

GREAT version 4.0.4 current (08/19/2019 to now)

Job Description

Job ID: 20240719-public-4.0.4-qoHtEr

Display name:

Test set: distfilter_DKO_K4me3_dcp.target.peaks.bed (1,207 genomic regions)
[Show in UCSC genome browser.](#) *How do I look at my regions in the genome?*

Background: Whole genome background

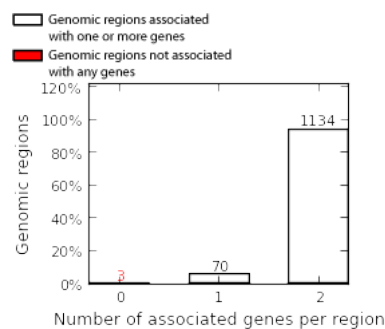
Assembly: Mouse: NCBI build 38 ([UCSC mm10, Dec. 2011](#)) *What gene set does GREAT use?*

Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included in 3 of all 1,207 genomic regions (0.2%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

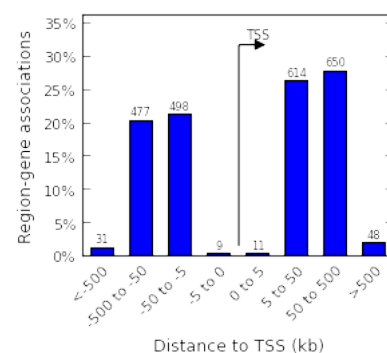
➤ Region-Gene Association Graphs

What do these graphs illustrate?

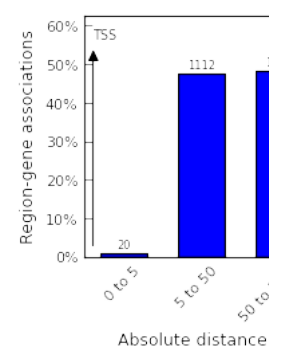
Number of associated genes per region

[Download as PDF.](#)

Binned by orientation and distance to TSS

[Download as PDF.](#)

Binned by absolute distance to

[Download as PDF.](#)

Global Controls

Global Export 

Which data is exported by each option?

⊕ Ensembl Genes (no terms)

- GO Biological Process (9 terms)

Table controls: Export

Shown top rows in this table:

Term annotation count: Min: Max:

Visualize this table: [select one]

Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Other Genes
dopaminergic neuron differentiation	93	3.5712e-6	5.0266e-4	3.1727	22	1.82%	222	2.0544e-3	3.7587	
endoplasmic reticulum calcium ion homeostasis	120	3.9613e-5	4.3212e-3	5.0834	10	0.83%	292	8.8337e-3	3.9936	
dorsal spinal cord development	137	8.9604e-5	8.5614e-3	4.2019	11	0.91%	462	4.6582e-2	3.7274	
putrescine biosynthetic process	139	9.1482e-5	8.6151e-3	11.4507	5	0.41%	415	3.1397e-2	7.0997	
dorsal/ventral pattern formation	146	1.1424e-4	1.0243e-2	2.1203	31	2.57%	189	6.4175e-4	2.6081	
regulation of endoribonuclease activity	155	1.3129e-4	1.1088e-2	31.7011	3	0.25%	398	2.7194e-2	10.6496	
monounsaturated fatty acid biosynthetic process	208	3.5173e-4	2.2135e-2	22.6110	3	0.25%	248	4.0924e-3	10.6496	
regulation of ARF protein signal transduction	218	4.4175e-4	2.6525e-2	4.1164	9	0.75%	322	1.3805e-2	4.6592	
positive regulation of mitochondrial calcium ion concentration	237	5.8222e-4	3.2157e-2	7.6301	5	0.41%	436	3.6695e-2	5.3248	

The test set of 1,207 genomic regions picked 2,009 (9%) of all 21,395 genes.
GO Biological Process has 13,090 terms covering 17,925 (84%) of all 21,395 genes, and 1,163,819 term - gene associations.
13,090 ontology terms (100%) were tested using an annotation count range of [1, Inf].

● **GO Cellular Component (1 term)**

Table controls: Export

Shown top rows in this table: 20 Set

Term annotation count: Min: 1 Max: Inf Set

Visualize this table: [select one]

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Gene
apicolateral plasma membrane	52	1.9691e-4	6.4147e-3	4.1675	10	0.83%	39	3.4674e-2	4.1415	

The test set of 1,207 genomic regions picked 2,009 (9%) of all 21,395 genes.

GO Cellular Component has 1,694 terms covering 19,074 (89%) of all 21,395 genes, and 371,380 term - gene associations.

1,694 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Molecular Function (4 terms)

Table controls: Export Shown top rows in this table: 20 Set Term annotation count: Min: 1 Max: Inf Set Visualize this table: [select one]

Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Ontology
palmitoyl-CoA 9-desaturase activity	71	3.5173e-4	2.0465e-2	22.6110	3	0.25%	32	1.0009e-2	10.6496	
ARF guanyl-nucleotide exchange factor activity	74	3.8828e-4	2.1676e-2	3.8195	10	0.83%	39	1.8490e-2	4.4840	
frizzled binding	80	6.4653e-4	3.3385e-2	2.8133	14	1.16%	55	4.0223e-2	3.0828	
signal transducer activity, downstream of receptor	83	6.9600e-4	3.4641e-2	2.0370	26	2.15%	44	2.7661e-2	2.2590	

The test set of 1,207 genomic regions picked 2,009 (9%) of all 21,395 genes.

GO Molecular Function has 4,131 terms covering 17,189 (80%) of all 21,395 genes, and 227,341 term - gene associations.

4,131 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Human Phenotype (no terms)

Mouse Phenotype Single KO (20+ terms)

Table controls: Export Shown top rows in this table: 20 Set Term annotation count: Min: 1 Max: Inf Set Visualize this table: [select one]

Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Ontology
abnormal mean corpuscular volume	11	1.9207e-7	1.6011e-4	2.4632	42	3.48%	351	3.9536e-2	1.6999	
abnormal rhombomere morphology	12	4.3977e-7	3.3606e-4	5.5536	14	1.16%	260	1.8716e-2	4.3851	
increased neuron number	16	7.7990e-7	4.4698e-4	2.9413	28	2.32%	104	4.3992e-4	3.1130	
abnormal neuromere morphology	18	1.4471e-6	7.3724e-4	5.0107	14	1.16%	296	2.4730e-2	4.1415	
absent supraoccipital bone	23	3.2934e-6	1.3131e-3	6.8154	10	0.83%	331	3.3860e-2	5.3248	
decreased sensitivity to induced cell death	26	3.9699e-6	1.4001e-3	3.1512	22	1.82%	284	2.1459e-2	2.3512	
abnormal lymph node cortex morphology	35	8.3346e-6	2.1837e-3	3.6272	17	1.41%	301	2.6028e-2	2.7782	
decreased erythrocyte cell number	41	1.2526e-5	2.8016e-3	2.1450	39	3.23%	307	2.8988e-2	1.8153	
abnormal rhombomere 4 morphology	43	1.2882e-5	2.7471e-3	9.4133	7	0.58%	243	1.3532e-2	8.5197	
abnormal skin condition	44	1.3571e-5	2.8283e-3	2.0492	43	3.56%	141	1.6561e-3	2.0708	
abnormal lymph node B cell domain morphology	46	1.6693e-5	3.3278e-3	3.5985	16	1.33%	321	3.0884e-2	2.8572	
sparse hair	65	6.4972e-5	9.1661e-3	2.5467	23	1.91%	287	2.1813e-2	2.2821	
abnormal optic tract morphology	67	6.9342e-5	9.4905e-3	5.3036	9	0.75%	331	3.3860e-2	5.3248	
abnormal corpora quadrigemina morphology	76	1.1987e-4	1.4464e-2	2.8108	18	1.49%	166	3.8543e-3	3.7789	
abnormal wound healing	90	1.7162e-4	1.7486e-2	2.0177	33	2.73%	365	4.4237e-2	1.8337	
increased heart weight	113	2.7456e-4	2.2281e-2	2.0137	31	2.57%	288	2.1790e-2	1.8993	
abnormal styloid process morphology	120	3.3780e-4	2.5814e-2	3.8891	10	0.83%	245	1.4287e-2	5.3248	
abnormal heart ventricle wall thickness	128	3.6390e-4	2.6070e-2	2.0058	30	2.49%	202	8.5592e-3	2.1137	
abnormal ear development	130	3.8902e-4	2.7441e-2	2.1987	24	1.99%	125	1.2876e-3	3.2150	
increased cochlear hair cell number	147	5.5696e-4	3.4743e-2	3.1708	12	0.99%	327	3.2589e-2	3.9235	

The test set of 1,207 genomic regions picked 2,009 (9%) of all 21,395 genes.

Mouse Phenotype Single KO has 9,170 terms covering 9,466 (44%) of all 21,395 genes, and 551,620 term - gene associations.

9,170 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype (20+ terms)

Table controls: Export Shown top rows in this table: 20 Set Term annotation count: Min: 1 Max: Inf Set Visualize this table: [select one]

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Bejerano Lab

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
abnormal mean corpuscular volume	22	5.4022e-7	2.3512e-4	2.2614	46	3.81%	563	4.4649e-2	1.6083	
abnormal spinal cord dorsal horn morphology	26	1.5472e-6	5.6979e-4	6.5611	11	0.91%	236	2.7045e-3	5.0116	
increased neuron number	27	1.6767e-6	5.9461e-4	2.3755	38	3.15%	189	7.4497e-4	2.4882	
small scala media	29	2.0765e-6	6.8561e-4	6.3604	11	0.91%	380	1.6689e-2	5.9164	
absent supraoccipital bone	35	3.2934e-6	9.0098e-4	6.8154	10	0.83%	444	2.6358e-2	5.3248	
abnormal fibroblast physiology	36	4.1809e-6	1.1120e-3	2.0023	51	4.23%	340	1.0904e-2	1.7258	
increased monocyte cell number	53	1.4787e-5	2.6713e-3	2.2367	35	2.90%	428	2.2945e-2	1.8521	
abnormal rhombomere 4 morphology	60	2.2189e-5	3.5410e-3	8.6386	7	0.58%	423	2.2532e-2	7.0997	
increased sensory neuron number	63	2.4719e-5	3.7569e-3	2.5319	26	2.15%	202	1.1570e-3	3.0174	
decreased sensitivity to induced cell death	77	6.3230e-5	7.8627e-3	2.5514	23	1.91%	516	3.8043e-2	2.0836	
abnormal corpora quadrigemina morphology	111	1.5705e-4	1.3547e-2	2.6611	19	1.57%	203	1.1624e-3	3.8726	
abnormal physiological neovascularization	121	1.8127e-4	1.4345e-2	3.6010	12	0.99%	558	4.4490e-2	3.1554	
increased cardiomyocyte apoptosis	126	2.0907e-4	1.5888e-2	2.5263	20	1.66%	356	1.3125e-2	2.5765	
abnormal tectum morphology	147	2.9010e-4	1.8896e-2	2.3991	21	1.74%	191	8.3443e-4	3.5499	
abnormal cardiomyocyte apoptosis	181	5.0137e-4	2.6523e-2	2.2474	22	1.82%	396	1.8778e-2	2.3211	
increased response of heart to induced stress	188	5.5736e-4	2.8387e-2	2.5444	17	1.41%	386	1.7108e-2	2.8399	
enlarged myocardial fiber	203	7.1589e-4	3.3767e-2	2.3457	19	1.57%	211	1.4249e-3	2.8611	
sparse hair	211	7.8481e-4	3.5614e-2	2.0527	25	2.07%	507	3.5680e-2	2.0094	
abnormal styloid process morphology	215	8.2108e-4	3.6567e-2	3.2210	11	0.91%	271	4.2622e-3	5.3248	
abnormal optic tract morphology	230	9.5665e-4	3.9826e-2	3.3896	10	0.83%	482	3.2065e-2	4.2598	

The test set of 1,207 genomic regions picked 2,009 (9%) of all 21,395 genes.
Mouse Phenotype has 9,575 terms covering 9,654 (45%) of all 21,395 genes, and 705,265 term - gene associations.
9,575 ontology terms (100%) were tested using an annotation count range of [1, Inf].