

GW_113

Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1609 (947 + / 662 -)
 # genes with fdr < 0.1 = 1360 (834 + / 526 -)
 # genes with fdr < 0.05 = 1115 (712 + / 403 -)
 # genes with fdr < 0.01 = 722 (501 + / 221 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.86

Global Genelist

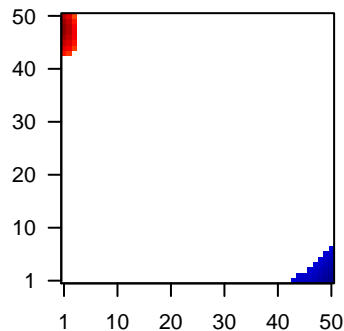
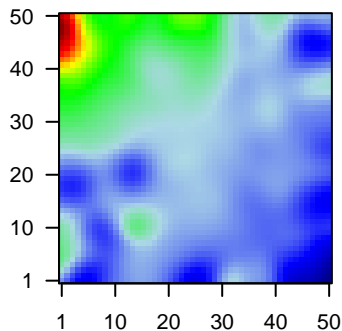
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.09	2e-16	4e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	222	2.07	2e-16	4e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	242	1.65	2e-16	4e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
4	341405	-1.29	2e-16	4e-14	30 x 1 ankyrin repeat domain 33 [Source:HGNC Symbol;Acc:13788]
5	360	1.32	2e-16	4e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
6	151516	1.95	2e-16	4e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
7	650	1.27	2e-16	4e-14	1 x 4 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10
8	387695	1.99	2e-16	4e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
9	283422	1.5	2e-16	4e-14	9 x 50
10	92747	1.41	2e-16	4e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
11	760	1.58	2e-16	4e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	810	-1.61	2e-16	4e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
13	51806	-1.29	2e-16	4e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
14	8900	1.69	2e-16	4e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
15	970	1.45	2e-16	4e-14	33 x 2 CD70 molecule [Source:HGNC Symbol;Acc:11937]
16	1041	1.68	2e-16	4e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
17	10370	1.31	2e-16	4e-14	46 x 9 Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo
18	9076	1.31	2e-16	4e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
19	84518	1.42	2e-16	4e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
20	1672	-1.26	2e-16	4e-14	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]

Global Geneset Analysis

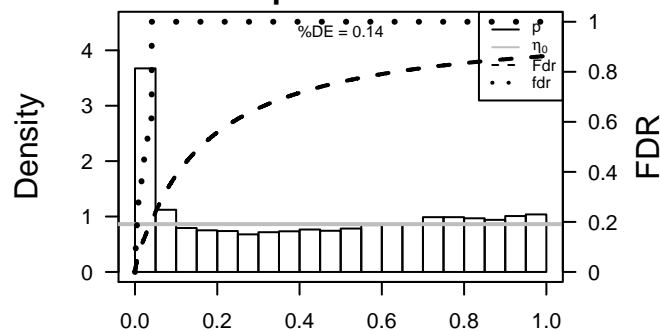
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	21.79	NULL	135	H.Tiss WIRTH_Mucosa
2	18.5	NULL	572	Disease GUDJ_psooriasis up
3	15.27	NULL	42	BP keratinization
4	13.5	NULL	21	CC cornified envelope
5	13.4	NULL	53	BP keratinocyte differentiation
6	10.92	NULL	76	BP epidermis development
7	9.73	NULL	714	Chr 6
8	8.94	NULL	280	Chr Chr 13
9	8.92	NULL	21	CC desmosome
10	8.11	NULL	6	Lymphoma_AVE_MHCCII BL DN
11	8.03	NULL	10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
12	7.15	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	7.07	NULL	866	Chr Chr 12
14	7.04	NULL	10	CC MHC class I protein complex
15	7.03	NULL	44	CC keratin filament
16	6.99	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
17	6.84	NULL	10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
18	6.81	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
19	6.51	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	6.44	NULL	38	BP epithelial cell differentiation
<i>Underexpressed</i>				
1	-9.71	NULL	918	Chr Chr 17
2	-7.89	NULL	633	Chr Chr 9
3	-7.1	NULL	36	BP muscle filament sliding
4	-6.59	NULL	153	MF structural constituent of ribosome
5	-6.48	NULL	127	H.Tiss WIRTH_Muscle
6	-6.17	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
7	-6.17	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
8	-6.15	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
9	-5.94	NULL	167	CC ribosome
10	-5.62	NULL	602	Chr Chr 10
11	-5.62	NULL	92	BP translational elongation
12	-5.58	NULL	44	MF structural constituent of muscle
13	-5.53	NULL	92	BP viral life cycle
14	-5.33	NULL	87	BP translational termination
15	-5.26	NULL	81	BP viral transcription
16	-5.23	NULL	16	H.Tiss WIRTH_Hippocampus
17	-5.12	NULL	743	Chr Chr 7
18	-4.95	NULL	417	H.Tiss WIRTH_Immune system
19	-4.9	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
20	-4.8	NULL	5	GSEA C2NAKAMURA_ALVEOLAR_EPITHELIUM

Profile

Regulated Spots



p-values



GW_113

Local Summary

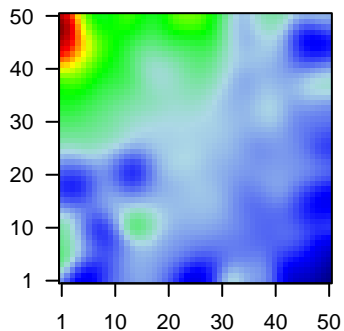
%DE = 0.79
 # metagenes = 23
 # genes = 312
 # genes in genesets = 304

genes with $fdr < 0.1 = 226$ (202 + / 24 -)
 # genes with $fdr < 0.05 = 198$ (179 + / 19 -)
 # genes with $fdr < 0.01 = 184$ (167 + / 17 -)

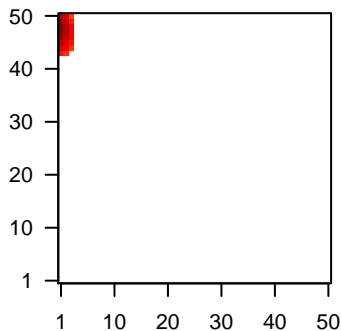
<r> metagenes = 0.9
 <r> genes = 0.38

<FC> = 0.58
 <shrinkage-t> = 20.6
 <p-value> = 0
 <fdr> = 0.32

Profile



Spot



Local Genelist

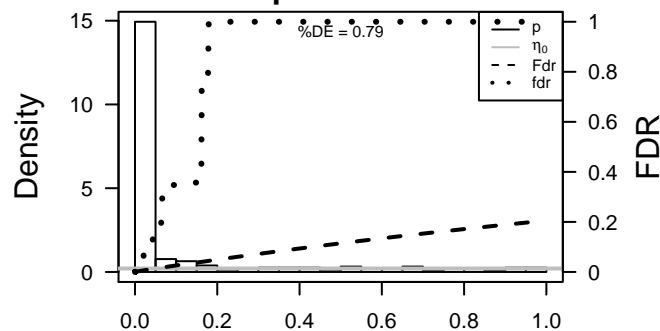
Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.09	2e-16	3e-16	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	222	2.07	2e-16	3e-16	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	242	1.65	2e-16	3e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syrr
4	360	1.32	2e-16	3e-16	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
5	151516	1.95	2e-16	3e-16	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
6	387695	1.99	2e-16	3e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	760	1.58	2e-16	3e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	810	-1.61	2e-16	3e-16	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
9	1041	1.68	2e-16	3e-16	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
10	84518	1.42	2e-16	3e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
11	1672	-1.26	2e-16	3e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
12	93099	1.31	2e-16	3e-16	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
13	1828	1.73	2e-16	3e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	2167	2.67	2e-16	3e-16	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
15	9982	1.24	2e-16	3e-16	1 x 47 fibroblast growth factor binding protein 1 [Source:HGNC Sym
16	2697	1.31	2e-16	3e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
17	2706	1.52	2e-16	3e-16	1 x 47 gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
18	10804	1.91	2e-16	3e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
19	2941	1.27	2e-16	3e-16	3 x 50 glutathione S-transferase alpha 4 [Source:HGNC Symbol;Ac
20	3489	1.5	2e-16	3e-16	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	39.87	NULL	88 / 135	H.Tiss WIRTH_Mucosa
2	31.59	NULL	18 / 21	CC cornified envelope
3	27.34	NULL	24 / 53	BP keratinocyte differentiation
4	26.97	NULL	20 / 42	BP keratinization
5	25.71	NULL	113 / 572	Disease GUDJ_psooriasis up
6	20.44	NULL	12 / 21	CC desmosome
7	19.1	NULL	27 / 76	BP epidermis development
8	16.63	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
9	14.43	NULL	3 / 8	GSEA C2LU_CDX2_TARGETS_DN
10	14.29	NULL	5 / 10	MF RAGE receptor binding
11	13.86	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
12	13.26	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
13	13.24	NULL	21 / 82	CC intermediate filament
14	13.02	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	12.99	NULL	13 / 44	CC keratin filament
16	12.66	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	12.45	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
18	12.26	NULL	10 / 19	BP peptide cross-linking
19	12.21	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
20	12.06	NULL	30 / 186	MF structural molecule activity
21	11.99	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
22	11.84	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
23	11.75	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
24	11.13	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
25	11.09	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
26	11.02	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
27	10.87	NULL	10 / 52	BP negative regulation of endopeptidase activity
28	10.71	NULL	3 / 15	MF interleukin-1 receptor binding
29	10.52	NULL	7 / 29	BP regulation of proteolysis
30	10.34	NULL	3 / 15	CC connexon complex
31	10.16	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
32	9.81	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
33	9.74	NULL	4 / 21	CC gap junction
34	9.67	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
35	9.51	NULL	4 / 10	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
36	9.4	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
37	9.16	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
38	9.13	NULL	2 / 12	MF fatty acid binding
39	8.83	NULL	5 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
40	8.71	NULL	5 / 23	MF peptidase inhibitor activity

p-values



GW_113

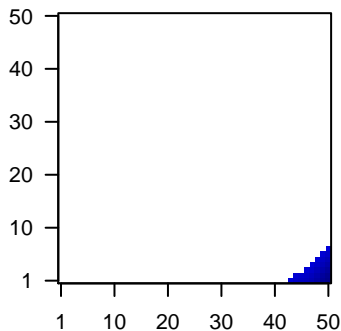
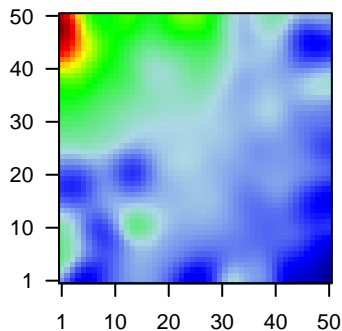
Local Summary

%DE = 0.71
 # metagenes = 30
 # genes = 465
 # genes in genesets = 462
 # genes with $fdr < 0.1$ = 250 (25 + / 225 -)
 # genes with $fdr < 0.05$ = 142 (12 + / 130 -)
 # genes with $fdr < 0.01$ = 105 (10 + / 95 -)

$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.46
 $\langle FC \rangle = -0.25$
 $\langle \text{shrinkage-t} \rangle = -8.91$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.63$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	6364	1.2	5e-15 4e-13	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc:6364]
2	65108	-1.2	5e-15 3e-11	44 x 1 MARCKS-like 1 [Source:HGNC Symbol;Acc:7142]
3	260436	-1.12	3e-13 7e-10	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:260436]
4	23180	-1.05	6e-12 3e-08	50 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
5	347733	-0.95	4e-10 3e-08	50 x 5 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
6	347	-0.95	5e-10 2e-07	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
7	83641	-0.92	2e-09 2e-07	50 x 1 family with sequence similarity 107, member B [Source:HGNC Symbol;Acc:83641]
8	9709	0.9	4e-09 2e-07	48 x 5 homocysteine-inducible, endoplasmic reticulum stress-inducible protein 1 [Source:HGNC Symbol;Acc:9709]
9	6363	-0.89	5e-09 3e-06	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:6363]
10	169044	-0.85	3e-08 6e-06	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298]
11	3059	-0.82	7e-08 6e-06	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:3059]
12	57484	-0.8	2e-07 6e-06	50 x 2 ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
13	1805	-0.8	2e-07 6e-06	50 x 5 dermatopontin [Source:HGNC Symbol;Acc:3011]
14	5730	-0.79	2e-07 8e-06	50 x 1 prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:5730]
15	3488	-0.79	3e-07 2e-05	50 x 7 insulin-like growth factor binding protein 5 [Source:HGNC Symbol;Acc:3488]
16	11322	-0.78	4e-07 2e-05	44 x 1 transmembrane channel-like 6 [Source:HGNC Symbol;Acc:11322]
17	84446	-0.77	5e-07 2e-05	43 x 1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:185]
18	5176	-0.76	6e-07 3e-05	50 x 5 serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pig) member 1 [Source:HGNC Symbol;Acc:5176]
19	4033	0.75	9e-07 3e-05	49 x 1 lymphoid-restricted membrane protein [Source:HGNC Symbol;Acc:4033]
20	341	-0.75	1e-06 6e-05	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-20.89	NULL	108 / 417	H.Tiss WIRTH_Immune system
2	-18.79	NULL	125 / 553	Cancer Lembecke_Colonc Inflammation
3	-12.89	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
4	-12.29	NULL	7 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
5	-12.15	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
6	-10.94	NULL	2 / 5	GSEA C2NAKAMURA_ALVEOLAR_EPITHELIUM
7	-10.68	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
8	-9.83	NULL	55 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
9	-9.83	NULL	55 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
10	-9.83	NULL	55 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	-9.83	NULL	55 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
12	-9.81	NULL	19 / 74	BP regulation of immune response
13	-9.72	NULL	6 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
14	-9.55	NULL	68 / 312	BP immune response
15	-9.48	NULL	7 / 13	MMML C2SCIEJ_MMML 6
16	-9.32	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDDP_SIGNATURE
17	-9.29	NULL	9 / 28	Lymphoma GAVE_Immune response 1
18	-9.21	NULL	32 / 162	CC external side of plasma membrane
19	-9.17	NULL	4 / 13	BP positive regulation of endocytosis
20	-9.12	NULL	6 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
21	-8.98	NULL	5 / 12	BP dendritic cell chemotaxis
22	-8.9	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_ACCEPTED
23	-8.72	NULL	4 / 13	Cancer GENTLES_modul17
24	-8.63	NULL	4 / 14	BP ruffle organization
25	-8.62	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
26	-8.52	NULL	4 / 14	BP lipid transporter activity
27	-8.45	NULL	5 / 17	MF positive regulation of neutrophil chemotaxis
28	-8.42	NULL	5 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
29	-8.28	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
30	-8.18	NULL	3 / 3	MMML C2SCIEJ_MMML 7
31	-7.97	NULL	3 / 12	GSEA C2HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
32	-7.96	NULL	3 / 11	BP negative regulation of lipid catabolic process
33	-7.95	NULL	5 / 14	GSEA C2WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
34	-7.75	NULL	4 / 15	GSEA C2DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_UP
35	-7.62	NULL	8 / 55	Glio OL vs. MOG- OL
36	-7.55	NULL	4 / 13	GSEA C2KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
37	-7.55	NULL	7 / 11	GSEA C2BIOCARTA_THelper_PATHWAY
38	-7.47	NULL	8 / 13	Cancer GENTLES_modul18
39	-7.37	NULL	4 / 18	BP cellular response to cytokine stimulus
40	-7.32	NULL	5 / 22	BP positive regulation of phosphatidylinositol 3-kinase activity

p-values

