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

Warning: Your set hits a large fraction of the genes in the genome, which often does not work well with the GREAT Significant by Both view due to a saturation of the gene-based hype...
See our *tips for handling large datasets* or try the Significant By Region-based Binomial view.

⊖ Job Description

|	
Job ID:	20250409-public-4.0.4-t9mokl
Display name:	species_pancreas_parsed.bed
Test set:	species_pancreas_parsed.bed (27,353 genomic regions)
	Show in UCSC genome browser.　　*How do I look at my regions in the genome?*
Background:	Whole genome background
Assembly:	Human: GRCh38 (UCSC hg38, Dec. 2013)　　*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 inclu...
	11 of all 27,353 genomic regions (0%) 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
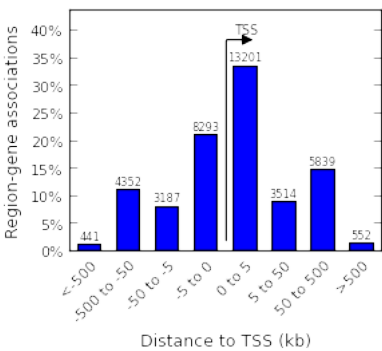
What do these graphs illustrate?

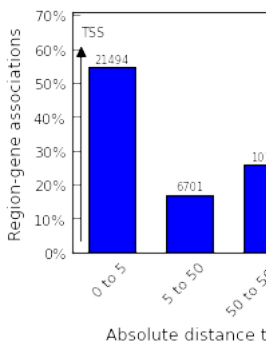**Number of associated genes per region**
Download as PDF.
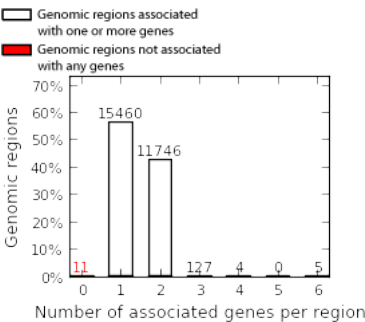
Binned by orientation and distance to TSS
Download as PDF.

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 (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	Hyper Ob Ge
endoplasmic reticulum unfolded protein response	31	6.6580e-37	2.8262e-34	2.0787	373	1.36%	544	1.9449e-5	1.3627	
snRNA metabolic process	55	2.1239e-28	5.0815e-26	2.2047	247	0.90%	748	4.8814e-4	1.3548	
regulation of pri-miRNA transcription from RNA polymerase II promoter	62	1.2927e-27	2.7436e-25	2.2335	233	0.85%	804	8.7237e-4	1.5721	
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	73	1.6903e-25	3.0469e-23	2.1007	246	0.90%	507	8.5779e-6	1.4979	
signal transduction involved in mitotic G1 DNA damage checkpoint	77	3.6696e-25	6.2713e-23	2.0812	248	0.91%	486	5.9308e-6	1.5010	
ncRNA transcription	81	4.4879e-25	7.2910e-23	2.0022	272	0.99%	515	9.4260e-6	1.4133	
cellular component disassembly involved in execution phase of apoptosis	84	2.8935e-24	4.5328e-22	3.0957	113	0.41%	1,172	1.3850e-2	1.4937	
snRNA transcription from RNA polymerase II promoter	86	4.0126e-24	6.1397e-22	2.1355	223	0.82%	724	3.5284e-4	1.3991	
apoptotic nuclear changes	110	1.0267e-21	1.2283e-19	3.0015	105	0.38%	1,314	2.7927e-2	1.4775	
positive regulation of pri-miRNA transcription from RNA polymerase II promoter	115	5.2109e-21	5.9627e-19	2.5311	135	0.49%	1,017	5.3526e-3	1.6041	
cytoplasmic translation	117	8.5383e-21	9.6030e-19	2.6128	126	0.46%	446	2.1713e-6	1.6100	
IRE1-mediated unfolded protein response	121	1.2817e-20	1.3939e-18	2.2104	174	0.64%	756	5.3521e-4	1.4266	

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	
regulation of receptor biosynthetic process	130	**6.2865e-20**	**6.3634e-18**	3.0792	92	0.34%	1,331	**2.9073e-2**	1.5197	
cytoplasmic sequestering of protein	144	**3.9118e-19**	**3.5747e-17**	2.6392	113	0.41%	1,260	**2.2004e-2**	1.3855	
positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	193	**1.5988e-16**	**1.0901e-14**	2.3285	122	0.45%	1,307	**2.7608e-2**	1.5830	
ER-nucleus signaling pathway	225	**3.7956e-15**	**2.2199e-13**	2.1010	139	0.51%	1,077	**8.4927e-3**	1.4474	
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	278	**3.0961e-13**	**1.4655e-11**	2.5975	77	0.28%	1,342	**3.0751e-2**	1.6886	
ER overload response	280	**3.3006e-13**	**1.5512e-11**	3.1596	56	0.20%	1,342	**3.0751e-2**	1.6886	
hepatocyte apoptotic process	322	**4.1695e-12**	**1.7039e-10**	2.5477	72	0.26%	1,229	**1.9878e-2**	1.6886	
histone H2A ubiquitination	359	**2.2658e-11**	**8.3051e-10**	2.0934	101	0.37%	1,174	**1.3839e-2**	1.5351	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
GO Biological Process has 13,159 terms covering 16,804 (89%) of all 18,777 genes, and 1,256,055 term - gene associations.
13,159 ontology terms (100%) were tested using an annotation count range of [1, Inf].

⊖ GO Cellular Component (7 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	
COPI-coated vesicle	78	**3.6570e-12**	**8.1016e-11**	2.3587	84	0.31%	200	**6.8720e-3**	1.5417	
nuclear ubiquitin ligase complex	79	**7.8905e-12**	**1.7259e-10**	2.0832	107	0.39%	257	**3.0629e-2**	1.3509	
mitochondrial large ribosomal subunit	82	**1.8730e-11**	**3.9470e-10**	2.0593	106	0.39%	280	**4.6402e-2**	1.2913	
intrinsic component of mitochondrial outer membrane	94	**1.1241e-10**	**2.0665e-9**	2.2999	76	0.28%	249	**2.8891e-2**	1.4683	
integral component of mitochondrial outer membrane	97	**2.3333e-10**	**4.1567e-9**	2.2902	74	0.27%	272	**3.9276e-2**	1.4583	
COPI-coated vesicle membrane	152	**3.7887e-7**	**4.3071e-6**	2.0709	59	0.22%	234	**2.0250e-2**	1.5830	
CD40 receptor complex	197	**8.9994e-6**	**7.8939e-5**	2.4143	32	0.12%	240	**2.2580e-2**	1.6886	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
GO Cellular Component has 1,728 terms covering 17,911 (95%) of all 18,777 genes, and 382,522 term - gene associations.
1,728 ontology terms (100%) were tested using an annotation count range of [1, Inf].

⊖ GO Molecular Function (5 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	
mitogen-activated protein kinase binding	17	**3.4213e-17**	**8.4970e-15**	2.3069	130	0.48%	124	**4.7474e-4**	1.6260	
myosin V binding	20	**2.0763e-15**	**4.3830e-13**	2.6896	86	0.31%	215	**3.3700e-2**	1.5893	
NF-kappaB binding	26	**5.8021e-14**	**9.4217e-12**	2.2458	109	0.40%	115	**3.1352e-4**	1.6283	
cyclin-dependent protein serine/threonine kinase inhibitor activity	49	**4.9884e-11**	**4.2982e-9**	2.9663	50	0.18%	220	**3.5628e-2**	1.6886	
protein kinase B binding	57	**2.4401e-10**	**1.8074e-8**	3.1178	43	0.16%	220	**3.5628e-2**	1.6886	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
GO Molecular Function has 4,222 terms covering 16,729 (89%) of all 18,777 genes, and 230,772 term - gene associations.
4,222 ontology terms (100%) were tested using an annotation count range of [1, Inf].

⊖ Human Phenotype (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]

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	
Death in infancy	1	**2.4361e-22**	**1.6256e-18**	2.1741	197	0.72%	296	**3.7123e-4**	1.4474	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
Human Phenotype has 6,673 terms covering 3,390 (18%) of all 18,777 genes, and 255,152 term - gene associations.
6,673 ontology terms (100%) were tested using an annotation count range of [1, Inf].

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	O G
abnormal bone mineral density of femur	24	1.9006e-13	7.2516e-11	2.8752	66	0.24%	965	5.0268e-2	1.6886	
decreased cellular sensitivity to ultraviolet irradiation	42	4.7881e-12	1.0439e-9	2.9800	55	0.20%	782	2.1739e-2	1.6886	
delayed embryo turning	44	5.3603e-12	1.1156e-9	2.1406	102	0.37%	728	1.5530e-2	1.5351	
increased incidence of tumors by ionizing radiation induction	78	4.9482e-10	5.8090e-8	2.5921	56	0.20%	929	4.3045e-2	1.5760	
embryonic lethality between somite formation and embryo turning, incomplete penetrance	106	7.0970e-9	6.1309e-7	2.1588	70	0.26%	695	1.4109e-2	1.5948	
abnormal hypoglossal nerve topology	129	2.9541e-8	2.0970e-6	2.0668	71	0.26%	695	1.4109e-2	1.5948	
absent hypoglossal nerve	168	1.3273e-7	7.2347e-6	2.2264	54	0.20%	929	4.3045e-2	1.5760	
thin hypoglossal nerve	200	2.6678e-7	1.2214e-5	2.0517	62	0.23%	571	6.1748e-3	1.6886	
reduced sympathetic cervical ganglion size	387	2.2607e-5	5.3492e-4	2.0027	44	0.16%	703	1.4315e-2	1.6886	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
Mouse Phenotype Single KO has 9,157 terms covering 9,525 (51%) of all 18,777 genes, and 563,371 term - gene associations.
9,157 ontology terms (100%) were tested using an annotation count range of [1, Inf].

⊖ **Mouse Phenotype (11 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	O G
increased hemangioma incidence	20	5.4273e-19	2.5945e-16	2.3231	143	0.52%	617	3.2891e-4	1.5796	
decreased cellular sensitivity to ultraviolet irradiation	51	9.9525e-15	1.8658e-12	2.9300	71	0.26%	856	4.3007e-3	1.6886	
increased renal carcinoma incidence	75	1.7714e-12	2.2582e-10	3.6610	43	0.16%	1,330	3.8082e-2	1.6886	
abnormal frontal lobe morphology	87	5.5121e-12	6.0576e-10	2.3256	85	0.31%	1,275	3.2747e-2	1.5760	
increased kidney tumor incidence	98	2.1843e-11	2.1310e-9	2.4898	70	0.26%	1,183	2.2162e-2	1.5830	
abnormal small intestinal crypt cell proliferation	99	2.8419e-11	2.7446e-9	2.0761	102	0.37%	1,044	1.1307e-2	1.5351	
abnormal hypoglossal nerve topology	225	2.9541e-8	1.2553e-6	2.0668	71	0.26%	1,019	1.0047e-2	1.5948	
absent hypoglossal nerve	275	1.3273e-7	4.6147e-6	2.2264	54	0.20%	1,275	3.2747e-2	1.5760	
thin hypoglossal nerve	308	2.6678e-7	8.2814e-6	2.0517	62	0.23%	856	4.3007e-3	1.6886	
abnormal base-excision repair	346	8.1333e-7	2.2475e-5	2.4388	39	0.14%	1,330	3.8082e-2	1.6886	
reduced sympathetic cervical ganglion size	553	2.2607e-5	3.9086e-4	2.0027	44	0.16%	1,024	1.0261e-2	1.6886	

The test set of 27,353 genomic regions picked 11,120 (59%) of all 18,777 genes.
Mouse Phenotype has 9,561 terms covering 9,709 (52%) of all 18,777 genes, and 718,378 term - gene associations.
9,561 ontology terms (100%) were tested using an annotation count range of [1, Inf].