

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-w9HV7r

 Display name:
 species\_liver\_parsed.bed

Test set: species\_liver\_parsed.bed (38,051 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

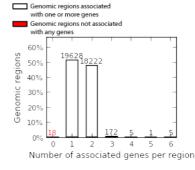
18 of all 38,051 genomic regions (0%) are not associated with any genes.

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

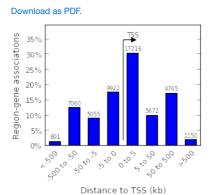
#### • Region-Gene Association Graphs

What do these graphs illustrate?

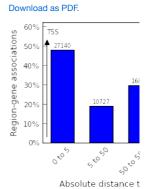
# Number of associated genes per region Download as PDF.



#### Binned by orientation and distance to TSS



#### Binned by absolute distance to



- Ensembl Genes (no terms)
- **□** GO Biological Process (17 terms)

Table controls: Export Shown top re	ows 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 C
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	57	3.9728e-37	9.1716e-35	2.0004	414	1.09%	536	1.9906e-6	1.3282
intrinsic apoptotic signaling pathway in response to DNA damage	64	1.2562e-35	2.5829e-33	2.1016	351	0.92%	924	8.1227e-4	1.3232
snRNA metabolic process	74	7.3696e-33	1.3105e-30	2.0917	326	0.86%	1,476	2.0480e-2	1.2208
IRE1-mediated unfolded protein response	77	2.9079e-32	4.9694e-30	2.3195	254	0.67%	1,116	4.5442e-3	1.3118
snRNA transcription from RNA polymerase II promoter	82	3.8236e-30	6.1359e-28	2.0789	302	0.79%	1,328	1.1541e-2	1.2608
regulation of receptor biosynthetic process	89	1.5503e-28	2.2922e-26	3.1518	131	0.34%	1,500	2.2562e-2	1.4456
alpha-linolenic acid metabolic process	101	3.4718e-27	4.5233e-25	4.0813	89	0.23%	1,625	3.4465e-2	1.5216
ER-nucleus signaling pathway	157	5.9987e-23	5.0278e-21	2.1840	201	0.53%	1,149	5.2398e-3	1.3912
histone monoubiquitination	222	8.8260e-20	5.2316e-18	2.1512	177	0.47%	1,651	3.6356e-2	1.3586
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	254	5.6765e-19	2.9408e-17	2.3468	140	0.37%	1,565	2.7860e-2	1.3642
positive regulation of triglyceride metabolic process	349	5.5306e-16	2.0853e-14	2.6336	93	0.24%	1,594	3.0846e-2	1.4416
regulation of cholesterol homeostasis	438	1.1702e-13	3.5157e-12	2.5264	84	0.22%	1,750	4.8714e-2	1.5216
hematopoietic stem cell differentiation	452	1.8288e-13	5.3243e-12	2.5205	83	0.22%	1,750	4.8714e-2	1.5216
'de novo' posttranslational protein folding	713	1.0950e-9	2.0209e-8	2.1567	78	0.20%	1,167	5.8709e-3	1.5216

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	Name	Rank	P-Value	FDR Q-Val	Enrichment 2.5394	Region Hits	Coverage 0.12%	1,750	4.8714e-2	Enrichment 1.5216	G€
chaperone me	ediated protein folding requiring	877	2.0847e-8	3.1280e-7							
proteasome a	ssembly	1,087	4.2890e-7	5.1922e-6	2.1963	51	0.13%	1,625	3.4465e-2	1.5216	
	ation of transcription elongation	1,229	1.8502e-6	1.9811e-5	2.2471	43	0.11%	1,435	1.6844e-2	1.5216	

The test set of 38,051 genomic regions picked 12,340 (66%) 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 (2 terms)

Table controls: Export Shown top rows				s in this table: 20 Set			Term annotation count: Min: 1			Set	Visualize this	table: [select	[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 Ge	
COPI-coated	l vesicle			130	1.9323e-10	2.5684e-9	2.0185	100	0.26%	145	7.5852e-4	1.5216		
proteasome subcomplex	regulatory par	ticle, ba	se	263	8.7946e-6	5.7783e-5	2.3798	33	0.09%	242	4.6259e-2	1.5216		

The test set of 38,051 genomic regions picked 12,340 (66%) 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 (no terms)

# □ Human Phenotype (3 terms)

Table controls: Export Shown top rows				s in this	table: 20	Set Ter	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	OI Ge	
Abnormal gly	ycosylation			19	7.1656e-16	2.5166e-13	2.6219	93	0.24%	578	1.3980e-2	1.4525		
Abnormal pr	otein N-linked g	lycosyla	tion	24	4.0585e-15	1.1284e-12	2.5746	91	0.24%	605	1.9484e-2	1.4492		
Abnormal iso	pelectric focusin	ng of ser	um	38	1.3779e-13	2.4196e-11	2.4720	87	0.23%	641	2.6774e-2	1.4456		

The test set of 38,051 genomic regions picked 12,340 (66%) 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].

# ● Mouse Phenotype Single KO (3 terms)

Table controls:	le controls: Export Shown top ro		Shown top rows	ws in this table: 20 Se		Set Te	rm 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	OI Ge
delayed emb	ryo turning			114	4.5714e-16	3.6720e-14	2.1422	142	0.37%	921	1.2040e-2	1.4525	
thin hypoglos	ssal nerve			123	3.7798e-15	2.8140e-13	2.4263	102	0.27%	975	1.7251e-2	1.5216	
increased sq	uamous cell ca	arcinoma in	cidence	127	6.0878e-15	4.3894e-13	2.0412	147	0.39%	498	3.3152e-4	1.5216	

The test set of 38,051 genomic regions picked 12,340 (66%) 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 (4 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
abnormal circulating phospholipid level	138	2.5185e-16	1.7449e-14	2.2152	134	0.35%	1,595	3.1321e-2	1.3893	
thin hypoglossal nerve	162	3.7798e-15	2.2308e-13	2.4263	102	0.27%	1,324	1.3264e-2	1.5216	
abnormal frontal lobe morphology	297	8.6792e-11	2.7940e-9	2.0258	103	0.27%	1,324	1.3264e-2	1.5216	

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Name

Rank P-Value FDR Q-Val Enrichment Region Hits Coverage

Rank FDR Q-Val Enrichment Ge

5.6905e-6

increased keratinocyte apoptosis 619 **3.6842e-7**The test set of 38,051 genomic regions picked 12,340 (66%) 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].



# Bejerano Lab



2.0317

62

0.16%

1,523

2.6719e-2

1.5216

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