

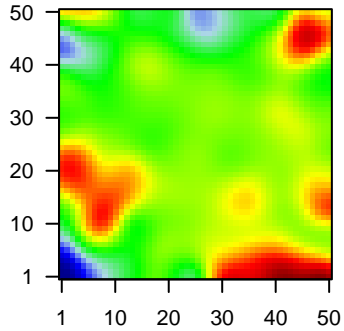
GW_230

Global Summary

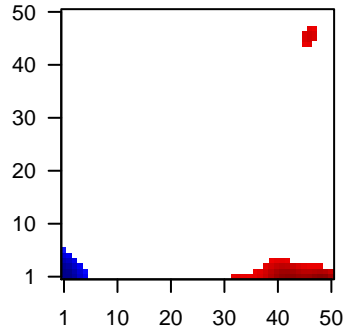
%DE = 0.15
 # genes with $fdr < 0.2$ = 1744 (943 + / 801 -)
 # genes with $fdr < 0.1$ = 1427 (772 + / 655 -)
 # genes with $fdr < 0.05$ = 1155 (637 + / 518 -)
 # genes with $fdr < 0.01$ = 750 (422 + / 328 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.85

Profile



Regulated Spots



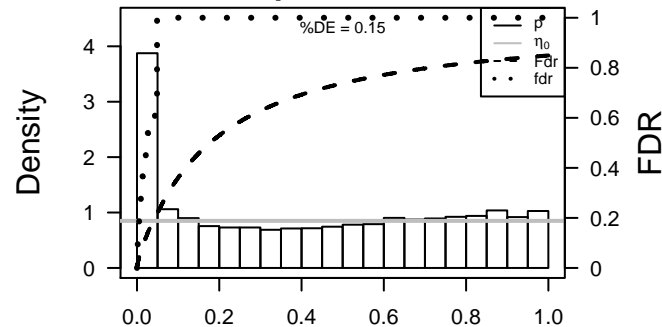
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	58	-1.4	2e-16 5e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	113146	-1.39	2e-16 5e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
3	218	1.81	2e-16 5e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	55107	-1.82	2e-16 5e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
5	360	1.37	2e-16 5e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	655	1.46	2e-16 5e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
7	148304	1.65	2e-16 5e-14	1 x 41 chromosome 1 open reading frame 74 [Source:HGNC Symbc
8	57172	1.39	2e-16 5e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
9	1056	1.34	2e-16 5e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
10	1290	-1.42	2e-16 5e-14	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
11	49860	1.81	2e-16 5e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
12	1571	1.57	2e-16 5e-14	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
13	1672	-1.51	2e-16 5e-14	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
14	2052	1.48	2e-16 5e-14	9 x 50 epoxide hydrolase 1, microsomal (xenobiotic) [Source:HGNC
15	2167	-1.77	2e-16 5e-14	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
16	3169	1.65	2e-16 5e-14	50 x 12 forkhead box A1 [Source:HGNC Symbol;Acc:5021]
17	163351	1.39	2e-16 5e-14	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
18	10457	-1.51	2e-16 5e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
19	3040	-2.32	2e-16 5e-14	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
20	3043	-2.6	2e-16 5e-14	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.56	NULL	1720	Chr Chr 1
2	11.58	NULL	15	CC MHC class II protein complex
3	10.34	NULL	417	H.Tiss WIRTH_Immune system
4	10.11	NULL	135	H.Tiss WIRTH_Mucosa
5	8.99	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
6	8.99	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
7	8.47	NULL	51	BP type I interferon signaling pathway
8	8.2	NULL	1135	Chr Chr 19
9	8	NULL	949	CC nucleoplasm
10	7.81	NULL	47	BP antigen processing and presentation
11	7.47	NULL	52	Chr Chr HSCHR6_MHC_QBL
12	7.14	NULL	149	BP DNA replication
13	7.1	NULL	204	BP cytokine-mediated signaling pathway
14	7.01	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
15	6.9	NULL	4640	CC nucleus
16	6.88	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
17	6.8	NULL	298	BP DNA repair
18	6.64	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
19	6.56	NULL	123	BP defense response to virus
20	6.47	NULL	12	GSEA C2ZHU_CMV_8_HR_UP
<i>Underexpressed</i>				
1	-15.41	NULL	250	LymphomaENZ_Stromal signature 1
2	-13.69	NULL	242	BP extracellular matrix organization
3	-12.91	NULL	190	CC extracellular matrix
4	-10.67	NULL	534	Chr Chr 8
5	-10.4	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	-10.18	NULL	16	MMML C6SCIEJ_MMML 1
7	-10.03	NULL	183	CC proteinaceous extracellular matrix
8	-9.94	NULL	1182	CC extracellular region
9	-8.93	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
10	-8.71	NULL	280	Chr Chr 13
11	-8.59	NULL	403	BP cell adhesion
12	-8.27	NULL	957	Chr Chr 11
13	-8.21	NULL	64	BP collagen catabolic process
14	-8.08	NULL	69	BP extracellular matrix disassembly
15	-8.07	NULL	57	MF extracellular matrix structural constituent
16	-7.9	NULL	683	CC extracellular space
17	-7.76	NULL	83	CC basement membrane
18	-7.59	NULL	4	MMML C6SCIEJ_MMML 23
19	-7.49	NULL	11	MMML C6SCIEJ_MMML 31
20	-7.14	NULL	37	BP collagen fibril organization

p-values



GW_230

Local Summary

%DE = 0.7
 # metagenes = 49
 # genes = 726
 # genes in genesets = 694

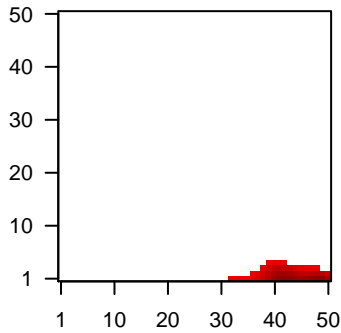
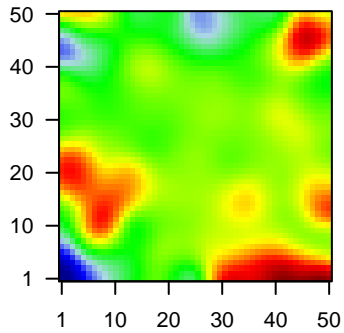
genes with $fdr < 0.1$ = 320 (311 + / 9 -)
 # genes with $fdr < 0.05$ = 300 (293 + / 7 -)
 # genes with $fdr < 0.01$ = 206 (201 + / 5 -)

<r> metagenes = 0.8
 <r> genes = 0.31

<FC> = 0.35
 <shrinkage-t> = 12.45
 <p-value> = 0
 <fdr> = 0.56

Profile

Spot



Local Genelist

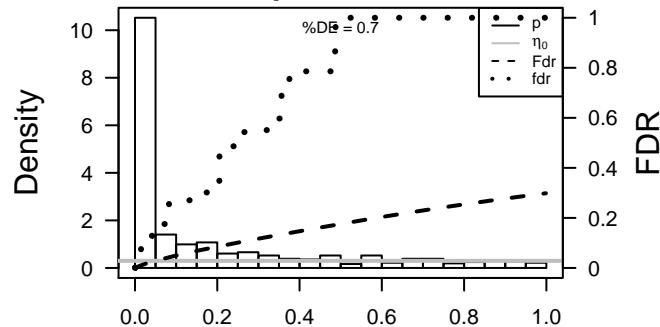
Rank	ID	log(FC)	fdr	p-value	Description
1	57172	1.39	2e-16	8e-15	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
2	3108	1.51	2e-16	8e-15	50 x 1 major histocompatibility complex, class II, DM alpha [Source:l
3	3119	1.52	2e-16	8e-15	49 x 1 major histocompatibility complex, class II, DQ beta 1 [Source:
4	3127	2.16	2e-16	8e-15	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:
5	3128	1.63	2e-16	8e-15	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
6	10537	1.43	2e-16	8e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
7	3123	1.32	1e-15	1e-12	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
8	393	1.28	7e-15	1e-12	49 x 1 Rho GTPase activating protein 4 [Source:HGNC Symbol;Acc:
9	126306	1.26	2e-14	1e-12	49 x 1 junctional sarcoplasmic reticulum protein 1 [Source:HGNC S
10	3627	1.25	2e-14	1e-12	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
11	23225	1.25	3e-14	1e-12	44 x 1 nucleoporin 210kDa [Source:HGNC Symbol;Acc:30052]
12	54855	1.25	3e-14	1e-12	49 x 1 family with sequence similarity 46, member C [Source:HGNC
13	972	1.24	4e-14	4e-12	50 x 1 CD74 molecule, major histocompatibility complex, class II inv
14	10964	1.23	6e-14	2e-11	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
15	3543	1.11	2e-13	2e-11	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC S
16	115361	1.2	3e-13	2e-11	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
17	728294	1.2	3e-13	4e-11	40 x 1 D-2-hydroxyglutarate dehydrogenase [Source:HGNC Symbc
18	11040	1.18	6e-13	4e-11	49 x 1 pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
19	51755	1.18	6e-13	1e-10	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242:
20	51237	1.16	1e-12	1e-10	48 x 1 marginal zone B and B1 cell-specific protein [Source:HGNC :

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	34.68	NULL	14 / 15	CC MHC class II protein complex
2	24.05	NULL	24 / 47	BP antigen processing and presentation
3	21.56	NULL	121 / 417	H.Tiss WIRTH_Immune system
4	21.36	NULL	36 / 51	BP type I interferon signaling pathway
5	20.62	NULL	14 / 23	CC integral to luminal side of endoplasmic reticulum membrane
6	20.46	NULL	88 / 312	BP immune response
7	20.13	NULL	30 / 60	BP interferon-gamma-mediated signaling pathway
8	19.96	NULL	14 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
9	18.63	NULL	13 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
10	18.02	NULL	59 / 204	BP cytokine-mediated signaling pathway
11	17.86	NULL	10 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	17.84	NULL	14 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
13	17.76	NULL	13 / 16	GSEA C2JUROSEVIC_RESPONSE_TO_IMIQUMOD
14	17.11	NULL	15 / 32	CC ER to Golgi transport vesicle membrane
15	17.1	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
16	16.5	NULL	3 / 3	MMML C2SCIEJ_MMML_7
17	15.57	NULL	43 / 123	BP defense response to virus
18	15.49	NULL	17 / 52	Chr Chr HSCR6_MHC_QBL
19	15.41	NULL	10 / 28	CC transport vesicle membrane
20	15.01	NULL	11 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
21	14.64	NULL	23 / 60	BP T cell costimulation
22	14.62	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
23	13.98	NULL	5 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
24	13.95	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
25	13.95	NULL	109 / 553	Cancer Lembecke_Colonc Inflammation
26	13.79	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
27	13.27	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
28	13.13	NULL	9 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
29	13.12	NULL	5 / 12	GSEA C2ZHU_CMV_8_HR_UP
30	12.87	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
31	12.81	NULL	9 / 35	CC trans-Golgi network membrane
32	12.16	NULL	23 / 84	BP T cell receptor signaling pathway
33	12.14	NULL	31 / 74	BP regulation of immune response
34	12.04	NULL	6 / 12	BP immunoglobulin mediated immune response
35	11.79	NULL	5 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
36	11.72	NULL	16 / 87	BP antigen processing and presentation of exogenous peptide antigen
37	11.72	NULL	9 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
38	11.48	NULL	9 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
39	11.4	NULL	8 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
40	11.35	NULL	35 / 109	BP response to virus

p-values



GW_230

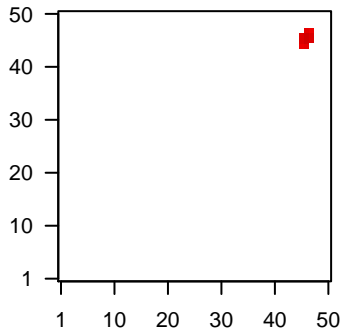
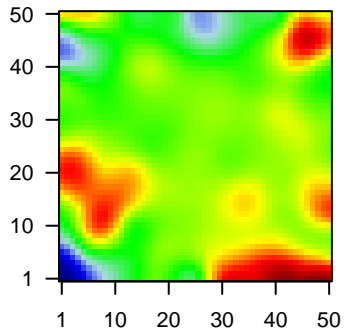
Local Summary

%DE = 0.88
 # metagenes = 10
 # genes = 108
 # genes in genesets = 108
 # genes with $fdr < 0.1 = 76$ (74 + / 2 -)
 # genes with $fdr < 0.05 = 67$ (67 + / 0 -)
 # genes with $fdr < 0.01 = 52$ (52 + / 0 -)

<r> metagenes = 0.98
 <r> genes = 0.36
 <FC> = 0.47
 <shrinkage-t> = 16.51
 <p-value> = 0
 <fdr> = 0.43

Profile

Spot



Local Genelist

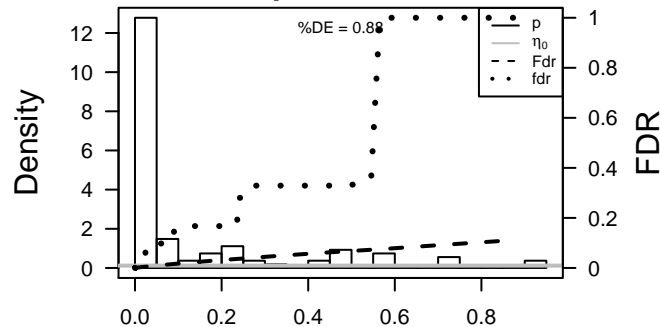
Rank	ID	log(FC)	fdr	p-value	Description
1	3787	1.78	2e-16	3e-15	46 x 45 potassium voltage-gated channel, delayed-rectifier, subfamil
2	116028	1.3	3e-15	3e-14	46 x 47 RecQ mediated genome instability 2 [Source:HGNC Symbol;]
3	285498	1.29	5e-15	2e-12	46 x 44 ring finger protein 212 [Source:HGNC Symbol;Acc:27729]
4	10388	1.22	1e-13	6e-12	47 x 46 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
5	283212	1.18	7e-13	6e-12	46 x 44 kelch-like family member 35 [Source:HGNC Symbol;Acc:265
6	113802	1.17	1e-12	6e-11	46 x 46 HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:HC
7	84215	1.13	6e-12	5e-10	46 x 45 zinc finger protein 541 [Source:HGNC Symbol;Acc:25294]
8	23580	1.07	9e-11	5e-10	47 x 45 CDC42 effector protein (Rho GTPase binding) 4 [Source:HG
9	57570	1.07	9e-11	5e-10	46 x 45 tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:23141]
10	8914	1.06	1e-10	2e-09	46 x 47 timeless circadian clock [Source:HGNC Symbol;Acc:11813]
11	128178	1.04	3e-10	1e-08	47 x 45 EDAR-associated death domain [Source:HGNC Symbol;Acc
12	54457	1	1e-09	1e-08	46 x 44 TAF7-like RNA polymerase II, TATA box binding protein (TBP
13	1870	0.98	2e-09	3e-08	46 x 45 E2F transcription factor 2 [Source:HGNC Symbol;Acc:3114]
14	1029	0.96	5e-09	3e-08	45 x 45 cyclin-dependent kinase inhibitor 2A [Source:HGNC Symbol;
15	80020	0.95	7e-09	4e-08	46 x 45 FAD-dependent oxidoreductase domain containing 2 [Source
16	4174	0.94	1e-08	1e-07	46 x 46 minichromosome maintenance complex component 5 [Source
17	580	0.92	2e-08	1e-07	46 x 45 BRCA1 associated RING domain 1 [Source:HGNC Symbol;A
18	55723	0.91	3e-08	2e-05	46 x 47 anti-silencing function 1B histone chaperone [Source:HGNC
19	55329	0.78	2e-06	2e-05	46 x 45 meiosis-specific nuclear structural 1 [Source:HGNC Symbol;
20	246777	0.77	3e-06	6e-05	45 x 45 sperm equatorial segment protein 1 [Source:HGNC Symbol;A

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	18.07	NULL	3 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
2	15.36	NULL	3 / 20	CC synaptonemal complex
3	14.48	NULL	4 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
4	14.4	NULL	3 / 13	GSEA C2SA_REG_CASCADE_OF_CYCLIN_EXPR
5	13.58	NULL	4 / 16	GSEA C2KEGG_BASE_EXCISION_REPAIR
6	13.39	NULL	2 / 10	CC lateral element
7	13.26	NULL	3 / 15	GSEA C2SA_G1_AND_S_PHASES
8	12.99	NULL	6 / 30	BP DNA strand elongation involved in DNA replication
9	12.88	NULL	1 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPlicON
10	12.87	NULL	3 / 13	GSEA C2NADERI_BREAST_CANCER_PROGNOSIS_UP
11	12.81	NULL	3 / 10	GSEA C2REACTOME_GLOBAL_GENOMIC_NER
12	12.77	NULL	3 / 16	GSEA C2KEGG_BLADDER_CANCER
13	12.55	NULL	4 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
14	12.29	NULL	5 / 22	BP DNA replication initiation
15	12.16	NULL	5 / 16	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_UP
16	11.67	NULL	1 / 5	MMML C2SCIEJ_MMML_20
17	11.61	NULL	13 / 149	BP DNA replication
18	11.57	NULL	1 / 12	GSEA C2YAGI_AML_WITH_INV_16_TRANSLOCATION
19	11.27	NULL	3 / 15	GSEA C2REACTOME_G1_PHASE
20	11.11	NULL	4 / 15	GSEA C2KEGG_DNA_REPLICATION
21	10.92	NULL	2 / 11	GSEA C2REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC:ORIGIN_C
22	10.91	NULL	5 / 24	MF DNA helicase activity
23	10.84	NULL	3 / 16	GSEA C2YAGING_PREMATURE_DN
24	10.38	NULL	2 / 12	GSEA C2REACTOME_ASSOCIATION_OF_LICENSING_FACTORS_WITH
25	10.36	NULL	2 / 9	miRNA target-24
26	10.1	NULL	3 / 15	GSEA C2REACTOME_EXTENSION_OF_TELOMERES
27	10	NULL	2 / 12	GSEA C2FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_DN
28	9.78	NULL	1 / 16	GSEA C2KIM_MYC_AMPLIFICATION_TARGETS_UP
29	9.76	NULL	19 / 370	BP mitotic cell cycle
30	9.73	NULL	3 / 16	GSEA C2REACTOME_TELOMERE_MAINTENANCE
31	9.34	NULL	1 / 6	GSEA C2OHM_EMBRYONIC_CARCINOMA_DN
32	9.24	NULL	4 / 28	MF core promoter binding
33	9.18	NULL	2 / 16	BP cell cycle checkpoint
34	9.13	NULL	1 / 18	MF delayed rectifier potassium channel activity
35	9.08	NULL	3 / 18	BP nucleotide-excision repair, DNA gap filling
36	8.84	NULL	3 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
37	8.63	NULL	21 / 530	Cancer Lembecke_Normal vs Adenoma
38	8.38	NULL	1 / 10	BP piRNA metabolic process
39	8.34	NULL	3 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
40	8.3	NULL	3 / 21	BP telomere maintenance via semi-conservative replication

p-values



GW_230

Local Summary

%DE = 0.87
 # metagenes = 20
 # genes = 330
 # genes in genesets = 327
 # genes with $fdr < 0.1$ = 245 (18 + / 227 -)
 # genes with $fdr < 0.05$ = 226 (16 + / 210 -)
 # genes with $fdr < 0.01$ = 188 (12 + / 176 -)

<r> metagenes = 0.94

<r> genes = 0.35

<FC> = -0.5

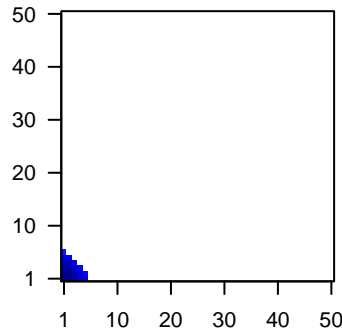
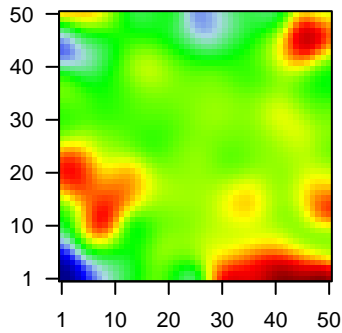
<shrinkage-t> = -17.55

<p-value> = 0

<fdr> = 0.35

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	55107	-1.82	2e-16	9e-16	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
2	1290	-1.42	2e-16	9e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
3	3040	-2.32	2e-16	9e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3043	-2.6	2e-16	9e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
5	4319	-1.41	2e-16	9e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy]
6	4316	-2.15	2e-16	9e-16	2 x 1 matrix metalloproteinase 7 (matrilysin, uterine) [Source:HGNC]
7	12	-1.41	2e-16	9e-16	1 x 1
8	6696	-1.36	2e-16	9e-16	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125]
9	23213	-1.78	2e-16	9e-16	2 x 1 sulfatase 1 [Source:HGNC Symbol;Acc:20391]
10	7045	-1.56	2e-16	9e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HG]
11	3371	-1.6	2e-16	9e-16	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
12	3918	-1.34	4e-16	1e-14	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
13	8076	-1.33	4e-16	1e-14	4 x 1 microfibrillar associated protein 5 [Source:HGNC Symbol;Acc]
14	857	-1.33	7e-16	1e-13	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A]
15	3039	-1.29	5e-15	1e-13	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
16	3685	-1.29	5e-15	3e-13	1 x 4 integrin, alpha V [Source:HGNC Symbol;Acc:6150]
17	5054	-1.26	2e-14	3e-13	1 x 2 serpin peptidase inhibitor, clade E (hexin, plasminogen activa
18	7058	-1.26	2e-14	3e-13	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
19	6423	-1.25	3e-14	3e-13	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Ac
20	10631	-1.24	4e-14	3e-13	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-32.43	NULL	15 / 16	MMML C6S CIEJ_MMML 1
2	-30.12	NULL	65 / 190	CC extracellular matrix
3	-29.67	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
4	-29.16	NULL	75 / 242	BP extracellular matrix organization
5	-29.05	NULL	77 / 250	Lympho ENZ_Stromal signature 1
6	-25.02	NULL	2 / 4	MMML C6S CIEJ_MMML 23
7	-22.79	NULL	12 / 19	MF extracellular matrix binding
8	-21.59	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
9	-20.5	NULL	6 / 10	GSEA C2LEON_SMAD6_TARGETS_UP
10	-20.09	NULL	39 / 183	CC proteinaceous extracellular matrix
11	-20.06	NULL	32 / 69	BP extracellular matrix disassembly
12	-19.79	NULL	29 / 64	BP collagen catabolic process
13	-19.24	NULL	15 / 37	BP collagen fibril organization
14	-19.14	NULL	6 / 11	MMML C6S CIEJ_MMML 31
15	-18.89	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
16	-18.86	NULL	8 / 11	MF platelet-derived growth factor binding
17	-18.85	NULL	21 / 57	MF extracellular matrix structural constituent
18	-17.92	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
19	-17.01	NULL	3 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
20	-16.84	NULL	23 / 119	Lympho BOSOWSKI_green total
21	-16.5	NULL	60 / 403	BP cell adhesion
22	-16.46	NULL	5 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
23	-16.13	NULL	8 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
24	-15.99	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
25	-15.98	NULL	17 / 68	Glio cultured astroglia vs. in vivo astrocytes
26	-15.77	NULL	8 / 12	miRNA target-29c
27	-15.65	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
28	-15.47	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
29	-15.46	NULL	82 / 683	CC extracellular space
30	-15.36	NULL	117 / 1182	CC extracellular region
31	-15.26	NULL	7 / 16	MF fibronectin binding
32	-15.1	NULL	3 / 7	GSEA C2DASU_IL6_SIGNALING_DN
33	-15.09	NULL	3 / 14	CC endocytic vesicle lumen
34	-15.03	NULL	13 / 35	Glio Colman_survival_associated
35	-14.83	NULL	2 / 10	CC hemoglobin complex
36	-14.81	NULL	25 / 83	CC basement membrane
37	-14.8	NULL	4 / 7	GSEA C2WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
38	-14.53	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
39	-14.49	NULL	6 / 10	GSEA C2ERRECCCHIA_RESPONSE_TO_TGFB1_C4
40	-14.22	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP

