

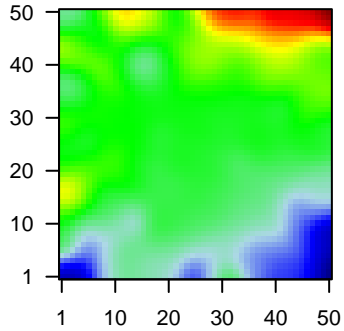
GW_150

Global Summary

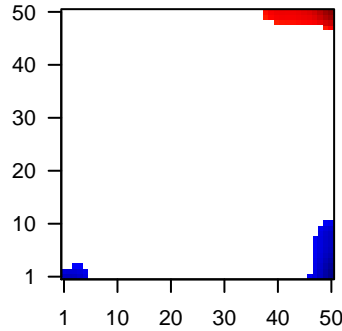
%DE = 0.12
 # genes with fdr < 0.2 = 1304 (655 + / 649 -)
 # genes with fdr < 0.1 = 1001 (500 + / 501 -)
 # genes with fdr < 0.05 = 772 (376 + / 396 -)
 # genes with fdr < 0.01 = 467 (227 + / 240 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.16
 <fdr> = 0.88

Profile



Regulated Spots



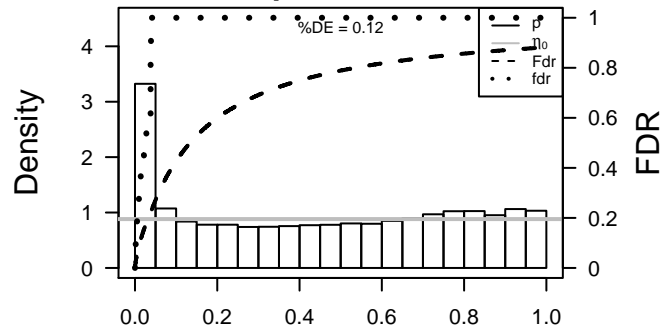
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	8644	1.85	2e-16 9e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
2	1109	1.57	2e-16 9e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy]
3	218	2.13	2e-16 9e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
4	501	-1.58	2e-16 9e-14	6 x 46 aldehyde dehydrogenase 7 family, member A1 [Source:HGNC]
5	445	1.77	2e-16 9e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75]
6	655	1.69	2e-16 9e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10]
7	10974	-1.68	2e-16 9e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2]
8	51806	-1.83	2e-16 9e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
9	1673	-1.76	2e-16 9e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
10	115572	-1.53	2e-16 9e-14	1 x 48 family with sequence similarity 46, member B [Source:HGNC]
11	2353	-1.52	2e-16 9e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:-]
12	10457	1.63	2e-16 9e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A]
13	2938	1.65	2e-16 9e-14	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Ac]
14	2944	1.85	2e-16 9e-14	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4]
15	283120	-1.97	2e-16 9e-14	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
16	3040	-1.95	2e-16 9e-14	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
17	3043	-2.19	2e-16 9e-14	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
18	3123	1.86	2e-16 9e-14	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
19	8988	1.68	2e-16 9e-14	1 x 4 heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248]
20	3486	2.27	2e-16 9e-14	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Sy]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.09	NULL	534	Chr Chr 8
2	9.7	NULL	1318	CC mitochondrion
3	9.52	NULL	699	Chr Chr 5
4	9.3	NULL	1233	TF KIM_MYC targets
5	9.24	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
6	9.24	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
7	7.58	NULL	370	BP mitotic cell cycle
8	7.14	NULL	83	BP respiratory electron transport chain
9	7.05	NULL	304	CC mitochondrial inner membrane
10	6.9	NULL	152	BP cellular metabolic process
11	6.78	NULL	530	Cancer Lembecke_Normal vs Adenoma
12	6.33	NULL	8	GSEA C2L10_CD_X2_TARGETS_DN
13	6.04	NULL	579	CC nucleolus
14	5.91	NULL	1253	BP small molecule metabolic process
15	5.86	NULL	44	BP tRNA aminoacylation for protein translation
16	5.86	NULL	25	BP glutathione derivative biosynthetic process
17	5.83	NULL	649	BP gene expression
18	5.81	NULL	949	CC nucleoplasm
19	5.8	NULL	298	BP DNA repair
20	5.73	NULL	618	Chr Chr 4
<i>Underexpressed</i>				
1	-16.92	NULL	633	Chr Chr 9
2	-13.33	NULL	519	Chr Chr 14
3	-10.67	NULL	553	Cancer Lembecke_Colonc Inflammation
4	-9.26	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
5	-9.26	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
6	-9.26	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
7	-9.26	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
8	-9.15	NULL	280	Chr Chr 13
9	-8.46	NULL	1135	Chr Chr 19
10	-8.25	NULL	312	BP immune response
11	-8.03	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
12	-7.94	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
13	-7.47	NULL	250	LymphomaL14_ENZ_Stromal signature 1
14	-7.46	NULL	1182	CC extracellular region
15	-7.32	NULL	190	CC extracellular matrix
16	-7.29	NULL	269	BP inflammatory response
17	-7.27	NULL	683	CC extracellular space
18	-7.08	NULL	4	MMML C6CIEJ_MMML 23
19	-7	NULL	2659	CC plasma membrane
20	-6.74	NULL	14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G4

p-values



GW_150

Local Summary

%DE = 0.6
 # metagenes = 39
 # genes = 592
 # genes in genesets = 586

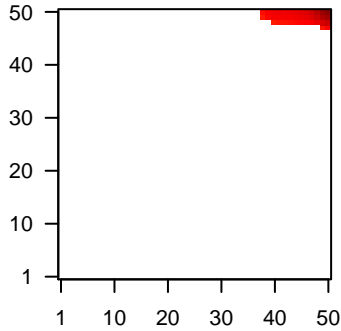
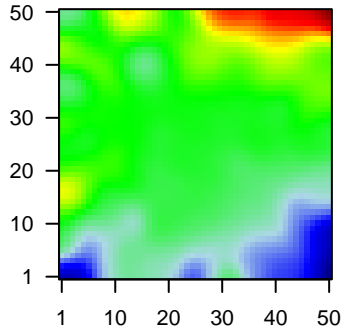
genes with $fdr < 0.1 = 231$ (217 + / 14 -)
 # genes with $fdr < 0.05 = 180$ (169 + / 11 -)
 # genes with $fdr < 0.01 = 93$ (89 + / 4 -)

<r> metagenes = 0.81
 <r> genes = 0.25

<FC> = 0.31
 <shrinkage-t> = 10.85
 <p-value> = 0.01
 <fdr> = 0.65

Profile

Spot



Local Genelist

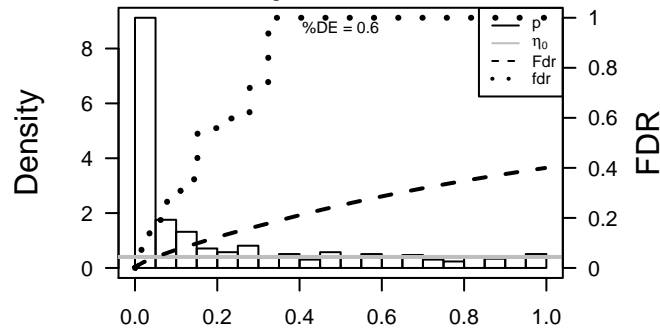
Rank	ID	log(FC)	fdr	p-value	Description
1	445	1.77	2e-16	9e-15	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75]
2	655	1.69	2e-16	9e-15	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1C
3	2938	1.65	2e-16	9e-15	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc:1C
4	2944	1.85	2e-16	9e-15	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
5	3866	2.05	2e-16	9e-15	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
6	4922	1.92	2e-16	9e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
7	216	1.48	4e-16	4e-13	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
8	875	1.48	4e-16	4e-13	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15]
9	339512	1.44	2e-15	4e-12	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
10	94234	1.39	2e-14	9e-12	50 x 50 forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
11	80896	1.37	6e-14	3e-11	50 x 50 N-acetylneuraminate pyruvate lyase (dihydrodipicolinate pyru
12	3856	1.33	2e-13	3e-11	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
13	2946	1.32	4e-13	3e-11	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Synt
14	2719	1.32	5e-13	1e-08	50 x 50 glypican 3 [Source:HGNC Symbol;Acc:4451]
15	55244	1.2	4e-11	1e-08	50 x 50 solute carrier family 47 (multidrug and toxin extrusion), memb
16	4780	1.18	9e-11	2e-08	50 x 50 nuclear factor, erythroid 2-like 2 [Source:HGNC Symbol;Acc:1C
17	79190	1.16	2e-10	3e-08	50 x 47 iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
18	4915	1.15	3e-10	3e-08	50 x 50 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
19	8492	1.14	4e-10	3e-07	50 x 47 protease, serine, 12 (neurotrypsin, motopsin) [Source:HGNC
20	57110	1.1	2e-09	2e-06	50 x 50 HRAS-like suppressor [Source:HGNC Symbol;Acc:14922]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	18.8	NULL	76 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	18.8	NULL	76 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	17.18	NULL	11 / 14	MMML C2GACIEJ_MMML_4
4	14.16	NULL	14 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	13.17	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
6	13.07	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
7	12.77	NULL	9 / 34	BP glutathione metabolic process
8	12.67	NULL	5 / 20	MF glutathione transferase activity
9	12.59	NULL	13 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
10	11.9	NULL	7 / 25	BP glutathione derivative biosynthetic process
11	11.75	NULL	4 / 13	BP regulation of blood vessel size
12	11.54	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
13	11.11	NULL	3 / 11	MF glutathione binding
14	11.11	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
15	11.09	NULL	10 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	11.03	NULL	10 / 16	Cancer WOLFER_overlap_genes
17	10.73	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
18	10.49	NULL	9 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
19	10.34	NULL	82 / 370	BP mitotic cell cycle
20	10.31	NULL	4 / 15	GSEA C2REACTOME_Glutathione_CONJUGATION
21	10.23	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHIA
22	10.19	NULL	11 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
23	10.19	NULL	5 / 15	Cancer BEN-PORATH_UP
24	9.86	NULL	81 / 530	Cancer Lembcke_Normal vs Adenoma
25	9.57	NULL	6 / 15	GSEA C2KEGG_Glutathione_METABOLISM
26	9.36	NULL	22 / 57	Glio developing astrocytes
27	9.09	NULL	10 / 30	BP DNA strand elongation involved in DNA replication
28	9.08	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
29	8.9	NULL	1 / 5	GSEA C2NIELSEN_SCHWANNOMA_DN
30	8.77	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_E2F1_UP
31	8.62	NULL	19 / 66	CC condensed chromosome kinetochore
32	8.46	NULL	7 / 15	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
33	8.29	NULL	13 / 119	BP xenobiotic metabolic process
34	8.28	NULL	2 / 14	CC membrane-bounded vesicle
35	8.25	NULL	3 / 6	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_DN
36	8.24	NULL	7 / 11	BP mitotic metaphase plate congression
37	8.24	NULL	8 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
38	8.17	NULL	16 / 100	Lymphoma OSOLOWSKI_blue total
39	8.04	NULL	44 / 232	BP mitosis
40	7.87	NULL	6 / 11	GSEA C2REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION

p-values



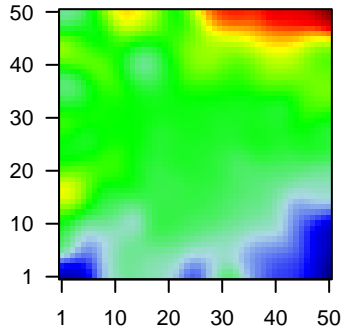
GW_150

Local Summary

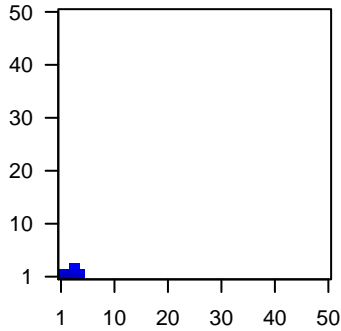
%DE = 0.7
 # metagenes = 12
 # genes = 197
 # genes in genesets = 196
 # genes with $fdr < 0.1 = 84$ (5 + / 79 -)
 # genes with $fdr < 0.05 = 74$ (3 + / 71 -)
 # genes with $fdr < 0.01 = 52$ (3 + / 49 -)

<r> metagenes = 0.98
 <r> genes = 0.45
 <FC> = -0.36
 <shrinkage-t> = -12.77
 <p-value> = 0
 <fdr> = 0.61

Profile



Spot



Local Genelist

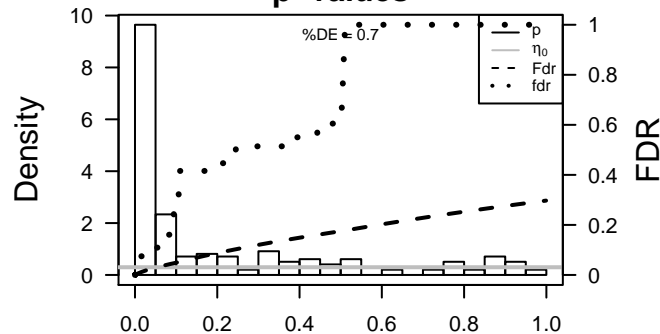
Rank	ID	log(FC)	fdr	p-value	Description
1	3040	-1.95	2e-16	3e-15	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	3043	-2.19	2e-16	3e-15	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
3	4314	-1.6	2e-16	3e-15	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
4	12	-1.49	2e-16	3e-15	1 x 1
5	4318	-1.44	2e-15	8e-12	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 9:
6	3039	-1.34	1e-13	1e-10	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
7	4060	1.28	2e-12	7e-10	2 x 1 lumican [Source:HGNC Symbol;Acc:6724]
8	2919	-1.21	3e-11	7e-10	1 x 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimula
9	3956	-1.2	3e-11	7e-10	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
10	4320	1.2	4e-11	8e-08	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
11	1397	-1.09	2e-09	8e-08	4 x 3 cysteine-rich protein 2 [Source:HGNC Symbol;Acc:2361]
12	5054	-1.08	3e-09	4e-07	1 x 2 serpin peptidase inhibitor, clade E (nexin, plasminogen activa
13	91663	-1.04	9e-09	2e-06	2 x 1 myeloid-associated differentiation marker [Source:HGNC Syr
14	6515	-0.99	5e-08	2e-06	3 x 1 solute carrier family 2 (facilitated glucose transporter), membx
15	6696	-0.98	8e-08	3e-06	2 x 1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125:
16	3553	-0.96	1e-07	4e-06	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
17	7431	-0.95	2e-07	3e-05	4 x 1 vimentin [Source:HGNC Symbol;Acc:12692]
18	3569	-0.9	7e-07	7e-05	1 x 1 interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:f
19	4312	-0.86	2e-06	7e-05	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:H
20	7076	-0.83	5e-06	7e-05	4 x 1 TIMP metalloproteinase inhibitor 1 [Source:HGNC Symbol;Acc

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-37.09	NULL	2 / 4	MMML C69CIEJ_MMML_23
2	-28.59	NULL	10 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
3	-24.09	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
4	-23.27	NULL	6 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
5	-22.77	NULL	3 / 11	MF oxygen transporter activity
6	-22.07	NULL	59 / 190	CC extracellular matrix
7	-21.96	NULL	2 / 10	CC hemoglobin complex
8	-21.19	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
9	-20.83	NULL	2 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
10	-20.06	NULL	2 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1T1_FUSION_SUSTAINED
11	-19.95	NULL	64 / 250	LymphomaL1ENZ_Stromal signature 1
12	-19.27	NULL	3 / 14	CC endocytic vesicle lumen
13	-18.95	NULL	2 / 3	GSEA C2KONDO_HYPOXIA
14	-18.84	NULL	5 / 19	MF peroxidase activity
15	-17.72	NULL	29 / 69	BP extracellular matrix disassembly
16	-17.18	NULL	56 / 242	BP extracellular matrix organization
17	-17.05	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
18	-16.87	NULL	5 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
19	-16.75	NULL	3 / 19	BP hydrogen peroxide catabolic process
20	-16.67	NULL	5 / 10	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
21	-16.48	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
22	-16.43	NULL	3 / 13	GSEA C2SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
23	-16.12	NULL	6 / 11	Glio Phillips MES up vs Prolif & PN
24	-16.06	NULL	2 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
25	-15.8	NULL	26 / 64	BP collagen catabolic process
26	-15.53	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
27	-15.37	NULL	4 / 29	BP positive regulation of cell death
28	-15.11	NULL	5 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
29	-14.71	NULL	4 / 16	GSEA C2U_TUMOR_VASCULATURE_UP
30	-14.25	NULL	6 / 16	GSEA C2JEN_BREAST_CARCINOMA_METAPLASTIC
31	-14.21	NULL	4 / 14	GSEA C2WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
32	-14.21	NULL	4 / 26	BP positive regulation of nitric oxide biosynthetic process
33	-14.18	NULL	2 / 22	BP bicarbonate transport
34	-14.14	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
35	-14.12	NULL	4 / 26	MF oxygen binding
36	-14.11	NULL	2 / 6	GSEA C2BIOCARTA_IL5_PATHWAY
37	-14.01	NULL	83 / 1182	CC extracellular region
38	-13.76	NULL	4 / 14	GSEA C2DANG_REGULATED_BY_MYC_DN
39	-13.59	NULL	3 / 15	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
40	-13.57	NULL	4 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH

p-values



GW_150

Local Summary

%DE = 0.75
 # metagenes = 41
 # genes = 566
 # genes in genesets = 563

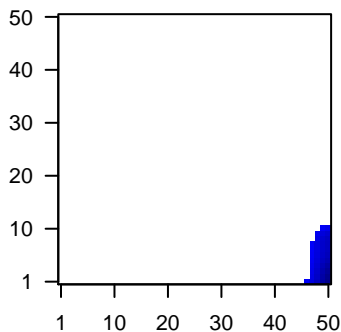
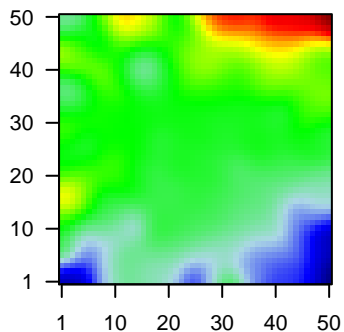
genes with $fdr < 0.1 = 279$ (31 + / 248 -)
 # genes with $fdr < 0.05 = 219$ (26 + / 193 -)
 # genes with $fdr < 0.01 = 131$ (16 + / 115 -)

$\langle r \rangle$ metagenes = 0.85
 $\langle r \rangle$ genes = 0.35

$\langle FC \rangle = -0.29$
 $\langle \text{shrinkage-t} \rangle = -10.16$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.63$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5920	1.67	2e-16	3e-14	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Sour
2	6192	-1.45	1e-15	2e-12	50 x 9 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:
3	3512	1.4	1e-14	8e-12	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobu
4	10232	-1.36	7e-14	2e-11	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
5	10628	-1.31	2e-13	2e-09	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
6	2878	-1.22	2e-11	2e-09	50 x 9 glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
7	3543	1.11	3e-11	3e-07	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
8	1675	-1.09	2e-09	3e-07	50 x 9 complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
9	10365	-1.06	6e-09	3e-07	50 x 3 Kruppel-like factor 2 [Source:HGNC Symbol;Acc:6347]
10	92304	-1.04	1e-08	3e-07	50 x 10 secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
11	2934	-1.04	1e-08	3e-07	50 x 9 gelsolin [Source:HGNC Symbol;Acc:4620]
12	3120	-1.03	1e-08	3e-07	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:
13	25891	1.03	1e-08	6e-07	50 x 8 peptidase domain containing associated with muscle regener
14	260436	-1.02	2e-08	6e-07	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
15	1363	1.02	2e-08	2e-06	50 x 7 carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
16	5341	-1	4e-08	2e-06	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
17	57172	0.99	5e-08	2e-06	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
18	54102	-0.98	6e-08	2e-06	50 x 10 chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2l
19	347733	-0.98	7e-08	2e-06	50 x 5 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
20	9235	-0.97	8e-08	4e-06	46 x 1 interleukin 32 [Source:HGNC Symbol;Acc:16830]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.97	NULL	14 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-16.89	NULL	128 / 553	Cancer Lembecke_Colonic Inflammation
3	-14.95	NULL	98 / 417	H.Tiss WIRTH_Immune system
4	-14.8	NULL	59 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
5	-14.8	NULL	59 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
6	-14.8	NULL	59 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
7	-14.8	NULL	59 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
8	-13	NULL	5 / 9	GSEA C2MILICIC_FAMILY_ADENOMATOUS_POLYPOSIIS_DN
9	-12.17	NULL	3 / 7	MMML C6SCIEJ_MMML 5
10	-11.58	NULL	7 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
11	-11.51	NULL	12 / 15	CC MHC class II protein complex
12	-11.31	NULL	64 / 312	BP immune response
13	-11.31	NULL	3 / 8	GSEA C2RUNNE_GENDER_EFFECT_UP
14	-11.2	NULL	12 / 43	MF chemokine activity
15	-10.89	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
16	-10.7	NULL	5 / 14	BP ruffle organization
17	-10.57	NULL	3 / 5	GSEA C2NAKAMURA_ALVEOLAR_EPITHELIUM
18	-10.48	NULL	7 / 16	GSEA C2BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
19	-10.4	NULL	4 / 11	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
20	-10.18	NULL	4 / 7	GSEA C2BIOCARTA_COMP_PATHWAY
21	-10.11	NULL	4 / 12	GSEA C2HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
22	-10.03	NULL	75 / 683	CC extracellular space
23	-9.93	NULL	5 / 12	BP dendritic cell chemotaxis
24	-9.86	NULL	7 / 8	BP Donson-migration tethering and rolling-associated with LTS in HGA
25	-9.75	NULL	6 / 20	BP actin filament polymerization
26	-9.54	NULL	4 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
27	-9.45	NULL	4 / 8	GSEA C2REACTOME_COMPLEMENT_CASCADE
28	-9.45	NULL	4 / 8	GSEA C2REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
29	-9.43	NULL	4 / 10	BP actin polymerization or depolymerization
30	-9.3	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNAATURE
31	-8.82	NULL	4 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
32	-8.42	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
33	-8.33	NULL	14 / 76	BP defense response
34	-8.28	NULL	3 / 14	GSEA C2WINPENPINCKX_MELANOMA_METASTASIS_DN
35	-8.04	NULL	4 / 16	GSEA C2BROWNE_HCMV_INFECTION_2HR_UP
36	-8.02	NULL	6 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
37	-7.82	NULL	4 / 15	GSEA C2SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
38	-7.81	NULL	3 / 14	GSEA C2GOLUB_ALL_VS_AML_DN
39	-7.74	NULL	105 / 1182CC	extracellular region
40	-7.65	NULL	2 / 7	GSEA C2LEE_NAIVE_T_LYMPHOCYTE

p-values

