

GW_119

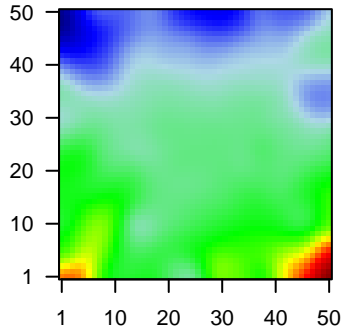
Global Summary

%DE = 0.13
 # genes with fdr < 0.2 = 1613 (979 + / 634 -)
 # genes with fdr < 0.1 = 1157 (730 + / 427 -)
 # genes with fdr < 0.05 = 933 (605 + / 328 -)
 # genes with fdr < 0.01 = 685 (468 + / 217 -)

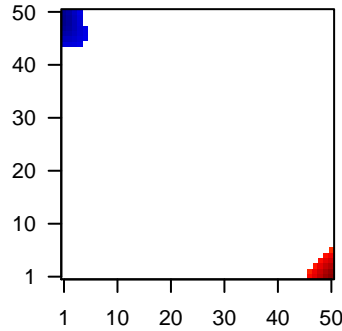
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.87

Profile



Regulated Spots



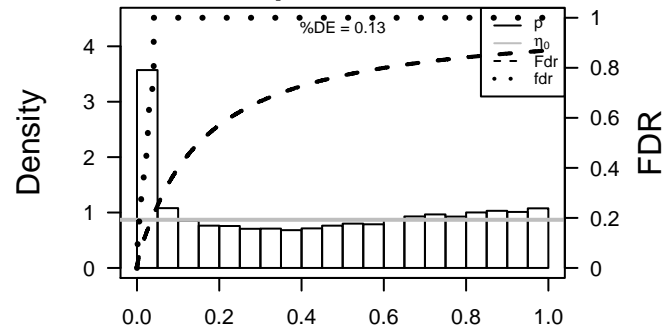
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	72	1.56	2e-16 4e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	124	1.81	2e-16 4e-14	50 x 11 alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	1.46	2e-16 4e-14	50 x 12 alcohol dehydrogenase 1C (class I), gamma polypeptide [Soc
4	57016	-2.27	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
5	441282	-1.47	2e-16 4e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
6	220	2.03	2e-16 4e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
7	242	-1.37	2e-16 4e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrn
8	55107	1.67	2e-16 4e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
9	366	1.74	2e-16 4e-14	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
10	445328	-2.23	2e-16 4e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
11	387695	-1.5	2e-16 4e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Syml
12	339512	1.53	2e-16 4e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Syml
13	92291	2.2	2e-16 4e-14	50 x 11 calpain 13 [Source:HGNC Symbol;Acc:16663]
14	6358	1.43	2e-16 4e-14	50 x 7 chemokine (C-C motif) ligand 14 [Source:HGNC Symbol;Acc
15	6363	2.48	2e-16 4e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
16	6366	1.48	2e-16 4e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
17	414062	1.88	2e-16 4e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbc
18	595	1.3	2e-16 4e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
19	1236	1.61	2e-16 4e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
20	930	1.67	2e-16 4e-14	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.74	NULL	553	Cancer Lembecke_Colonin Inflammation
2	16.52	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
3	16.52	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
4	16.52	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
5	16.52	NULL	265	Glio wilscher_GBM_Verhaak-PNmt_expression_B_down
6	13.56	NULL	312	BP immune response
7	13.05	NULL	190	CC extracellular matrix
8	12.94	NULL	683	CC extracellular space
9	12.93	NULL	43	MF chemokine activity
10	12.11	NULL	269	BP inflammatory response
11	11.87	NULL	250	Lymphoid_TENZ_Stromal signature 1
12	11.38	NULL	417	H.Tiss WIRTH_Immune system
13	11.31	NULL	1182	CC extracellular region
14	10.81	NULL	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
15	10.35	NULL	111	BP chemotaxis
16	9.46	NULL	717	Chr Chr 16
17	9.26	NULL	7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
18	9.13	NULL	2659	CC plasma membrane
19	9.13	NULL	242	BP extracellular matrix organization
20	9.09	NULL	4	MMML C6CIEJ_MMML 23
<i>Underexpressed</i>				
1	-13.83	NULL	135	H.Tiss WIRTH_Mucosa
2	-7.91	NULL	21	CC desmosome
3	-7.59	NULL	633	Chr Chr 9
4	-7.57	NULL	21	CC cornified envelope
5	-7.26	NULL	232	Chr Chr 18
6	-6.91	NULL	10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
7	-6.38	NULL	53	BP keratinocyte differentiation
8	-5.68	NULL	42	BP keratinization
9	-5.61	NULL	16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
10	-5.57	NULL	192	miRNA target-miR-394
11	-5.44	NULL	1318	CC mitochondrion
12	-5.37	NULL	262	miRNA target-miR-391
13	-5.01	NULL	303	miRNA target-miR-392b
14	-4.91	NULL	603	miRNA target-miR-392a
15	-4.9	NULL	217	miRNA target-miR-392m
16	-4.9	NULL	370	BP mitotic cell cycle
17	-4.89	NULL	300	miRNA target-miR-391
18	-4.88	NULL	311	miRNA target-miR-392c
19	-4.83	NULL	16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_C
20	-4.81	NULL	436	miRNA target-miR-392n

p-values



GW_119

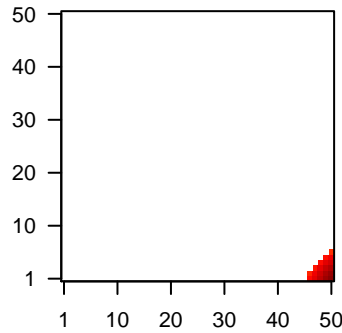
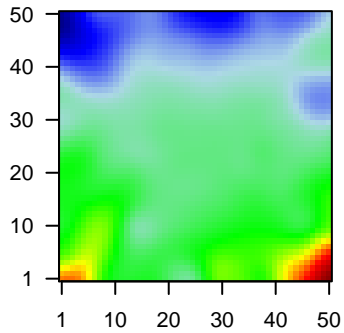
Local Summary

%DE = 0.85
 # metagenes = 20
 # genes = 323
 # genes in genesets = 321
 # genes with $fdr < 0.1 = 230$ (220 + / 10 -)
 # genes with $fdr < 0.05 = 230$ (220 + / 10 -)
 # genes with $fdr < 0.01 = 197$ (192 + / 5 -)

<r> metagenes = 0.97
 <r> genes = 0.53
 <FC> = 0.58
 <shrinkage-t> = 20.19
 <p-value> = 0
 <fdr> = 0.32

Profile

Spot



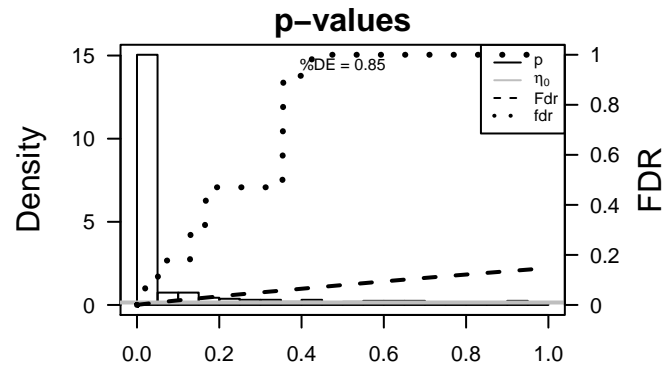
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	6363	2.48	2e-16	7e-16	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:10342]
2	6366	1.48	2e-16	7e-16	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc:10343]
3	1236	1.61	2e-16	7e-16	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:10344]
4	930	1.67	2e-16	7e-16	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
5	1593	1.39	2e-16	7e-16	50 x 3 cytochrome P450, family 27, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:10345]
6	2532	2.29	2e-16	7e-16	50 x 5 Duffy blood group, atypical chemokine receptor [Source:HGNC Symbol;Acc:10346]
7	2219	1.74	2e-16	7e-16	50 x 5 ficolin (collagen/fibrinogen domain containing) 1 [Source:HGNC Symbol;Acc:10347]
8	3128	1.38	2e-16	7e-16	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene) [Source:HGNC Symbol;Acc:10348]
9	3385	1.4	2e-16	7e-16	50 x 1 intercellular adhesion molecule 3 [Source:HGNC Symbol;Acc:10349]
10	4050	1.67	2e-16	7e-16	50 x 1 lymphotoxin beta (TNF superfamily, member 3) [Source:HGNC Symbol;Acc:10350]
11	256236	1.49	2e-16	7e-16	50 x 1 napsin B aspartic peptidase, pseudogene [Source:HGNC Symbol;Acc:256236]
12	11040	1.36	2e-16	7e-16	49 x 1 pim-2 oncogene [Source:HGNC Symbol;Acc:8987]
13	5341	1.78	2e-16	7e-16	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
14	5730	2.57	2e-16	7e-16	50 x 1 prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:10351]
15	10537	2.26	2e-16	7e-16	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	7450	1.5	2e-16	7e-16	50 x 6 von Willebrand factor [Source:HGNC Symbol;Acc:12726]
17	3936	1.35	4e-16	2e-14	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:10352]
18	54855	1.33	9e-16	2e-14	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:54855]
19	606724	1.33	1e-15	5e-14	50 x 1
20	7454	1.31	3e-15	5e-14	50 x 1 Wiskott-Aldrich syndrome [Source:HGNC Symbol;Acc:12731]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.8	NULL	92 / 417	H.Tiss WIRTH_Immune system
2	24.83	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSI
3	22.73	NULL	103 / 553	Cancer Lembecke_Colonc Inflammation
4	18.84	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
5	17.81	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
6	16.76	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
7	16.52	NULL	46 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
8	16.52	NULL	46 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
9	16.52	NULL	46 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
10	16.52	NULL	46 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	15.46	NULL	5 / 12	BP dendritic cell chemotaxis
12	15.28	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
13	14.86	NULL	4 / 14	BP ruffle organization
14	14.83	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
15	14.61	NULL	2 / 4	MMML C2SCIEJ_MMML 2
16	13.74	NULL	55 / 312	BP immune response
17	13.44	NULL	19 / 74	BP regulation of immune response
18	12.95	NULL	5 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
19	12.61	NULL	3 / 14	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_DN
20	12.48	NULL	4 / 13	BP positive regulation of endocytosis
21	12.43	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
22	12.42	NULL	4 / 22	BP positive regulation of phosphatidylinositol 3-kinase activity
23	12.4	NULL	2 / 10	BP positive regulation of chemotaxis
24	12.21	NULL	3 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
25	11.9	NULL	28 / 162	CC external side of plasma membrane
26	11.78	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
27	11.72	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
28	11.47	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
29	11.37	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
30	11.17	NULL	2 / 12	BP positive regulation of receptor-mediated endocytosis
31	11.09	NULL	6 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
32	11.05	NULL	5 / 14	GSEA C2WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
33	10.99	NULL	4 / 13	BP lymph node development
34	10.88	NULL	5 / 15	GSEA C2JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
35	10.84	NULL	4 / 12	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
36	10.65	NULL	2 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
37	10.63	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
38	10.55	NULL	1 / 5	miRNA target-205
39	10.52	NULL	3 / 11	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
40	10.5	NULL	17 / 60	BP T cell costimulation



GW_119

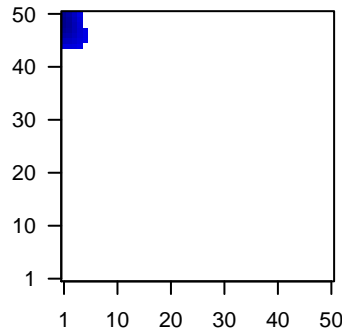
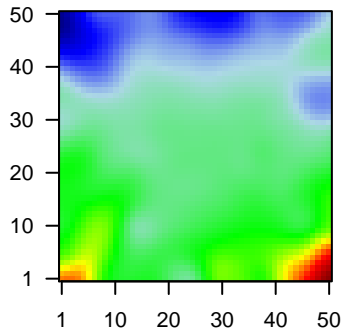
Local Summary

%DE = 0.8
 # metagenes = 31
 # genes = 370
 # genes in genesets = 362
 # genes with $fdr < 0.1$ = 247 (35 + / 212 -)
 # genes with $fdr < 0.05$ = 239 (34 + / 205 -)
 # genes with $fdr < 0.01$ = 195 (23 + / 172 -)

$\langle r \rangle$ metagenes = 0.92
 $\langle r \rangle$ genes = 0.4
 $\langle FC \rangle = -0.4$
 $\langle \text{shrinkage-t} \rangle = -14.17$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.4$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	57016	-2.27	2e-16	9e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
2	441282	-1.47	2e-16	9e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
3	220	2.03	2e-16	9e-16	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC]
4	242	-1.37	2e-16	9e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syn]
5	445328	-2.23	2e-16	9e-16	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:Hi]
6	387695	-1.5	2e-16	9e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
7	93099	-1.36	2e-16	9e-16	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
8	1828	-1.65	2e-16	9e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
9	5653	1.74	2e-16	9e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63]
10	3848	-1.43	2e-16	9e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
11	3868	-1.39	2e-16	9e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
12	192666	1.95	2e-16	9e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
13	388533	-4.35	2e-16	9e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC]
14	114569	-1.56	2e-16	9e-16	4 x 50 mal, T-cell differentiation protein 2 (gene/pseudogene) [Sour]
15	5317	-1.44	2e-16	9e-16	1 x 46 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [E]
16	374897	-1.49	2e-16	9e-16	1 x 49 suprabasin [Source:HGNC Symbol;Acc:24950]
17	5275	-1.79	2e-16	9e-16	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 13 [E]
18	6701	-1.73	2e-16	9e-16	1 x 49 small proline-rich protein 2B [Source:HGNC Symbol;Acc:112]
19	7053	-2.02	2e-16	9e-16	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
20	6706	-1.33	9e-16	3e-13	1 x 48 small proline-rich protein 2G [Source:HGNC Symbol;Acc:112]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-35.47	NULL	103 / 135	H.Tiss WIRTH_Mucosa
2	-22.7	NULL	13 / 21	CC desmosome
3	-21.51	NULL	19 / 21	CC cornified envelope
4	-17.68	NULL	26 / 53	BP keratinocyte differentiation
5	-15.4	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
6	-14.96	NULL	20 / 42	BP keratinization
7	-14.79	NULL	128 / 572	Disease GUUDJ_pсориазис up
8	-14.3	NULL	12 / 19	BP peptide cross-linking
9	-12.75	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	-11.49	NULL	3 / 12	BP cellular aldehyde metabolic process
11	-10.82	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
12	-10.48	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
13	-10.08	NULL	8 / 29	BP regulation of proteolysis
14	-9.95	NULL	3 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
15	-9.87	NULL	6 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
16	-8.55	NULL	6 / 13	BP negative regulation of peptidase activity
17	-8.3	NULL	8 / 16	GSEA C2JAEGER_METASTASIS_DN
18	-8.21	NULL	2 / 12	GSEA C2ODONNELL_METASTASIS_DN
19	-7.9	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
20	-7.88	NULL	29 / 76	BP epidermis development
21	-7.46	NULL	2 / 9	GSEA C2GOUYER_TUMOR_INVASIVENESS
22	-7.28	NULL	11 / 52	BP negative regulation of endopeptidase activity
23	-7.19	NULL	2 / 11	MF gamma-catenin binding
24	-7.05	NULL	2 / 16	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_UP
25	-6.97	NULL	3 / 25	BP protein tetramerization
26	-6.96	NULL	3 / 15	GSEA C2CROMER_METASTASIS_DN
27	-6.95	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
28	-6.94	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
29	-6.86	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
30	-6.83	NULL	3 / 16	GSEA C2AMIT_SERULM_RESPONSE_480_MCF10A
31	-6.72	NULL	3 / 15	BP fibrinolysis
32	-6.59	NULL	16 / 232	Chr Chr 18
33	-6.49	NULL	3 / 13	TF Tissue/AQUERIZAS_Skin
34	-6.44	NULL	4 / 46	BP cellular component disassembly involved in execution phase of ap
35	-6.42	NULL	2 / 15	GSEA C2I_AMPLIFIED_IN_LUNG_CANCER
36	-6.28	NULL	8 / 16	GSEA C2OLDREN_GEFITINIB_RESISTANCE_DN
37	-6.25	NULL	1 / 12	GSEA C2ONDER_CDH1_TARGETS_1_UP
38	-6.2	NULL	9 / 100	BP cell-cell adhesion
39	-5.99	NULL	2 / 10	GSEA C2KIM_MYCL1_AMPLIFICATION_TARGETS_UP
40	-5.96	NULL	1 / 13	GSEA C2BRUECKNER_TARGETS_OF_MIRLET7A3_DN

p-values

