

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:

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:

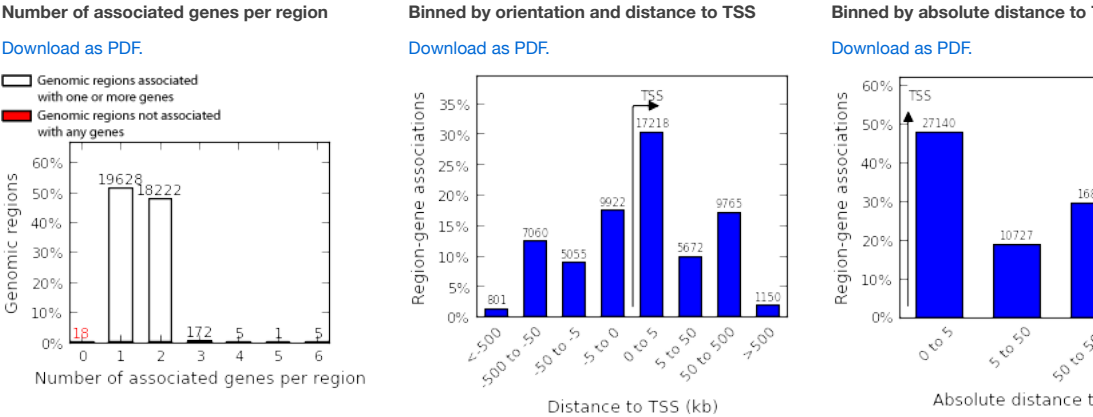
Human: GRCh38 ([UCSC hg38, Dec. 2013](#)) [What gene set does GREAT use?](#)

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 included. 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.](#) [How are my regions associated with genes?](#)

Region-Gene Association Graphs

What do these graphs illustrate?



Global Controls

Global Export

▼

Which data is exported by each option?

Ensembl Genes (no terms)

GO Biological Process (17 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	Other
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	

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].

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

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].

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


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].

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

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].

Green 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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[Overview](#) [News](#) [Use GREAT](#) [Demo](#) [Video](#) [How to Cite](#) [Help](#) [Forum](#)

Bejerano Lab

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
increased keratinocyte apoptosis	619	3.6842e-7	5.6905e-6	2.0317	62	0.16%	1,523	2.6719e-2	1.5216	

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].



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