

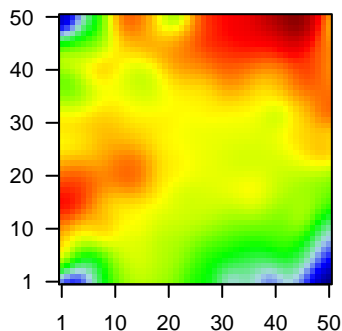
GW_309

Global Summary

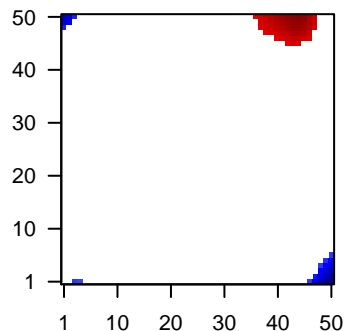
%DE = 0.15
 # genes with $fdr < 0.2$ = 1590 (596 + / 994 -)
 # genes with $fdr < 0.1$ = 1239 (423 + / 816 -)
 # genes with $fdr < 0.05$ = 1081 (336 + / 745 -)
 # genes with $fdr < 0.01$ = 695 (161 + / 534 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.12
 <fdr> = 0.85

Profile



Regulated Spots



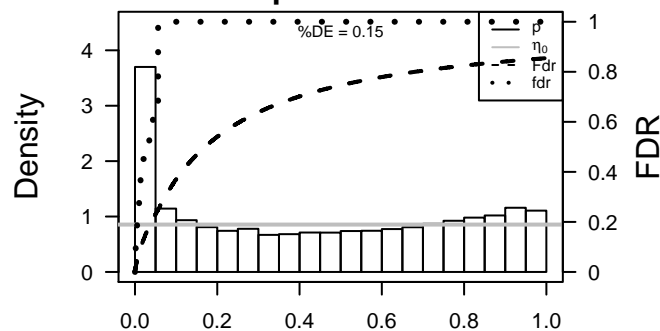
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	-2.02	2e-16	6e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Metagene]
2	633	-1.9	2e-16	6e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	684	-2.31	2e-16	6e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:1044]
4	6364	-2.31	2e-16	6e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:1044]
5	4680	-2.12	2e-16	6e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
6	629	-2.1	2e-16	6e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
7	22802	-2.25	2e-16	6e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20197]
8	1277	-2.61	2e-16	6e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
9	1278	-2.53	2e-16	6e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
10	1281	-2.57	2e-16	6e-14	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
11	1291	-2.19	2e-16	6e-14	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
12	1293	-2.33	2e-16	6e-14	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
13	1396	-2.03	2e-16	6e-14	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:1230]
14	49860	-2.22	2e-16	6e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	1673	-2.11	2e-16	6e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	1843	-2.06	2e-16	6e-14	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30193]
17	2353	-3.04	2e-16	6e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:1230]
18	2354	-2.37	2e-16	6e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:1230]
19	10457	2.06	2e-16	6e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;Acc:1230]
20	283120	-1.99	2e-16	6e-14	25 x 1 H19, imprinted maternally expressed transcript (non-protein coding)

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.25	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	14.25	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	13.46	NULL	1233	TF KIM_MYC targets
4	13.05	NULL	370	BP mitotic cell cycle
5	11.04	NULL	1318	CC mitochondrion
6	10.9	NULL	649	BP gene expression
7	10.37	NULL	530	Cancer Lembecke_Normal vs Adenoma
8	10.34	NULL	949	CC nucleoplasm
9	8.78	NULL	595	MF RNA binding
10	8.71	NULL	287	BP viral process
11	8.55	NULL	717	Chr Chr 16
12	8.35	NULL	242	BP RNA metabolic process
13	8.29	NULL	219	BP mRNA metabolic process
14	8.16	NULL	232	BP mitosis
15	8	NULL	149	BP DNA replication
16	7.93	NULL	253	BP translation
17	7.87	NULL	4640	CC nucleus
18	7.79	NULL	298	BP DNA repair
19	7.54	NULL	579	CC nucleolus
20	7.17	NULL	128	BP translational initiation
<i>Underexpressed</i>				
1	-23.06	NULL	553	Cancer Lembecke_Colonc Inflammation
2	-20.01	NULL	1182	CC extracellular region
3	-18.62	NULL	312	BP immune response
4	-17.97	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
5	-17.97	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
6	-17.97	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
7	-17.97	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
8	-16.69	NULL	683	CC extracellular space
9	-15.89	NULL	572	Disease GUDJ_psooriasis up
10	-15.86	NULL	250	LymphomaL1_ENZ_Stromal signature 1
11	-14.53	NULL	135	H.Tiss WIRTH_Mucosa
12	-13.8	NULL	269	BP inflammatory response
13	-13.69	NULL	21	CC cornified envelope
14	-12.96	NULL	16	GSEA_C23_CROONQUIST_STROMAL_STIMULATION_UP
15	-12.63	NULL	190	CC extracellular matrix
16	-11.44	NULL	42	BP keratinization
17	-11.35	NULL	129	BP response to lipopolysaccharide
18	-11.08	NULL	51	BP type I interferon signaling pathway
19	-11.04	NULL	15	CC MHC class II protein complex
20	-10.88	NULL	2659	CC plasma membrane

p-values



GW_309

Local Summary

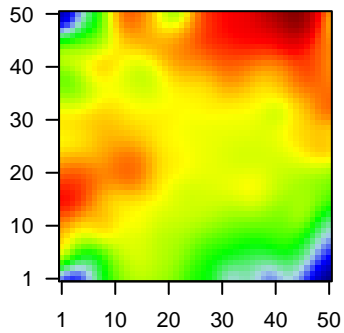
%DE = 0.76
 # metagenes = 53
 # genes = 693
 # genes in genesets = 681

genes with $fdr < 0.1$ = 349 (345 + / 4 -)
 # genes with $fdr < 0.05$ = 211 (207 + / 4 -)
 # genes with $fdr < 0.01$ = 112 (110 + / 2 -)

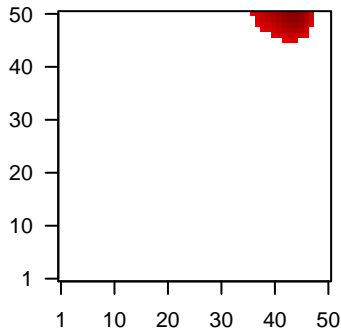
$\langle r \rangle$ metagenes = 0.88
 $\langle r \rangle$ genes = 0.3

$\langle FC \rangle = 0.44$
 $\langle \text{shrinkage-t} \rangle = 15.57$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.66$

Profile



Spot



Local Genelist

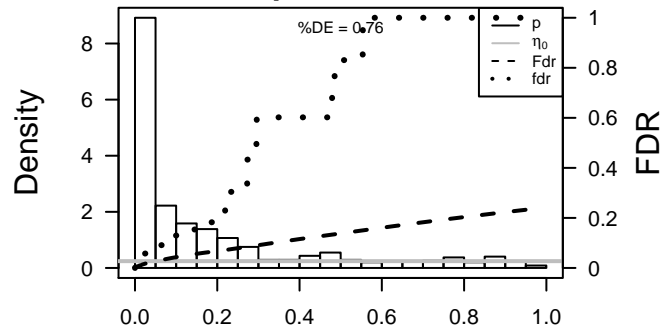
Rank	ID	log(FC)	fdr	p-value	Description
1	23480	1.62	1e-12	2e-08	39 x 50 Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
2	55915	1.56	1e-10	4e-07	38 x 50 LanC lantibiotic synthetase component C-like 2 (bacterial) [S
3	51659	1.45	3e-09	6e-07	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
4	7298	1.4	9e-09	6e-07	46 x 48 thymidylate synthetase [Source:HGNC Symbol;Acc:12441]
5	494514	1.39	1e-08	1e-05	46 x 48 chromosome 18 open reading frame 56 [Source:HGNC Symt
6	4172	1.31	8e-08	2e-05	46 x 47 minichromosome maintenance complex component 3 [Source
7	3161	1.26	2e-07	3e-05	43 x 50 hyaluronan-mediated motility receptor (RHAMM) [Source:HG
8	5984	1.24	4e-07	1e-04	46 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syr
9	10403	1.17	1e-06	1e-04	44 x 50 NDC80 kinetochore complex component [Source:HGNC Sym
10	29899	1.16	2e-06	1e-04	41 x 50 G-protein signaling modulator 2 [Source:HGNC Symbol;Acc:
11	7153	1.15	2e-06	1e-04	45 x 49 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
12	908	1.12	4e-06	1e-04	40 x 50 chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
13	54107	1.11	5e-06	1e-04	43 x 45 polymerase (DNA directed), epsilon 3, accessory subunit [So
14	81831	1.11	5e-06	1e-04	42 x 50 neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Sym
15	7037	1.01	5e-06	1e-04	47 x 50 transferrin receptor [Source:HGNC Symbol;Acc:11763]
16	3376	1.1	6e-06	2e-04	41 x 50 isoleucyl-tRNA synthetase [Source:HGNC Symbol;Acc:5330]
17	5713	1.09	7e-06	2e-04	38 x 50 proteasome (prosome, macropain) 26S subunit, non-ATPase
18	64785	1.08	9e-06	2e-04	44 x 48 GINS complex subunit 3 (Psf3 homolog) [Source:HGNC Sym
19	84823	1.08	9e-06	4e-04	44 x 49 lamin B2 [Source:HGNC Symbol;Acc:6638]
20	86	1.06	1e-05	4e-04	46 x 50 actin-like 6A [Source:HGNC Symbol;Acc:24124]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	43.37	NULL	100 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	43.37	NULL	100 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	26.98	NULL	118 / 370	BP mitotic cell cycle
4	22.52	NULL	13 / 16	GSEA C27FARMER_BREAST_CANCER_CLUSTER_2
5	21.55	NULL	50 / 149	BP DNA replication
6	21.28	NULL	13 / 14	MMML C69SCIEJ_MMML_4
7	21.13	NULL	120 / 530	Cancer Lembecke_Normal vs Adenoma
8	20.06	NULL	15 / 16	GSEA C27FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
9	19.47	NULL	16 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
10	19.08	NULL	14 / 15	GSEA C27FINETTI_BREAST_CANCER_KINOME_RED
11	18.54	NULL	8 / 11	GSEA C2KALMA_E2F1_TARGETS
12	18.29	NULL	18 / 30	BP DNA strand elongation involved in DNA replication
13	18.17	NULL	24 / 57	Glio developing astrocytes
14	18.11	NULL	10 / 14	GSEA C27ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
15	17.97	NULL	11 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
16	17.83	NULL	12 / 13	GSEA C2ROONQUIST_IL6_DEPRIVATION_DN
17	17.73	NULL	66 / 232	BP mitosis
18	17.24	NULL	9 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
19	17.18	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	16.72	NULL	11 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
21	16.24	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
22	16.11	NULL	13 / 18	BP spindle organization
23	15.81	NULL	11 / 16	Cancer WOLFER_overlap genes
24	15.57	NULL	9 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
25	15.49	NULL	9 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
26	15.42	NULL	146 / 949	CC nucleoplasm
27	15.3	NULL	25 / 56	CC chromosome, centromeric region
28	15.18	NULL	43 / 148	BP G1/S transition of mitotic cell cycle
29	14.75	NULL	11 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
30	14.75	NULL	12 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
31	14.65	NULL	12 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
32	14.5	NULL	11 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
33	14.48	NULL	9 / 15	GSEA C2BOVAULT_LIVER_CANCER_SUBCLASS_G23_UP
34	14.33	NULL	9 / 16	GSEA C2KEGG_MISMATCH_REPAIR
35	14.25	NULL	8 / 11	BP mitotic metaphase plate congression
36	14.24	NULL	10 / 13	GSEA C2WINNENPENNINCKX_MELANOMA_METASTASIS_UP
37	14.21	NULL	11 / 15	GSEA C2CHANG_CYCLING_GENES
38	14.09	NULL	11 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
39	13.99	NULL	8 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
40	13.75	NULL	11 / 21	BP telomere maintenance via semi-conservative replication

p-values



GW_309

Local Summary

%DE = 0.97
 # metagenes = 2
 # genes = 65
 # genes in genesets = 65
 # genes with $fdr < 0.1$ = 60 (3 + / 57 -)
 # genes with $fdr < 0.05$ = 57 (3 + / 54 -)
 # genes with $fdr < 0.01$ = 55 (2 + / 53 -)

<r> metagenes = 1

<r> genes = 0.58

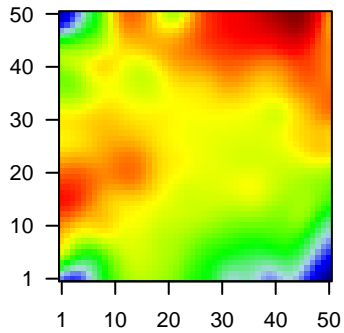
<FC> = -1.04

<shrinkage-t> = -36.53

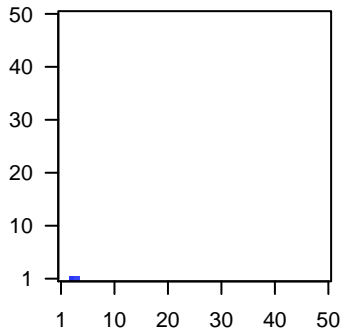
<p-value> = 0

<fdr> = 0.17

Profile



Spot



Local Genelist

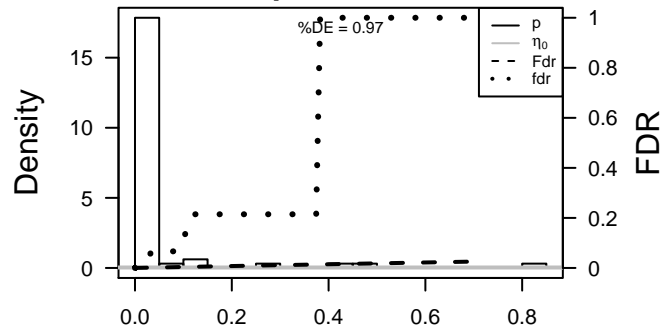
Rank	ID	log(FC)	fdr	p-value	Description
1	59	-2.02	2e-16	1e-16	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	633	-1.9	2e-16	1e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
3	3040	-2.4	2e-16	1e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	7076	-2.13	2e-16	1e-16	4 x 1 TIMP metalloproteinase inhibitor 1 [Source:HGNC Symbol;Acc:2]
5	1490	-1.97	4e-16	4e-16	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2]
6	6515	-1.97	7e-16	2e-14	3 x 1 solute carrier family 2 (facilitated glucose transporter), membr
7	6678	-1.87	2e-14	2e-14	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC Symbol;Acc:1044]
8	115908	-1.86	2e-14	2e-14	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symbol;Acc:1044]
9	1462	-1.85	3e-14	6e-13	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
10	1513	-1.77	3e-13	1e-12	4 x 1 cathepsin K [Source:HGNC Symbol;Acc:2536]
11	5159	-1.71	2e-12	1e-12	3 x 1 platelet-derived growth factor receptor, beta polypeptide [Source:HGNC Symbol;Acc:1044]
12	6423	-1.71	2e-12	1e-12	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:1044]
13	165	-1.71	2e-12	2e-12	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
14	7431	-1.7	3e-12	1e-11	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]
15	23452	-1.65	1e-11	1e-11	3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490]
16	11167	-1.64	2e-11	4e-11	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
17	7070	-1.61	4e-11	2e-09	4 x 1 Thy-1 cell surface antigen [Source:HGNC Symbol;Acc:11801]
18	7169	-1.48	1e-09	3e-09	3 x 1 tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
19	2199	-1.45	2e-09	8e-09	4 x 1 fibulin 2 [Source:HGNC Symbol;Acc:3601]
20	6876	-1.41	6e-09	1e-08	3 x 1 transgelin [Source:HGNC Symbol;Acc:11553]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-49.86	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
2	-37.31	NULL	1 / 2	miRNA target-18
3	-29.79	NULL	7 / 19	MF extracellular matrix binding
4	-28.27	NULL	28 / 250	Lymphoma ENZ_Stromal signature 1
5	-26.71	NULL	3 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
6	-25.41	NULL	3 / 5	GSEA C2COLLER_MYC_TARGETS_DN
7	-24.35	NULL	22 / 190	CC extracellular matrix
8	-24.05	NULL	3 / 11	BP dermatan sulfate biosynthetic process
9	-23.53	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_CARCINOMA
10	-22.82	NULL	4 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
11	-21.12	NULL	3 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
12	-21.07	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
13	-20.7	NULL	3 / 14	BP chondroitin sulfate catabolic process
14	-19.88	NULL	3 / 11	GSEA C2CLAUS_PGR_POSITIVE_MENINGIOMA_DN
15	-19.67	NULL	3 / 15	Cancer LIU_PROSTATE_CANCER_DN
16	-19.63	NULL	2 / 8	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
17	-18.93	NULL	4 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_CARCINOMA
18	-18.33	NULL	3 / 15	GSEA C2MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS
19	-18.25	NULL	2 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
20	-17.82	NULL	19 / 242	BP extracellular matrix organization
21	-17.76	NULL	2 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
22	-17.45	NULL	3 / 11	MMML C6SCIEJ_MMML 31
23	-17.4	NULL	1 / 4	MMML C6SCIEJ_MMML 23
24	-16.55	NULL	5 / 16	MMML C6SCIEJ_MMML 1
25	-16.39	NULL	3 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
26	-16.21	NULL	3 / 21	MF glycosaminoglycan binding
27	-16.16	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
28	-16.04	NULL	2 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CANCER
29	-15.95	NULL	3 / 20	BP positive regulation of collagen biosynthetic process
30	-15.65	NULL	1 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
31	-15.57	NULL	12 / 183	CC proteinaceous extracellular matrix
32	-15.42	NULL	2 / 14	GSEA C2MAINA_VHL_TARGETS_DN
33	-15.35	NULL	3 / 13	GSEA C2ZIRN_TRETINOIN_RESPONSE_UP
34	-14.9	NULL	2 / 14	CC endocytic vesicle lumen
35	-14.83	NULL	1 / 5	GSEA C2PASTURAL_RIZ1_TARGETS_UP
36	-14.73	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
37	-14.62	NULL	3 / 25	BP chondroitin sulfate biosynthetic process
38	-14.58	NULL	2 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HEL4
39	-14.51	NULL	2 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
40	-14.45	NULL	10 / 69	BP extracellular matrix disassembly

p-values



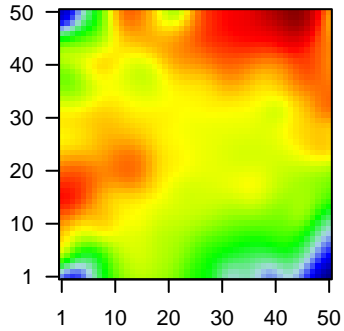
GW_309

Local Summary

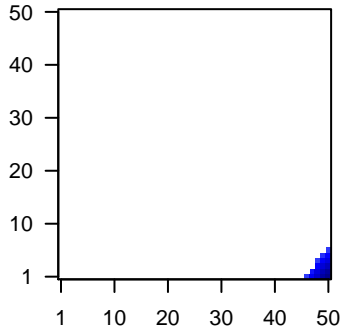
%DE = 0.95
 # metagenes = 18
 # genes = 312
 # genes in genesets = 310
 # genes with $fdr < 0.1$ = 289 (5 + / 284 -)
 # genes with $fdr < 0.05$ = 264 (4 + / 260 -)
 # genes with $fdr < 0.01$ = 229 (3 + / 226 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.53
 $\langle FC \rangle = -0.82$
 $\langle \text{shrinkage-t} \rangle = -28.61$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.29$

Profile



Spot



Local Genelist

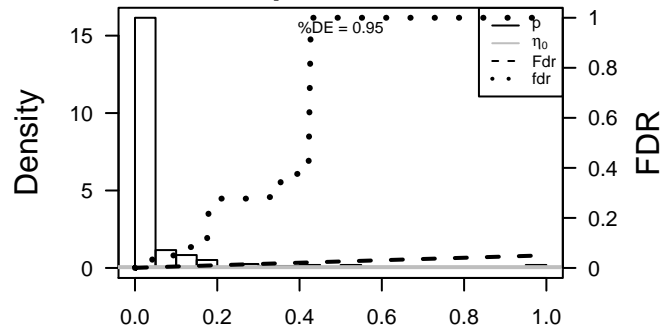
Rank	ID	log(FC)	fdr	p-value	Description
1	6364	-2.31	2e-16	6e-16	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:10342]
2	1396	-2.03	2e-16	6e-16	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:10342]
3	3109	-2.01	2e-16	6e-16	50 x 1 major histocompatibility complex, class II, DM beta [Source:HGNC Symbol;Acc:10342]
4	3113	-2.12	2e-16	6e-16	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:10342]
5	3122	-2.25	2e-16	6e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:10342]
6	3543	-3.32	2e-16	6e-16	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:10342]
7	894	-1.95	1e-15	2e-14	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
8	3512	-1.94	1e-15	2e-14	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin heavy chain [Source:HGNC Symbol;Acc:1583]
9	972	-1.92	3e-15	2e-13	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:1583]
10	5552	-1.86	2e-14	2e-13	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
11	2634	-1.84	4e-14	2e-13	47 x 1 guanylate binding protein 2, interferon-inducible [Source:HGNC Symbol;Acc:9361]
12	713	-1.83	5e-14	5e-13	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:9361]
13	3108	-1.82	8e-14	7e-13	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:9361]
14	241	-1.8	1e-13	3e-12	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:9361]
15	8404	-1.76	5e-13	3e-12	50 x 6 SPARC-like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
16	2	-1.76	5e-13	7e-12	50 x 5 alpha-2-macroglobulin [Source:HGNC Symbol;Acc:7]
17	5996	-1.73	1e-12	7e-12	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:7]
18	4283	-1.72	1e-12	3e-11	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:7]
19	7450	-1.69	4e-12	3e-11	50 x 6 von Willebrand factor [Source:HGNC Symbol;Acc:12726]
20	3689	-1.68	6e-12	3e-11	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:12726]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-33.52	NULL	12 / 15	CC MHC class II protein complex
2	-25.55	NULL	54 / 312	BP immune response
3	-24.65	NULL	89 / 417	H.Tiss WIRTH_Immune system
4	-22.08	NULL	99 / 553	Cancer Lembcke_Coloniac Inflammation
5	-21.04	NULL	15 / 47	BP antigen processing and presentation
6	-18.56	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
7	-18.55	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
8	-18.37	NULL	43 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
9	-18.37	NULL	43 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
10	-18.37	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	-18.37	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
12	-17.59	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
13	-17.47	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
14	-17.01	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
15	-16.95	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
16	-16.72	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
17	-16.01	NULL	15 / 60	BP T cell costimulation
18	-15.9	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
19	-15.54	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
20	-15.51	NULL	4 / 8	GSEA C2GRAHAM_CML QUIESCENT_VS_NORMAL_DIVIDING_DN
21	-15.28	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
22	-14.96	NULL	7 / 28	CC transport vesicle membrane
23	-14.91	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
24	-14.81	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
25	-14.79	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
26	-14.71	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
27	-14.61	NULL	9 / 35	CC trans-Golgi network membrane
28	-14.11	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
29	-14	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
30	-13.96	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
31	-13.94	NULL	5 / 12	BP immunoglobulin mediated immune response
32	-13.87	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
33	-13.63	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
34	-13.48	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
35	-13.42	NULL	18 / 74	BP regulation of immune response
36	-13.26	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
37	-13.02	NULL	14 / 87	BP antigen processing and presentation of exogenous peptide antigen
38	-12.82	NULL	4 / 8	LymphomaMASCQUE_ABC UP
39	-12.79	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
40	-12.75	NULL	28 / 162	CC external side of plasma membrane

p-values



GW_309

Local Summary

%DE = 0.94
 # metagenes = 6
 # genes = 131
 # genes in genesets = 128

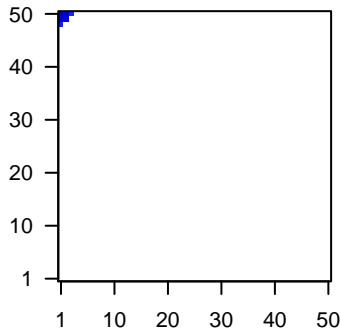
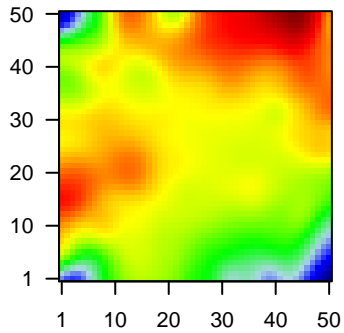
genes with $fdr < 0.1 = 119$ (5 + / 114 -)
 # genes with $fdr < 0.05 = 119$ (5 + / 114 -)
 # genes with $fdr < 0.01 = 111$ (4 + / 107 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.52

$\langle FC \rangle = -1.16$
 $\langle \text{shrinkage-t} \rangle = -40.96$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.12$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4680	-2.12	2e-16	9e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
2	22802	-2.25	2e-16	9e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
3	49860	-2.22	2e-16	9e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
4	1673	-2.11	2e-16	9e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
5	3934	-2.9	2e-16	9e-17	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]
6	4118	-2.31	2e-16	9e-17	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
7	5266	-1.93	2e-16	9e-17	1 x 49 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Ac
8	6278	-2.57	2e-16	9e-17	1 x 49 S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
9	6280	-2.42	2e-16	9e-17	1 x 49 S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:
10	6286	-2.65	2e-16	9e-17	1 x 50 S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
11	6337	-2.06	2e-16	9e-17	3 x 50 sodium channel, non-voltage-gated 1 alpha subunit [Source:
12	1992	-2.16	2e-16	9e-17	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Sc
13	6590	-2.1	2e-16	9e-17	1 x 49 secretory leukocyte peptidase inhibitor [Source:HGNC Symbo
14	6698	-2.04	2e-16	9e-17	1 x 50 small proline-rich protein 1A [Source:HGNC Symbol;Acc:112
15	6700	-2.82	2e-16	9e-17	1 x 50 small proline-rich protein 2A [Source:HGNC Symbol;Acc:112
16	6702	-2.2	2e-16	9e-17	1 x 50
17	6704	-2.38	2e-16	9e-17	1 x 50 small proline-rich protein 2E [Source:HGNC Symbol;Acc:112
18	6705	-2.75	2e-16	9e-17	1 x 50 small proline-rich protein 2F [Source:HGNC Symbol;Acc:112
19	6706	-2	2e-16	9e-17	1 x 48 small proline-rich protein 2G [Source:HGNC Symbol;Acc:112
20	6707	-2.35	2e-16	9e-17	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-47.32	NULL	62 / 135	H.Tiss WIRTH_Mucosa
2	-44.43	NULL	13 / 21	CC cornified envelope
3	-35.46	NULL	15 / 42	BP keratinization
4	-33.41	NULL	17 / 53	BP keratinocyte differentiation
5	-28.09	NULL	4 / 10	MF RAGE receptor binding
6	-27.77	NULL	63 / 572	Disease GUDJ_poriasis up
7	-27.48	NULL	16 / 76	BP epidermis development
8	-25.04	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
9	-24.48	NULL	7 / 19	BP peptide cross-linking
10	-18.61	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	-17.96	NULL	6 / 13	BP negative regulation of peptidase activity
12	-17.34	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
13	-16.67	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
14	-16.13	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
15	-15.34	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
16	-14.42	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_
17	-14.4	NULL	2 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
18	-13.98	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
19	-13.91	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
20	-13.89	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
21	-13.3	NULL	5 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
22	-13.09	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
23	-12.99	NULL	8 / 52	BP negative regulation of endopeptidase activity
24	-12.94	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
25	-12.68	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
26	-12.51	NULL	2 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
27	-12.49	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
28	-12.45	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
29	-12.37	NULL	3 / 16	GSEA C2IAEGER_METASTASIS_DN
30	-12.14	NULL	2 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
31	-12.13	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
32	-11.8	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
33	-11.75	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
34	-11.65	NULL	1 / 5	miRNA target-196a
35	-11.58	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
36	-11.55	NULL	4 / 23	MF peptidase inhibitor activity
37	-11.46	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
38	-10.91	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
39	-10.56	NULL	40 / 1182	CC extracellular region
40	-10.39	NULL	2 / 16	GSEA C2MURATA_VIRULENCE_OF_H_PILORI

p-values

