

GW_138

Global Summary

%DE = 0.13
 # genes with fdr < 0.2 = 1653 (919 + / 734 -)
 # genes with fdr < 0.1 = 1399 (795 + / 604 -)
 # genes with fdr < 0.05 = 1193 (690 + / 503 -)
 # genes with fdr < 0.01 = 824 (491 + / 333 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.87

Global Genelist

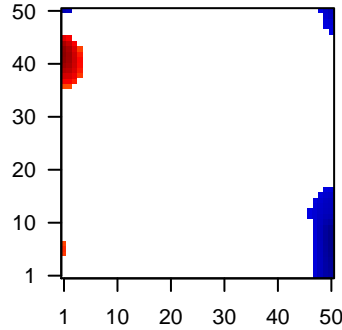
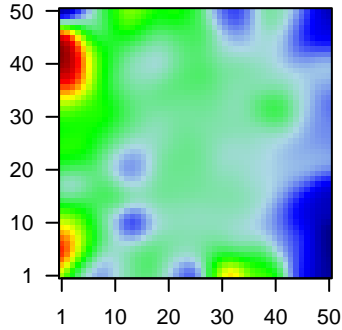
Rank	ID	log(FC)	fdr	p-value	Description	Metagene
1	79852	-1.23	2e-16	3e-14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	-1.71	2e-16	3e-14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	216	-1.4	2e-16	3e-14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC]
4	501	-1.43	2e-16	3e-14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC]
5	23780	1.45	2e-16	3e-14	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
6	10409	1.26	2e-16	3e-14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
7	329	1.92	2e-16	3e-14	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
8	330	1.86	2e-16	3e-14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
9	85016	1.31	2e-16	3e-14	50 x 25	chromosome 11 open reading frame 70 [Source:HGNC Synt
10	260436	-1.33	2e-16	3e-14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
11	760	1.31	2e-16	3e-14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	51806	-1.63	2e-16	3e-14	4 x 50	calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
13	57172	-1.37	2e-16	3e-14	49 x 1	calcium/calmodulin-dependent protein kinase IG [Source:HG
14	55450	1.33	2e-16	3e-14	1 x 4	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Si
15	131076	-1.34	2e-16	3e-14	1 x 16	coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
16	595	1.31	2e-16	3e-14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
17	908	1.43	2e-16	3e-14	40 x 50	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
18	970	1.5	2e-16	3e-14	33 x 2	CD70 molecule [Source:HGNC Symbol;Acc:11937]
19	1048	-1.23	2e-16	3e-14	2 x 50	carcinoembryonic antigen-related cell adhesion molecule 5 [
20	51142	1.29	2e-16	3e-14	38 x 50	coiled-coil-helix-coiled-coil-helix domain containing 2 [Sour

Global Geneset Analysis

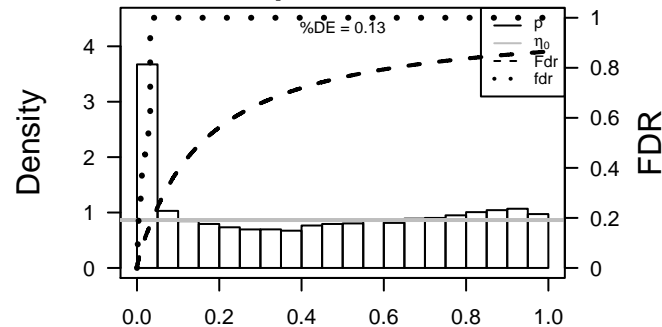
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	8.23	NULL	16	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_UP
2	8.17	NULL	15	GSEA C2SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
3	7.9	NULL	12	BP hemidesmosome assembly
4	7.84	NULL	633	Chr Chr 9
5	7.37	NULL	51	BP type I interferon signaling pathway
6	7.22	NULL	14	GSEA C2BIOCARTA_DEATH_PATHWAY
7	7.08	NULL	15	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_DN
8	6.92	NULL	15	BP fibrinolysis
9	6.87	NULL	15	GSEA C2AIGNER_ZEB1_TARGETS
10	6.86	NULL	699	Chr Chr 5
11	6.84	NULL	7	GSEA C2GAUTSCHI_SRC_SIGNALING
12	6.61	NULL	957	Chr Chr 11
13	6.53	NULL	16	GSEA C2MOERLE_IFNA_RESPONSE
14	6.19	NULL	13	GSEA C2SUZUKI_AMPLIFIED_IN_ORAL_CANCER
15	5.97	NULL	15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
16	5.83	NULL	8	GSEA C2NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
17	5.76	NULL	11	GSEA C2ST_TUMOR_NECROSIS_FACTOR_PATHWAY
18	5.74	NULL	449	Chr Chr 20
19	5.7	NULL	29	BP regulation of proteolysis
20	5.7	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
<i>Underexpressed</i>				
1	-12.92	NULL	618	Chr Chr 4
2	-9.49	NULL	1135	Chr Chr 19
3	-6.73	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
4	-6.7	NULL	187	Chr Chr 21
5	-6.5	NULL	92	BP translational elongation
6	-6.22	NULL	81	BP viral transcription
7	-6.18	NULL	87	BP translational termination
8	-6.06	NULL	42	BP keratinization
9	-5.81	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
10	-5.7	NULL	15	GSEA C2KEGG_Glutathione_Metabolism
11	-5.68	NULL	37	CC cytosolic small ribosomal subunit
12	-5.66	NULL	83	BP respiratory electron transport chain
13	-5.65	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
14	-5.47	NULL	92	BP viral life cycle
15	-5.47	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
16	-5.36	NULL	153	MF structural constituent of ribosome
17	-5.32	NULL	12	BP cellular aldehyde metabolic process
18	-5.32	NULL	9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
19	-5.29	NULL	128	BP translational initiation
20	-5.19	NULL	25	CC small ribosomal subunit

Profile

Regulated Spots



p-values



GW_138

Local Summary

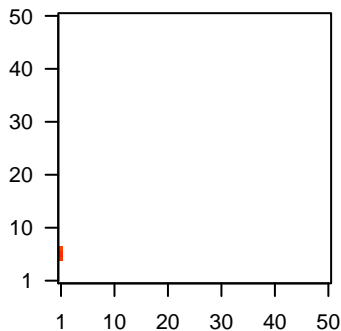
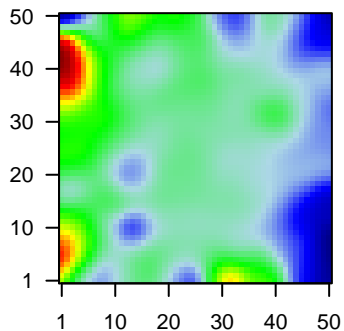
%DE = 0.8
 # metagenes = 3
 # genes = 98
 # genes in genesets = 96
 # genes with $fdr < 0.1$ = 66 (61 + / 5 -)
 # genes with $fdr < 0.05$ = 60 (56 + / 4 -)
 # genes with $fdr < 0.01$ = 52 (49 + / 3 -)

<r> metagenes = 0.99
 <r> genes = 0.33

<FC> = 0.41
 <shrinkage-t> = 14.24
 <p-value> = 0
 <fdr> = 0.42

Profile

Spot



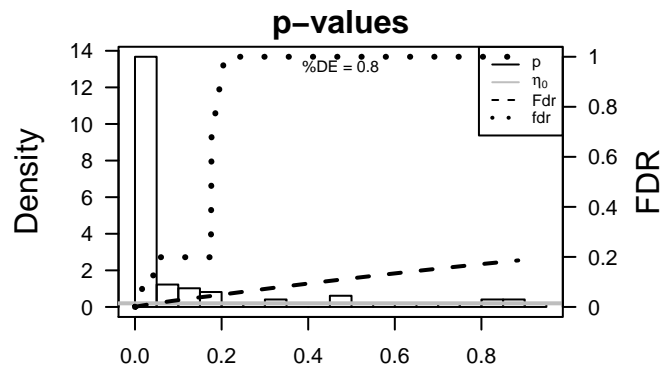
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	595	1.31	2e-16	4e-15	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
2	3486	1.14	2e-14	5e-12	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Sy
3	4430	1.08	5e-13	5e-12	1 x 5 myosin IB [Source:HGNC Symbol;Acc:7596]
4	153572	1.08	5e-13	5e-11	1 x 5 iroquois homeobox 2 [Source:HGNC Symbol;Acc:14359]
5	9388	1.04	3e-12	8e-11	1 x 5 lipase, endothelial [Source:HGNC Symbol;Acc:6623]
6	6385	1.03	7e-12	2e-09	1 x 7 syndecan 4 [Source:HGNC Symbol;Acc:10661]
7	169611	0.97	1e-10	4e-09	1 x 5 olfactomedin-like 2A [Source:HGNC Symbol;Acc:27270]
8	2201	0.94	3e-10	6e-09	1 x 5 fibrillin 2 [Source:HGNC Symbol;Acc:3604]
9	10808	0.91	1e-09	6e-09	1 x 7 heat shock 105kDa/110kDa protein 1 [Source:HGNC Symbol
10	375790	0.91	1e-09	6e-09	1 x 7 agrin [Source:HGNC Symbol;Acc:329]
11	22943	0.9	2e-09	6e-09	1 x 7 dickkopf1 WNT signaling pathway inhibitor 1 [Source:HGNC S
12	2195	0.9	2e-09	7e-08	1 x 5 FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
13	1012	0.87	5e-09	3e-07	1 x 5 cadherin 13 [Source:HGNC Symbol;Acc:1753]
14	91283	0.84	2e-08	5e-07	1 x 5 Myb/SANT-like DNA-binding domain containing 3 [Source:H
15	54972	0.82	4e-08	9e-07	1 x 7 transmembrane protein 132A [Source:HGNC Symbol;Acc:31
16	10468	0.78	2e-07	9e-07	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
17	8727	0.78	2e-07	9e-07	1 x 5 catenin (cadherin-associated protein), alpha-like 1 [Source:t
18	3691	0.77	2e-07	9e-07	1 x 7 integrin, beta 4 [Source:HGNC Symbol;Acc:6158]
19	4651	0.77	2e-07	9e-07	1 x 6 myosin X [Source:HGNC Symbol;Acc:7593]
20	4000	0.77	3e-07	2e-06	1 x 6 lamin A/C [Source:HGNC Symbol;Acc:6636]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	33.92	NULL	1 / 2	miRNA target-16-1
2	26.94	NULL	2 / 4	miRNA target-195
3	25.57	NULL	3 / 9	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_DN
4	25.03	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
5	20.9	NULL	4 / 16	GSEA C2ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
6	20.78	NULL	2 / 6	miRNA target7b
7	20.57	NULL	1 / 4	miRNA target-20a
8	20.14	NULL	4 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
9	17.79	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
10	17.79	NULL	1 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
11	17.79	NULL	1 / 5	miRNA target-15a
12	16.99	NULL	3 / 16	MF fibronectin binding
13	14.97	NULL	1 / 4	MML C2CIEJ_MMML 44
14	14.72	NULL	3 / 14	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
15	14.68	NULL	3 / 15	GSEA C2NIDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
16	14.65	NULL	2 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
17	14.41	NULL	2 / 11	miRNA target-16
18	14.41	NULL	1 / 7	miRNA target-17-5p
19	14.04	NULL	5 / 49	CC filopodium
20	13.95	NULL	2 / 14	GSEA C2ENGELMANN_CANCER_PROGENITORS_UP
21	13.28	NULL	1 / 8	GSEA C2ZHAN_MULTIPLE_MYELOMA_SPIKED
22	13.15	NULL	2 / 13	GSEA C2CHIN_BREAST_CANCER_COPY_NUMBER_UP
23	12.96	NULL	3 / 12	BP hemidesmosome assembly
24	12.67	NULL	2 / 15	GSEA C2SUNG_METASTASIS_STROMA_UP
25	12.66	NULL	1 / 3	GSEA C2VICENT_METASTASIS_DN
26	12.61	NULL	2 / 16	GSEA C2SWEET_KRAS_TARGETS_UP
27	12.59	NULL	2 / 12	MF heparan sulfate proteoglycan binding
28	12.54	NULL	2 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_DN
29	12.54	NULL	2 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_32HR_DN
30	12.54	NULL	2 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_48HR_DN
31	12.51	NULL	2 / 14	GSEA C2BIOCARTA_G1_PATHWAY
32	12.37	NULL	1 / 9	GSEA C2MARKS_HDAC_TARGETS_DN
33	12.3	NULL	2 / 12	BP keratinocyte proliferation
34	12.28	NULL	2 / 14	GSEA C2SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
35	12.14	NULL	1 / 6	GSEA C2SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
36	12.11	NULL	4 / 32	BP glycosaminoglycan biosynthetic process
37	12.02	NULL	2 / 15	GSEA C2KEGG_GLIOMA
38	12.02	NULL	2 / 15	GSEA C2BIOCARTA_CELLCYCLE_PATHWAY
39	12.02	NULL	2 / 15	GSEA C2REACTOME_G1_PHASE
40	11.85	NULL	3 / 14	GSEA C2CLIMENT_BREAST_CANCER_COPY_NUMBER_UP



GW_138

Local Summary

%DE = 0.79
 # metagenes = 34
 # genes = 372
 # genes in genesets = 365

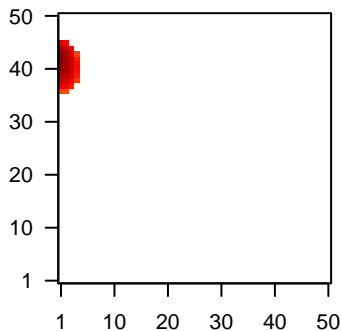
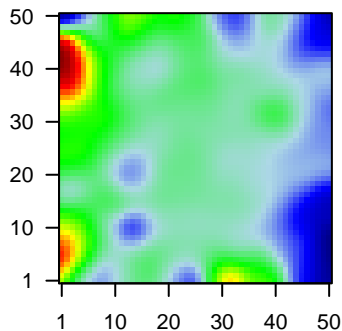
genes with $fdr < 0.1$ = 235 (220 + / 15 -)
 # genes with $fdr < 0.05$ = 206 (191 + / 15 -)
 # genes with $fdr < 0.01$ = 162 (154 + / 8 -)

<r> metagenes = 0.95
 <r> genes = 0.3

<FC> = 0.4
 <shrinkage-t> = 14.04
 <p-value> = 0
 <fdr> = 0.45

Profile

Spot



Local Genelist

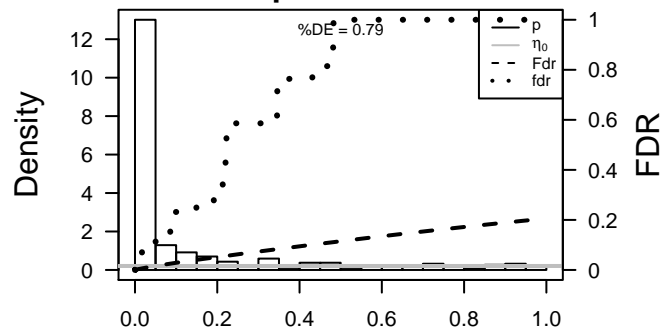
Rank	ID	log(FC)	fdr	p-value	Description
1	760	1.31	2e-16	1e-15	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	2152	1.6	2e-16	1e-15	1 x 43 coagulation factor III (thromboplastin, tissue factor) [Source:H
3	3229	1.37	2e-16	1e-15	1 x 42 homeobox C13 [Source:HGNC Symbol;Acc:5125]
4	3397	1.47	2e-16	1e-15	2 x 45 inhibitor of DNA binding 1, dominant negative helix-loop-heli
5	3861	1.44	2e-16	1e-15	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
6	150696	1.23	2e-16	1e-15	2 x 45 prominin 2 [Source:HGNC Symbol;Acc:20685]
7	5742	1.23	2e-16	1e-15	4 x 42 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H s
8	2810	1.13	2e-16	1e-15	1 x 45 stratifin [Source:HGNC Symbol;Acc:10773]
9	8140	1.46	2e-16	1e-15	1 x 43 solute carrier family 7 (amino acid transporter light chain, L s)
10	780851	1.97	2e-16	1e-15	2 x 39 small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
11	780853	1.91	2e-16	1e-15	2 x 39 small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc
12	780854	1.4	2e-16	1e-15	2 x 39 small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
13	83882	1.7	2e-16	1e-15	1 x 43 tetraspanin 10 [Source:HGNC Symbol;Acc:29942]
14	80326	1.33	2e-16	1e-15	1 x 40 wingless-type MMTV integration site family, member 10A [So
15	54626	1.2	9e-16	6e-14	1 x 44 hes family bHLH transcription factor 2 [Source:HGNC Symbol
16	50805	1.18	2e-15	6e-14	1 x 43 iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
17	1308	1.18	3e-15	6e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	146802	1.18	3e-15	1e-13	1 x 45 solute carrier family 47 (multidrug and toxin extrusion), memb
19	2760	1.17	5e-15	1e-11	1 x 40 GM2 ganglioside activator [Source:HGNC Symbol;Acc:4367]
20	7280	1.09	3e-13	1e-11	1 x 45 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	16.5	NULL	5 / 12	BP hemidesmosome assembly
2	10.59	NULL	2 / 8	GSEA C2L1U_CDX2_TARGETS_DN
3	10.31	NULL	60 / 572	Disease GUDJ_pсориаз up
4	9.86	NULL	1 / 2	Disease BCHETNIA_EBM down
5	9.62	NULL	3 / 7	MMML C2GACIEJ_MMML 9
6	9.29	NULL	1 / 4	GSEA C2DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
7	9.01	NULL	3 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
8	8.63	NULL	7 / 44	BP skin development
9	8.59	NULL	2 / 11	BP positive regulation of positive chemotaxis
10	8.3	NULL	3 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
11	8.29	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
12	8.15	NULL	12 / 76	BP epidermis development
13	7.99	NULL	1 / 6	GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP
14	7.93	NULL	9 / 82	MF structural constituent of cytoskeleton
15	7.93	NULL	3 / 16	GSEA C2SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP
16	7.89	NULL	7 / 70	BP cell junction assembly
17	7.67	NULL	4 / 15	GSEA C2KOBAYASHI_EGFR_SIGNALING_6HR_DN
18	7.62	NULL	3 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP
19	7.43	NULL	3 / 15	GSEA C2BROWNE_HCMV_INFECTION_2HR_DN
20	7.4	NULL	3 / 13	GSEA C2WANG_METHYLATED_IN_BREAST_CANCER
21	7.35	NULL	13 / 135	H.Tiss WIRTH_Mucosa
22	7.29	NULL	1 / 6	miRNA target-mir-146
23	7.05	NULL	2 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
24	6.99	NULL	3 / 11	GSEA C2LEI_MYB_TARGETS
25	6.98	NULL	4 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
26	6.98	NULL	3 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
27	6.85	NULL	1 / 2	miRNA target-mir-659
28	6.82	NULL	1 / 4	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
29	6.79	NULL	1 / 6	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_21
30	6.79	NULL	12 / 82	CC intermediate filament
31	6.72	NULL	3 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
32	6.69	NULL	1 / 7	GSEA C2GAUTSCHI_SRC_SIGNALING
33	6.61	NULL	1 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
34	6.6	NULL	2 / 10	MF neutral amino acid transmembrane transporter activity
35	6.48	NULL	2 / 13	BP intermediate filament cytoskeleton organization
36	6.43	NULL	2 / 25	BP response to zinc ion
37	6.31	NULL	2 / 13	GSEA C2NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON
38	6.29	NULL	3 / 16	GSEA C2HARRIS_HYPOXIA
39	6.29	NULL	2 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
40	6.18	NULL	4 / 35	BP hair follicle development

p-values



GW_138

Local Summary

%DE = 0.71
 # metagenes = 67
 # genes = 828
 # genes in genesets = 819

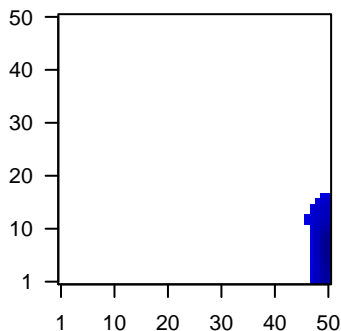
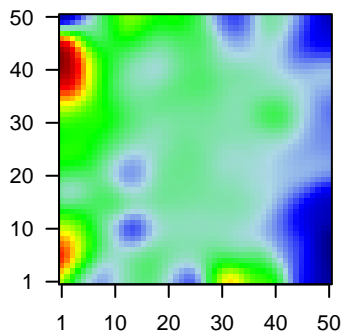
 # genes with $fdr < 0.1$ = 401 (73 + / 328 -)
 # genes with $fdr < 0.05$ = 311 (57 + / 254 -)
 # genes with $fdr < 0.01$ = 208 (42 + / 166 -)

 $\langle r \rangle$ metagenes = 0.78
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle = -0.21$
 $\langle \text{shrinkage-t} \rangle = -7.36$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.6$

Profile

Spot



Local Genelist

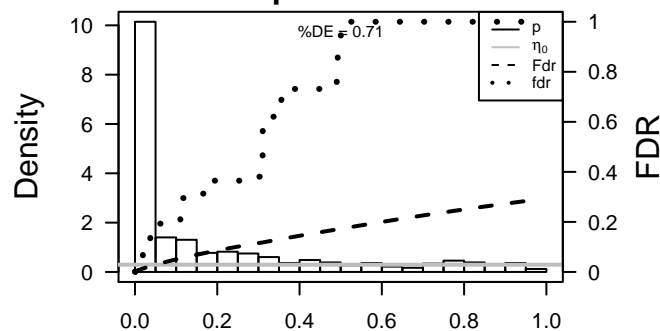
Rank	ID	log(FC)	fdr	p-value	Description
1	330	1.86	2e-16	9e-15	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:10410]
2	260436	-1.33	2e-16	9e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:10410]
3	57172	-1.37	2e-16	9e-15	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HGNC Symbol;Acc:10410]
4	2878	-1.48	2e-16	9e-15	50 x 9 glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Acc:10410]
5	3543	-1.75	2e-16	9e-15	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:10410]
6	6228	-1.64	2e-16	9e-15	50 x 14 ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
7	3512	-1.17	6e-15	9e-13	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin J [Source:HGNC Symbol;Acc:10410]
8	1396	1.16	8e-15	4e-12	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:10410]
9	6363	-1.14	2e-14	1e-11	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:10410]
10	3128	1.12	8e-14	2e-11	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo) [Source:HGNC Symbol;Acc:10410]
11	23641	1.1	2e-13	2e-11	50 x 11 leucine zipper, down-regulated in cancer 1 [Source:HGNC Symbol;Acc:10410]
12	2568	-1.1	2e-13	9e-11	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:10410]
13	7177	1.07	9e-13	9e-11	50 x 7 tryptase alpha/beta 1 [Source:HGNC Symbol;Acc:12019]
14	6542	-1.07	1e-12	8e-10	50 x 16 solute carrier family 7 (cationic amino acid transporter, y+ sys) member 1 [Source:HGNC Symbol;Acc:12019]
15	4781	-1.03	5e-12	8e-10	50 x 8 nuclear factor I/B [Source:HGNC Symbol;Acc:7785]
16	25840	-1.02	8e-12	2e-09	50 x 11 methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
17	51755	-1	2e-11	2e-09	49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:24222]
18	1359	0.99	4e-11	2e-09	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:25931]
19	84952	-0.99	4e-11	3e-09	50 x 10 cingulin-like 1 [Source:HGNC Symbol;Acc:25931]
20	10232	0.98	6e-11	3e-09	50 x 11 mesothelin [Source:HGNC Symbol;Acc:7371]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.86	NULL	14 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	-11.49	NULL	128 / 553	Cancer_Lembcke_Colonic_Inflammation
3	-11.07	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
4	-9.95	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	-9.68	NULL	102 / 417	H.Tiss_WIRTH_Immune_system
6	-8.94	NULL	4 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
7	-8.51	NULL	6 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARINOMA_WITH_LMP1_DN
8	-8.43	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
9	-8.16	NULL	1 / 6	H.Tiss_WIRTH_Bone_marrow
10	-7.89	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARINOMA_VS_LOBULAR_DN
11	-7.74	NULL	4 / 14	MF_selenium_binding
12	-7.67	NULL	5 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARINOMA_VS_LOBULAR_DN
13	-7.61	NULL	7 / 8	Glio_Donson-migration_tethering_and_rolling-associated_with_LTS_in_HGA
14	-7.58	NULL	7 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
15	-7.48	NULL	3 / 7	MMML_C2CIEJ_MMML_5
16	-7.47	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDP_SIGNATURE
17	-7.42	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
18	-7.3	NULL	6 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
19	-7.04	NULL	3 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
20	-7.03	NULL	4 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
21	-6.94	NULL	3 / 8	GSEA C2RUNNE_GENDER_EFFECT_UP
22	-6.81	NULL	4 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARINOMA_VS_DUCTAL_DN
23	-6.79	NULL	5 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
24	-6.78	NULL	5 / 12	BP_dendritic_cell_chemotaxis
25	-6.55	NULL	6 / 37	CC_cytosolic_small_ribosomal_subunit
26	-6.53	NULL	5 / 14	GSEA C2LIEN_BREAST_CARINOMA_METAPLASTIC_VS_DUCTAL_DN
27	-6.44	NULL	6 / 15	Cancer_GENTLES_modul13
28	-6.4	NULL	5 / 16	GSEA C2BROWNE_HCMV_INFECTION_2HR_UP
29	-6.24	NULL	5 / 12	GSEA C2HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
30	-6.22	NULL	9 / 16	GSEA C2SU_THYMUS
31	-6.15	NULL	5 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_DN
32	-6.06	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
33	-6.02	NULL	3 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DIFFERENTIATED_WELL
34	-6.02	NULL	4 / 11	GSEA C2GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
35	-5.99	NULL	2 / 5	GSEA C2ALK_AML_WITH_T_8_21_TRANSLOCATION
36	-5.88	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
37	-5.84	NULL	5 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
38	-5.8	NULL	4 / 11	GSEA C2APPEL_IMATINIB_RESPONSE
39	-5.79	NULL	6 / 15	Glio_Donson-chemokines/cytokines-associated_with_LTS_in_HGA
40	-5.76	NULL	4 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN

p-values



GW_138

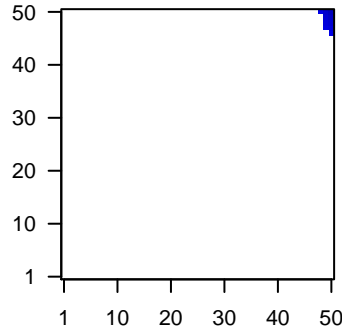
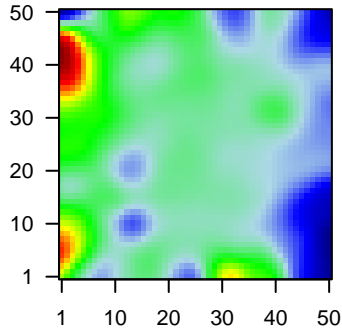
Local Summary

%DE = 0.68
 # metagenes = 10
 # genes = 178
 # genes in genesets = 177
 # genes with $fdr < 0.1$ = 70 (18 + / 52 -)
 # genes with $fdr < 0.05$ = 65 (17 + / 48 -)
 # genes with $fdr < 0.01$ = 53 (14 + / 39 -)

<r> metagenes = 0.98
 <r> genes = 0.28
 <FC> = -0.21
 <shrinkage-t> = -7.3
 <p-value> = 0
 <fdr> = 0.61

Profile

Spot



Local Genelist

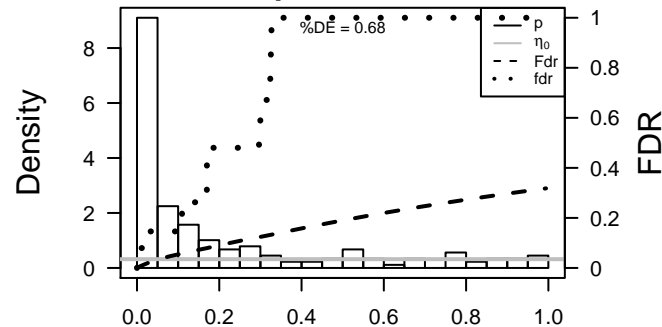
Rank	ID	log(FC)	fdr	p-value	Description
1	216	-1.4	2e-16	3e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	2944	-1.38	2e-16	3e-15	50 x 50 glutathione S-transferase mu 1 [Source:HGNC Symbol;Acc:4
3	2946	-1.34	2e-16	3e-15	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr
4	26227	-2.06	2e-16	3e-15	50 x 46 phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
5	3880	1.18	2e-15	7e-14	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
6	4922	-1.18	3e-15	7e-14	50 x 50 neurtensin [Source:HGNC Symbol;Acc:8038]
7	875	-1.17	4e-15	1e-13	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15:
8	26047	-1.17	6e-15	1e-13	50 x 50 contactin associated protein-like 2 [Source:HGNC Symbol;Ac
9	154664	-1.16	8e-15	4e-13	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Soi
10	214	1.15	2e-14	4e-12	50 x 50 activated leukocyte cell adhesion molecule [Source:HGNC S
11	339512	-1.12	8e-14	1e-11	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Synt
12	4953	-1.09	3e-13	3e-11	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
13	84707	-1.07	7e-13	3e-10	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
14	10643	-1.02	1e-11	3e-10	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:t
15	56963	-1.01	1e-11	3e-10	50 x 50 repulsive guidance molecule family member a [Source:HGNC
16	2304	-1.01	2e-11	1e-09	50 x 50 forkhead box E1 (thyroid transcription factor 2) [Source:HGNC
17	256764	0.98	5e-11	1e-09	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
18	1528	-0.98	7e-11	5e-08	50 x 50 cytochrome b5 type A (microsomal) [Source:HGNC Symbol;A
19	7345	-0.9	2e-09	5e-08	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
20	11166	-0.9	2e-09	2e-07	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-26.39	NULL	5 / 15	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
2	-21.53	NULL	3 / 11	MF glutathione binding
3	-21.53	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
4	-18.71	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
5	-18.33	NULL	5 / 20	MF glutathione transferase activity
6	-17.47	NULL	6 / 25	BP glutathione derivative biosynthetic process
7	-17.03	NULL	2 / 14	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
8	-15.75	NULL	4 / 13	BP regulation of blood vessel size
9	-15.75	NULL	8 / 34	BP glutathione metabolic process
10	-15.72	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
11	-13.81	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
12	-13.81	NULL	2 / 15	GSEA C2LEE_LIVER_CANCER_E2F1_UP
13	-13.56	NULL	2 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
14	-13.14	NULL	3 / 19	BP cellular amino acid biosynthetic process
15	-12.87	NULL	4 / 15	GSEA C2REACTOME_GLYCINE_SERINE_AND_THREONINE_METABOLISM
16	-12.69	NULL	3 / 16	GSEA C2BOYAUULT_LIVER_CANCER_SUBCLASS_G1_DN
17	-12.42	NULL	3 / 12	GSEA C2HELLER_SILENCED_BY_METHYLATION_DN
18	-12.16	NULL	2 / 16	GSEA C2PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
19	-12.16	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
20	-12.01	NULL	3 / 16	GSEA C2KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
21	-11.77	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
22	-11.74	NULL	11 / 119	BP xenobiotic metabolic process
23	-11.39	NULL	2 / 18	BP glutamine metabolic process
24	-10.76	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
25	-10.68	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
26	-10.37	NULL	1 / 15	BP spinal cord development
27	-10.37	NULL	1 / 15	GSEA C2VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_UP
28	-10.37	NULL	1 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_UP
29	-10.01	NULL	1 / 16	GSEA C2HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN
30	-9.88	NULL	1 / 6	GSEA C2SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
31	-9.56	NULL	2 / 15	GSEA C2REACTOME_PHASE_II_CONJUGATION
32	-9.42	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
33	-9.33	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
34	-9.33	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
35	-9.25	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
36	-9.23	NULL	1 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
37	-9.15	NULL	2 / 12	GSEA C2KAYO_AGING_MUSCLE_UP
38	-9.13	NULL	9 / 237	MF enzyme binding
39	-8.91	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
40	-8.79	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP

p-values



GW_138

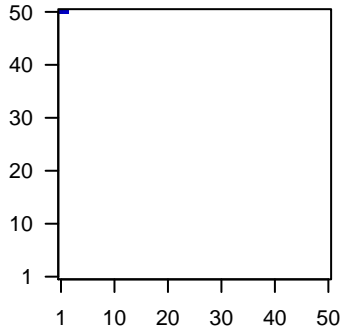
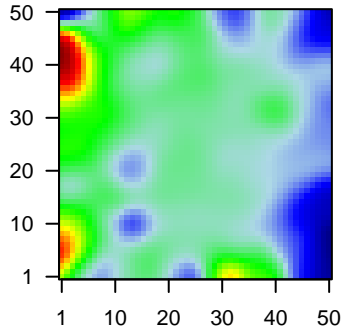
Local Summary

%DE = 0.85
 # metagenes = 2
 # genes = 71
 # genes in genesets = 70
 # genes with $fdr < 0.1$ = 55 (9 + / 46 -)
 # genes with $fdr < 0.05$ = 48 (7 + / 41 -)
 # genes with $fdr < 0.01$ = 48 (7 + / 41 -)

<r> metagenes = 1
 <r> genes = 0.58
 <FC> = -0.57
 <shrinkage-t> = -20.27
 <p-value> = 0
 <fdr> = 0.28

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-1.71	2e-16	2e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	1048	-1.23	2e-16	2e-16	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
3	84518	-2.15	2e-16	2e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
4	49860	-2.03	2e-16	2e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
5	1672	1.31	2e-16	2e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
6	5653	-2.06	2e-16	2e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:631
7	4118	-2.22	2e-16	2e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
8	342897	-1.92	2e-16	2e-16	1 x 50 non-specific cytotoxic cell receptor protein 1 homolog (zebraf
9	51458	-1.83	2e-16	2e-16	1 x 50 Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
10	5275	1.73	2e-16	2e-16	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 13 [E
11	5055	1.51	2e-16	2e-16	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 2 [Sc
12	6702	-1.87	2e-16	2e-16	1 x 50
13	6707	-1.25	2e-16	2e-16	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126
14	7053	-1.93	2e-16	2e-16	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	144568	-1.21	7e-16	3e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
16	26085	-1.18	4e-15	2e-13	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6:
17	8644	-1.14	2e-14	3e-13	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
18	79755	-1.12	6e-14	3e-13	1 x 50 zinc finger protein 750 [Source:HGNC Symbol;Acc:25843]
19	4680	-1.11	9e-14	3e-12	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
20	84651	-1.09	4e-13	5e-12	1 x 50 serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-30.75	NULL	39 / 135	H.Tiss WIRTH_Mucosa
2	-17.52	NULL	4 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
3	-15.76	NULL	11 / 42	BP keratinization
4	-14.33	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
5	-13.61	NULL	3 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
6	-13.19	NULL	2 / 15	MF retinol dehydrogenase activity
7	-12.62	NULL	10 / 21	CC cornified envelope
8	-12.49	NULL	12 / 53	BP keratinocyte differentiation
9	-12.4	NULL	1 / 11	Glio VERHAAK_Brain
10	-12.35	NULL	4 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	-11.75	NULL	9 / 122	MF serine-type endopeptidase activity
12	-11.74	NULL	1 / 12	MF channel activity
13	-11.52	NULL	2 / 38	BP myelination
14	-11.16	NULL	1 / 13	GSEA C2HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
15	-11.15	NULL	2 / 13	H.Tiss WIRTH_Tonsil
16	-10.87	NULL	1 / 10	BP homeostatic process
17	-10.87	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
18	-10.77	NULL	1 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
19	-10.5	NULL	7 / 19	BP peptide cross-linking
20	-10.5	NULL	29 / 572	Disease GUDJ_pсориаzis up
21	-10.22	NULL	1 / 15	BP positive regulation of extrinsic apoptotic signaling pathway via deat
22	-10.22	NULL	1 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
23	-10.22	NULL	1 / 15	GSEA C2BIOCARTA_MAL_PATHWAY
24	-10.19	NULL	1 / 12	GSEA C2ODONNELL_METASTASIS_DN
25	-10.19	NULL	1 / 12	GSEA C2SYED ESTRADIOL_RESPONSE
26	-10.11	NULL	3 / 39	BP retinoid metabolic process
27	-9.92	NULL	1 / 14	BP tissue regeneration
28	-9.82	NULL	1 / 16	Cancer GENTLES_modul11
29	-9.5	NULL	1 / 15	BP hormone metabolic process
30	-9.32	NULL	2 / 55	Glio OL vs. MOG- OL
31	-9.3	NULL	1 / 8	GSEA C2JU_CDX2_TARGETS_DN
32	-9.13	NULL	1 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
33	-9.03	NULL	1 / 12	MF retinol binding
34	-8.98	NULL	2 / 15	GSEA C2L_AMPLIFIED_IN_LUNG_CANCER
35	-8.8	NULL	1 / 17	Disease BCHETNIA_EBM up
36	-8.79	NULL	1 / 14	MF ankyrin binding
37	-8.58	NULL	1 / 13	BP retinoic acid metabolic process
38	-8.53	NULL	2 / 12	BP cellular aldehyde metabolic process
39	-7.67	NULL	9 / 76	BP epidermis development
40	-7.38	NULL	3 / 38	BP epithelial cell differentiation

