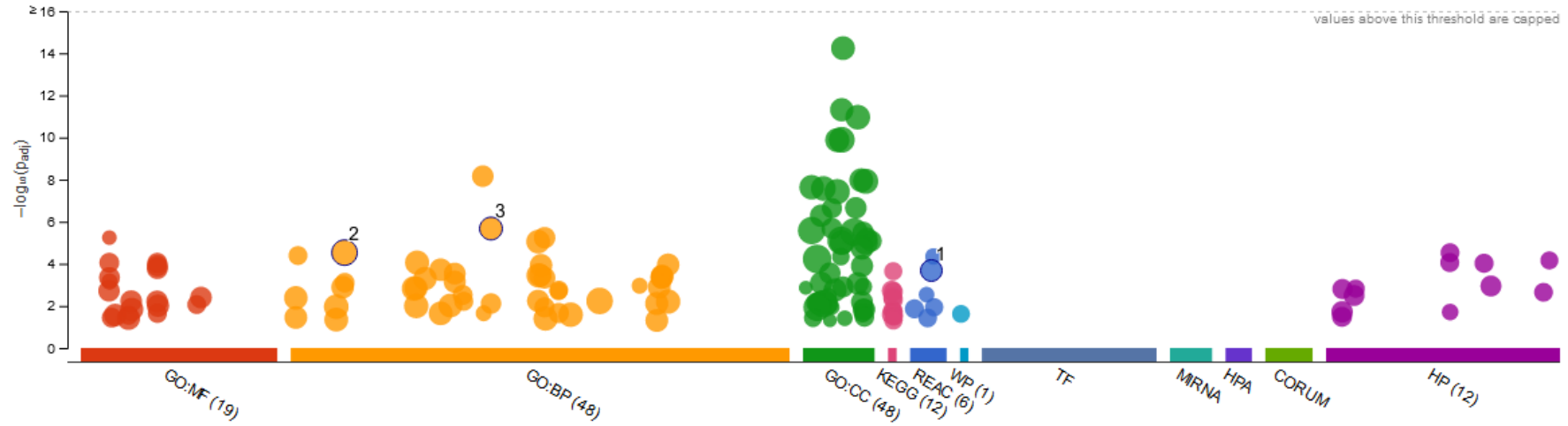
Numeric IDs treated as

ENTREZGENE_ACC

Data sources

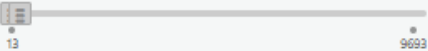
Custom GMT

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ID	Source	Term ID	Term Name	Padj (query_1)
1	REAC	REAC:R-HSA-11...	Neuronal System	2.087×10^{-4}
2	GO:BP	GO:0007399	nervous system development	2.938×10^{-5}
3	GO:BP	GO:0043269	regulation of ion transport	2.117×10^{-6}

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Should match... Term size 13  200 ×

Legend

GO:MF		stats											
Term name	Term ID	P _{adj}	$-\log_{10}(P_{adj})$	T	Q	T∩Q	U	AAKI	ACIN	ADDS	AEPI	AKI	
voltage-gated sodium channel activity	GO:0005248	5.693×10^{-6}		19	153	6	18098						
voltage-gated channel activity	GO:0022832	8.869×10^{-5}		199	153	12	18098						
voltage-gated ion channel activity	GO:0005244	8.869×10^{-5}		199	153	12	18098						
sodium channel activity	GO:0005272	6.956×10^{-4}		40	153	6	18098						
ion channel binding	GO:0044325	8.643×10^{-3}		127	153	8	18098						
voltage-gated cation channel activity	GO:0022843	2.259×10^{-2}		145	153	8	18098						
sodium ion transmembrane transporter activity	GO:0015081	2.745×10^{-2}		149	153	8	18098						
calmodulin binding	GO:0005516	3.608×10^{-2}		200	153	9	18098						

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source	term_name	term_id	adjusted_p	negative	term_size	query_size	intersect	effective	intersections
GO:MF	growth f	GO:0019	0.000693	3.159	137	71	7	17516	IGFBP3,IGFBP4,IGFBP5,GHR,COL3A1,COL6A1,COL2A1
GO:MF	insulin-lik	GO:0031	0.001816	2.741	8	71	3	17516	IGFBP3,IGFBP4,IGFBP5
GO:MF	insulin-lik	GO:0031	0.00705	2.158	12	71	3	17516	IGFBP3,IGFBP4,IGFBP5
GO:MF	platelet-	GO:0046	0.00705	2.158	12	71	3	17516	COL3A1,COL6A1,COL2A1
GO:MF	extracell	GO:0005	0.020021	1.6385	155	71	6	17516	MGP,EFEMP1,FBN2,COL3A1,COL6A1,COL2A1
GO:BP	tissue de	GO:0005	4.04E-09	8.334	1980	73	32	17622	GJA1,MGP,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,ELF5,GATA3,SEMA3C,CRABP2,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	cellular d	GO:0046	8.76E-07	6.0575	4306	73	43	17622	GJA1,IGFBP3,CLU,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,NCAM2,SEMA3C,RHOA,CRABP2,MECOM,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	cell diffe	GO:0030	3.55E-07	6.0201	4127	73	42	17622	GJA1,IGFBP3,CLU,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,NCAM2,SEMA3C,CRABP2,MECOM,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	animal or	GO:0046	3.69E-06	5.0135	3502	73	37	17622	GJA1,PRLR,LCP1,MGP,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,SEMA3C,MECOM,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,INHBB,HLA-B,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	anatomic	GO:0046	2.45E-05	4.6105	5813	73	48	17622	GJA1,IGFBP3,PRLR,CLU,FAT1,LCP1,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,IGFBP4,OLFML3,ELF5,GATA3,NCAM2,SEMA3C,RHOA,CRABP2,MECOM,TFAM,TFEB,TFE3,TFEB1,TFE2L1,TFE2L2,TFE2L3,TFE2L4,TFE2L5,TFE2L6,TFE2L7,TFE2L8,TFE2L9,TFE2L10,TFE2L11,TFE2L12,TFE2L13,TFE2L14,TFE2L15,TFE2L16,TFE2L17,TFE2L18,TFE2L19,TFE2L20,TFE2L21,TFE2L22,TFE2L23,TFE2L24,TFE2L25,TFE2L26,TFE2L27,TFE2L28,TFE2L29,TFE2L30,TFE2L31,TFE2L32,TFE2L33,TFE2L34,TFE2L35,TFE2L36,TFE2L37,TFE2L38,TFE2L39,TFE2L40,TFE2L41,TFE2L42,TFE2L43,TFE2L44,TFE2L45,TFE2L46,TFE2L47,TFE2L48,TFE2L49,TFE2L50,TFE2L51,TFE2L52,TFE2L53,TFE2L54,TFE2L55,TFE2L56,TFE2L57,TFE2L58,TFE2L59,TFE2L60,TFE2L61,TFE2L62,TFE2L63,TFE2L64,TFE2L65,TFE2L66,TFE2L67,TFE2L68,TFE2L69,TFE2L70,TFE2L71,TFE2L72,TFE2L73,TFE2L74,TFE2L75,TFE2L76,TFE2L77,TFE2L78,TFE2L79,TFE2L80,TFE2L81,TFE2L82,TFE2L83,TFE2L84,TFE2L85,TFE2L86,TFE2L87,TFE2L88,TFE2L89,TFE2L90,TFE2L91,TFE2L92,TFE2L93,TFE2L94,TFE2L95,TFE2L96,TFE2L97,TFE2L98,TFE2L99,TFE2L100
GO:BP	system d	GO:0046	3.23E-05	4.431	4801	73	43	17622	GJA1,PRLR,CLU,LCP1,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,IGFBP4,ELF5,GATA3,NCAM2,SEMA3C,CRABP2,MECOM,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	developr	GO:0032	6.83E-05	4.1658	6205	73	43	17622	GJA1,IGFBP3,PRLR,CLU,FAT1,LCP1,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,IGFBP4,OLFML3,ELF5,GATA3,NCAM2,SEMA3C,RHOA,CRABP2,MECOM,TFAM,TFEB,TFE3,TFEB1,TFE2L1,TFE2L2,TFE2L3,TFE2L4,TFE2L5,TFE2L6,TFE2L7,TFE2L8,TFE2L9,TFE2L10,TFE2L11,TFE2L12,TFE2L13,TFE2L14,TFE2L15,TFE2L16,TFE2L17,TFE2L18,TFE2L19,TFE2L20,TFE2L21,TFE2L22,TFE2L23,TFE2L24,TFE2L25,TFE2L26,TFE2L27,TFE2L28,TFE2L29,TFE2L30,TFE2L31,TFE2L32,TFE2L33,TFE2L34,TFE2L35,TFE2L36,TFE2L37,TFE2L38,TFE2L39,TFE2L40,TFE2L41,TFE2L42,TFE2L43,TFE2L44,TFE2L45,TFE2L46,TFE2L47,TFE2L48,TFE2L49,TFE2L50,TFE2L51,TFE2L52,TFE2L53,TFE2L54,TFE2L55,TFE2L56,TFE2L57,TFE2L58,TFE2L59,TFE2L60,TFE2L61,TFE2L62,TFE2L63,TFE2L64,TFE2L65,TFE2L66,TFE2L67,TFE2L68,TFE2L69,TFE2L70,TFE2L71,TFE2L72,TFE2L73,TFE2L74,TFE2L75,TFE2L76,TFE2L77,TFE2L78,TFE2L79,TFE2L80,TFE2L81,TFE2L82,TFE2L83,TFE2L84,TFE2L85,TFE2L86,TFE2L87,TFE2L88,TFE2L89,TFE2L90,TFE2L91,TFE2L92,TFE2L93,TFE2L94,TFE2L95,TFE2L96,TFE2L97,TFE2L98,TFE2L99,TFE2L100
GO:BP	multicell	GO:0001	7.26E-05	4.1392	5339	73	45	17622	GJA1,PRLR,CLU,LCP1,MGP,EFHD1,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,IGFBP4,OLFML3,ELF5,GATA3,NCAM2,SEMA3C,CRABP2,MECOM,TRPS1,SLC7A11,KAZN,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	anatomic	GO:0005	0.000135	3.8639	2631	73	30	17622	GJA1,CLU,FAT1,MGP,MSX1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,SEMA3C,RHOA,CRABP2,MEIS1,IGFBP5,MEOX1,PAX8,PGR,GPNMB,SEMA3A,NR2F2,AGR2,GHR
GO:BP	gland de	GO:0046	0.000677	3.1633	446	73	12	17622	GJA1,PRLR,MSX1,ANXA1,ELF5,GATA3,SEMA3C,IGFBP5,PAX8,PGR,SEMA3A,CLDN1
GO:BP	epitheliu	GO:0060	0.001085	2.9646	1237	73	19	17622	GJA1,MSX1,CDH2,ANXA1,ELF5,GATA3,SEMA3C,SLC7A11,KAZN,IGFBP5,MEOX1,PAX8,PGR,SEMA3A,CLDN1,NR2F2,AGR2,KRT19,COL2A1
GO:BP	regulatio	GO:0045	0.001272	2.8955	1739	73	23	17622	GJA1,IGFBP3,MSX1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,SEMA3C,CRABP2,TRPS1,MEIS1,IGFBP5,PAX8,HLA-B,SEMA3A,GHR,RCAN1,CCDC88A,COL3A1
GO:BP	animal or	GO:0005	0.001277	2.834	1002	73	17	17622	GJA1,MGP,MSX1,EFEMP1,CDH2,FBN2,GATA3,SEMA3C,MEIS1,IGFBP5,PAX8,PGR,SEMA3A,GHR,COL3A1,COL6A1,COL2A1
GO:BP	regulatio	GO:0050	0.001789	2.7475	2615	73	28	17622	GJA1,IGFBP3,MGP,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,ELF5,GATA3,SEMA3C,RHOA,CRABP2,TRPS1,MEIS1,IGFBP5,PAX8,HLA-B,GPNMB,SEMA3A,AGR2,GHR,FAT2,NCAM2,SEMA3C,CRABP2,MECOM
GO:BP	mammary	GO:0030	0.005715	2.243	145	73	7	17622	GJA1,PRLR,MSX1,ELF5,GATA3,IGFBP5,PGR
GO:BP	cellular r	GO:0071	0.006026	2.22	1386	73	19	17622	GJA1,PRLR,FBXO32,MSX1,HDAC3,ANXA1,FBN2,GATA3,IGFBP5,PAX8,INHBB,PGR,CLDN1,NR2F2,GHR,COL3A1,COL6A1,COL2A1,SESN3
GO:BP	cell deat	GO:0006	0.015171	1.819	2235	73	24	17622	GJA1,IGFBP3,PRLR,MUC1,CLU,MSX1,NUPR1,ANXA1,PREX1,GATA3,TRIM2,EEF1A2,MECOM,KAZN,PAX8,INHBB,GPNMB,SEMA3A,BNIP1,AGR2,GHR,MAGEA3,KRT19,COL2A1
GO:BP	multicell	GO:0032	0.015342	1.8141	7484	73	50	17622	GJA1,IGFBP3,PRLR,CLU,LCP1,MGP,EFHD1,FBXO32,MSX1,NUPR1,EFEMP1,CDH2,HDAC3,ANXA1,FBN2,PREX1,IGFBP4,OLFML3,ELF5,GATA3,FAT2,NCAM2,SEMA3C,CRABP2,MECOM
GO:BP	skeletal	GO:0001	0.019895	1.7012	513	73	11	17622	MGP,MSX1,EFEMP1,FBN2,IGFBP4,TRPS1,MEIS1,GHR,COL3A1,COL6A1,COL2A1
GO:BP	limb dev	GO:0060	0.021348	1.6706	177	73	7	17622	GJA1,MSX1,FBN2,SEMA3C,CRABP2,NR2F2,COL2A1
GO:BP	appenda	GO:0046	0.021348	1.6706	177	73	7	17622	GJA1,MSX1,FBN2,SEMA3C,CRABP2,NR2F2,COL2A1
GO:BP	cellular r	GO:0071	0.021366	1.6703	2612	73	26	17622	GJA1,PRLR,MUC1,CLU,LCP1,FBXO32,MSX1,HDAC3,ANXA1,FBN2,GATA3,RHOA,IGFBP5,PAX8,INHBB,HLA-B,PGR,SLC16A1,CLDN1,NR2F2,AGR2,GHR,COL3A1,COL6A1,COL2A1,SESN3
GO:BP	embryo	GO:0005	0.022449	1.6488	976	73	15	17622	GJA1,MSX1,EFEMP1,FBN2,ELF5,GATA3,SEMA3C,CRABP2,MEOX1,PAX8,SEMA3A,NR2F2,KRT19,COL6A1,COL2A1
GO:BP	regulatio	GO:0010	0.022472	1.6484	3508	73	31	17622	GJA1,IGFBP3,PRLR,MUC1,CLU,MSX1,EFEMP1,CDH2,ANXA1,FBN2,PREX1,IGFBP4,GATA3,RHOA,CRABP2,MECOM,IGFBP5,PAX8,INHBB,GPNMB,CACNG4,SLC16A1,SEMA3A,NETO2,TFAM,TFEB,TFE3,TFEB1,TFE2L1,TFE2L2,TFE2L3,TFE2L4,TFE2L5,TFE2L6,TFE2L7,TFE2L8,TFE2L9,TFE2L10,TFE2L11,TFE2L12,TFE2L13,TFE2L14,TFE2L15,TFE2L16,TFE2L17,TFE2L18,TFE2L19,TFE2L20,TFE2L21,TFE2L22,TFE2L23,TFE2L24,TFE2L25,TFE2L26,TFE2L27,TFE2L28,TFE2L29,TFE2L30,TFE2L31,TFE2L32,TFE2L33,TFE2L34,TFE2L35,TFE2L36,TFE2L37,TFE2L38,TFE2L39,TFE2L40,TFE2L41,TFE2L42,TFE2L43,TFE2L44,TFE2L45,TFE2L46,TFE2L47,TFE2L48,TFE2L49,TFE2L50,TFE2L51,TFE2L52,TFE2L53,TFE2L54,TFE2L55,TFE2L56,TFE2L57,TFE2L58,TFE2L59,TFE2L60,TFE2L61,TFE2L62,TFE2L63,TFE2L64,TFE2L65,TFE2L66,TFE2L67,TFE2L68,TFE2L69,TFE2L70,TFE2L71,TFE2L72,TFE2L73,TFE2L74,TFE2L75,TFE2L76,TFE2L77,TFE2L78,TFE2L79,TFE2L80,TFE2L81,TFE2L82,TFE2L83,TFE2L84,TFE2L85,TFE2L86,TFE2L87,TFE2L88,TFE2L89,TFE2L90,TFE2L91,TFE2L92,TFE2L93,TFE2L94,TFE2L95,TFE2L96,TFE2L97,TFE2L98,TFE2L99,TFE2L100
GO:BP	cell migr	GO:0016	0.026179	1.5821	1533	73	19	17622	GJA1,IGFBP3,FAT1,LCP1,CDH2,HDAC3,ANXA1,PREX1,GATA3,FAT2,SEMA3C,SLC7A11,IGFBP5,GPNMB,SLC16A1,SEMA3A,NR2F2,CCDC88A,COL3A1
GO:BP	regulatio	GO:0020	0.026596	1.5752	3536	73	31	17622	GJA1,IGFBP3,PRLR,MUC1,CLU,MSX1,EFEMP1,CDH2,ANXA1,FBN2,PREX1,IGFBP4,GATA3,RHOA,CRABP2,MECOM,IGFBP5,PAX8,INHBB,GPNMB,CACNG4,SLC16A1,SEMA3A,NETO2,TFAM,TFEB,TFE3,TFEB1,TFE2L1,TFE2L2,TFE2L3,TFE2L4,TFE2L5,TFE2L6,TFE2L7,TFE2L8,TFE2L9,TFE2L10,TFE2L11,TFE2L12,TFE2L13,TFE2L14,TFE2L15,TFE2L16,TFE2L17,TFE2L18,TFE2L19,TFE2L20,TFE2L21,TFE2L22,TFE2L23,TFE2L24,TFE2L25,TFE2L26,TFE2L27,TFE2L28,TFE2L29,TFE2L30,TFE2L31,TFE2L32,TFE2L33,TFE2L34,TFE2L35,TFE2L36,TFE2L37,TFE2L38,TFE2L39,TFE2L40,TFE2L41,TFE2L42,TFE2L43,TFE2L44,TFE2L45,TFE2L46,TFE2L47,TFE2L48,TFE2L49,TFE2L50,TFE2L51,TFE2L52,TFE2L53,TFE2L54,TFE2L55,TFE2L56,TFE2L57,TFE2L58,TFE2L59,TFE2L60,TFE2L61,TFE2L62,TFE2L63,TFE2L64,TFE2L65,TFE2L66,TFE2L67,TFE2L68,TFE2L69,TFE2L70,TFE2L71,TFE2L72,TFE2L73,TFE2L74,TFE2L75,TFE2L76,TFE2L77,TFE2L78,TFE2L79,TFE2L80,TFE2L81,TFE2L82,TFE2L83,TFE2L84,TFE2L85,TFE2L86,TFE2L87,TFE2L88,TFE2L89,TFE2L90,TFE2L91,TFE2L92,TFE2L93,TFE2L94,TFE2L95,TFE2L96,TFE2L97,TFE2L98,TFE2L99,TFE2L100
GO:BP	growth	GO:0040	0.031831	1.4372	1005	73	15	17622	GJA1,IGFBP3,MSX1,ANXA1,IGFBP4,GATA3,SEMA3C,CRABP2,MEIS1,IGFBP5,SEMA3A,BNIP1,AGR2,GHR,COL6A1
GO:BP	epithelial	GO:0030	0.033068	1.4806	763	73	13	17622	GJA1,CDH2,ANXA1,ELF5,GATA3,SLC7A11,KAZN,PAX8,PGR,CLDN1,NR2F2,AGR2,KRT19
GO:BP	insulin-lik	GO:0046	0.040347	1.3942	37	73	4	17622	IGFBP3,IGFBP4,IGFBP5,GHR
GO:BP	muscle c	GO:0061	0.041474	1.3822	664	73	12	17622	GJA1,IGFBP3,MSX1,NUPR1,CDH2,HDAC3,MEIS1,IGFBP5,NR2F2,RCAN1,KRT19,COL3A1
GO:BP	positiv	GO:0044	0.047334	1.3248	13	73	3	17622	IGFBP3,IGFBP4,IGFBP5
GO:CC	extracell	GO:0044	8.84E-05	4.0535	3634	74	34	18745	LDHB,IGFBP3,MUC1,CLU,FAT1,LCP1,MGP,SERPINA6,EFEMP1,CDH2,ANXA1,FBN2,IGFBP4,HIST1H2BK,OLFML3,FAT2,SEMA3C,AHNAK,CRABP2,PSAT1,IGFBP5,INHBB,HLA-B,SLC16A1,SEMA3A,KIAA1324,TPM4
GO:CC	anchorio	GO:0070	0.000488	3.312	552	74	12	18745	GJA1,FAT1,LCP1,CDH2,ANXA1,FAT2,STXBP6,RHOA,AHNAK,KAZN,TMEM47,TPM4
GO:CC	extracell	GO:0005	0.000956	3.0197	3434	74	31	18745	LDHB,IGFBP3,MUC1,CLU,FAT1,LCP1,MGP,SERPINA6,EFEMP1,ANXA1,IGFBP4,HIST1H2BK,FAT2,SEMA3C,AHNAK,CRABP2,PSAT1,IGFBP5,INHBB,HLA-B,SLC16A1,SEMA3A,KIAA1324,TPM4
GO:CC	collagen	GO:0062	0.001829	2.7377	330	74	9	18745	CLU,MGP,EFEMP1,CDH2,ANXA1,FBN2,COL3A1,COL6A1,COL2A1
GO:CC	adherens	GO:0005	0.002442	2.6123	537	74	11	18745	GJA1,FAT1,LCP1,CDH2,ANXA1,FAT2,STXBP6,RHOA,AHNAK,TMEM47,TPM4
GO:CC	extracell	GO:0005	0.002822	2.5434	4475	74	35	18745	LDHB,IGFBP3,PRLR,MUC1,CLU,FAT1,LCP1,MGP,SERPINA6,EFEMP1,ANXA1,FBN2,IGFBP4,HIST1H2BK,OLFML3,FAT2,SEMA3C,AHNAK,CRABP2,PSAT1,IGFBP5,INHBB,HLA-B,SLC16A1,SEMA3A,KIAA1324,TPM4
GO:CC	cell-cell	GO:0005	0.003251	2.488	450	74	10	18745	GJA1,FAT1,CDH2,ANXA1,FAT2,STXBP6,AHNAK,KAZN,TMEM47,CLDN1
GO:CC	sarcole	GO:0042	0.004227	2.3739	132	74	6	18745	CDH2,ANXA1,AHNAK,CACNG4,KRT19,COL6A1
GO:CC	extracell	GO:1903	0.018539	1.7319	2153	74	21	18745	LDHB,MUC1,CLU,FAT1,LCP1,MGP,SERPINA6,EFEMP1,ANXA1,OLFML3,FAT2,SEMA3C,AHNAK,CRABP2,PSAT1,HLA-B,SLC16A1,KIAA1324,TPM4,KRT19,COL6A1
GO:CC	extracell	GO:0044	0.018794	1.726	2155	74	21	18745	LDHB,MUC1,CLU,FAT1,LCP1,MGP,SERPINA6,EFEMP1,ANXA1,OLFML3,FAT2,SEMA3C,AHNAK,CRABP2,PSAT1,HLA-B,SLC16A1,KIAA1324,TPM4,KRT19,COL6A1
GO:CC	cell-cell	GO:0005	0.02508	1.6007	112	74	5	18745	GJA1,CDH2,ANXA1,FAT2,STXBP6
GO:CC	insulin-lik	GO:0046	0.028502	1.5451	4	74	2	18745	IGFBP3,IGFBP5
GO:CC	extracell	GO:0031	0.040871	1.3886	431	74	9	18745	CLU,MGP,EFEMP1,CDH2,ANXA1,FBN2,COL3A1,COL6A1,COL2A1
GO:CC	growth f	GO:0036	0.047382	1.3244	5	74	2	18745	IGFBP3,IGFBP5
GO:CC	insulin-lik	GO:0016	0.047382	1.3244	5	74	2	18745	IGFBP3,IGFBP5

EnrichR

Transcription Pathways Ontologies Disease/Drugs **Cell Types** Misc Legacy Crowd

Description No description available (95 genes)



Human Gene Atlas

CardiacMyocytes
colon
Fetalliver
SmoothMuscle
BronchialEpithelialCells

Mouse Gene Atlas

osteoblast_day21
mammary_gland_lact
uterus
ovary
epidermis

ARCHS4 Tissues

RENAL CORTEX
SKIN (BULK TISSUE)
BREAST (BULK TISSUE)
ENDOMETRIUM (BULK)
MAMMARY GLAND

ARCHS4 Cell-lines

T47D
MCF7
NHBE
BT474
RT4

Allen Brain Atlas up

Lingula (I), molecular layer
Nodulus (X)
Nodulus (X), molecular layer
external globus pallidum
superficial stratum of m2B

Allen Brain Atlas down

Gigantocellular reticular nucleus
intermediate tier of thalamus
mantle zone of ITth
r2 part of the trigeminal motor nucleus
superficial stratum of r2Lim

GTEx Tissue Sample Gene Expression Profiles up

GTEx-S4UY-0726-SM-4AD6X_breast_female_4
GTEx-XMD3-0008-SM-4AT4V_skin_female_50
GTEx-R55C-1026-SM-48FCM_stomach_male_4
GTEx-S4P3-1126-SM-4AD52_vagina_female_4
GTEx-XLM4-0008-SM-4AT4W_skin_male_60-6

GTEx Tissue Sample Gene Expression Profiles down

GTEx-TMZ5-0001-SM-3P61Q_blood_male_60
GTEx-WFJO-0002-SM-3P61X_blood_male_30-3
GTEx-XS85-0002-SM-46MVA_blood_male_50-5
GTEx-UPK5-0003-SM-3NMDI_blood_male_40-4
GTEx-XGQ4-0004-SM-4AT5S_blood_male_50-5

Cancer Cell Line Encyclopedia

T47D_BREAST
BT483_BREAST
HCC1500_BREAST
CAMA1_BREAST
BT474_BREAST

EnrichR

GO Biological Process 2017b

Bar Graph

Table

Clustergram



Click the bars to sort. Now sorted by **p-value ranking**.

SVG PNG JPG

mesenchymal to epithelial transition involved in metanephros morphogenesis (GO:0003337)

positive regulation of insulin-like growth factor receptor signaling pathway (GO:0043568)

negative regulation of insulin-like growth factor receptor signaling pathway (GO:0043569)

protocatechuate catabolic process, meta-cleavage (GO:0019617)

negative regulation of thyroid hormone receptor activity (GO:1904168)

mesenchymal to epithelial transition involved in renal vesicle formation (GO:0072036)

negative regulation of ferrichrome biosynthetic process in response to iron (GO:0097739)

mesenchymal to epithelial transition involved in mesonephros morphogenesis (GO:0061261)

cellular response to iron(III) ion (GO:0071283)

negative regulation of leukocyte proliferation (GO:0070664)

EnrichR

GO Biological Process 2017b

Bar Graph

Table

Clustergram



Enriched Terms are the columns, input genes are the rows, and cells in the matrix indicate if a gene is associated with a term.



Row Order

Cluster Sum

Column Order

Cluster Sum

Gene Search

Combined Score

P-Value

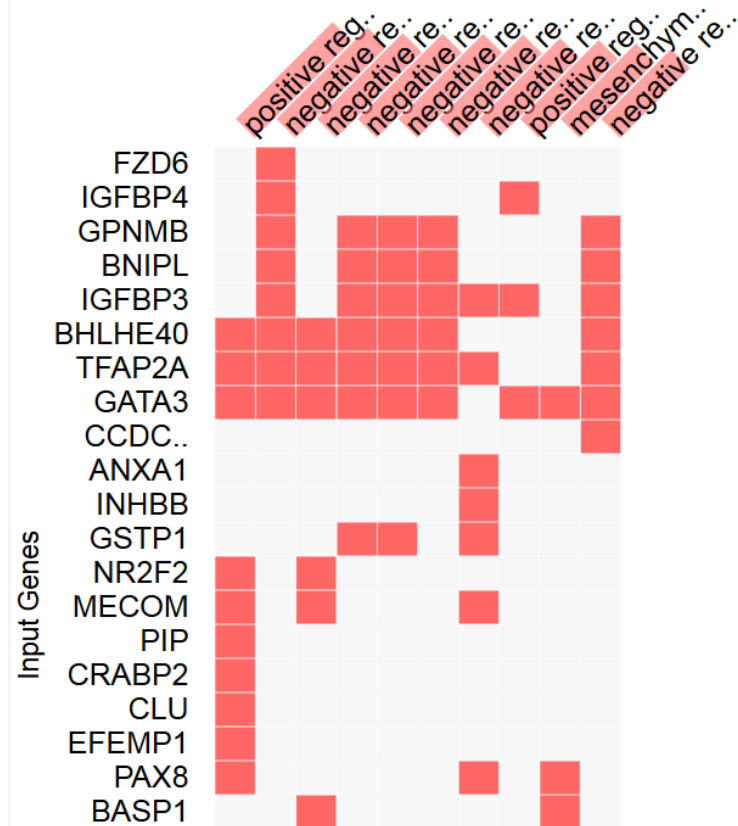
Z-score

Top Enriched Terms: 10

Top rows sum: 20 rows



Enriched Terms



EnrichR

GO Biological Process 2017b

Bar Graph

Table

Clustergram



Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Adjusted p-value	Z-score	Combined score
1	positive regulation of transcription, DNA-templated (GO:0045893)	0.002814	0.05952	-6.83	40.13
2	negative regulation of canonical Wnt signaling pathway involved in controlling type B pancreatic cell proliferation (GO:2000080)	0.0007846	0.05799	-5.29	37.81
3	negative regulation of transcription by competitive promoter binding (GO:0010944)	0.0008223	0.05799	-5.00	35.52
4	negative regulation of leukocyte proliferation (GO:0070664)	0.0004032	0.05799	-4.52	35.29
5	negative regulation of fibroblast proliferation (GO:0048147)	0.0005062	0.05799	-4.65	35.25
6	negative regulation of smooth muscle cell proliferation (GO:0048662)	0.0006053	0.05799	-4.71	34.92
7	negative regulation of apoptotic process (GO:0043066)	0.001717	0.05799	-5.26	33.46
8	positive regulation of insulin-like growth factor receptor signaling pathway (GO:0043568)	0.00008045	0.05799	-3.46	32.65
9	mesenchymal to epithelial transition involved in metanephros morphogenesis (GO:0003337)	0.00001216	0.03271	-2.76	31.22
10	negative regulation of cell proliferation (GO:0008285)	0.002928	0.05952	-4.95	28.85

Showing 1 to 10 of 2,690 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

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