



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 hypothesis. See our [tips for handling large datasets](#) or try the [Significant By Region-based Binomial](#) view.

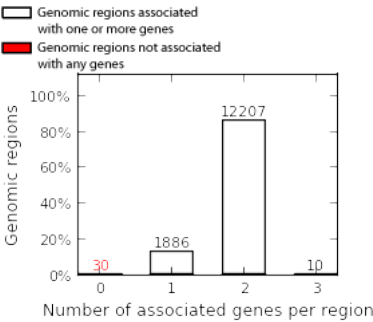
Job Description

Job ID: 20250414-public-4.0.4-HzgVds
Display name: `mouse_pancreas_unique_parsed.t`
Test set: mouse_pancreas_unique_parsed.bed (14,133 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 included. 30 of all 14,133 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?](#)

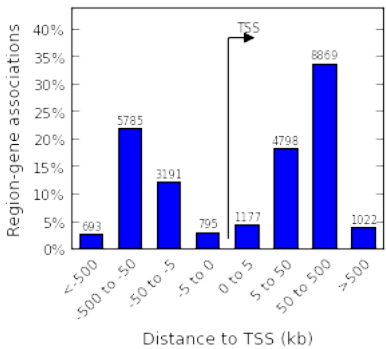
Region-Genes Association Graphs

What do these graphs illustrate?

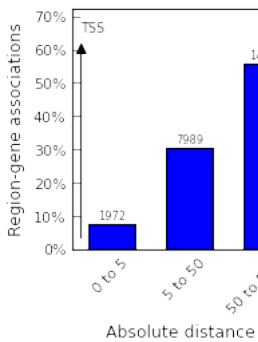
Number of associated genes per region
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Binned by orientation and distance to TSS
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Binned by absolute distance to TSS
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Global Controls [Global Export](#) [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: [Set](#) Term annotation count: Min: Max: [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	Ol
myeloid cell differentiation	176	1.2322e-46	9.2128e-45	2.0084	512	3.62%	490	3.9996e-5	1.4128	
regulation of Notch signaling pathway	283	2.3824e-30	1.1078e-28	2.1702	273	1.93%	425	9.7511e-6	1.7220	
corticosteroid receptor signaling pathway	288	8.2812e-30	3.7837e-28	5.5138	72	0.51%	1,451	4.2372e-2	2.1609	
myeloid leukocyte differentiation	291	1.2269e-29	5.5482e-28	2.0707	297	2.10%	496	4.5148e-5	1.5865	
regulation of muscle adaptation	308	2.3311e-28	9.9594e-27	2.0692	284	2.01%	446	1.3955e-5	1.7264	
CD4-positive, alpha-beta T cell differentiation	313	4.6975e-28	1.9749e-26	2.7786	156	1.10%	696	1.0663e-3	1.8417	
CD4-positive, alpha-beta T cell activation	326	6.1354e-27	2.4766e-25	2.6981	157	1.11%	721	1.2950e-3	1.8059	
regulation of cardiac muscle hypertrophy	349	3.1336e-25	1.1815e-23	2.1942	219	1.55%	504	5.6595e-5	1.8656	
regulation of muscle hypertrophy	355	4.4519e-25	1.6502e-23	2.1703	223	1.58%	454	1.7386e-5	1.8908	
actin filament bundle organization	374	4.4624e-24	1.5701e-22	2.4119	171	1.21%	368	2.1828e-6	1.9067	
T-helper cell differentiation	383	9.2461e-24	3.1767e-22	2.9285	120	0.85%	601	2.9634e-4	2.0420	
alpha-beta T cell differentiation	399	1.2719e-22	4.1948e-21	2.2035	193	1.37%	437	1.2835e-5	1.8739	
cellular response to vascular endothelial growth factor stimulus	411	4.0713e-22	1.3035e-20	2.5062	145	1.03%	660	6.2622e-4	1.9280	
regulation of multicellular organism growth	423	1.0811e-21	3.3633e-20	2.0358	222	1.57%	675	8.2858e-4	1.5965	
alpha-beta T cell differentiation involved in immune response	434	1.7755e-21	5.3835e-20	2.6617	126	0.89%	524	7.8685e-5	2.0708	
actin filament bundle assembly	448	1.0763e-20	3.1614e-19	2.3420	154	1.09%	437	1.2835e-5	1.8739	

Great

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Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
T cell differentiation involved in immune response	449	1.1692e-20	3.4268e-19	2.5989	126	0.89%	844	3.0226e-3	1.8036	
alpha-beta T cell activation	453	1.4178e-20	4.1186e-19	2.0544	205	1.45%	410	6.7335e-6	1.8458	
cellular response to glucocorticoid stimulus	454	1.5016e-20	4.3524e-19	2.0070	217	1.54%	942	5.9072e-3	1.5396	
Fc receptor mediated stimulatory signaling pathway	458	2.3323e-20	6.7010e-19	2.0699	199	1.41%	693	9.5376e-4	1.5652	

The test set of 14,133 genomic regions picked 7,724 (41%) 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 (6 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	Ol
extrinsic component of cytoplasmic side of plasma membrane	58	3.6245e-27	1.0798e-25	2.0311	284	2.01%	60	1.2266e-6	1.6281	
cortical actin cytoskeleton	87	4.5966e-18	9.1299e-17	2.1366	162	1.15%	92	1.0599e-4	1.7017	
myosin complex	90	1.1435e-17	2.1955e-16	2.0621	172	1.22%	144	8.7838e-3	1.4723	
platelet dense tubular network membrane	142	3.1111e-10	3.7859e-9	3.4401	37	0.26%	180	4.4854e-2	2.1609	
node of Ranvier	165	8.3364e-9	8.7305e-8	2.2698	62	0.44%	138	4.8357e-3	2.1069	
zonula adherens	218	2.0785e-6	1.6475e-5	3.0216	25	0.18%	145	9.7494e-3	2.4310	

The test set of 14,133 genomic regions picked 7,724 (41%) 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 (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	Ol
protein phosphorylated amino acid binding	102	9.5913e-15	3.9701e-13	2.0368	145	1.03%	189	4.7673e-2	1.5470	
phosphatidylinositol 3-kinase binding	107	4.4880e-14	1.7709e-12	2.0651	133	0.94%	160	1.6901e-2	1.7604	
14-3-3 protein binding	111	9.1299e-14	3.4727e-12	2.2761	104	0.74%	104	5.4944e-4	2.0420	
phosphotyrosine binding	137	4.8075e-12	1.4815e-10	2.0105	119	0.84%	169	2.3643e-2	1.6670	
I-SMAD binding	148	8.2656e-11	2.3579e-9	2.3935	71	0.50%	119	2.0162e-3	2.4310	
AP-2 adaptor complex binding	245	1.3807e-7	2.3793e-6	2.6624	38	0.27%	166	2.0807e-2	2.4310	
glucocorticoid receptor binding	250	1.5715e-7	2.6540e-6	2.0191	67	0.47%	133	5.9821e-3	2.2440	
ankyrin binding	273	4.8406e-7	7.4860e-6	2.0832	57	0.40%	167	2.2907e-2	1.9192	
muscle alpha-actinin binding	404	3.8180e-5	3.9900e-4	2.0304	40	0.28%	184	4.0431e-2	1.8908	
profilin binding	410	4.7249e-5	4.8655e-4	2.2101	32	0.23%	188	4.7586e-2	2.1879	
arginine binding	702	3.2972e-3	1.9830e-2	2.1507	17	0.12%	187	4.4926e-2	2.4310	

The test set of 14,133 genomic regions picked 7,724 (41%) 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 (2 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	Ol
Abnormality of adipose tissue	56	1.0099e-15	1.2034e-13	2.1705	134	0.95%	26	2.2073e-2	1.6207	
Gastrointestinal hemorrhage	203	2.5118e-9	8.2566e-8	2.3286	63	0.45%	44	3.4227e-2	1.8700	

The test set of 14,133 genomic regions picked 7,724 (41%) 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].

Visualize this table: [select one]

The test set of 14,133 genomic regions picked 7,724 (41%) 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].

Visualize this table: [select one]

3/4



9,561 ontology terms (100%) were tested using an annotation count range of [1, inf].

**Bejerano Lab**

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