

GW_056

Global Summary

%DE = 0.13
 # genes with fdr < 0.2 = 1343 (769 + / 574 -)
 # genes with fdr < 0.1 = 1103 (662 + / 441 -)
 # genes with fdr < 0.05 = 906 (568 + / 338 -)
 # genes with fdr < 0.01 = 570 (392 + / 178 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.14
 <fdr> = 0.87

Global Genelist

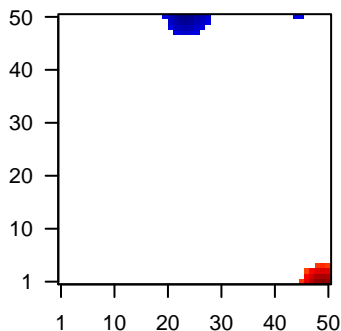
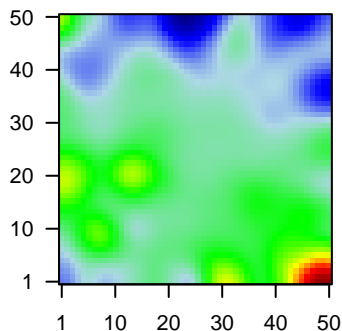
Rank	ID	log(FC)	fdr	Description
		p-value	Metagene	
1	92591	1.87	2e-16 6e-14	48 x 2 ankryn repeat and SOCS box containing 16 [Source:HGNC S
2	387695	1.5	2e-16 6e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
3	57172	2.83	2e-16 6e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
4	6363	1.86	2e-16 6e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
5	6366	1.5	2e-16 6e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
6	6355	1.47	2e-16 6e-14	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:
7	939	1.46	2e-16 6e-14	49 x 1 CD27 molecule [Source:HGNC Symbol;Acc:11922]
8	1675	1.38	2e-16 6e-14	50 x 9 complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
9	1277	-1.49	2e-16 6e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
10	51755	2.35	2e-16 6e-14	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	49860	1.46	2e-16 6e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
12	9547	2.1	2e-16 6e-14	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
13	84259	1.96	2e-16 6e-14	5 x 42 DCN1, defective in cullin neddylation 1, domain containing 5 [
14	1673	1.35	2e-16 6e-14	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
15	1958	-1.69	2e-16 6e-14	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
16	2167	1.35	2e-16 6e-14	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
17	54855	2.38	2e-16 6e-14	49 x 1 family with sequence similarity 46, member C [Source:HGNC
18	51303	1.69	2e-16 6e-14	49 x 3 FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
19	2353	-1.59	2e-16 6e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:f
20	3002	1.41	2e-16 6e-14	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associati

Global Geneset Analysis

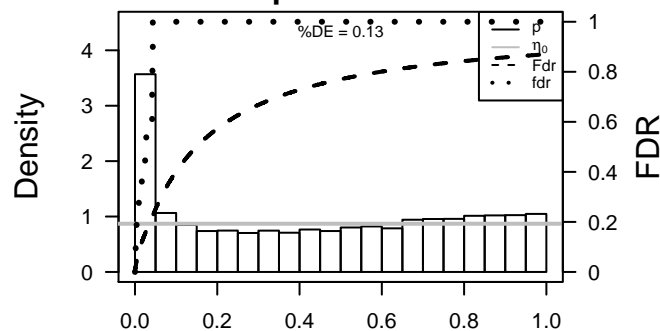
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.65	NULL	4	MMML C69CIEJ_MMML_23
2	10.75	NULL	553	Cancer Lembecke_Colonic Inflammation
3	10.15	NULL	417	H.Tiss WIRTH_Immune system
4	10	NULL	957	Chr Chr 11
5	9.55	NULL	1135	Chr Chr 19
6	9.05	NULL	16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
7	8.89	NULL	312	BP immune response
8	8.58	NULL	21	CC cornified envelope
9	8.51	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	8.09	NULL	42	BP keratinization
11	8.09	NULL	135	H.Tiss WIRTH_Mucosa
12	8.02	NULL	10	CC hemoglobin complex
13	7.77	NULL	51	BP type I interferon signaling pathway
14	7.65	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
15	7.37	NULL	74	BP regulation of immune response
16	7.26	NULL	11	MF oxygen transporter activity
17	7.11	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
18	6.68	NULL	11	GSEA C2BIOCARTA_AHSP_PATHWAY
19	6.5	NULL	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSI_DN
20	6.4	NULL	5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
<i>Underexpressed</i>				
1	-10.07	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-9.43	NULL	436	miRNA target-starB346n
3	-9.36	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
4	-9.15	NULL	262	miRNA target-starB346l
5	-8.47	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
6	-8.47	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
7	-8	NULL	24	TF Tissue/AQUERIZAS_Trachea
8	-7.94	NULL	370	BP mitotic cell cycle
9	-7.32	NULL	315	miRNA target-starB346e
10	-7.31	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
11	-7.23	NULL	313	miRNA target-starB346f
12	-7.21	NULL	217	miRNA target-starB346m
13	-7.02	NULL	421	miRNA target-starB346g
14	-7.01	NULL	470	miRNA 3UTR/CAC-17-5P--20A--106A--106B--20B--519D
15	-6.99	NULL	335	miRNA target-starB346a-5p
16	-6.96	NULL	321	miRNA target-starB346a-5p
17	-6.78	NULL	310	miRNA target-starB346e
18	-6.77	NULL	324	miRNA target-starB346a
19	-6.73	NULL	12	miRNA target-starB346c
20	-6.72	NULL	368	miRNA target-starB346a

Profile

Regulated Spots



p-values



GW_056

Local Summary

%DE = 0.88
 # metagenes = 19
 # genes = 296
 # genes in genesets = 293

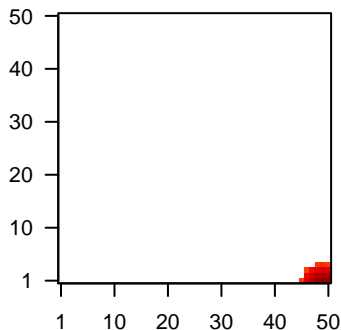
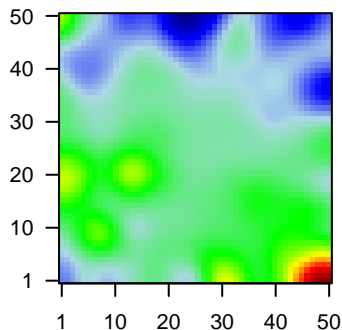
genes with $fdr < 0.1$ = 231 (219 + / 12 -)
 # genes with $fdr < 0.05$ = 207 (197 + / 10 -)
 # genes with $fdr < 0.01$ = 175 (168 + / 7 -)

<r> metagenes = 0.99
 <r> genes = 0.57

<FC> = 0.56
 <shrinkage-t> = 19.48
 <p-value> = 0
 <fdr> = 0.32

Profile

Spot



Local Genelist

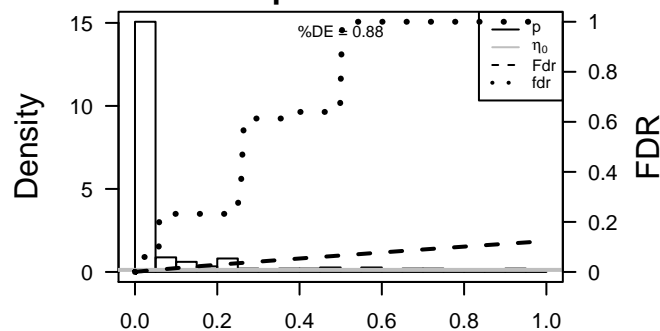
Rank	ID	log(FC)	fdr	p-value	Description
1	92591	1.87	2e-16	5e-16	ankyrin repeat and SOCS box containing 16 [Source:HGNC S
2	57172	2.83	2e-16	5e-16	calcium/calmodulin-dependent protein kinase IG [Source:HG
3	6363	1.86	2e-16	5e-16	chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
4	6366	1.5	2e-16	5e-16	chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
5	939	1.46	2e-16	5e-16	CD27 molecule [Source:HGNC Symbol;Acc:11922]
6	51755	2.35	2e-16	5e-16	cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242
7	54855	2.38	2e-16	5e-16	family with sequence similarity 46, member C [Source:HGNC
8	51303	1.69	2e-16	5e-16	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Acc
9	3002	1.41	2e-16	5e-16	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
10	3128	1.6	2e-16	5e-16	major histocompatibility complex, class II, DR beta 6 (pseudo
11	3512	1.41	2e-16	5e-16	immunoglobulin J polypeptide, linker protein for immunoglobu
12	91353	1.79	2e-16	5e-16	
13	126306	2.07	2e-16	5e-16	junctional sarcoplasmic reticulum protein 1 [Source:HGNC S
14	51237	1.96	2e-16	5e-16	marginal zone B and B1 cell-specific protein [Source:HGNC :
15	11040	2.12	2e-16	5e-16	pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
16	170679	1.8	2e-16	5e-16	psoriasis susceptibility 1 candidate 1 [Source:HGNC Symbol;
17	5730	1.37	2e-16	5e-16	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
18	6748	1.65	2e-16	5e-16	signal sequence receptor, delta [Source:HGNC Symbol;Acc:1
19	3385	1.33	4e-16	3e-13	intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc
20	608	1.26	2e-14	3e-13	tumor necrosis factor receptor superfamily, member 17 [Sour

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	27.16	NULL	97 / 417	H.Tiss WIRTH_Immune system
2	22	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
3	21.48	NULL	99 / 553	Cancer Lembecke_Colonic Inflammation
4	19.6	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	16.27	NULL	13 / 15	CC MHC class II protein complex
6	16.04	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
7	16	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
8	15.55	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
9	15.32	NULL	56 / 312	BP immune response
10	15.3	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
11	14.92	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
12	14.54	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
13	14.31	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
14	14.08	NULL	19 / 60	BP T cell costimulation
15	13.69	NULL	2 / 7	GSEA C2IZUKA_LIVER_CANCER_PROGRESSION_G2_G3_DN
16	13.43	NULL	7 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
17	13.18	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDDP_SIGNATURE
18	13.12	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
19	13.04	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
20	12.98	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
21	12.91	NULL	5 / 12	BP dendritic cell chemotaxis
22	12.88	NULL	5 / 13	GSEA C2HAHTOLA_CTL_PATHOGENESIS
23	12.81	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
24	12.81	NULL	7 / 16	LymphomaWRIGHT_ABC UP
25	12.79	NULL	18 / 74	BP regulation of immune response
26	12.73	NULL	1 / 2	GSEA C2GUTIERREZ_MULTIPLE_MYELOMA_UP
27	12.56	NULL	5 / 12	BP immunoglobulin mediated immune response
28	12.26	NULL	45 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
29	12.26	NULL	45 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
30	12.26	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
31	12.26	NULL	45 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
32	11.9	NULL	5 / 11	BP positive regulation of B cell differentiation
33	11.3	NULL	2 / 10	BP positive regulation of chemotaxis
34	11.05	NULL	27 / 204	BP cell surface receptor signaling pathway
35	11.04	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
36	10.94	NULL	4 / 13	BP lymph node development
37	10.81	NULL	4 / 22	BP positive regulation of phosphatidylinositol 3-kinase activity
38	10.78	NULL	4 / 8	LymphomaMASCQUE_ABC UP
39	10.75	NULL	5 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
40	10.56	NULL	3 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D

p-values



GW_056

Local Summary

%DE = 0.89
 # metagenes = 29
 # genes = 368
 # genes in genesets = 363

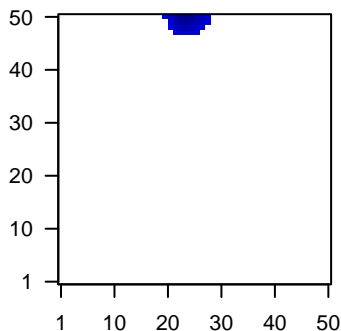
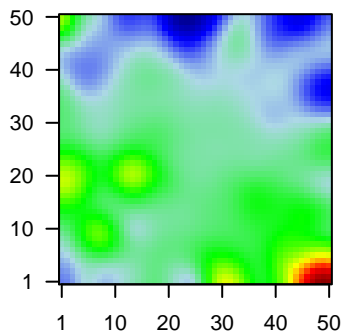
genes with $fdr < 0.1$ = 286 (9 + / 277 -)
 # genes with $fdr < 0.05$ = 241 (7 + / 234 -)
 # genes with $fdr < 0.01$ = 130 (6 + / 124 -)

$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.26

$\langle FC \rangle = -0.35$
 $\langle \text{shrinkage-t} \rangle = -12.27$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.57$

Profile

Spot



Local Genelist

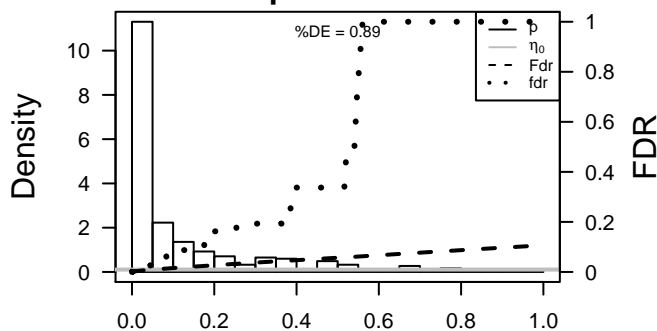
Rank	ID	log(FC)	fdr	p-value	Description
1	1958	-1.69	2e-16	2e-15	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
2	2353	-1.59	2e-16	2e-15	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3238]
3	114908	1.36	2e-16	2e-15	26 x 50 transmembrane protein 123 [Source:HGNC Symbol;Acc:3013]
4	10413	1.57	2e-16	2e-15	26 x 50 Yes-associated protein 1 [Source:HGNC Symbol;Acc:16262]
5	2354	-1.26	1e-14	5e-11	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:3238]
6	8553	-1.07	1e-12	3e-10	22 x 50 basic helix-loop-helix family, member e40 [Source:HGNC Symbol;Acc:3238]
7	1843	-1.03	8e-12	2e-09	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3013]
8	23645	-1.08	5e-11	4e-09	22 x 50 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:3238]
9	3725	-1.05	1e-10	2e-08	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
10	678	-1.01	6e-10	4e-08	23 x 50 ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:12862]
11	7538	-0.98	2e-09	3e-07	22 x 50 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
12	10787	-0.94	1e-08	1e-06	25 x 50 NCK-associated protein 1 [Source:HGNC Symbol;Acc:7666]
13	8349	-0.89	5e-08	1e-06	21 x 50 histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760]
14	51030	-0.89	6e-08	2e-06	26 x 50 trans-golgi network vesicle protein 23 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:51030]
15	5782	-0.87	1e-07	2e-06	25 x 50 protein tyrosine phosphatase, non-receptor type 12 [Source:HGNC Symbol;Acc:5782]
16	3716	-0.86	2e-07	2e-06	25 x 49 Janus kinase 1 [Source:HGNC Symbol;Acc:6190]
17	57162	-0.86	2e-07	9e-06	23 x 50 pellino E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:57162]
18	467	-0.83	4e-07	9e-06	22 x 50 activating transcription factor 3 [Source:HGNC Symbol;Acc:7147]
19	11260	-0.81	7e-07	9e-06	25 x 50 exportin, tRNA [Source:HGNC Symbol;Acc:12826]
20	665	-0.81	9e-07	5e-05	24 x 50 BCL2/adenovirus E1B 19kDa interacting protein 3-like [Source:HGNC Symbol;Acc:665]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-32.34	NULL	6 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	-25.59	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
3	-22.95	NULL	7 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
4	-22.19	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
5	-21.05	NULL	6 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
6	-20.29	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
7	-18.59	NULL	4 / 14	BP response to light stimulus
8	-17.96	NULL	4 / 14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
9	-17.7	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
10	-17.26	NULL	7 / 16	GSEA C2AMIT_DELAYED_EARLY_GENES
11	-15.64	NULL	4 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
12	-15.37	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
13	-14.87	NULL	2 / 8	GSEA C2EMELYANOV_GR_TARGETS_DN
14	-14.79	NULL	5 / 16	GSEA C2UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
15	-14.45	NULL	2 / 5	miRNA target-101
16	-14.38	NULL	6 / 16	TF Tissue/AQUERIZAS_Pancreas
17	-14.28	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
18	-14.15	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
19	-13.84	NULL	3 / 15	BP response to corticosterone
20	-13.45	NULL	5 / 30	BP cellular response to hormone stimulus
21	-13.43	NULL	4 / 8	MMML C2SCIEJ_MMML_50
22	-13.39	NULL	1 / 4	GSEA C2GARASHI_ATF4_TARGETS_UP
23	-13.35	NULL	3 / 12	GSEA C2BIOCARTA_ARENERF2_PATHWAY
24	-13.34	NULL	2 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_API_FAMILY_OF_TRANSCRIPTION_FACTORS
25	-13.27	NULL	5 / 39	BP response to cAMP
26	-13.04	NULL	4 / 19	MF R-SMAD binding
27	-13.04	NULL	3 / 12	GSEA C2BIOCARTA_DREAM_PATHWAY
28	-12.88	NULL	3 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
29	-12.56	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
30	-12.38	NULL	2 / 12	TF Tissue/AQUERIZAS_Kidney
31	-12.3	NULL	4 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_DN
32	-12.26	NULL	4 / 30	BP cellular response to calcium ion
33	-12.13	NULL	5 / 39	TF Tissue/AQUERIZAS_Thyroid
34	-12.1	NULL	1 / 5	GSEA C2TURJANSKI_MAPK11_TARGETS
35	-12.09	NULL	2 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_DN
36	-11.71	NULL	3 / 15	GSEA C2NGA_TP53_TARGETS
37	-11.52	NULL	2 / 13	BP SMAD protein signal transduction
38	-11.42	NULL	4 / 15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
39	-11.39	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
40	-11.38	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY

p-values



GW_056

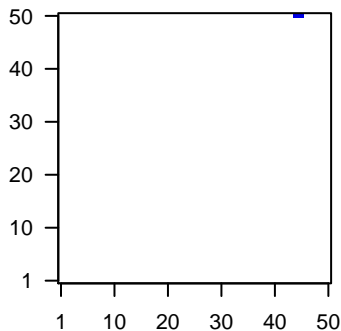
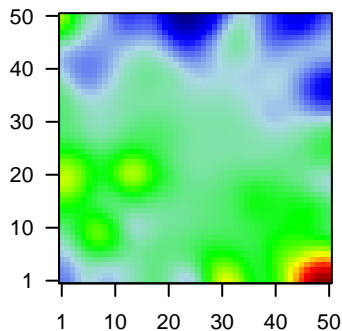
Local Summary

%DE = 0.83
 # metagenes = 2
 # genes = 43
 # genes in genesets = 43
 # genes with $fdr < 0.1 = 33$ (1 + / 32 -)
 # genes with $fdr < 0.05 = 33$ (1 + / 32 -)
 # genes with $fdr < 0.01 = 16$ (0 + / 16 -)

<r> metagenes = 1
 <r> genes = 0.56
 <FC> = -0.35
 <shrinkage-t> = -12.38
 <p-value> = 0.01
 <fdr> = 0.57

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	51659	-0.88	7e-08	2e-04	44 x 50 GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
2	29028	-0.7	2e-05	3e-04	44 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Sym
3	9833	-0.65	7e-05	3e-04	44 x 50 maternal embryonic leucine zipper kinase [Source:HGNC Syr
4	63979	-0.64	1e-04	6e-04	45 x 50 fidgetin-like 1 [Source:HGNC Symbol;Acc:13286]
5	10733	-0.61	2e-04	6e-04	44 x 50 polo-like kinase 4 [Source:HGNC Symbol;Acc:11397]
6	890	-0.59	3e-04	6e-04	44 x 50 cyclin A2 [Source:HGNC Symbol;Acc:1578]
7	23350	-0.59	4e-04	1e-03	45 x 50 U2 snRNP-associated SURP domain containing [Source:HG
8	55635	-0.56	7e-04	1e-03	44 x 50 DEP domain containing 1 [Source:HGNC Symbol;Acc:22949]
9	10728	-0.55	8e-04	1e-03	45 x 50 prostaglandin E synthase 3 (cytosolic) [Source:HGNC Symbc
10	983	-0.55	9e-04	7e-03	44 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:1722]
11	29980	-0.51	2e-03	7e-03	44 x 50 downstream neighbor of SON [Source:HGNC Symbol;Acc:29
12	22974	-0.48	3e-03	7e-03	44 x 50 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:1:
13	6790	-0.47	4e-03	7e-03	44 x 50 aurora kinase A [Source:HGNC Symbol;Acc:11393]
14	4085	-0.46	5e-03	1e-02	44 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC S
15	9493	-0.45	7e-03	1e-02	44 x 50 kinesin family member 23 [Source:HGNC Symbol;Acc:6392]
16	7272	-0.43	8e-03	1e-02	44 x 50 TTK protein kinase [Source:HGNC Symbol;Acc:12401]
17	8833	-0.43	9e-03	3e-02	45 x 50 guanine monophosphate synthase [Source:HGNC Symbol;Acc
18	144455	-0.4	1e-02	3e-02	45 x 50 E2F transcription factor 7 [Source:HGNC Symbol;Acc:23820]
19	83461	-0.38	2e-02	3e-02	44 x 50 cell division cycle associated 3 [Source:HGNC Symbol;Acc:1:
20	10635	-0.38	2e-02	5e-02	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169:

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-40.14	NULL	6 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
2	-39.98	NULL	26 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
3	-39.98	NULL	26 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
4	-34.18	NULL	5 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
5	-27.08	NULL	5 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
6	-25.98	NULL	4 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
7	-24.67	NULL	10 / 57	Glio developing astrocytes
8	-24.18	NULL	4 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
9	-22.05	NULL	5 / 18	BP spindle organization
10	-21.44	NULL	4 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
11	-21.37	NULL	4 / 15	GSEA C2Y_AGING_MIDDLE_DN
12	-20.12	NULL	3 / 14	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP
13	-19.96	NULL	4 / 14	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
14	-19.06	NULL	3 / 15	GSEA C2OLSSON_E2F3_TARGETS_DN
15	-17.45	NULL	2 / 9	GSEA C2BIOCARTA_RANMS_PATHWAY
16	-17.4	NULL	3 / 14	MMML C2SCIEJ_MMML_4
17	-17.29	NULL	2 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN
18	-16.5	NULL	23 / 530	Cancer Lembecke_Normal vs Adenoma
19	-16.39	NULL	2 / 11	BP trophoblast giant cell differentiation
20	-16.01	NULL	2 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
21	-15.95	NULL	4 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
22	-15.7	NULL	2 / 9	GSEA C2CHUANG_OXIDATIVE_STRESS_RESPONSE_DN
23	-15.6	NULL	2 / 12	BP regulation of double-strand break repair via homologous recombina
24	-15.34	NULL	2 / 15	GSEA C2REACTOME_CYCLIN_A1_ASSOCIATED_EVENTS_DURING_G2
25	-15.11	NULL	2 / 16	Cancer WOLFER_overlap genes
26	-14.91	NULL	2 / 15	GSEA C2DODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
27	-14.68	NULL	3 / 15	GSEA C2CHANG_CYCLING_GENES
28	-14.57	NULL	21 / 572	Disease GUDJ_poriasis up
29	-14.4	NULL	2 / 9	GSEA C2SEMBA_FHIT_TARGETS_DN
30	-13.98	NULL	4 / 26	BP cellular response to ionizing radiation
31	-13.93	NULL	4 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
32	-13.8	NULL	4 / 30	BP mitotic spindle assembly checkpoint
33	-13.61	NULL	2 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
34	-13.25	NULL	3 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
35	-12.97	NULL	1 / 7	GSEA C2FIRESTEIN_CTNNB1_PATHWAY_AND_PROLIFERATION
36	-12.95	NULL	1 / 13	GSEA C2NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON
37	-12.74	NULL	1 / 6	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_DN
38	-12.69	NULL	8 / 56	CC chromosome, centromeric region
39	-12.67	NULL	16 / 370	BP mitotic cell cycle
40	-12.62	NULL	3 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN

