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: 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 inclu

30 of all 14,133 genomic regions (0.2%) are not associated with any genes.

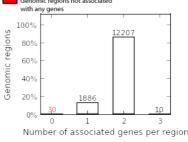
View all genomic region-gene associations. Which genes are my regions associated with? Revise the region-gene association rule. Which genes are my regions associated with genes?

# **○** Region-Gene Association Graphs

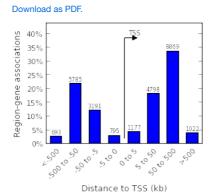
What do these graphs illustrate?

# Download as PDF. Genomic regions associated with one or more genes Genomic regions not associated with any genes 100%

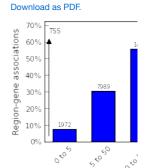
Number of associated genes per region



### Binned by orientation and distance to TSS



### Binned by absolute distance to



Absolute distance

- Ensembl Genes (no terms)
- GO Biological Process (20+ terms)

Table controls: Export Shown	top rows in this t	table: 20	Set Ter	m annotation c	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 I Fold OI Enrichment Ge
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 grov factor stimulus	wth 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

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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	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	<b>∨</b>	Shown top rov	ws in this	table: 20	Set Ter	m annotation c	count: Min: 1	Max: Inf	Set	Visualize this	table: [select	ct 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 Enrichmen	Ol nt Ge
extrinsic con plasma mem	nponent of cyt brane	oplasm	ic side of	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 comp	olex			90	1.1435e-17	2.1955e-16	2.0621	172	1.22%	144	8.7838e-3	1.4723	
platelet dens	e tubular netw	ork me	mbrane	142	3.1111e-10	3.7859e-9	3.4401	37	0.26%	180	4.4854e-2	2.1609	
node of Ranv	vier			165	8.3364e-9	8.7305e-8	2.2698	62	0.44%	138	4.8357e-3	2.1069	
zonula adher	ens			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.

# **○** GO Molecular Function (11 terms)

Table controls:	Export 🗸	Shown top rows in this	table: 20	Set Ter	m annotation c	ount: Min: 1	Max: Inf	Set	Visualize this	table: [select of	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	OI G€
protein phos	phorylated amino aci	d binding 102	9.5913e-15	3.9701e-13	2.0368	145	1.03%	189	4.7673e-2	1.5470	
phosphatidyl	linositol 3-kinase bino	ling 107	4.4880e-14	1.7709e-12	2.0651	133	0.94%	160	1.6901e-2	1.7604	
14-3-3 protei	n binding	111	9.1299e-14	3.4727e-12	2.2761	104	0.74%	104	5.4944e-4	2.0420	
phosphotyro	sine binding	137	4.8075e-12	1.4815e-10	2.0105	119	0.84%	169	2.3643e-2	1.6670	
I-SMAD bind	ing	148	8.2656e-11	2.3579e-9	2.3935	71	0.50%	119	2.0162e-3	2.4310	
AP-2 adaptor	r complex binding	245	1.3807e-7	2.3793e-6	2.6624	38	0.27%	166	2.0807e-2	2.4310	
glucocortico	id receptor binding	250	1.5715e-7	2.6540e-6	2.0191	67	0.47%	133	5.9821e-3	2.2440	
ankyrin bindi	ing	273	4.8406e-7	7.4860e-6	2.0832	57	0.40%	167	2.2907e-2	1.9192	
muscle alpha	a-actinin binding	404	3.8180e-5	3.9900e-4	2.0304	40	0.28%	184	4.0431e-2	1.8908	
profilin bindi	ng	410	4.7249e-5	4.8655e-4	2.2101	32	0.23%	188	4.7586e-2	2.1879	
arginine bind	ling	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.

# **○** Human Phenotype (2 terms)

Table controls: Export	Shown top rows in this	table: 20	Set Ter	m annotation c	ount: 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	OI Ge
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	

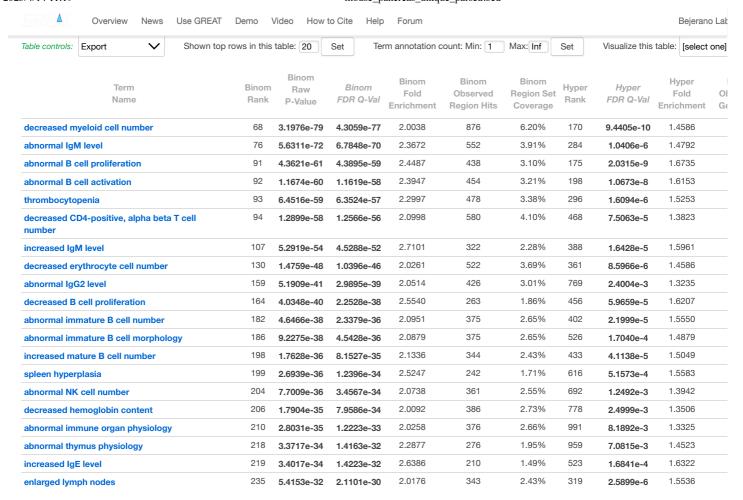
The test set of 14,133 genomic regions picked 7,724 (41%) of all 18,777 genes.

 $\textit{Human Phenotype} \ \text{has}\ 6,673\ \text{terms covering}\ 3,390\ (18\%)\ \text{of all}\ 18,777\ \text{genes, and}\ 255,152\ \text{term}\ \text{-}\ \text{gene}\ \text{associations}.$ 

 $6,\!673$  ontology terms (100%) were tested using an annotation count range of [1, Inf].

<sup>1,728</sup> ontology terms (100%) were tested using an annotation count range of [1, Inf].

<sup>4,222</sup> ontology terms (100%) were tested using an annotation count range of [1, Inf].



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, lnf].

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Table controls: Export S	hown top rows in this	table: 20	Set Ter	m annotation c	ount: 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 C Enrichment G
abnormal IgM level	89	1.3147e-79	1.4124e-77	2.2252	693	4.90%	340	3.2075e-8	1.4586
thymus hypoplasia	90	3.8405e-79	4.0799e-77	2.1518	741	5.24%	336	2.6959e-8	1.4943
increased IgM level	119	9.0740e-65	7.2905e-63	2.5281	438	3.10%	347	3.8543e-8	1.6038
abnormal B cell proliferation	136	8.4701e-59	5.9546e-57	2.1736	538	3.81%	296	5.0596e-9	1.5564
thrombocytopenia	138	1.6027e-58	1.1104e-56	2.1223	565	4.00%	344	3.6094e-8	1.5032
abnormal B cell activation	144	5.1746e-57	3.4357e-55	2.1128	556	3.93%	326	1.5479e-8	1.5179
decreased double-positive T cell number	r 164	1.1863e-53	6.9159e-52	2.0129	587	4.15%	281	2.5783e-9	1.5514
abnormal immature B cell number	191	1.7763e-48	8.8919e-47	2.0279	520	3.68%	421	3.9710e-7	1.5158
abnormal immature B cell morphology	193	1.0033e-47	4.9703e-46	2.0117	522	3.69%	475	2.0757e-6	1.4750
abnormal IgG2 level	202	2.8035e-45	1.3269e-43	2.0113	495	3.50%	973	1.2486e-3	1.3072
abnormal NK cell number	203	3.2180e-45	1.5156e-43	2.0772	457	3.23%	647	3.4083e-5	1.4434
increased autoantibody level	210	1.2382e-44	5.6374e-43	2.1485	417	2.95%	471	1.8435e-6	1.5006
increased anti-nuclear antigen antibody	level 218	3.0250e-43	1.3267e-41	2.2551	363	2.57%	453	1.1498e-6	1.5654
decreased type I pneumocyte number	219	3.7099e-43	1.6197e-41	4.1194	143	1.01%	922	8.6179e-4	2.2574
abnormal NK cell morphology	224	3.5594e-42	1.5192e-40	2.0031	465	3.29%	566	1.2313e-5	1.4557
abnormal interleukin-6 secretion	234	2.3091e-40	9.4348e-39	2.0167	437	3.09%	940	9.8266e-4	1.3295
abnormal single-positive T cell number	237	5.7677e-40	2.3268e-38	2.1314	379	2.68%	548	9.0426e-6	1.5313
abnormal type I pneumocyte morpholog	<b>y</b> 243	1.3795e-39	5.4277e-38	3.4755	161	1.14%	964	1.1432e-3	1.9890
abnormal pancreatic beta cell differentia	ation 253	1.2683e-38	4.7928e-37	3.2100	175	1.24%	1,510	1.1157e-2	1.8908
spleen hyperplasia	256	3.0672e-38	1.1455e-36	2.2126	333	2.36%	555	1.1033e-5	1.5567

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9,001 ontology terms (100%) were tested using an annotation count range of [1, Inf].



# Bejerano Lab



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