

GREAT version 3.0.0current (02/15/2015 to now)

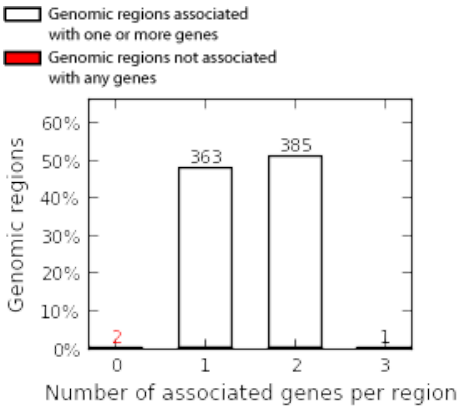
Job Description

Region-Gene Association Graphs

What do these graphs illustrate?

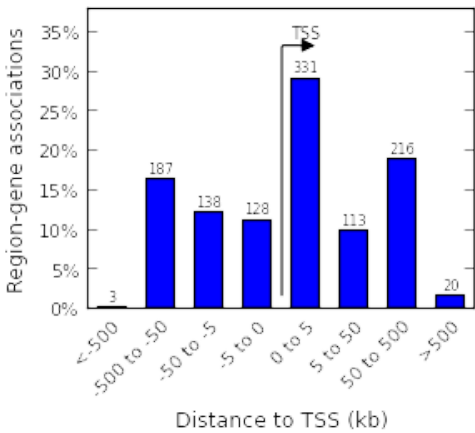
Number of associated genes per region

Download as PDF.



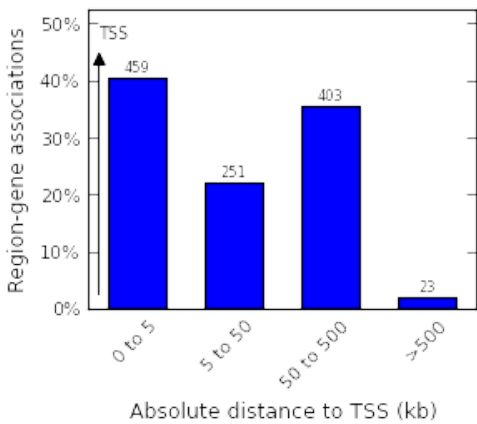
Binned by orientation and distance to TSS

Download as PDF.



Binned by absolute distance to TSS

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Global Controls

Global Export

 Which data is exported by each option?

GO Molecular Function (no terms)

Global controls

GO Biological Process (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
melanosome localization	2	8.6927e-14	4.5376e-10	14.3084	16	2.13%	1	4.8421e-3	13.4836	7	21	1.57%
pigment granule localization	3	1.6278e-13	5.6648e-10	13.7204	16	2.13%	2	3.4756e-3	12.8707	7	22	1.57%
melanosome transport	4	1.9499e-13	5.0893e-10	15.3316	15	2.00%	3	7.5430e-3	14.2767	6	17	1.35%
establishment of melanosome localization	5	3.8004e-13	7.9351e-10	14.6220	15	2.00%	4	8.3092e-3	13.4836	6	18	1.35%
pigment granule transport	6	3.8234e-13	6.6527e-10	14.6158	15	2.00%	4	8.3092e-3	13.4836	6	18	1.35%
establishment of pigment granule localization	8	7.2138e-13	9.4141e-10	13.9695	15	2.00%	6	7.9277e-3	12.7739	6	19	1.35%
cellular pigmentation	40	2.9002e-8	7.5695e-6	5.8978	16	2.13%	7	4.3500e-2	7.6528	7	37	1.57%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
GO Biological Process has 10,440 terms covering 15,441 (86%) of all 18,041 genes, and 950,065 term - gene associations.
10,440 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Cellular Component (no terms)

Global controls

Mouse Phenotype (no terms)

Global controls

Human Phenotype (no terms)

Global controls

Disease Ontology (1 term)

Global controls

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Visualize this table:

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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
Prader-Willi syndrome	18	4.2294e-7	5.2515e-5	7.4951	11	1.46%	1	1.8891e-4	16.6562	7	17	1.57%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
Disease Ontology has 2,235 terms covering 7,886 (44%) of all 18,041 genes, and 232,324 term - gene associations.
2,235 ontology terms (100%) were tested using an annotation count range of [1, Inf].

MSigDB Cancer Neighborhood (no terms)

Global controls

Placenta Disorders (no terms)

Global controls

PANTHER Pathway (1 term)

Global controls

Table controls:

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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
Alzheimer disease-amyloid secretase pathway	4	4.9511e-6	1.8814e-4	3.4458	19	2.53%	1	2.3435e-2	5.1366	8	63	1.79%

- +

BioCyc Pathway (no terms)

Global controls

+

MSigDB Pathway (no terms)

Global controls

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MGI Expression: Detected (no terms)

Global controls

-

MSigDB Perturbation (8 terms)

Global controls

Table controls:

Export

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Term annotation count: Min:1Max:InfSet

Visualize this table:

30%

[select one]

Term Name	Binom Rank	Binom Raw P-Value	<i>Binom FDR Q-Val</i>	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	<i>Hyper FDR Q-Val</i>	Hyper Fold Enrichment	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
Genes within amplicon 15q26 identified in a copy number alterations study of 191 breast tumor samples.	1	2.3338e-54	7.8510e-51	35.3896	46	6.13%	1	2.1072e-23	38.2034	17	18	3.81%
Genes whose expression profile is specific to Cluster III of urothelial cell carcinoma (UCC) tumors.	2	2.2178e-23	3.7303e-20	3.8703	77	10.25%	3	2.6226e-5	4.1010	22	217	4.93%
Genes commonly down-regulated in CD-1 and CD-2 clusters of multiple myeloma samples and which were higher expressed in the CD-1 group.	4	2.7097e-17	2.2788e-14	7.3841	31	4.13%	2	3.9185e-5	9.0808	11	49	2.47%
Protein biosynthesis, transport or catabolism genes up-regulated in hyperploid multiple myeloma (MM) compared to the non-hyperploid MM samples.	5	3.0620e-17	2.0601e-14	12.5287	22	2.93%	4	4.8831e-4	7.6322	10	53	2.24%
Amplification hot spot 3: colocolized fragile sites and cancer genes in the 15q21-q26 region.	6	9.6544e-14	5.4129e-11	21.8843	13	1.73%	10	1.9825e-2	30.3380	3	4	0.67%
Genes up-regulated in serrated vs conventional colorectal carcinoma (CRC) samples.	29	1.7311e-7	2.0080e-5	3.0865	29	3.86%	6	2.0190e-3	4.7375	13	111	2.91%
Genes down-regulated in Paneth cell (part of instiinal epithelium) of mice with hypomorphic (reduced function) form of ATG16L1 [GeneID=55054].	110	2.4537e-4	7.5038e-3	2.9589	15	2.00%	5	2.3807e-3	6.3204	10	64	2.24%
Top 50 up-regulated genes in cluster PR of multiple myeloma samples characterized by increased expression of proliferation and cell cycle genes.	118	3.1303e-4	8.9241e-3	4.3135	9	1.20%	11	2.8601e-2	6.4353	7	44	1.57%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
MSigDB Perturbation has 3,364 terms covering 17,091 (95%) of all 18,041 genes, and 358,104 term - gene associations.
3,364 ontology terms (100%) were tested using an annotation count range of [1, Inf].

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MSigDB Predicted Promoter Motifs (no terms)

Global controls

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MSigDB miRNA Motifs (no terms)

Global controls

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InterPro (1 term)

Global controls

Table controls:

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Term annotation count: Min:1Max:InfSet

Visualize this table:

30%

[select one]

Term Name	Binom Rank	Binom Raw P-Value	<i>Binom FDR Q-Val</i>	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	<i>Hyper FDR Q-Val</i>	Hyper Fold Enrichment	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
Golgin subfamily A	1	8.8375e-36	8.3267e-32	32.1172	31	4.13%	1	3.5717e-21	34.3831	17	20	3.81%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
InterPro has 9,422 terms covering 17,343 (96%) of all 18,041 genes, and 60,477 term - gene associations.
9,422 ontology terms (100%) were tested using an annotation count range of [1, Inf].

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TreeFam (1 term)

Global controls

Table controls:

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Term annotation count: Min:1Max:InfSet

Visualize this table:

30%

[select one]

Term Name	Binom Rank	Binom Raw P-Value	<i>Binom FDR Q-Val</i>	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	<i>Hyper FDR Q-Val</i>	Hyper Fold Enrichment	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
GOLGA2, GOLGA6A, GOLGA6B, GOLGA6C, GOLGA6D, ...	1	8.8375e-36	7.1814e-32	32.1172	31	4.13%	1	3.0804e-21	34.3831	17	20	3.81%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
TreeFam has 8,126 terms covering 13,550 (75%) of all 18,041 genes, and 13,551 term - gene associations.
8,126 ontology terms (100%) were tested using an annotation count range of [1, Inf].

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HGNC Gene Families (no terms)

Global controls

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Ensembl Genes (no terms)

Global controls

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MSigDB Oncogenic Signatures (no terms)

Global controls

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MSigDB Immunologic Signatures (1 term)

Global controls

great.stanford.edu/public/cgi-bin/greatWeb.php

2/3

Term Name	Binom Rank	Binom Raw P-Value	<i>Binom FDR Q-Val</i>	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	<i>Hyper FDR Q-Val</i>	Hyper Fold Enrichment	Hyper Observed Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
Genes down-regulated in comparison of untreated CD4 [GeneID=920] memory T cells from old donors versus those treated with TSST at 72 h.	27	1.7539e-8	1.2407e-6	3.1331	33	4.39%	1	2.0982e-2	3.4212	17	201	3.81%

The test set of 751 genomic regions picked 446 (2%) of all 18,041 genes.
MSigDB Immunologic Signatures has 1,910 terms covering 16,609 (92%) of all 18,041 genes, and 363,333 term - gene associations.
1,910 ontology terms (100%) were tested using an annotation count range of [1, Inf].



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