

# Results

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## Input Parameters [\[Hide Detail\]](#)

Number of genes in training set:	34																																																																																															
Number of genes in test set:	0																																																																																															
Correction and Cutoff:	<table border="1"> <thead> <tr> <th>category</th> <th>Correction</th> <th>Cutoff</th> <th>Min</th> <th>Max</th> </tr> </thead> <tbody> <tr> <td>GO: Molecular Function</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>GO: Biological Process</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>GO: Cellular Component</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Human Phenotype</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Mouse Phenotype</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Domain</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Pathway</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Pubmed</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Interaction</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Cytoband</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Transcription Factor Binding Site</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Gene Family</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Coexpression</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Coexpression Atlas</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Computational</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>MicroRNA</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Drug</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> <tr> <td>Disease</td> <td>FDR B&amp;H</td> <td>0.05</td> <td>1</td> <td>2000</td> </tr> </tbody> </table>	category	Correction	Cutoff	Min	Max	GO: Molecular Function	FDR B&H	0.05	1	2000	GO: Biological Process	FDR B&H	0.05	1	2000	GO: Cellular Component	FDR B&H	0.05	1	2000	Human Phenotype	FDR B&H	0.05	1	2000	Mouse Phenotype	FDR B&H	0.05	1	2000	Domain	FDR B&H	0.05	1	2000	Pathway	FDR B&H	0.05	1	2000	Pubmed	FDR B&H	0.05	1	2000	Interaction	FDR B&H	0.05	1	2000	Cytoband	FDR B&H	0.05	1	2000	Transcription Factor Binding Site	FDR B&H	0.05	1	2000	Gene Family	FDR B&H	0.05	1	2000	Coexpression	FDR B&H	0.05	1	2000	Coexpression Atlas	FDR B&H	0.05	1	2000	Computational	FDR B&H	0.05	1	2000	MicroRNA	FDR B&H	0.05	1	2000	Drug	FDR B&H	0.05	1	2000	Disease	FDR B&H	0.05	1	2000
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pValue Method:	Hypergeometric Probability Mass Function																																																																																															
Random sampling size in analysis:	0																																																																																															
Minimum feature count in test set:	2																																																																																															
Analysis took:	0 seconds																																																																																															
Analysis finished at:	Thu Apr 19 15:49:00 EDT 2018																																																																																															

## Training Results [\[Collapse All\]](#) [\[Download All\]](#) [\[Sparse Matrix\]](#) Display pValues and Scores as

 Scientific (4 significant digits)  Table row limit 

### 1: GO: Molecular Function [\[Display Chart\]](#) 34 input genes in category / 161 annotations before applied cutoff / 18661 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0015278	calcium-release channel activity		3.805E-4	3.063E-2	1.734E-1	6.126E-2	2	16
2	GO:0099604	ligand-gated calcium channel activity		3.805E-4	3.063E-2	1.734E-1	6.126E-2	2	16

### 2: GO: Biological Process [\[Display Chart\]](#) 34 input genes in category / 885 annotations before applied cutoff / 18623 genes in category

No results to display

### 3: GO: Cellular Component [\[Display Chart\]](#) 34 input genes in category / 146 annotations before applied cutoff / 19061 genes in category

No results to display

### 4: Human Phenotype [\[Display Chart\]](#) 10 input genes in category / 725 annotations before applied cutoff / 4707 genes in category

**category**

No results to display

**5: Mouse Phenotype** [Display Chart] 19 input genes in category / 477 annotations before applied cutoff / 9319 genes in category

No results to display

**6: Domain** [Display Chart] 34 input genes in category / 253 annotations before applied cutoff / 18735 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PF05483	Scp-1	1.818E-3	4.181E-2	2.556E-1	4.600E-1	1	1
2	IPR008496	DUF778	1.818E-3	4.181E-2	2.556E-1	4.600E-1	1	1
3	IPR030645	SEPT9	1.818E-3	4.181E-2	2.556E-1	4.600E-1	1	1
4	IPR003028	Na/ntran symport glycine GLY1	1.818E-3	4.181E-2	2.556E-1	4.600E-1	1	1
5	IPR029664	NIN	1.818E-3	4.181E-2	2.556E-1	4.600E-1	1	1

Show 6 more annotations

**7: Pathway** [Display Chart] 21 input genes in category / 137 annotations before applied cutoff / 12450 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M3008	Genes encoding structural ECM glycoproteins	2.890E-4	3.959E-2	2.178E-1	3.959E-2	4	196

**8: Pubmed** [Display Chart] 34 input genes in category / 1350 annotations before applied cutoff / 36332 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	11555487	Positional cloning of the mouse saccharin preference (Sac) locus.	1.765E-4	3.964E-3	3.086E-2	2.383E-1	2	21
2	24322204	Genome-wide association study of bipolar disorder accounting for effect of body mass index identifies a new risk allele in TCF7L2.	3.164E-4	3.964E-3	3.086E-2	4.272E-1	2	28
3	19851296	Assessment of a polymorphism of SDK1 with hypertension in Japanese Individuals.	3.200E-4	3.964E-3	3.086E-2	4.321E-1	3	142
4	20198315	Association of genetic variants with hemorrhagic stroke in Japanese individuals.	3.267E-4	3.964E-3	3.086E-2	4.410E-1	3	143
5	19724895	Association of gene polymorphisms with chronic kidney disease in Japanese individuals.	6.163E-4	3.964E-3	3.086E-2	8.320E-1	2	39

Show 45 more annotations

**9: Interaction** [Display Chart] 30 input genes in category / 668 annotations before applied cutoff / 17363 genes in category

No results to display

**10: Cytoband** [Display Chart] 33 input genes in category / 28 annotations before applied cutoff / 34661 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1p36.33	1p36.33	1.305E-6	3.655E-5	1.435E-4	3.655E-5	4	85
2	8p23.3	8p23.3	1.332E-4	1.865E-3	7.324E-3	3.730E-3	2	18
3	8q21.12	8q21.12	1.903E-3	1.598E-2	6.276E-2	5.329E-2	1	2
4	8q12-q13	8q12-q13	2.854E-3	1.598E-2	6.276E-2	7.990E-2	1	3
5	1p13-p12	1p13-p12	2.854E-3	1.598E-2	6.276E-2	7.990E-2	1	3

Show 2 more annotations

**11: Transcription Factor Binding Site** [Display Chart] 16 input genes in category / 200 annotations before applied cutoff /

**9770 genes in category**

No results to display

**12: Gene Family [Display Chart] 26 input genes in category / 29 annotations before applied cutoff / 18194 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 682	Zinc fingers FYVE-type Pleckstrin homology domain containing Rho guanine nucleotide exchange factors	genenames.org	3.069E-3	4.861E-2	1.926E-1	8.901E-2	3	206
2 677	Peptidyl arginine deiminases	genenames.org	7.126E-3	4.861E-2	1.926E-1	2.066E-1	1	5
3 1185	CD molecules Type I classical cadherins	genenames.org	7.126E-3	4.861E-2	1.926E-1	2.066E-1	1	5
4 658	Fibronectin type III domain containing I-set domain containing Myosin binding proteins	genenames.org	1.138E-2	4.861E-2	1.926E-1	3.299E-1	1	8
5 1230	WD repeat domain containing BEACH domain containing	genenames.org	1.279E-2	4.861E-2	1.926E-1	3.709E-1	1	9

[Show 11 more annotations](#)**13: Coexpression [Display Chart] 34 input genes in category / 2244 annotations before applied cutoff / 23137 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 17414055-Table2	Human pancreas Kim07 34genes	GeneSigDB	1.267E-5	2.843E-2	2.358E-1	2.843E-2	3	31
2 M4391	Genes up-regulated in the HMEC cells (primary mammary epithelium) upon expression of TP53 [GeneID=7157] off adenoviral vector.	MSigDB C2: CGP Curated Gene Sets (v6.0)	3.537E-5	3.969E-2	3.292E-1	7.938E-2	9	1172

**14: Coexpression Atlas [Display Chart] 33 input genes in category / 1642 annotations before applied cutoff / 23956 genes in category**

No results to display

**15: Computational [Display Chart] 16 input genes in category / 86 annotations before applied cutoff / 10037 genes in category**

No results to display

**16: MicroRNA [Display Chart] 34 input genes in category / 1945 annotations before applied cutoff / 19844 genes in category**

No results to display

**17: Drug [Display Chart] 34 input genes in category / 4571 annotations before applied cutoff / 22841 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 5667 UP	Metrapone [54-36-4]; Up 200; 17.6uM; MCF7; HT HG-U133A	Broad Institute CMAP Up	9.093E-6	2.320E-2	2.089E-1	4.157E-2	5	192
2 ctd:D019287	Zinc Sulfate	CTD	1.015E-5	2.320E-2	2.089E-1	4.639E-2	8	741

**18: Disease [Display Chart] 27 input genes in category / 342 annotations before applied cutoff / 16205 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 C0424711	Orbital separation diminished	DisGeNET Curated	6.619E-4	4.077E-2	2.615E-1	2.264E-1	2	23
2 cv:CN158704	Seckel syndrome 7	Clinical Variations	1.669E-3	4.077E-2	2.615E-1	5.707E-1	1	1
3 C0563305	IgA myeloma	DisGeNET BeFree	1.669E-3	4.077E-2	2.615E-1	5.707E-1	1	1
4 C1446219	Akinetic rigid syndrome	DisGeNET BeFree	1.669E-3	4.077E-2	2.615E-1	5.707E-1	1	1

5	OMIN:162100	AMYOTROPHY, HEREDITARY NEURALGIC; HNA	OMIM	1.669E- 3	4.077E- 2	2.615E- 1	5.707E-1	1	1
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[Show 18 more annotations](#)