

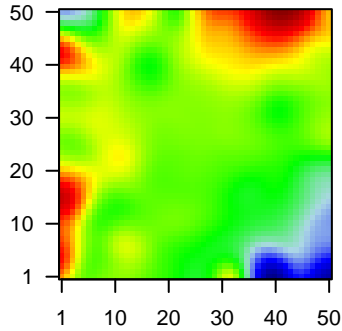
GW_283

Global Summary

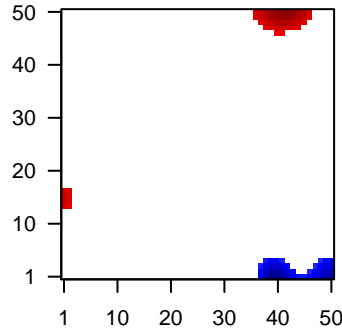
%DE = 0.14
 # genes with $fdr < 0.2$ = 1758 (942 + / 816 -)
 # genes with $fdr < 0.1$ = 1276 (682 + / 594 -)
 # genes with $fdr < 0.05$ = 1108 (585 + / 523 -)
 # genes with $fdr < 0.01$ = 672 (361 + / 311 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.86

Profile



Regulated Spots



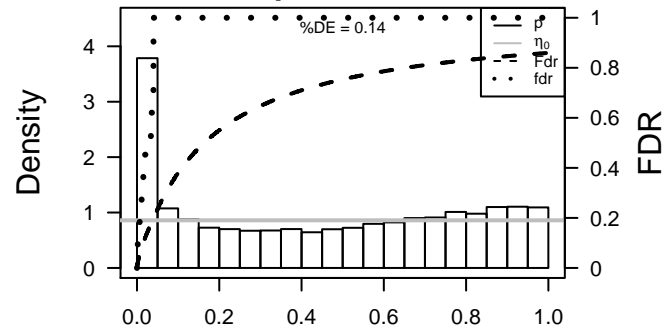
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.62	2e-16	1e-13	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
2	401138	2.68	2e-16	1e-13	1 x 5 amelotin [Source:HGNC Symbol;Acc:33188]
3	440	1.7	2e-16	1e-13	50 x 46 asparagine synthetase (glutamine-hydrolyzing) [Source:HGNC]
4	590	1.56	2e-16	1e-13	16 x 50 butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
5	8553	-1.61	2e-16	1e-13	22 x 50 basic helix-loop-helix family, member e40 [Source:HGNC Sy]
6	908	1.96	2e-16	1e-13	40 x 50 chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG]
7	643253	1.56	2e-16	1e-13	40 x 50
8	9547	-2.09	2e-16	1e-13	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;Ac]
9	6372	1.59	2e-16	1e-13	1 x 1 chemokine (C-X-C motif) ligand 6 [Source:HGNC Symbol;Ac]
10	1843	-1.8	2e-16	1e-13	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3C]
11	1958	-1.9	2e-16	1e-13	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
12	2167	2.35	2e-16	1e-13	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
13	8772	1.71	2e-16	1e-13	1 x 14 Fas (TNFRSF6)-associated via death domain [Source:HGNC]
14	641737	-1.52	2e-16	1e-13	40 x 1
15	2353	-1.42	2e-16	1e-13	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HG]
16	2354	-2.8	2e-16	1e-13	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source]
17	2631	1.79	2e-16	1e-13	39 x 50 glioblastoma amplified sequence [Source:HGNC Symbol;Acc]
18	3306	1.62	2e-16	1e-13	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]
19	5653	-1.69	2e-16	1e-13	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63]
20	9119	1.76	2e-16	1e-13	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.79	NULL	1233	TF KIM_MYC targets
2	9.68	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
3	9.68	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
4	8.92	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
5	8.31	NULL	504	Chr Chr 15
6	8.28	NULL	530	Cancer Lembcke_Normal vs Adenoma
7	8.02	NULL	370	BP mitotic cell cycle
8	7.45	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
9	7.29	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
10	7.23	NULL	8	GSEA C2ROETH_TERT_TARGETS_UP
11	6.59	NULL	534	Chr Chr 8
12	6.56	NULL	148	BP G1/S transition of mitotic cell cycle
13	6.39	NULL	4	MMML C2CIEJ_MMML 47
14	6.36	NULL	1318	CC mitochondrion
15	6.34	NULL	12	BP hemidesmosome assembly
16	6.33	NULL	253	BP translation
17	6.32	NULL	48	BP regulation of cellular amino acid metabolic process
18	6.29	NULL	14	GSEA C2RUIZ_TNC_TARGETS_DN
19	6.27	NULL	74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-
20	5.99	NULL	519	Chr Chr 14
<i>Underexpressed</i>				
1	-10.54	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-9.5	NULL	1135	Chr Chr 19
3	-9.06	NULL	417	H.Tiss WIRTH_Immune system
4	-8.39	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
5	-8.34	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
6	-8.2	NULL	16	GSEA C2UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
7	-8.18	NULL	633	Chr Chr 9
8	-7.82	NULL	15	CC MHC class II protein complex
9	-7.63	NULL	9	GSEA C2UTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
10	-7.45	NULL	553	Cancer Lembcke_Colonc Inflammation
11	-7.4	NULL	16	GSEA C2BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
12	-7.26	NULL	15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
13	-6.93	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
14	-6.82	NULL	24	TF Tissue/AQUERIZAS_Trachea
15	-6.79	NULL	14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
16	-6.63	NULL	16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
17	-6.63	NULL	312	BP immune response
18	-6.48	NULL	327	Lymphoma SPANG_CD40 6hrs UP
19	-6.13	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
20	-6.13	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up

p-values



GW_283

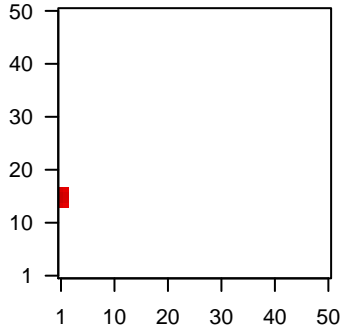
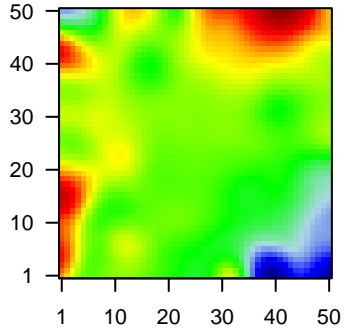
Local Summary

%DE = 0.8
 # metagenes = 8
 # genes = 113
 # genes in genesets = 113
 # genes with $fdr < 0.1 = 79$ (75 + / 4 -)
 # genes with $fdr < 0.05 = 55$ (52 + / 3 -)
 # genes with $fdr < 0.01 = 42$ (41 + / 1 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.32
 $\langle FC \rangle = 0.43$
 $\langle \text{shrinkage-t} \rangle = 15.15$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.52$

Profile

Spot



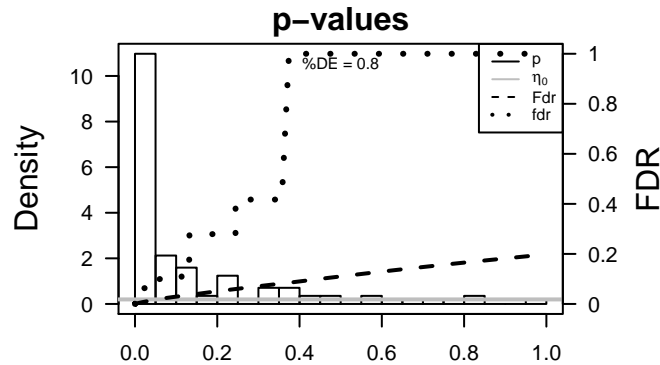
Local Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	8772	1.71	2e-16 2e-15	1 x 14 Fas (TNFRSF6)--associated via death domain [Source:HGNC
2	51373	1.97	2e-16 2e-15	1 x 16 28S ribosomal protein S17, mitochondrial; HCG1984214, isof
3	57761	1.31	3e-12 5e-09	1 x 17 tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]
4	93273	1.16	5e-10 5e-09	2 x 15 LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
5	283869	1.16	5e-10 5e-08	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
6	8345	1.09	5e-09 5e-08	1 x 15 histone cluster 1, H2bh [Source:HGNC Symbol;Acc:4755]
7	219927	1.09	5e-09 4e-07	1 x 15 mitochondrial ribosomal protein L21 [Source:HGNC Symbol;A
8	64979	1.03	4e-08 4e-07	1 x 16 mitochondrial ribosomal protein L36 [Source:HGNC Symbol;A
9	131076	1.02	4e-08 3e-06	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
10	991	0.96	3e-07 3e-06	1 x 16 cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
11	10963	0.94	4e-07 3e-06	1 x 16 stress-induced-phosphoprotein 1 [Source:HGNC Symbol;Ac
12	65003	0.93	6e-07 3e-06	2 x 17 mitochondrial ribosomal protein L11 [Source:HGNC Symbol;A
13	4715	0.93	6e-07 8e-06	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
14	3217	0.91	1e-06 8e-06	1 x 15 homeobox B7 [Source:HGNC Symbol;Acc:5118]
15	10248	0.9	1e-06 3e-05	1 x 16 processing of precursor 7, ribonuclease P/MPRP subunit (S. ce
16	10552	0.87	3e-06 3e-05	1 x 15 actin related protein 2/3 complex, subunit 1A, 41kDa [Source:
17	84948	0.86	5e-06 3e-05	1 x 16 tigger transposable element derived 5 [Source:HGNC Symbo
18	741	0.85	6e-06 2e-04	1 x 17 zinc finger, HIT-type containing 2 [Source:HGNC Symbol;Acc
19	26873	0.79	3e-05 2e-04	1 x 17 5-oxoprolinase (ATP-hydrolysing) [Source:HGNC Symbol;Ac
20	81037	0.78	3e-05 7e-04	1 x 14 CLPTM1-like [Source:HGNC Symbol;Acc:24308]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	17.17	NULL	1 / 3	GSEA C2WEBER_METHYLATED_LCP_IN_SPERM_DN
2	16.32	NULL	1 / 6	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_DN
3	14.59	NULL	2 / 8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
4	14.35	NULL	2 / 13	GSEA C2NADERI_BREAST_CANCER_PROGNOSIS_UP
5	12.82	NULL	1 / 9	GSEA C2BIOCARTA_RELA_PATHWAY
6	12.82	NULL	1 / 9	GSEA C2BIOCARTA_NFKB_PATHWAY
7	12.82	NULL	1 / 9	GSEA C2BIOCARTA_SODD_PATHWAY
8	12.82	NULL	1 / 9	GSEA C2REACTOME_DEATH_RECEPTOR_SIGNALLING
9	12.39	NULL	1 / 5	GSEA C2WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN
10	12.05	NULL	1 / 10	MF death receptor binding
11	12.05	NULL	1 / 10	BP positive regulation of macrophage differentiation
12	11.4	NULL	1 / 11	BP regulation of extrinsic apoptotic signaling pathway in absence of lig
13	11.4	NULL	1 / 11	GSEA C2HOFMANN_CELL_LYMPHOMA_DN
14	11.4	NULL	1 / 11	GSEA C2ST_TUMOR_NECROSIS_FACTOR_PATHWAY
15	10.84	NULL	1 / 12	GSEA C2BIOCARTA_FAS_PATHWAY
16	10.51	NULL	2 / 14	GSEA C2REACTOME_PI3K_AKT_SIGNALLING
17	10.36	NULL	2 / 11	BP positive regulation of ubiquitin-protein ligase activity
18	10.35	NULL	2 / 27	MF rRNA binding
19	10.34	NULL	1 / 13	BP lymph node development
20	10.34	NULL	1 / 13	GSEA C2BIOCARTA_TNFR1_PATHWAY
21	9.91	NULL	1 / 14	GSEA C2GENTILE_UV_RESPONSE_CLUSTER_D5
22	9.91	NULL	1 / 14	GSEA C2BIOCARTA_DEATH_PATHWAY
23	9.78	NULL	1 / 9	GSEA C2MARZEC_IL2_SIGNALLING_UP
24	9.73	NULL	2 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
25	9.73	NULL	2 / 16	GSEA C2REACTOME_TRKA_SIGNALLING_FROM_THE_PLASMA_MEMB
26	9.63	NULL	1 / 19	CC mitochondrial small ribosomal subunit
27	9.52	NULL	1 / 15	BP positive regulation of extrinsic apoptotic signaling pathway via deat
28	9.48	NULL	1 / 7	MMML C6SCIEJ_MMML_9
29	9.19	NULL	1 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
30	9.19	NULL	1 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
31	9.17	NULL	1 / 16	BP positive regulation of activated T cell proliferation
32	9.17	NULL	1 / 16	GSEA C2LAU_APOPTOSIS_CDKN2A_UP
33	9.17	NULL	1 / 16	GSEA C2BIOCARTA_CERAMIDE_PATHWAY
34	9.13	NULL	1 / 6	GSEA C2WAESCH_ANAPHASE_PROMOTING_COMPLEX
35	8.57	NULL	1 / 18	BP positive regulation of T cell mediated cytotoxicity
36	8.54	NULL	2 / 23	BP positive regulation of proteolysis
37	8.35	NULL	5 / 153	MF structural constituent of ribosome
38	8.33	NULL	3 / 34	BP positive regulation of protein binding
39	8.33	NULL	2 / 30	BP extrinsic apoptotic signaling pathway in absence of ligand
40	8.27	NULL	2 / 26	MF tumor necrosis factor receptor binding



GW_283

Local Summary

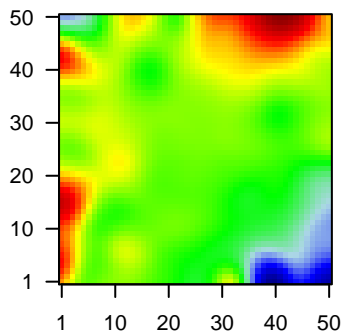
%DE = 0.69
 # metagenes = 40
 # genes = 549
 # genes in genesets = 538

genes with $fdr < 0.1 = 252$ (247 + / 5 -)
 # genes with $fdr < 0.05 = 199$ (198 + / 1 -)
 # genes with $fdr < 0.01 = 126$ (125 + / 1 -)

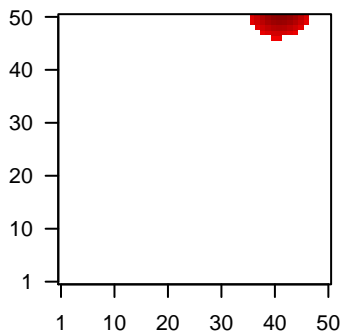
<r> metagenes = 0.91
 <r> genes = 0.32

<FC> = 0.37
 <shrinkage-t> = 12.83
 <p-value> = 0.01
 <fdr> = 0.62

Profile



Spot



Local Genelist

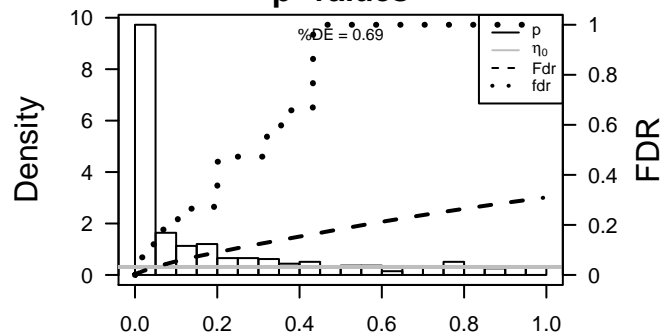
Rank	ID	log(FC)	fdr	p-value	Description
1	908	1.96	2e-16	8e-15	40 x 50 chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HGNC Symbol;Acc:11572]
2	643253	1.56	2e-16	8e-15	40 x 50
3	2631	1.79	2e-16	8e-15	39 x 50 glioblastoma amplified sequence [Source:HGNC Symbol;Acc:11572]
4	55915	1.8	2e-16	8e-15	38 x 50 LanC lantibiotic synthetase component C-like 2 (bacterial) [Source:HGNC Symbol;Acc:11572]
5	23480	1.83	2e-16	8e-15	39 x 50 Sec61 gamma subunit [Source:HGNC Symbol;Acc:18277]
6	51142	1.36	2e-15	3e-12	38 x 50 coiled-coil-helix-coiled-coil-helix domain containing 2 [Source:HGNC Symbol;Acc:11572]
7	113130	1.43	2e-14	1e-11	44 x 49 cell division cycle associated 5 [Source:HGNC Symbol;Acc:11572]
8	5723	1.39	1e-13	3e-10	37 x 50 phosphoserine phosphatase [Source:HGNC Symbol;Acc:957]
9	55789	1.31	2e-12	9e-10	44 x 50 DEP domain containing 1B [Source:HGNC Symbol;Acc:2490]
10	50810	1.28	7e-12	2e-08	46 x 50 Hepatoma-derived growth factor-related protein 3 [Source:HGNC Symbol;Acc:11572]
11	51504	1.2	1e-10	5e-08	38 x 50 tRNA methyltransferase 11-2 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:11572]
12	10884	1.17	4e-10	1e-07	40 x 50 mitochondrial ribosomal protein S30 [Source:HGNC Symbol;Acc:11572]
13	8500	1.14	1e-09	1e-06	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (P1) [Source:HGNC Symbol;Acc:11572]
14	6897	1.07	9e-09	1e-06	39 x 50 threonyl-tRNA synthetase [Source:HGNC Symbol;Acc:11572]
15	28998	1.05	2e-08	1e-06	39 x 50 mitochondrial ribosomal protein L13 [Source:HGNC Symbol;Acc:11572]
16	10797	1.04	3e-08	1e-06	43 x 50 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) [Source:HGNC Symbol;Acc:11572]
17	116832	1.02	4e-08	1e-06	46 x 50 ribosomal protein L39-like [Source:HGNC Symbol;Acc:17094]
18	4904	0.94	4e-08	1e-06	41 x 49 Y box binding protein 1 [Source:HGNC Symbol;Acc:8014]
19	55299	1.02	5e-08	7e-06	41 x 50 BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:11572]
20	1503	0.99	1e-07	7e-06	41 x 50 CTP synthase 1 [Source:HGNC Symbol;Acc:2519]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	27.38	NULL	79 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	27.38	NULL	79 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	19.51	NULL	12 / 14	MMML C2GSCIEJ_MMML_4
4	18.56	NULL	14 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
5	17.16	NULL	87 / 370	BP mitotic cell cycle
6	16.89	NULL	13 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
7	15.16	NULL	21 / 56	CC chromosome, centromeric region
8	14.45	NULL	10 / 13	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_UP
9	13.69	NULL	9 / 16	Cancer WOLFER_overlap genes
10	13.62	NULL	7 / 15	Cancer GENTLES_modul6
11	13.28	NULL	12 / 18	BP spindle organization
12	12.96	NULL	89 / 530	Cancer Lembcke_Normal vs Adenoma
13	12.41	NULL	8 / 11	BP mitotic metaphase plate congression
14	12.11	NULL	20 / 57	Glio developing astrocytes
15	11.8	NULL	5 / 10	CC zona pellucida receptor complex
16	11.55	NULL	47 / 232	BP mitosis
17	11.32	NULL	9 / 23	CC mitochondrial ribosome
18	11.11	NULL	7 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
19	10.94	NULL	7 / 16	GSEA C2BENPORATH_PROLIFERATION
20	10.89	NULL	6 / 15	GSEA C2REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED
21	10.55	NULL	69 / 572	Disease GUDJ_psooriasis_up
22	10.38	NULL	10 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
23	10.13	NULL	9 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
24	10.1	NULL	10 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
25	10.02	NULL	16 / 74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-
26	9.97	NULL	106 / 949	CC nucleoplasm
27	9.85	NULL	13 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
28	9.82	NULL	9 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
29	9.72	NULL	8 / 22	BP CENP-A containing nucleosome assembly at centromere
30	9.59	NULL	29 / 148	BP G1/S transition of mitotic cell cycle
31	9.35	NULL	19 / 86	CC condensed chromosome kinetochore
32	9.21	NULL	7 / 15	GSEA C2CHANG_CYCLING_GENES
33	9.19	NULL	14 / 35	BP mitotic nuclear envelope disassembly
34	9.12	NULL	8 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
35	8.82	NULL	9 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
36	8.75	NULL	7 / 16	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
37	8.65	NULL	7 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
38	8.42	NULL	5 / 9	GSEA C2BIOCARTA_RANMS_PATHWAY
39	8.31	NULL	10 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
40	8.29	NULL	5 / 15	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS

p-values



GW_283

Local Summary

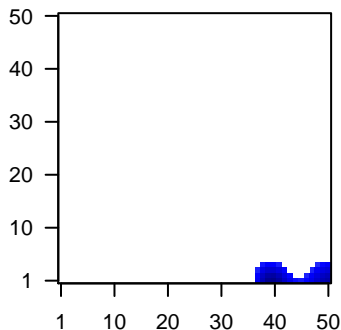
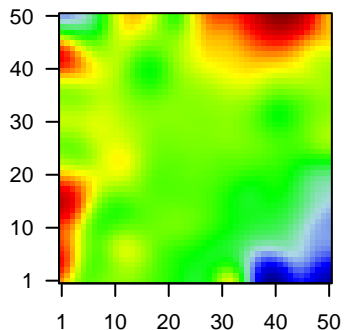
%DE = 0.93
 # metagenes = 43
 # genes = 645
 # genes in genesets = 614
 # genes with $fdr < 0.1$ = 531 (8 + / 523 -)
 # genes with $fdr < 0.05$ = 495 (7 + / 488 -)
 # genes with $fdr < 0.01$ = 339 (5 + / 334 -)

<r> metagenes = 0.82
 <r> genes = 0.36

<FC> = -0.5
 <shrinkage-t> = -17.48
 <p-value> = 0
 <fdr> = 0.45

Profile

Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	641737	-1.52	2e-16	4e-15	40 x 1
2	400818	-1.84	2e-16	4e-15	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
3	10628	-1.51	2e-16	4e-15	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
4	100132406	-1.52	4e-16	3e-13	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
5	3128	-1.45	8e-15	3e-13	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
6	3689	-1.44	1e-14	9e-13	50 x 1 integrin, beta 2 (complement component 3 receptor 3 and 4 s
7	3108	-1.4	6e-14	9e-13	50 x 1 major histocompatibility complex, class II, DM alpha [Source:l
8	25862	-1.4	6e-14	9e-13	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
9	894	-1.4	7e-14	1e-11	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
10	8837	-1.36	3e-13	3e-11	44 x 1 CASP8 and FADD-like apoptosis regulator [Source:HGNC S
11	3109	-1.33	1e-12	1e-10	50 x 1 major histocompatibility complex, class II, DM beta [Source:H
12	126205	-1.3	3e-12	1e-10	40 x 1 NLR family, pyrin domain containing 8 [Source:HGNC Symbo
13	3122	-1.2	6e-12	5e-10	50 x 1 major histocompatibility complex, class II, DR alpha [Source:l
14	972	-1.26	2e-11	1e-09	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
15	136051	-1.23	5e-11	1e-09	40 x 1 zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
16	57835	-1.22	7e-11	1e-09	40 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7I
17	250	-1.21	1e-10	3e-09	40 x 1 alkaline phosphatase, placental [Source:HGNC Symbol;Acc:4
18	255031	-1.18	2e-10	3e-09	40 x 1 long intergenic non-protein coding RNA 957 [Source:HGNC :
19	10365	-1.18	3e-10	3e-09	50 x 3 Kruppel-like factor 2 [Source:HGNC Symbol;Acc:6347]
20	3586	-1.09	3e-10	3e-09	40 x 1 interleukin 10 [Source:HGNC Symbol;Acc:5962]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-22.74	NULL	14 / 15	CC MHC class II protein complex
2	-18.34	NULL	98 / 417	H.Tiss WIRTH_Immune system
3	-15.79	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
4	-15.11	NULL	63 / 312	BP immune response
5	-14.65	NULL	103 / 553	Cancer Lembecke_Colonic Inflammation
6	-13.48	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
7	-13.42	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
8	-13.06	NULL	22 / 60	BP T cell costimulation
9	-12.51	NULL	17 / 47	BP antigen processing and presentation
10	-12.05	NULL	3 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
11	-11.92	NULL	47 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
12	-11.92	NULL	47 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
13	-11.92	NULL	47 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
14	-11.92	NULL	47 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
15	-11.86	NULL	8 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
16	-11.62	NULL	6 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
17	-11.27	NULL	5 / 12	BP immunoglobulin mediated immune response
18	-10.87	NULL	20 / 74	BP regulation of immune response
19	-10.79	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
20	-10.57	NULL	6 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
21	-10.4	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
22	-10.39	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
23	-10.38	NULL	3 / 8	GSEA C2INDSTEDT_DENDRITIC_CELL_MATURATION_D
24	-10.24	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
25	-9.84	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
26	-9.7	NULL	1 / 2	GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IIGA_PRODUC
27	-9.7	NULL	1 / 2	GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE
28	-9.7	NULL	1 / 2	GSEA C2KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
29	-9.67	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
30	-9.59	NULL	10 / 28	CC transport vesicle membrane
31	-9.47	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
32	-9.44	NULL	5 / 13	MMML C6SCIEJ_MMML 6
33	-9.4	NULL	1 / 2	miRNA target-193a
34	-9.13	NULL	3 / 10	GSEA C2HOSHIDA_LIVER_CANCER_SUBCLASS_S1
35	-9.11	NULL	38 / 316	Cancer SPANG_BCL6-index2
36	-9.08	NULL	10 / 35	CC trans-Golgi network membrane
37	-9.03	NULL	2 / 8	GSEA C2KEGG_CELL_ADHESION_MOLECULES_CAMS
38	-8.84	NULL	16 / 87	BP antigen processing and presentation of exogenous peptide antigen
39	-8.82	NULL	3 / 3	MMML C6SCIEJ_MMML 7
40	-8.82	NULL	4 / 10	BP negative thymic T cell selection

p-values

