

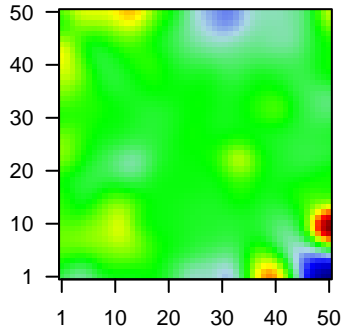
# GW\_225

## Global Summary

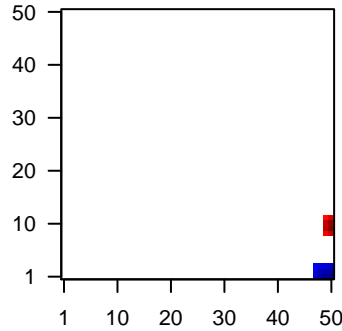
%DE = 0.13  
 # genes with fdr < 0.2 = 1584 ( 919 + / 665 - )  
 # genes with fdr < 0.1 = 1213 ( 747 + / 466 - )  
 # genes with fdr < 0.05 = 926 ( 602 + / 324 - )  
 # genes with fdr < 0.01 = 601 ( 425 + / 176 - )  
  
 # genes in genesets = 16332

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

Profile



Regulated Spots



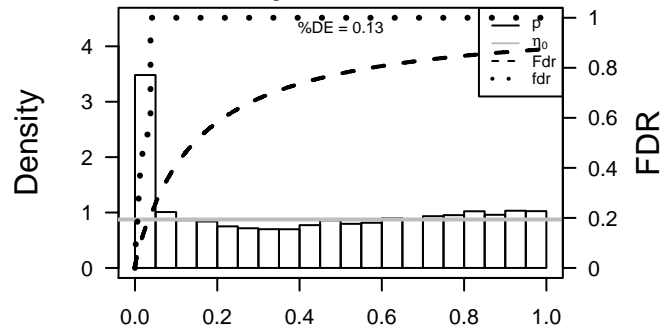
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	72	1.6	2e-16 3e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	131	-1.73	2e-16 3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	10551	3.15	2e-16 3e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	8644	1.58	2e-16 3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	1.68	2e-16 3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
6	347	1.45	2e-16 3e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
7	374569	1.57	2e-16 3e-14	4 x 50 asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
8	344905	1.49	2e-16 3e-14	50 x 50 ATPase type 13A5 [Source:HGNC Symbol;Acc:31789]
9	563	1.78	2e-16 3e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol
10	80341	3	2e-16 3e-14	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symb
11	387695	-2.46	2e-16 3e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symlt
12	149563	1.67	2e-16 3e-14	34 x 23 chromosome 1 open reading frame 64 [Source:HGNC Symbc
13	92747	4.8	2e-16 3e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
14	760	1.59	2e-16 3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	51806	2.41	2e-16 3e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
16	84290	-1.62	2e-16 3e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
17	6364	-1.57	2e-16 3e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
18	4680	1.56	2e-16 3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
19	1056	2.08	2e-16 3e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
20	84952	1.99	2e-16 3e-14	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	16.2	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	12.82	NULL	519	Chr Chr 14
3	9.09	NULL	13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
4	7.82	NULL	10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
5	7.74	NULL	5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
6	7.48	NULL	8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
7	7.25	NULL	13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
8	6.48	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	6.23	NULL	9	GSEA C2SOUYER_TATI_TARGETS_UP
10	6.19	NULL	37	BP digestion
11	5.93	NULL	386	Chr Chr 22
12	5.9	NULL	16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
13	5.4	NULL	13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
14	5.39	NULL	699	Chr Chr 5
15	5.37	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
16	5.31	NULL	7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
17	5.24	NULL	10	BP retinal metabolic process
18	5.22	NULL	15	GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
19	5.18	NULL	14	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
20	5.11	NULL	26	Disease BCHETNIA_EBM-DM up
<i>Underexpressed</i>				
1	-11.89	NULL	417	H.Tiss WIRTH_Immune system
2	-9.28	NULL	312	BP immune response
3	-8.74	NULL	47	BP antigen processing and presentation
4	-8.69	NULL	60	BP interferon-gamma-mediated signaling pathway
5	-8.6	NULL	553	Cancer Lembecke_Colonic Inflammation
6	-8.26	NULL	15	CC MHC class II protein complex
7	-7.88	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
8	-7.65	NULL	204	BP cytokine-mediated signaling pathway
9	-7.05	NULL	714	Chr Chr 6
10	-6.92	NULL	52	Chr Chr HSCHR6_MHC_QBL
11	-6.69	NULL	32	CC ER to Golgi transport vesicle membrane
12	-5.88	NULL	4	MMML C6SCIEJ_MMML_23
13	-5.82	NULL	74	BP antigen processing and presentation of exogenous peptide antigen
14	-5.78	NULL	6	Lymphoma BAVE_MHCII BL DN
15	-5.7	NULL	185	Cancer SPANG_LPS-index2
16	-5.64	NULL	60	BP T cell costimulation
17	-5.57	NULL	140	Lymphoma BAVE_BL-vs-DLBCL
18	-5.54	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
19	-5.47	NULL	70	BP antigen processing and presentation of exogenous peptide antigen
20	-5.47	NULL	84	BP T cell receptor signaling pathway

p-values



# GW\_225

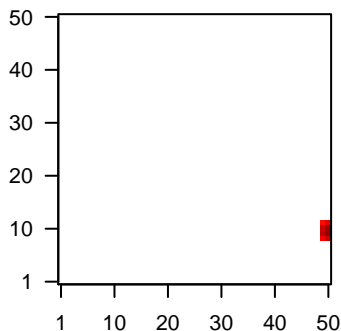
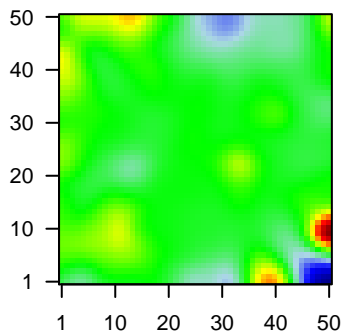
## Local Summary

%DE = 0.77  
 # metagenes = 8  
 # genes = 115  
 # genes in genesets = 114  
 # genes with  $fdr < 0.1 = 80$  ( 76 + / 4 - )  
 # genes with  $fdr < 0.05 = 71$  ( 70 + / 1 - )  
 # genes with  $fdr < 0.01 = 60$  ( 60 + / 0 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.34  
 $\langle FC \rangle = 0.87$   
 $\langle \text{shrinkage-t} \rangle = 30.54$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.38$

Profile

Spot



## Local Genelist

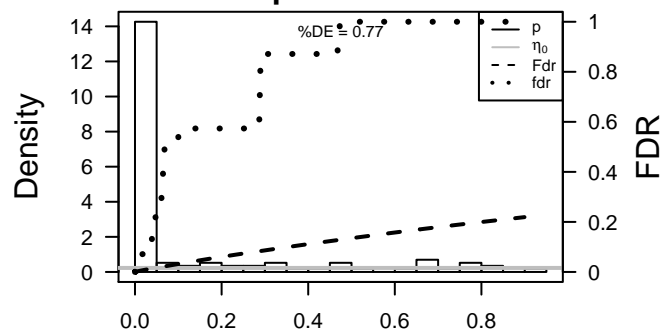
Rank	ID	log(FC)	fdr	p-value	Description
1	10551	3.15	2e-16	2e-16	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	563	1.78	2e-16	2e-16	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol]
3	80341	3	2e-16	2e-16	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symbol]
4	92747	4.8	2e-16	2e-16	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol]
5	84952	1.99	2e-16	2e-16	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]
6	9071	1.69	2e-16	2e-16	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
7	1755	1.79	2e-16	2e-16	50 x 10 deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:2033]
8	3158	1.65	2e-16	2e-16	50 x 10 3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
9	57535	1.71	2e-16	2e-16	50 x 10 KIAA1324 [Source:HGNC Symbol;Acc:29618]
10	3855	1.61	2e-16	2e-16	50 x 11 keratin 7 [Source:HGNC Symbol;Acc:6445]
11	124220	1.91	2e-16	2e-16	50 x 10 zymogen granule protein 16B [Source:HGNC Symbol;Acc:30203]
12	389816	2.75	2e-16	2e-16	50 x 10 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc:30203]
13	79083	1.92	2e-16	2e-16	50 x 10 melanophilin [Source:HGNC Symbol;Acc:29643]
14	10232	2.04	2e-16	2e-16	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]
15	94025	1.55	2e-16	2e-16	50 x 11 mucin 16, cell surface associated [Source:HGNC Symbol;Acc:7838]
16	4824	2.01	2e-16	2e-16	50 x 10 NK3 homeobox 1 [Source:HGNC Symbol;Acc:7838]
17	5284	2.57	2e-16	2e-16	50 x 10 polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:7838]
18	5304	1.55	2e-16	2e-16	50 x 10 prolactin-induced protein [Source:HGNC Symbol;Acc:8993]
19	8842	2.41	2e-16	2e-16	50 x 10 prominin 1 [Source:HGNC Symbol;Acc:9454]
20	11272	4.32	2e-16	2e-16	50 x 10 proline rich 4 (lacrima) [Source:HGNC Symbol;Acc:18020]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	50.42	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_DN
2	23.6	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	20.71	NULL	2 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
4	16.22	NULL	1 / 9	GSEA C2SOUYER_TATI_TARGETS_UP
5	14.57	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
6	13.73	NULL	2 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
7	12.98	NULL	1 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
8	12.51	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_CANCER_UP
9	11.82	NULL	4 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
10	11.53	NULL	2 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
11	10.66	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_CANCER_UP
12	9.77	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	9.69	NULL	3 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
14	9.36	NULL	1 / 15	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
15	9.36	NULL	1 / 15	GSEA C2LOPES_METHYLATED_IN_COLON_CANCER_UP
16	9.28	NULL	2 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_CANCER_UP
17	9.16	NULL	2 / 14	GSEA C2PENG_RAPAMYCIN_RESPONSE_UP
18	9.11	NULL	2 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
19	8.73	NULL	2 / 37	BP digestion
20	8.25	NULL	2 / 12	BP urogenital system development
21	8.14	NULL	1 / 10	BP negative regulation of blood coagulation
22	8.14	NULL	1 / 7	TF Tissue/AQUERIZAS_Appendix
23	8.13	NULL	2 / 16	GSEA C2WALK_AML_CLUSTER_9
24	8.03	NULL	1 / 15	GSEA C2LE_SKI_TARGETS_UP
25	7.47	NULL	2 / 16	GSEA C2FALVELLA_SMOKERS_WITH_LUNG_CANCER
26	7.44	NULL	1 / 17	Disease BChETNIA_EBM up
27	7.36	NULL	1 / 11	CC photoreceptor outer segment membrane
28	7.17	NULL	1 / 6	miRNA target-133a
29	7.1	NULL	1 / 13	GSEA C2NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
30	7.06	NULL	25 / 1182	CC extracellular region
31	7.05	NULL	19 / 683	CC extracellular space
32	6.97	NULL	1 / 12	BP retina layer formation
33	6.84	NULL	2 / 56	BP response to peptide hormone
34	6.74	NULL	2 / 13	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G3_DN
35	6.62	NULL	1 / 4	miRNA target-204
36	6.59	NULL	3 / 115	MF lipid binding
37	6.58	NULL	1 / 8	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_UP
38	6.58	NULL	1 / 8	GSEA C2ZHAN_MULTIPLE_MYELOMA_SPIKED
39	6.48	NULL	2 / 10	GSEA C2YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
40	6.42	NULL	1 / 10	GSEA C2MOHANKUMAR_TLX1_TARGETS_DN

p-values



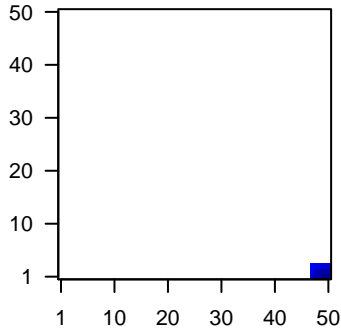
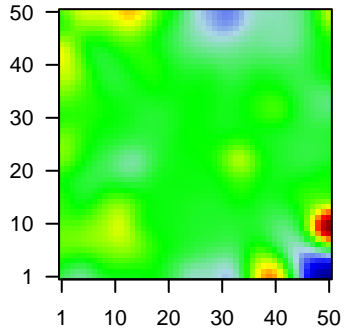
# GW\_225

## Local Summary

%DE = 0.91  
 # metagenes = 12  
 # genes = 231  
 # genes in genesets = 229  
  
 # genes with  $fdr < 0.1$  = 190 ( 8 + / 182 - )  
 # genes with  $fdr < 0.05$  = 169 ( 7 + / 162 - )  
 # genes with  $fdr < 0.01$  = 125 ( 6 + / 119 - )  
  
 $\langle r \rangle$  metagenes = 1  
 $\langle r \rangle$  genes = 0.63  
  
 $\langle FC \rangle = -0.41$   
 $\langle \text{shrinkage-t} \rangle = -14.44$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.45$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	929	1.33	2e-14	2e-12	50 x 3 CD14 molecule [Source:HGNC Symbol;Acc:1628]
2	3936	-1.29	1e-13	2e-10	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Syr
3	3122	-1.11	1e-11	2e-10	50 x 1 major histocompatibility complex, class II, DR alpha [Source:!
4	3113	-1.17	2e-11	2e-10	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source
5	3128	-1.16	2e-11	1e-09	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
6	241	-1.13	8e-11	2e-09	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HG!
7	23180	-1.11	2e-10	2e-09	50 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
8	5552	-1.1	3e-10	2e-08	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
9	9308	-1.06	1e-09	1e-07	50 x 3 CD83 molecule [Source:HGNC Symbol;Acc:1703]
10	3120	-1.01	7e-09	2e-07	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:
11	5341	-0.97	2e-08	2e-07	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
12	3512	0.97	2e-08	3e-06	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglo
13	5996	-0.89	3e-07	3e-06	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc
14	3125	-0.88	5e-07	3e-06	50 x 1 major histocompatibility complex, class II, DR beta 3 [Source:
15	962	-0.87	5e-07	3e-06	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
16	3620	-0.87	6e-07	2e-05	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:f
17	972	-0.83	2e-06	2e-05	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
18	7351	-0.8	4e-06	2e-05	50 x 1 uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
19	8728	-0.79	5e-06	2e-05	50 x 3 ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
20	9535	-0.79	6e-06	2e-05	50 x 1 glia maturation factor, gamma [Source:HGNC Symbol;Acc:43

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-34.61	NULL	12 / 15	CC MHC class II protein complex
2	-29.57	NULL	86 / 417	H.Tiss WIRTH_Immune system
3	-23.67	NULL	85 / 553	Cancer Lembcke_Colonc Inflammation
4	-22.49	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	-20.56	NULL	14 / 47	BP antigen processing and presentation
6	-20	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
7	-19.23	NULL	46 / 312	BP immune response
8	-19.03	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
9	-18.36	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
10	-17.91	NULL	38 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
11	-17.91	NULL	38 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
12	-17.91	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
13	-17.91	NULL	38 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
14	-17.08	NULL	7 / 28	CC transport vesicle membrane
15	-16	NULL	2 / 6	GSEA C2UDHU_LIVER_CANCER_METASTASIS_UP
16	-15.97	NULL	13 / 60	BP T cell costimulation
17	-15.92	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
18	-15.87	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
19	-15.18	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
20	-15.1	NULL	7 / 35	CC trans-Golgi network membrane
21	-14.7	NULL	8 / 16	GSEA C2SU_THYMUS
22	-14.52	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
23	-14.25	NULL	16 / 74	BP regulation of immune response
24	-14.18	NULL	5 / 12	BP dendritic cell chemotaxis
25	-14.06	NULL	2 / 6	GSEA C2UL_THYROID_CANCER_CLUSTER_4
26	-14.02	NULL	2 / 3	MMML C6SCIEJ_MMML_7
27	-13.9	NULL	12 / 87	BP antigen processing and presentation of exogenous peptide antigen
28	-13.75	NULL	23 / 162	CC external side of plasma membrane
29	-13.64	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
30	-13.25	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
31	-13.07	NULL	10 / 60	BP interferon-gamma-mediated signaling pathway
32	-13.04	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
33	-13	NULL	8 / 52	Chr Chr HSCR6_MHC_QBL
34	-12.96	NULL	7 / 46	CC endocytic vesicle membrane
35	-12.8	NULL	4 / 14	BP ruffle organization
36	-12.64	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
37	-12.63	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
38	-12.49	NULL	4 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
39	-12.29	NULL	3 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE
40	-12.28	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS

p-values

