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-LzsvKf Display name: mouse\_liver\_unique\_parsed.bed

Test set: mouse\_liver\_unique\_parsed.bed (28,811 genomic regions)

> Show in UCSC genome browser. How do I look at my regions in the genome?

Whole genome background Background:

Human: GRCh38 (UCSC hg38, Dec. 2013) Assembly: 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

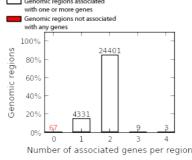
67 of all 28,811 genomic regions (0.2%) are not associated with any genes.

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?

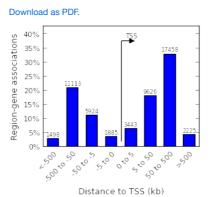
#### • Region-Gene Association Graphs

What do these graphs illustrate?

### Number of associated genes per region Download as PDF. Genomic regions associated

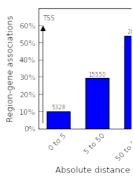


#### Binned by orientation and distance to TSS



## Binned by absolute distance to





Global Controls Global Export

Which data is exported by each option?

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

Table controls:	Export	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 O Enrichment G
lipid homeos	tasis	211	8.0602e-82	5.0268e-80	2.4714	585	2.03%	1,357	2.1052e-2	1.2571
regulation of process	cellular carbohydrate metabolic	270	1.1187e-65	5.4520e-64	2.0698	683	2.37%	651	9.2595e-5	1.3581
regulation of	steroid metabolic process	291	5.1760e-61	2.3406e-59	2.0958	615	2.13%	335	6.9288e-8	1.4963
regulation of	glucose metabolic process	310	1.7643e-58	7.4890e-57	2.1467	557	1.93%	684	1.5934e-4	1.3896
cellular respo	onse to epidermal growth factor	370	4.1721e-50	1.4838e-48	2.5888	325	1.13%	1,119	6.7702e-3	1.4813
response to	epidermal growth factor	382	9.9546e-49	3.4291e-47	2.4949	338	1.17%	1,069	5.0475e-3	1.4699
adrenal gland	d development	393	1.0147e-47	3.3975e-46	2.6730	292	1.01%	798	6.1921e-4	1.7332
secondary al	cohol metabolic process	412	8.0648e-46	2.5758e-44	2.0239	499	1.73%	595	4.2504e-5	1.3812
cholesterol n	netabolic process	414	9.1408e-46	2.9054e-44	2.0445	486	1.69%	639	7.9021e-5	1.3780
circadian reg	ulation of gene expression	415	1.1917e-45	3.7788e-44	2.1962	410	1.42%	1,367	2.2023e-2	1.3536
positive regu	lation of lipid biosynthetic proces	ss 442	5.3057e-43	1.5796e-41	2.1770	393	1.36%	1,167	8.8586e-3	1.3618
cholesterol h	omeostasis	458	5.1163e-42	1.4700e-40	2.3784	318	1.10%	1,233	1.2162e-2	1.3618
regulation of	plasma lipoprotein particle level	s 478	1.9998e-40	5.5054e-39	2.3038	326	1.13%	1,480	3.0037e-2	1.2934
platelet-deriv	ved growth factor receptor hway	507	3.7684e-38	9.7808e-37	2.3142	304	1.06%	1,239	1.2901e-2	1.4856

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Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment (
regulation of cellular response to insulin stimulus	533	1.4382e-36	3.5507e-35	2.0337	390	1.35%	625	6.2377e-5	1.4906
regulation of glucose import	584	2.5904e-33	5.8368e-32	2.0127	363	1.26%	1,338	1.8776e-2	1.3335
regulation of cholesterol metabolic process	612	2.3244e-32	4.9979e-31	2.3775	242	0.84%	1,140	7.3548e-3	1.4047
regulation of insulin receptor signaling pathway	635	3.7217e-31	7.7123e-30	2.0253	333	1.16%	555	2.2937e-5	1.5934
insulin-like growth factor receptor signaling pathway	637	4.0396e-31	8.3450e-30	2.4379	221	0.77%	1,446	2.6614e-2	1.6861
Wnt signaling pathway, calcium modulating pathway	646	7.6583e-31	1.5600e-29	2.0191	332	1.15%	1,437	2.5786e-2	1.4232

The test set of 28,811 genomic regions picked 10,341 (55%) 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	Ter	m annotation c	ount: Min: 1	Max: Inf	Set	Visualize this	table:	[select o	one]
	Term Name		Binom Rank	Binom Raw P-Value		inom R Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyr Fo Enrich	ld	OI Ge
actomyosin			50	5.4666e-51	1.88	93e-49	2.2287	445	1.54%	70	3.3936e-6	1.56	604	
stress fiber			51	7.8810e-48	2.67	03e-46	2.3647	368	1.28%	96	1.1080e-4	1.53	364	
actin filamen	t bundle		61	2.1307e-38	6.03	58e-37	2.1038	378	1.31%	89	3.8428e-5	1.53	340	
cortical actir	cytoskeleton		80	2.5755e-30	5.56	31e-29	2.0444	316	1.10%	118	6.9840e-4	1.45	526	
platelet dens	e granule		121	5.4738e-21	7.81	71e-20	2.5934	129	0.45%	140	7.0300e-3	1.64	128	
podosome			158	5.9854e-16	6.54	61e-15	2.0260	161	0.56%	157	1.8696e-2	1.50	027	
platelet dens	e granule lume	n	201	5.9658e-12	5.12	88e-11	2.5087	73	0.25%	169	2.9902e-2	1.68	361	

The test set of 28,811 genomic regions picked 10,341 (55%) 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 (8 terms)

Table controls:	Export	~	Shown top rows	in this	table: 20	Set Te	erm annotation o	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
steroid bindi	ng			54	1.0209e-47	7.9817e-46	2.0107	529	1.84%	123	2.0656e-3	1.3618	
signaling ada	ptor activity			56	7.7247e-47	5.8239e-45	2.0030	524	1.82%	194	2.9224e-2	1.3101	
sterol binding	9			103	2.0000e-26	8.1982e-25	2.2492	219	0.76%	142	3.9125e-3	1.4753	
Wnt-protein	binding			128	1.0221e-22	3.3713e-21	2.0241	238	0.83%	148	4.3935e-3	1.5815	
cholesterol t	ransporter activ	ity		146	7.0865e-21	2.0493e-19	2.8366	110	0.38%	200	3.2759e-2	1.6246	
cadherin bin	ding involved in	cell-ce	ell adhesion	158	1.5951e-18	4.2623e-17	2.2929	143	0.50%	110	8.2811e-4	1.8158	
cholesterol b	inding			185	2.8804e-16	6.5736e-15	2.0650	157	0.54%	152	7.6264e-3	1.4780	
sterol transp	orter activity			213	8.6272e-15	1.7101e-13	2.0778	139	0.48%	151	6.8640e-3	1.5737	

The test set of 28,811 genomic regions picked 10,341 (55%) 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 (7 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
Germinoma		244	1.8801e-18	5.1418e-17	2.2517	148	0.51%	470	3.6369e-2	1.8158	
Gonadoblasto	oma	267	8.0829e-18	2.0201e-16	2.4702	118	0.41%	470	3.6369e-2	1.8158	
Ovarian neopl	lasm	294	1.1396e-16	2.5867e-15	2.0667	161	0.56%	322	8.8545e-3	1.8158	
Focal segmen	ntal glomerulosclero	osis 311	3.8666e-16	8.2963e-15	2.0317	162	0.56%	474	3.6375e-2	1.4915	
Hypoalbumine	emia	322	1.0203e-15	2.1145e-14	2.4177	107	0.37%	456	3.4352e-2	1.5253	

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	Name		Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
Biconcave vert	tebral bodies		421	8.3527e-13	1.3239e-11	2.5093	79	0.27%	427	2.6809e-2	1.6947	
Prominent occ	iput		544	8.3390e-11	1.0229e-9	2.3618	73	0.25%	427	2.6809e-2	1.6947	

The test set of 28,811 genomic regions picked 10,341 (55%) 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 (20+ terms)

Table controls: Export Sho	own 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 O Enrichment G
abnormal fat-soluble vitamin level	236	1.0348e-50	4.0150e-49	3.0850	247	0.86%	1,618	4.5050e-2	1.3741
abnormal pulmonary alveolus epithelial ce morphology	II 271	2.2239e-46	7.5146e-45	2.0884	468	1.62%	591	1.7136e-4	1.5132
pale kidney	283	6.6412e-45	2.1489e-43	2.7202	266	0.92%	1,692	4.6495e-2	1.4058
abnormal eyelid fusion	287	1.2493e-44	3.9859e-43	2.8993	238	0.83%	493	3.6740e-5	1.8158
abnormal pulmonary alveolus epithelium morphology	302	2.6970e-43	8.1775e-42	2.0181	474	1.65%	623	2.7659e-4	1.4915
abnormal fibroblast migration	314	7.3729e-42	2.1501e-40	2.2170	367	1.27%	821	1.8542e-3	1.5058
abnormal Peyer's patch follicle morpholog	<b>325</b>	7.0276e-41	1.9800e-39	3.3848	173	0.60%	1,265	1.6993e-2	1.5253
abnormal type II pneumocyte morphology	333	5.8532e-40	1.6095e-38	2.1668	368	1.28%	955	4.1163e-3	1.4526
abnormal eyelid development	343	5.0893e-39	1.3587e-37	2.6651	238	0.83%	630	3.1326e-4	1.7368
decreased cell migration	348	1.1629e-38	3.0599e-37	2.1173	375	1.30%	845	2.1245e-3	1.4681
increased circulating bilirubin level	352	3.6887e-38	9.5960e-37	2.3564	293	1.02%	1,315	1.9264e-2	1.3316
decreased fibroblast cell migration	353	3.8965e-38	1.0108e-36	2.2110	335	1.16%	795	1.4081e-3	1.5564
abnormal cell adhesion	354	4.4454e-38	1.1499e-36	2.0778	386	1.34%	1,013	5.5061e-3	1.3849
abnormal liver sinusoid morphology	355	5.9240e-38	1.5281e-36	2.1772	345	1.20%	1,275	1.7293e-2	1.3206
abnormal vertebral body morphology	415	5.1456e-33	1.1354e-31	2.0207	356	1.24%	685	5.6697e-4	1.4795
enlarged liver sinusoidal spaces	432	2.2630e-32	4.7968e-31	2.4031	237	0.82%	1,068	7.3939e-3	1.4723
increased circulating aspartate transaminal level	<b>ase</b> 434	2.5080e-32	5.2917e-31	2.0143	351	1.22%	1,200	1.2729e-2	1.3229
decreased susceptibility to hepatic steator	sis 436	3.6550e-32	7.6763e-31	2.0169	348	1.21%	637	3.3167e-4	1.4526
failure of eyelid fusion	471	1.1366e-30	2.2098e-29	2.7319	177	0.61%	680	5.2795e-4	1.8158
abnormal fourth pharyngeal arch artery morphology	484	4.0412e-30	7.6458e-29	2.3953	221	0.77%	1,108	8.2845e-3	1.7023

The test set of 28,811 genomic regions picked 10,341 (55%) 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 (20+ 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	Ol Ge 1 0 3 3 4 3 1 1 2
	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	-
decreased liv	ver triglyceride level	279	7.9131e-59	2.7117e-57	2.2178	521	1.81%	746	3.7243e-5	1.4281	
abnormal pul	lmonary alveolus epith	elial cell 289	6.2119e-56	2.0551e-54	2.0116	622	2.16%	856	1.3579e-4	1.4250	
abnormal typ	pe II pneumocyte morp	hology 338	1.1498e-49	3.2523e-48	2.0871	503	1.75%	1,119	8.9581e-4	1.4093	
abnormal fibi	roblast migration	368	1.7007e-46	4.4187e-45	2.1728	428	1.49%	971	3.8211e-4	1.4953	
abnormal bro	own fat cell morpholog	y 386	1.4779e-44	3.6606e-43	2.0769	455	1.58%	672	1.4806e-5	1.5564	
enlarged live	r sinusoidal spaces	403	2.9419e-43	6.9794e-42	2.5116	295	1.02%	1,184	1.3424e-3	1.5058	
decreased su	usceptibility to hepatic	steatosis 405	3.6740e-43	8.6732e-42	2.1520	405	1.41%	731	3.2835e-5	1.4621	
decreased file	broblast cell migration	417	1.0400e-41	2.3846e-40	2.1663	385	1.34%	1,060	6.4047e-4	1.5202	
abnormal fat-	-soluble vitamin level	420	1.1372e-41	2.5887e-40	2.6017	266	0.92%	1,695	1.0784e-2	1.4031	
abnormal live	er sinusoid morphology	427	3.0769e-41	6.8896e-40	2.0489	434	1.51%	1,289	2.5218e-3	1.3502	
abnormal sar	rcomere morphology	436	1.4776e-40	3.2402e-39	2.1843	367	1.27%	1,344	3.0753e-3	1.3921	
small intestin	nal inflammation	454	7.8492e-39	1.6530e-37	2.4944	267	0.93%	1,784	1.4583e-2	1.3935	

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Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
abnormal endocrine pancreas development	458	1.2213e-38	2.5495e-37	2.1869	348	1.21%	929	2.6450e-4	1.6813	
abnormal Peyer's patch follicle morphology	462	2.3641e-38	4.8924e-37	2.9962	193	0.67%	1,788	1.4597e-2	1.4643	
decreased type I pneumocyte number	504	7.0978e-36	1.3465e-34	2.8121	199	0.69%	1,810	1.5448e-2	1.6861	
abnormal pancreatic beta cell differentiation	527	1.0440e-34	1.8940e-33	2.3664	263	0.91%	1,288	2.5158e-3	1.7149	
spontaneous skin ulceration	532	1.8156e-34	3.2630e-33	2.5326	229	0.79%	1,031	5.6106e-4	1.5434	
increased circulating bilirubin level	548	8.3894e-34	1.4637e-32	2.0646	346	1.20%	1,423	4.2492e-3	1.3379	
abnormal type I pneumocyte morphology	564	4.7932e-33	8.1254e-32	2.4567	232	0.81%	2,207	3.6641e-2	1.4856	
decreased liver cholesterol level	568	1.0455e-32	1.7598e-31	2.5899	208	0.72%	567	2.3005e-6	1.7590	

The test set of 28,811 genomic regions picked 10,341 (55%) 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



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