GW_052

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1821 (1078 + / 743 −)

genes with fdr < 0.1 = 1468 (882 + / 586 −)

genes with fdr < 0.05 = 1217 (757 + / 460 −)

genes with fdr < 0.01 = 861 (557 + / 304 −)

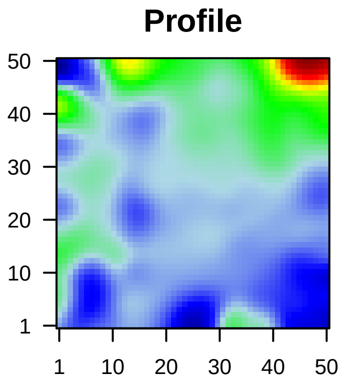
genes in genesets = 16332

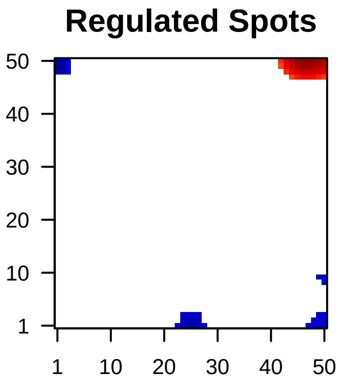
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

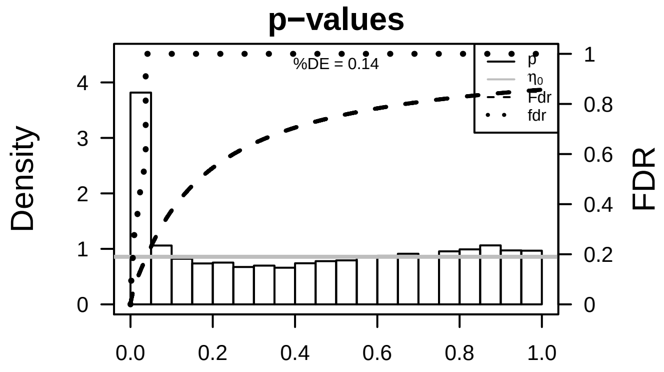
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.21	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	10840	1.45	2e−16	3e−14	50 x 12	aldehyde dehydrogenase 1 family, member L1 [Source:HGN
3	218	1.38	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	55107	1.54	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
5	445328	−1.44	2e−16	3e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
6	9070	1.28	2e−16	3e−14	47 x 46	ash2 (absent, small, or homeotic)−like (Drosophila) [Source:
7	483	1.49	2e−16	3e−14	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
8	149563	1.71	2e−16	3e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symb
9	92747	−1.17	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
10	260436	−1.18	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	8900	1.22	2e−16	3e−14	1 x 42	cyclin A1 [Source:HGNC Symbol;Acc:1577]
12	400916	1.26	2e−16	3e−14	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [So
13	9076	1.28	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
14	9071	1.41	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
15	26047	1.79	2e−16	3e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
16	54544	−1.56	2e−16	3e−14	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
17	1591	1.78	2e−16	3e−14	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
18	92196	1.49	2e−16	3e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	1672	−1.29	2e−16	3e−14	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
20	55894	−1.83	2e−16	3e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.87	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	12.87	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	12.54	NULL	914	Chr	Chr 3
4	8.3	NULL	370	BP	mitotic cell cycle
5	8.24	NULL	386	Chr	Chr 22
6	7.93	NULL	15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
7	6.98	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
8	6.97	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
9	6.91	NULL	16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
10	6.33	NULL	149	BP	DNA replication
11	6.32	NULL	13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
12	6.1	NULL	16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
13	6.07	NULL	15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
14	6.05	NULL	280	Chr	Chr 13
15	5.92	NULL	16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
16	5.9	NULL	16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
17	5.87	NULL	4640	CC	nucleus
18	5.67	NULL	14	GSEA C2	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP
19	5.56	NULL	13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
20	5.47	NULL	16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
Underexpressed					
1	−11.15	NULL	957	Chr	Chr 11
2	−7.18	NULL	1135	Chr	Chr 19
3	−6.72	NULL	42	BP	keratinization
4	−6.6	NULL	21	CC	cornified envelope
5	−6.51	NULL	4	MMML CGS	MACIEJ_MMML 23
6	−6.44	NULL	15	CC	MHC class II protein complex
7	−6.43	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
8	−5.85	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
9	−5.27	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
10	−5.08	NULL	21	CC	clathrin−coated endocytic vesicle membrane
11	−5.08	NULL	232	Chr	Chr 18
12	−5.01	NULL	1182	CC	extracellular region
13	−4.97	NULL	11	MF	oxygen transporter activity
14	−4.92	NULL	633	Chr	Chr 9
15	−4.8	NULL	36	BP	muscle filament sliding
16	−4.74	NULL	15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
17	−4.5	NULL	11	GSEA C2	BIOCARTA_AHSP_PATHWAY
18	−4.5	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
19	−4.4	NULL	16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
20	−4.4	NULL	44	MF	structural constituent of muscle

GW_052

Local Summary

%DE = 0.78

metagenes = 33

genes = 438

genes in genesets = 434

genes with fdr < 0.1 = 259 (238 + / 21 −)

genes with fdr < 0.05 = 236 (217 + / 19 −)

genes with fdr < 0.01 = 196 (181 + / 15 −)

<r> metagenes = 0.86

<r> genes = 0.28

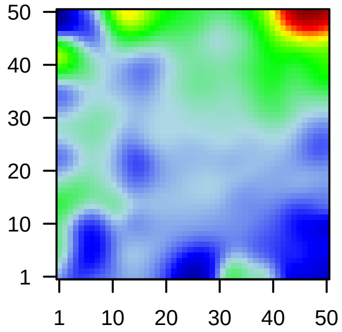
<FC> = 0.37

<shrinkage−t> = 12.79

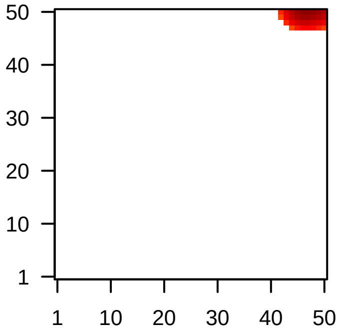
<p−value> = 0

<fdr> = 0.45

Profile



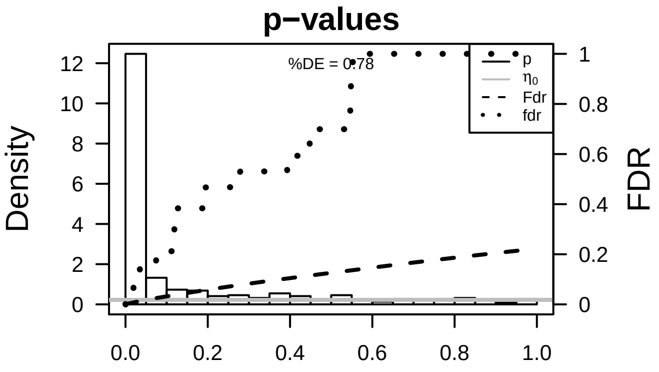
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.21	2e−16	2e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	400916	1.26	2e−16	2e−15	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [Sou
3	9076	1.28	2e−16	2e−15	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
4	26047	1.79	2e−16	2e−15	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
5	3866	1.35	2e−16	2e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
6	4171	1.43	2e−16	2e−15	46 x 48	minichromosome maintenance complex component 2 [Source
7	9918	1.33	2e−16	2e−15	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
8	4922	3.87	2e−16	2e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
9	5096	1.23	2e−16	2e−15	49 x 50	propionyl CoA carboxylase, beta polypeptide [Source:HGNC
10	139728	2.09	2e−16	2e−15	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
11	10721	1.21	2e−16	2e−15	46 x 48	polymerase (DNA directed), theta [Source:HGNC Symbol;Acc
12	7546	1.58	2e−16	2e−15	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
13	9582	1.12	2e−15	8e−14	46 x 49	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
14	214	−1.11	2e−15	8e−14	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
15	655	1.11	3e−15	8e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
16	339512	1.1	3e−15	3e−12	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
17	6565	1.06	3e−14	3e−12	50 x 50	solute carrier family 15 (oligopeptide transporter), member 2 [
18	80896	1.04	1e−13	3e−12	50 x 50	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
19	200810	1.04	1e−13	3e−12	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransferas
20	6596	1.04	1e−13	1e−11	46 x 50	helicase−like transcription factor [Source:HGNC Symbol;Acc:

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.55	NULL	86 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	29.55	NULL	86 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	20.7	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
4	19.41	NULL	11 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
5	17.03	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
6	16.98	NULL	12 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
7	16.46	NULL	10 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
8	16.39	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
9	15.72	NULL	10 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
10	15.42	NULL	7 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
11	14.96	NULL	4 / 13	BP	regulation of blood vessel size
12	14.94	NULL	81 / 370	BP	mitotic cell cycle
13	14.87	NULL	8 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
14	14.48	NULL	23 / 57	Glio	developing astrocytes
15	14.19	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
16	13.85	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
17	13.76	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
18	13.53	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
19	13.36	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
20	13.32	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
21	13.27	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
22	13.16	NULL	10 / 16	Cancer	WOLFER_overlap genes
23	13.15	NULL	1 / 11	Glio	neurons_glio
24	13.12	NULL	6 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
25	12.86	NULL	86 / 530	Cancer	Lembcke_Normal vs Adenoma
26	12.8	NULL	9 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	12.76	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
28	12.72	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
29	12.48	NULL	7 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
30	12.46	NULL	5 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
31	12.37	NULL	77 / 914	Chr	Chr 3
32	12.31	NULL	9 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
33	12.25	NULL	35 / 149	BP	DNA replication
34	12.24	NULL	6 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
35	12.24	NULL	7 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
36	12.15	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
37	11.94	NULL	7 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
38	11.79	NULL	6 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
39	11.72	NULL	8 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
40	11.5	NULL	8 / 15	GSEA C2	CHANG_CYCLING_GENES

GW_052

Local Summary

%DE = 0.67

metagenes = 14

genes = 106

genes in genesets = 106

genes with fdr < 0.1 = 39 (6 + / 33 −)

genes with fdr < 0.05 = 25 (4 + / 21 −)

genes with fdr < 0.01 = 16 (3 + / 13 −)

<r> metagenes = 0.96

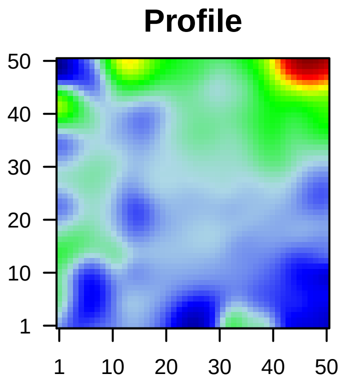
<r> genes = 0.61

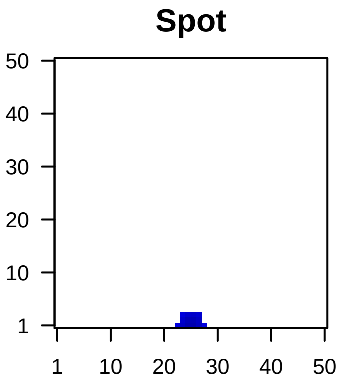
<FC> = −0.23

<shrinkage−t> = −8.06

<p−value> = 0.02

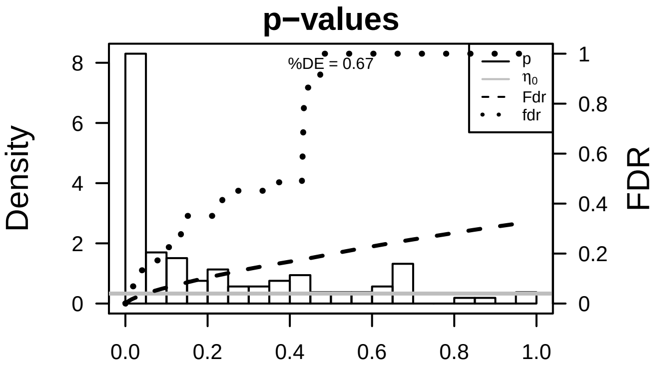
<fdr> = 0.69





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	283120	−1.77	2e−16	8e−15	25 x 1	H19, imprinted maternally expressed transcript (non−protein
2	1917	−0.91	7e−11	3e−09	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
3	2318	−0.89	2e−10	3e−09	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
4	58	−0.88	3e−10	4e−05	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
5	70	−0.66	2e−06	4e−05	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
6	1410	0.66	2e−06	2e−04	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
7	6588	−0.62	1e−05	2e−04	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
8	84940	0.61	1e−05	3e−04	25 x 1	coronin 6 [Source:HGNC Symbol;Acc:21356]
9	4151	−0.59	2e−05	3e−04	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
10	274	−0.58	3e−05	3e−04	26 x 1	bridging integrator 1 [Source:HGNC Symbol;Acc:1052]
11	5269	−0.57	4e−05	8e−04	28 x 1	serpin peptidase inhibitor, clade B (ovalbumin), member 6 [S
12	115265	−0.56	6e−05	9e−04	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
13	8736	−0.55	9e−05	9e−04	25 x 1	myomesin 1 [Source:HGNC Symbol;Acc:7613]
14	4608	−0.53	1e−04	9e−04	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
15	388115	−0.53	1e−04	7e−03	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Sym
16	22998	0.5	4e−04	7e−03	24 x 1	LIM and calponin homology domains 1 [Source:HGNC Symb
17	1158	−0.48	5e−04	1e−02	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
18	4620	−0.46	1e−03	1e−02	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
19	10486	0.45	1e−03	1e−02	24 x 1	CAP, adenylate cyclase−associated protein, 2 (yeast) [Source
20	222166	−0.44	2e−03	1e−02	24 x 1	maturin, neural progenitor differentiation regulator homolog (



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−40.55	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
2	−37.67	NULL	23 / 36	BP	muscle filament sliding
3	−37.35	NULL	55 / 127	H.Tiss	WIRTH_Muscle
4	−35.02	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	−33.12	NULL	10 / 12	CC	myosin filament
6	−31.42	NULL	22 / 44	MF	structural constituent of muscle
7	−25.19	NULL	12 / 37	CC	sarcomere
8	−22.82	NULL	8 / 13	CC	muscle myosin complex
9	−21.11	NULL	23 / 84	BP	muscle contraction
10	−19.36	NULL	8 / 16	CC	M band
11	−18.49	NULL	15 / 34	CC	myofibril
12	−15.71	NULL	7 / 12	MF	titin binding
13	−15.56	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
14	−15.13	NULL	3 / 15	Cancer	BEN−PORATH_UP
15	−15.01	NULL	9 / 37	BP	cardiac muscle contraction
16	−14.6	NULL	21 / 88	CC	Z disc
17	−14.43	NULL	7 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
18	−14.21	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
19	−14.02	NULL	7 / 15	BP	striated muscle contraction
20	−13.2	NULL	2 / 12	BP	muscle fiber development
21	−12.09	NULL	3 / 18	CC	costamere
22	−12.01	NULL	2 / 10	BP	heart contraction
23	−11.97	NULL	8 / 42	CC	myosin complex
24	−11.92	NULL	2 / 20	MF	myosin binding
25	−11.83	NULL	4 / 16	MF	microfilament motor activity
26	−10.96	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
27	−10.77	NULL	4 / 14	BP	adult heart development
28	−10.52	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
29	−10.52	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
30	−10.39	NULL	5 / 26	BP	ventricular cardiac muscle tissue morphogenesis
31	−10.35	NULL	3 / 15	BP	actin filament−based movement
32	−10.3	NULL	4 / 11	CC	A band
33	−10.11	NULL	2 / 14	GSEA C2	BIOCARTA_UCALPAIN_PATHWAY
34	−9.96	NULL	6 / 12	BP	skeletal muscle contraction
35	−9.92	NULL	1 / 10	GSEA C2	BIOCARTA_EPHA4_PATHWAY
36	−9.73	NULL	2 / 15	GSEA C2	BIOCARTA_INTEGRIN_PATHWAY
37	−9.68	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
38	−9.68	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
39	−9.62	NULL	3 / 37	CC	actin filament
40	−9.62	NULL	7 / 21	BP	sarcomere organization

GW_052

Local Summary

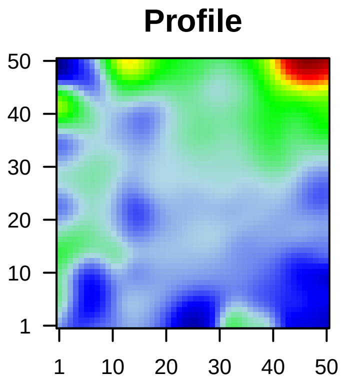
%DE = 0.52
metagenes = 9
genes = 209
genes in genesets = 207

genes with fdr < 0.1 = 35 (7 + / 28 −)
genes with fdr < 0.05 = 28 (6 + / 22 −)
genes with fdr < 0.01 = 21 (5 + / 16 −)

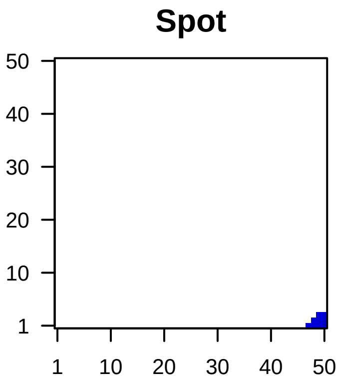
<r> metagenes = 1
<r> genes = 0.63

<FC> = −0.14
<shrinkage−t> = −4.74
<p−value> = 0.04
<fdr> = 0.79

Profile



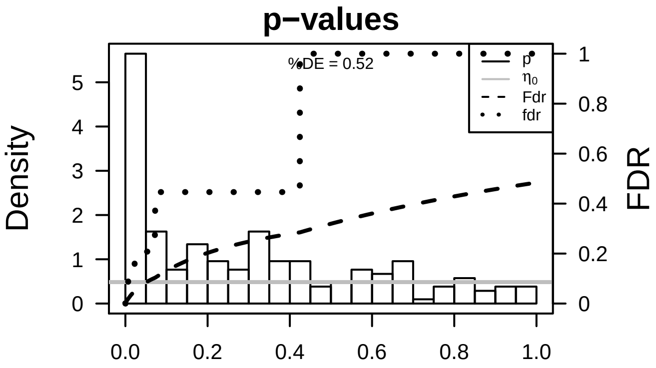
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.18	2e−16	1e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	5996	1.16	2e−16	1e−14	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
3	3126	−1	1e−12	2e−06	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
4	3108	−0.79	2e−08	4e−06	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
5	341	−0.76	6e−08	2e−05	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
6	348	−0.73	2e−07	8e−05	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	3543	0.63	1e−06	8e−05	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
8	57484	−0.67	2e−06	8e−05	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
9	3120	−0.65	3e−06	8e−05	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
10	3002	0.65	3e−06	7e−04	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
11	80833	0.61	1e−05	7e−04	47 x 1	apolipoprotein L, 3 [Source:HGNC Symbol;Acc:14868]
12	83641	−0.59	2e−05	7e−04	50 x 1	family with sequence similarity 107, member B [Source:HGN
13	54855	−0.59	3e−05	1e−03	49 x 1	family with sequence similarity 46, member C [Source:HGNC
14	3109	−0.57	4e−05	1e−03	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
15	1593	−0.57	5e−05	1e−03	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sour
16	55365	−0.56	6e−05	2e−03	50 x 3	transmembrane protein 176A [Source:HGNC Symbol;Acc:24
17	23180	−0.55	9e−05	2e−03	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
18	3689	−0.55	1e−04	3e−03	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
19	10537	−0.53	1e−04	3e−03	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
20	10563	−0.53	2e−04	8e−03	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−35.05	NULL	12 / 15	CC	MHC class II protein complex
2	−23.71	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
3	−20.37	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
4	−19.52	NULL	14 / 47	BP	antigen processing and presentation
5	−19.36	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
6	−17.54	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
7	−17.36	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
8	−17.36	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
9	−17.36	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
10	−16.72	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	−15.66	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
12	−15.09	NULL	7 / 28	CC	transport vesicle membrane
13	−14.68	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen
14	−14.16	NULL	2 / 8	GSEA C2	KEGG_CELL_ADHESION_MOLECULES_CAMS
15	−14.06	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
16	−13.98	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
17	−13.9	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
18	−13.62	NULL	2 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
19	−13.41	NULL	7 / 35	CC	trans−Golgi network membrane
20	−13.35	NULL	2 / 11	BP	high−density lipoprotein particle remodeling
21	−13.35	NULL	2 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
22	−12.96	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
23	−12.43	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
24	−12.01	NULL	1 / 4	GSEA C2	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY
25	−12.01	NULL	1 / 4	GSEA C2	REACTOME_DOWNSTREAM_TCR_SIGNALING
26	−12.01	NULL	1 / 4	GSEA C2	REACTOME_TCR_SIGNALING
27	−11.76	NULL	2 / 14	CC	very−low−density lipoprotein particle
28	−11.61	NULL	5 / 12	BP	immunoglobulin mediated immune response
29	−11.6	NULL	7 / 46	CC	endocytic vesicle membrane
30	−11.52	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
31	−11.34	NULL	2 / 15	BP	cholesterol efflux
32	−11.34	NULL	2 / 15	CC	high−density lipoprotein particle
33	−10.94	NULL	9 / 60	BP	interferon−gamma−mediated signaling pathway
34	−10.48	NULL	13 / 60	BP	T cell costimulation
35	−10.44	NULL	2 / 13	MMML CGS	MACIEJ_MMML 6
36	−10.17	NULL	2 / 8	GSEA C2	HELLER_SILENCED_BY_METHYLATION_UP
37	−10.15	NULL	33 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
38	−10.15	NULL	33 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
39	−10.15	NULL	33 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
40	−10.15	NULL	33 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down

GW_052

Local Summary

%DE = 0.93

metagenes = 3

genes = 64

genes in genesets = 63

genes with fdr < 0.1 = 54 (7 + / 47 −)

genes with fdr < 0.05 = 40 (5 + / 35 −)

genes with fdr < 0.01 = 30 (5 + / 25 −)

<r> metagenes = 0.99

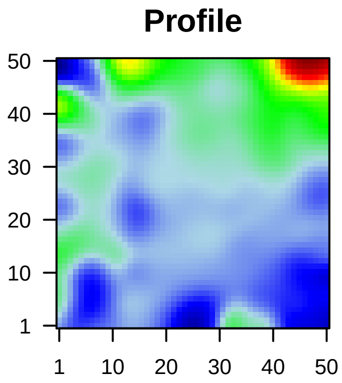
<r> genes = 0.42

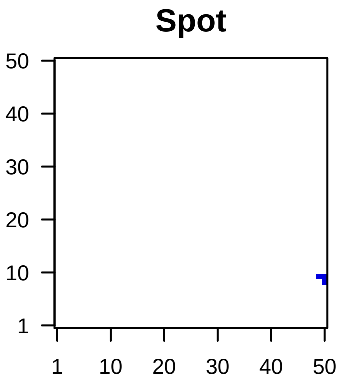
<FC> = −0.28

<shrinkage−t> = −9.66

<p−value> = 0

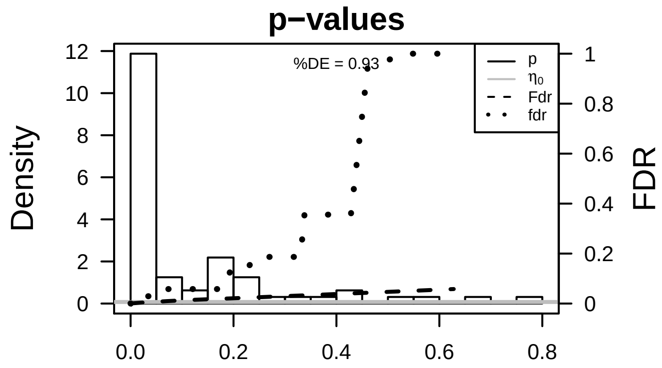
<fdr> = 0.51





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	92747	−1.17	2e−16	1e−15	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
2	6192	1.05	7e−14	3e−12	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
3	7033	−1	8e−13	9e−10	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
4	8842	−0.89	2e−10	6e−09	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
5	92304	−0.84	2e−09	6e−09	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
6	283229	−0.83	3e−09	7e−08	50 x 10	EF−hand calcium binding domain 4A [Source:HGNC Symbol;
7	2878	0.79	2e−08	1e−07	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
8	389816	−0.77	4e−08	3e−07	50 x 10	leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
9	140032	0.74	1e−07	3e−07	49 x 10	ribosomal protein S4, Y−linked 2 [Source:HGNC Symbol;Acc
10	5284	−0.73	2e−07	5e−07	50 x 10	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
11	256691	−0.72	3e−07	5e−07	50 x 9	MAM domain containing 2 [Source:HGNC Symbol;Acc:23673
12	5918	−0.71	4e−07	3e−06	50 x 9	retinoic acid receptor responder (tazarotene induced) 1 [Sour
13	11272	−0.67	2e−06	3e−06	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
14	4824	−0.67	2e−06	8e−06	50 x 10	NK3 homeobox 1 [Source:HGNC Symbol;Acc:7838]
15	79083	−0.65	4e−06	1e−05	50 x 10	melanophilin [Source:HGNC Symbol;Acc:29643]
16	84952	−0.63	7e−06	1e−04	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
17	124220	−0.57	5e−05	1e−04	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
18	7018	0.56	6e−05	2e−04	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
19	1755	−0.54	1e−04	5e−04	50 x 10	deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
20	7103	−0.5	3e−04	5e−04	50 x 10	tetraspanin 8 [Source:HGNC Symbol;Acc:11855]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.84	NULL	10 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−18.75	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	−15.31	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
4	−14.34	NULL	2 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
5	−13.38	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
6	−12.89	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
7	−10.86	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
8	−10.66	NULL	1 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
9	−10.66	NULL	1 / 7	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
10	−10.48	NULL	2 / 12	BP	urogenital system development
11	−10.33	NULL	1 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
12	−10.12	NULL	1 / 11	CC	photoreceptor outer segment membrane
13	−10.02	NULL	1 / 7	TF Tissue	VAQUERIZAS_Appendix
14	−9.61	NULL	1 / 12	BP	retina layer formation
15	−8.47	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
16	−8.1	NULL	1 / 16	CC	microvillus membrane
17	−8.1	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
18	−7.96	NULL	2 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
19	−7.94	NULL	2 / 14	GSEA C2	PENG_RAPAMYCIN_RESPONSE_UP
20	−7.91	NULL	1 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
21	−7.91	NULL	1 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
22	−7.78	NULL	1 / 10	CC	microtubule plus−end
23	−7.78	NULL	1 / 10	Cancer	LIU_BREAST_CANCER
24	−7.56	NULL	1 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
25	−7.49	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
26	−7.17	NULL	2 / 53	Glio	Christensen_hypermethylated_in_primary_glioblastoma
27	−7.1	NULL	1 / 20	CC	stereocilium
28	−6.77	NULL	1 / 12	CC	apical junction complex
29	−6.73	NULL	1 / 15	CC	interstitial matrix
30	−6.72	NULL	1 / 22	MF	cadherin binding
31	−6.69	NULL	1 / 15	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
32	−6.69	NULL	1 / 15	GSEA C2	ZIRN_TRETINOIN_RESPONSE_WT1_UP
33	−6.55	NULL	1 / 14	BP	pharyngeal system development
34	−6.55	NULL	1 / 23	CC	brush border
35	−6.43	NULL	2 / 64	Glio	Christensen_hypermethylated_in_grade2_astrocytoma
36	−6.39	NULL	1 / 24	BP	photoreceptor cell maintenance
37	−6.31	NULL	2 / 37	BP	digestion
38	−6.17	NULL	1 / 14	GSEA C2	PEREZ_TP53_AND_TP63_TARGETS
39	−6.04	NULL	1 / 16	BP	negative regulation of mitotic cell cycle
40	−6.04	NULL	1 / 16	MF	protein kinase activator activity

GW_052

Local Summary

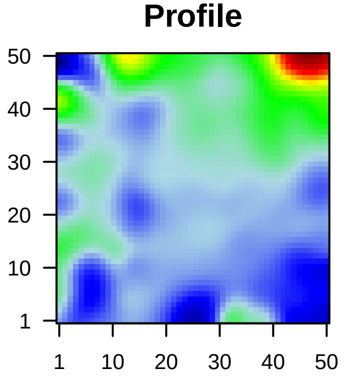
%DE = 0.86
metagenes = 9
genes = 141
genes in genesets = 138

genes with fdr < 0.1 = 105 (35 + / 70 −)
genes with fdr < 0.05 = 100 (33 + / 67 −)
genes with fdr < 0.01 = 90 (30 + / 60 −)

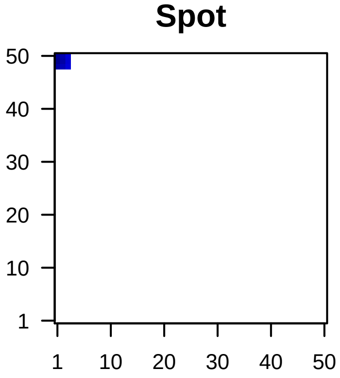
<r> metagenes = 0.99
<r> genes = 0.51

<FC> = −0.3
<shrinkage−t> = −10.4
<p−value> = 0
<fdr> = 0.31

Profile



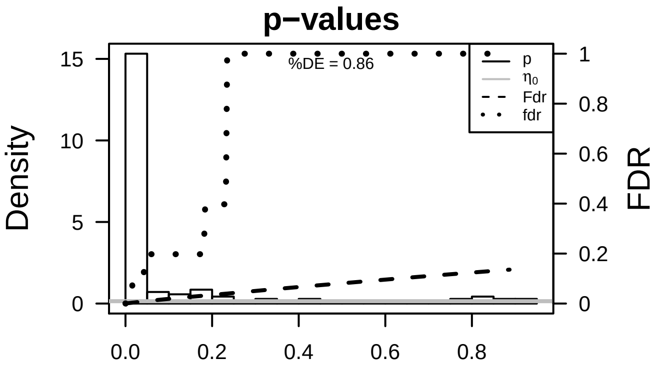
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	1.38	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
2	54544	−1.56	2e−16	2e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
3	92196	1.49	2e−16	2e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
4	1672	−1.29	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
5	414325	−2.67	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
6	1673	−2.19	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
7	1828	−1.19	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
8	26525	−1.17	2e−16	2e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
9	43849	−1.61	2e−16	2e−16	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
10	192666	−1.16	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
11	3851	1.56	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
12	84648	−1.9	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
13	3934	−1.34	2e−16	2e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
14	84659	−1.6	2e−16	2e−16	1 x 48	ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc:
15	6278	−1.9	2e−16	2e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
16	338324	−1.23	2e−16	2e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
17	5055	−1.27	2e−16	2e−16	1 x 50	serpin peptidase inhibitor, clade B (ovalbumin), member 2 [Sc
18	6590	−1.42	2e−16	2e−16	1 x 49	secretory leukocyte peptidase inhibitor [Source:HGNC Symbo
19	84651	−1.33	2e−16	2e−16	1 x 50	serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
20	6701	−1.28	2e−16	2e−16	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.67	NULL	14 / 21	CC	cornified envelope
2	−18.73	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
3	−17.6	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
4	−16.6	NULL	16 / 42	BP	keratinization
5	−15.26	NULL	66 / 572	Disease	GUDJ_psoriasis up
6	−14.18	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
7	−13.65	NULL	5 / 10	MF	RAGE receptor binding
8	−13.31	NULL	19 / 53	BP	keratinocyte differentiation
9	−13.22	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
10	−12.62	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
11	−12.42	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
12	−12.16	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
13	−11.84	NULL	7 / 73	BP	defense response to bacterium
14	−11.8	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
15	−11.75	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
16	−11.27	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	−10.76	NULL	4 / 27	BP	response to bacterium
18	−10.66	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
19	−10.54	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
20	−10.07	NULL	3 / 63	CC	Golgi lumen
21	−9.97	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
22	−9.84	NULL	16 / 76	BP	epidermis development
23	−9.82	NULL	2 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
24	−9.82	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_B_DN
25	−9.66	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
26	−9.45	NULL	8 / 52	BP	negative regulation of endopeptidase activity
27	−9.35	NULL	3 / 16	GSEA C2	JAEGER_METASTASIS_DN
28	−9.16	NULL	42 / 1182	CC	extracellular region
29	−9.07	NULL	3 / 76	BP	defense response
30	−8.78	NULL	1 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
31	−8.05	NULL	3 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
32	−7.95	NULL	3 / 15	GSEA C2	FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP
33	−7.87	NULL	4 / 23	MF	peptidase inhibitor activity
34	−7.69	NULL	1 / 16	BP	response to reactive oxygen species
35	−7.47	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
36	−7.41	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
37	−7.32	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
38	−7.29	NULL	2 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
39	−7.26	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
40	−7.13	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_