GREAT version 4.0.4 current (08/19/2019 to now)

Job Description

Job ID: 20250210-public-4.0.4-X2dyH7

Display name: K4me3_distal_CpG_plus_Double_

Test set: K4me3_distal_CpG_plus_Double_KO_vs_F_F.bed (2,578 genomic regions)
Show in UCSC genome browser. *How do I look at my regions in the genome?*

Background: Whole genome background

Assembly: Mouse: NCBI build 38 (UCSC mm10, Dec. 2011) *What gene set does GREAT use?*

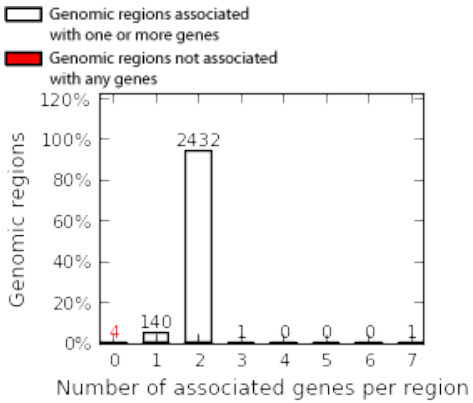
Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included.
4 of all 2,578 genomic regions (0.2%) are not associated with any genes.
View all genomic region-gene associations. *Which genes are 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?

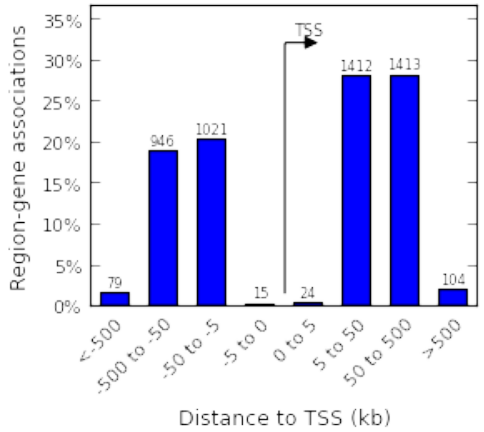
Number of associated genes per region

Download as PDF.



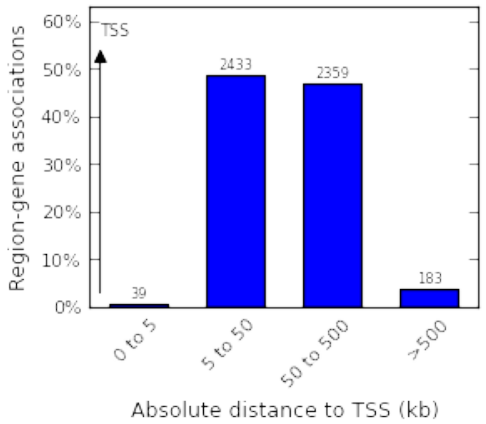
Binned by orientation and distance to TSS

Download as PDF.



Binned by absolute distance to TSS

Download as PDF.



Global Controls

Global Export *Which data is exported by each option?*

GO Biological Process (20+ terms)

Global controls

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	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
neural precursor cell proliferation	141	**1.2143e-10**	**1.1273e-8**	2.4089	68	2.64%	262	**1.3536e-6**	2.5394	35	80	0.95%
dopaminergic neuron differentiation	150	**1.7016e-9**	**1.4849e-7**	2.9033	43	1.67%	276	**2.7858e-6**	3.4144	20	34	0.54%
dorsal/ventral pattern formation	157	**2.8782e-9**	**2.3997e-7**	2.2096	69	2.68%	214	**1.4985e-7**	2.4876	42	98	1.14%
negative regulation of Notch signaling pathway	160	**4.9008e-9**	**4.0095e-7**	4.1917	25	0.97%	468	**9.7439e-4**	2.8143	16	33	0.43%
skeletal muscle tissue development	161	**5.5006e-9**	**4.4722e-7**	2.0087	83	3.22%	287	**3.8797e-6**	2.0879	50	139	1.36%
cell proliferation in forebrain	171	**9.6434e-9**	**7.3820e-7**	2.8551	40	1.55%	263	**1.4372e-6**	3.5178	20	33	0.54%
negative regulation of pathway-restricted SMAD protein phosphorylation	183	**2.8477e-8**	**2.0370e-6**	4.9244	19	0.74%	834	**2.4782e-2**	3.3859	7	12	0.19%
negative regulation of protein binding	210	**1.0805e-7**	**6.7352e-6**	2.3607	48	1.86%	675	**9.3839e-3**	1.8681	28	87	0.76%
response to laminar fluid shear stress	216	**1.6584e-7**	**1.0050e-5**	4.3847	19	0.74%	525	**1.9313e-3**	4.2214	8	11	0.22%
positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	223	**2.6096e-7**	**1.5318e-5**	4.4729	18	0.70%	735	**1.5110e-2**	3.0729	9	17	0.24%
mesoderm morphogenesis	229	**3.9193e-7**	**2.2403e-5**	2.2332	49	1.90%	436	**5.3954e-4**	2.2388	27	70	0.73%
mesoderm formation	235	**5.0270e-7**	**2.8002e-5**	2.2801	46	1.78%	474	**1.0609e-3**	2.2325	25	65	0.68%
skeletal muscle cell differentiation	244	**6.0196e-7**	**3.2294e-5**	2.3970	41	1.59%	418	**3.3029e-4**	2.3788	25	61	0.68%
cell junction assembly	248	**6.7038e-7**	**3.5384e-5**	2.0517	57	2.21%	652	**8.1462e-3**	1.8033	32	103	0.87%
metanephros morphogenesis	254	**9.4887e-7**	**4.8901e-5**	2.6440	33	1.28%	598	**4.5414e-3**	2.7947	13	27	0.35%
endothelial cell differentiation	271	**1.8674e-6**	**9.0202e-5**	2.0741	51	1.98%	380	**1.5468e-4**	2.3059	29	73	0.79%
positive regulation of morphogenesis of an epithelium	272	**1.9073e-6**	**9.1791e-5**	2.5158	34	1.32%	334	**2.7695e-5**	3.1510	19	35	0.52%
rostrocaudal neural tube patterning	279	**2.3964e-6**	**1.1243e-4**	4.0058	17	0.66%	496	**1.2802e-3**	4.0184	9	13	0.24%
apoptotic mitochondrial changes	285	**2.6831e-6**	**1.2323e-4**	2.6044	31	1.20%	913	**3.7446e-2**	1.8242	22	70	0.60%
epithelial cell morphogenesis	299	**3.5206e-6**	**1.5413e-4**	2.5686	31	1.20%	859	**2.7306e-2**	2.1766	15	40	0.41%

13,090 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Cellular Component (4 terms)

Global controls

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	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
ruffle	40	**2.2685e-8**	**9.6072e-7**	2.0933	69	2.68%	42	**1.3354e-4**	1.8517	52	163	1.41%
ruffle membrane	58	**2.5096e-6**	**7.3298e-5**	2.3764	37	1.44%	46	**7.8217e-4**	2.1236	30	82	0.81%
brush border	71	**1.1396e-5**	**2.7190e-4**	2.0547	44	1.71%	78	**3.3504e-2**	1.6656	33	115	0.90%
apicolateral plasma membrane	124	**8.6801e-4**	**1.1858e-2**	2.7317	14	0.54%	61	**7.1758e-3**	3.2247	10	18	0.27%

The test set of 2,578 genomic regions picked 3,686 (17%) of all 21,395 genes.
GO Cellular Component has 1,694 terms covering 19,074 (89%) of all 21,395 genes, and 371,380 term - gene associations.
1,694 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Molecular Function (7 terms)

Global controls

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	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
signal transducer activity, downstream of receptor	71	**8.0580e-7**	**4.6884e-5**	2.0541	56	2.17%	38	**4.8603e-5**	2.2279	38	99	1.03%
frizzled binding	78	**2.3111e-6**	**1.2240e-4**	2.7284	29	1.12%	78	**1.4774e-2**	2.4440	16	38	0.43%
ARF guanyl-nucleotide exchange factor activity	85	**6.5348e-6**	**3.1759e-4**	3.3977	19	0.74%	57	**5.4870e-3**	3.3604	11	19	0.30%
co-SMAD binding	106	**2.9729e-5**	**1.1586e-3**	3.8219	14	0.54%	82	**1.6642e-2**	4.0631	7	10	0.19%
palmitoyl-CoA 9-desaturase activity	151	**2.1402e-4**	**5.8550e-3**	14.1151	4	0.16%	95	**3.8258e-2**	5.8044	4	4	0.11%
HMG box domain binding	158	**2.5010e-4**	**6.5390e-3**	2.5685	19	0.74%	92	**3.5056e-2**	2.9022	10	20	0.27%
R-SMAD binding	182	**6.9346e-4**	**1.5740e-2**	2.4237	18	0.70%	97	**4.5795e-2**	2.6603	11	24	0.30%

The test set of 2,578 genomic regions picked 3,686 (17%) of all 21,395 genes.
GO Molecular Function has 4,131 terms covering 17,189 (80%) of all 21,395 genes, and 227,341 term - gene associations.
4,131 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]

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	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
Cleft lip	16	**7.5070e-8**	**3.0962e-5**	2.1345	61	2.37%	40	**6.4680e-4**	2.1107	36	99	0.98%
Abnormality of the shoulder	19	**1.2727e-7**	**4.4202e-5**	3.2414	28	1.09%	91	**4.5709e-3**	2.8086	15	31	0.41%
Cleft upper lip	39	**1.4246e-6**	**2.4104e-4**	2.0151	56	2.17%	45	**9.2149e-4**	2.1220	34	93	0.92%
Choanal atresia	41	**2.1515e-6**	**3.4628e-4**	2.8618	27	1.05%	213	**3.7849e-2**	2.3218	14	35	0.38%
Polyhydramnios	42	**2.2852e-6**	**3.5905e-4**	2.1954	44	1.71%	136	**1.1971e-2**	1.9128	29	88	0.79%
Abnormality of the vagina	65	**1.3025e-5**	**1.3223e-3**	2.2601	35	1.36%	174	**2.1162e-2**	2.3218	16	40	0.43%
Abnormality of the choanae	86	**3.2241e-5**	**2.4740e-3**	2.3215	30	1.16%	133	**1.1242e-2**	2.4067	17	41	0.46%
Genital neoplasm	112	**6.5030e-5**	**3.8315e-3**	2.1660	32	1.24%	236	**5.0105e-2**	2.1766	15	40	0.41%
Abnormal localization of kidney	114	**6.7110e-5**	**3.8847e-3**	2.2267	30	1.16%	205	**3.5408e-2**	2.1451	17	46	0.46%
Abnormality of the larynx	125	**8.0575e-5**	**4.2537e-3**	2.0362	36	1.40%	94	**4.8590e-3**	2.1658	25	67	0.68%
Sandal gap	134	**1.0925e-4**	**5.3802e-3**	2.7460	19	0.74%	231	**4.6378e-2**	2.5539	11	25	0.30%
Germ cell neoplasia	144	**1.3113e-4**	**6.0091e-3**	2.5549	21	0.81%	162	**1.8794e-2**	3.0549	10	19	0.27%
Vesicoureteral reflux	167	**1.9823e-4**	**7.8332e-3**	2.0886	30	1.16%	44	**8.8944e-4**	2.8278	19	39	0.52%
Abnormal larynx morphology	173	**2.0557e-4**	**7.8413e-3**	2.0041	33	1.28%	63	**2.3675e-3**	2.3839	23	56	0.62%
Mitral valve prolapse	184	**2.3177e-4**	**8.3122e-3**	2.2433	25	0.97%	236	**5.0105e-2**	2.1766	15	40	0.41%
Down-sloping shoulders	199	**3.0107e-4**	**9.9839e-3**	2.6074	18	0.70%	193	**2.9010e-2**	3.0729	9	17	0.24%
Cardiomegaly	208	**3.3041e-4**	**1.0482e-2**	2.6734	17	0.66%	213	**3.7849e-2**	2.3218	14	35	0.38%
Abnormal mitral valve morphology	217	**3.8147e-4**	**1.1601e-2**	2.0635	28	1.09%	164	**1.9405e-2**	2.2230	18	47	0.49%
Iris coloboma	236	**5.5741e-4**	**1.5586e-2**	2.0424	27	1.05%	234	**4.7534e-2**	2.2573	14	36	0.38%
Webbed neck	243	**5.9692e-4**	**1.6210e-2**	2.0033	28	1.09%	152	**1.6542e-2**	2.2057	19	50	0.52%

The test set of 2,578 genomic regions picked 3,686 (17%) of all 21,395 genes.
Human Phenotype has 6,599 terms covering 3,215 (15%) of all 21,395 genes, and 244,972 term - gene associations.
6,599 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype Single KO (20+ terms)

Global controls

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	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
abnormal mean corpuscular volume	34	**1.2477e-12**	**3.3650e-10**	2.3614	86	3.34%	357	**1.1809e-3**	1.6350	60	213	1.63%
decreased erythrocyte cell number	39	**2.4186e-12**	**5.6869e-10**	2.2919	89	3.45%	212	**6.7260e-5**	1.8469	56	176	1.52%
abnormal wound healing	49	**3.1762e-11**	**5.9441e-9**	2.2901	80	3.10%	356	**1.1254e-3**	1.7682	46	151	1.25%
increased mean corpuscular volume	62	**3.6577e-10**	**5.4098e-8**	2.5733	57	2.21%	513	**6.8291e-3**	1.7020	39	133	1.06%
increased neuron number	69	**9.6732e-10**	**1.2856e-7**	2.6067	53	2.06%	203	**4.3261e-5**	2.5004	28	65	0.76%
abnormal epidermis stratum corneum morphology	89	**5.4668e-9**	**5.6327e-7**	2.4987	52	2.02%	390	**1.9160e-3**	1.8514	37	116	1.00%
small scala media	116	**7.1643e-8**	**5.6635e-6**	5.1919	17	0.66%	539	**9.0285e-3**	4.3533	6	8	0.16%
increased monocyte cell number	125	**1.5561e-7**	**1.1415e-5**	2.1853	55	2.13%	808	**3.7226e-2**	1.5962	33	120	0.90%
abnormal vascular wound healing	133	**2.5136e-7**	**1.7331e-5**	2.5507	39	1.51%	499	**5.7959e-3**	2.1385	21	57	0.57%
increased cochlear outer hair cell number	134	**2.5150e-7**	**1.7211e-5**	3.6229	23	0.89%	526	**8.2142e-3**	3.2650	9	16	0.24%
increased cochlear hair cell number	145	**4.0444e-7**	**2.5577e-5**	3.2165	26	1.01%	388	**1.7893e-3**	3.3604	11	19	0.30%
increased sensory neuron number	148	**4.3660e-7**	**2.7051e-5**	2.5662	37	1.44%	220	**9.0126e-5**	2.9806	19	37	0.52%
abnormal epidermis stratum granulosum morphology	167	**9.0855e-7**	**4.9889e-5**	2.5625	35	1.36%	776	**3.3715e-2**	1.8724	20	62	0.54%
abnormal corpora quadrigemina morphology	168	**9.3721e-7**	**5.1156e-5**	2.5589	35	1.36%	490	**5.1835e-3**	2.6213	14	31	0.38%
thin myocardium	172	**1.0021e-6**	**5.3428e-5**	2.1997	47	1.82%	420	**2.7231e-3**	2.0353	27	77	0.73%
abnormal pharyngeal arch artery morphology	175	**1.0974e-6**	**5.7506e-5**	2.2603	44	1.71%	195	**2.9255e-5**	2.9022	22	44	0.60%
short scala media	177	**1.2361e-6**	**6.4041e-5**	5.0915	14	0.54%	840	**4.1410e-2**	4.6435	4	5	0.11%
abnormal cochlear inner hair cell number	182	**1.3819e-6**	**6.9628e-5**	2.6925	31	1.20%	351	**1.0895e-3**	3.0097	14	27	0.38%
lung hemorrhage	188	**1.5705e-6**	**7.6601e-5**	2.4992	35	1.36%	507	**6.4038e-3**	2.2713	18	46	0.49%
increased pulmonary respiratory rate	191	**1.6901e-6**	**8.1142e-5**	3.7412	19	0.74%	871	**4.4874e-2**	2.4185	10	24	0.27%

The test set of 2,578 genomic regions picked 3,686 (17%) of all 21,395 genes.
Mouse Phenotype Single KO has 9,170 terms covering 9,466 (44%) of all 21,395 genes, and 551,620 term - gene associations.
9,170 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype (20+ terms)

Global controls

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

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Gene Hits	Genes	Coverage
abnormal mean corpuscular volume	62	1.0862e-12	1.6775e-10	2.2326	97	3.76%	532	8.5743e-4	1.5873	67	245	1.82%
decreased erythrocyte cell number	88	4.1674e-11	4.5344e-9	2.0425	102	3.96%	400	1.6779e-4	1.6763	67	232	1.82%
extramedullary hematopoiesis	104	5.7051e-10	5.2525e-8	2.1732	78	3.03%	422	2.8813e-4	1.7755	52	170	1.41%
increased mean corpuscular volume	121	2.8271e-9	2.2372e-7	2.3647	60	2.33%	806	6.9019e-3	1.6361	42	149	1.14%
increased neuron number	144	1.8916e-8	1.2578e-6	2.0780	71	2.75%	337	4.1957e-5	2.1156	39	107	1.06%
absent midbrain-hindbrain boundary	159	3.5747e-8	2.1527e-6	4.8520	19	0.74%	1,102	2.5214e-2	3.4826	6	10	0.16%
colitis	164	4.4157e-8	2.5781e-6	2.1845	60	2.33%	889	1.0603e-2	1.6286	39	139	1.06%
thin myocardium	165	4.4506e-8	2.5827e-6	2.0944	66	2.56%	312	1.9658e-5	2.1766	39	104	1.06%
increased sensory neuron number	177	6.9593e-8	3.7647e-6	2.3253	51	1.98%	305	1.6230e-5	2.6120	27	60	0.73%
small scala media	179	7.5938e-8	4.0621e-6	4.8729	18	0.70%	611	1.8263e-3	4.5145	7	9	0.19%
brachypodia	188	1.3074e-7	6.6589e-6	6.1690	14	0.54%	1,045	2.1398e-2	4.1460	5	7	0.14%
abnormal vascular wound healing	206	2.8406e-7	1.3203e-5	2.3813	44	1.71%	747	5.4516e-3	1.9901	24	70	0.65%
decreased IgG1 level	209	3.3203e-7	1.5212e-5	2.0543	60	2.33%	1,064	2.1738e-2	1.5478	40	150	1.09%
lung hemorrhage	219	5.4370e-7	2.3771e-5	2.4069	41	1.59%	526	8.0258e-4	2.3017	23	58	0.62%
abnormal lymphatic vessel morphology	231	7.6844e-7	3.1852e-5	2.0890	54	2.09%	317	2.3210e-5	2.3992	31	75	0.84%
decreased fetal cardiomyocyte proliferation	232	7.7724e-7	3.2078e-5	3.6347	21	0.81%	624	2.0842e-3	3.4144	10	17	0.27%
abnormal Mullerian duct morphology	233	7.7788e-7	3.1966e-5	2.6233	34	1.32%	687	3.5747e-3	2.3218	18	45	0.49%
abnormal occipital bone morphology	242	9.8609e-7	3.9016e-5	2.0115	58	2.25%	341	4.4937e-5	2.2082	35	92	0.95%
abnormal pulmonary circulation	244	9.9418e-7	3.9013e-5	2.1217	51	1.98%	383	9.8833e-5	2.2492	31	80	0.84%
abnormal spinal cord dorsal horn morphology	250	1.1938e-6	4.5723e-5	4.4682	16	0.62%	858	9.4684e-3	3.0729	9	17	0.24%

The test set of 2,578 genomic regions picked 3,686 (17%) of all 21,395 genes.
Mouse Phenotype has 9,575 terms covering 9,654 (45%) of all 21,395 genes, and 705,265 term - gene associations.
9,575 ontology terms (100%) were tested using an annotation count range of [1, Inf].