GW_102

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1715 (931 + / 784 −)

genes with fdr < 0.1 = 1304 (728 + / 576 −)

genes with fdr < 0.05 = 928 (547 + / 381 −)

genes with fdr < 0.01 = 596 (393 + / 203 −)

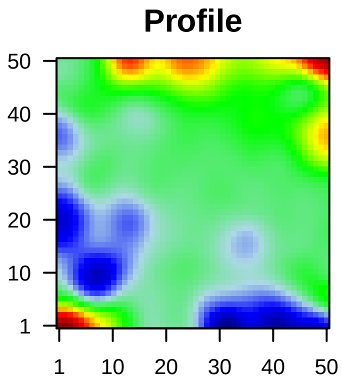
genes in genesets = 16332

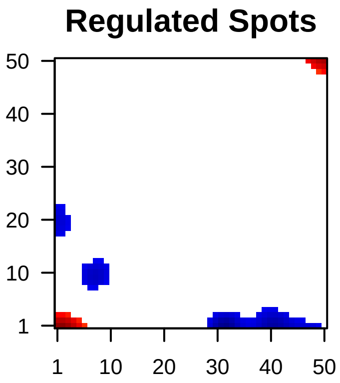
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



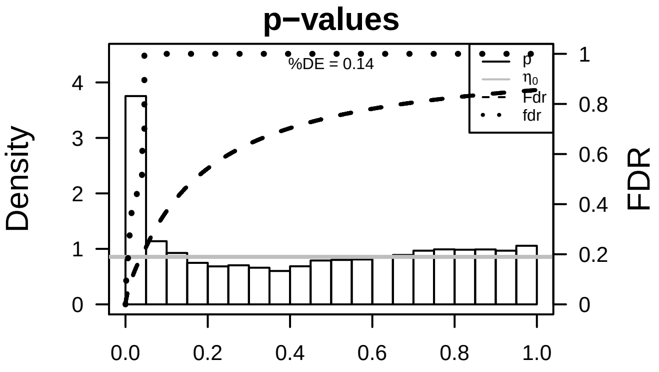


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.97	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	1.63	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	1.8	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
4	1109	1.88	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
5	218	1.74	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	55107	2.59	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
7	483	1.45	2e−16	4e−14	13 x 50	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HG
8	56271	1.41	2e−16	4e−14	50 x 12	brain expressed, X−linked 4 [Source:HGNC Symbol;Acc:2547
9	205428	1.45	2e−16	4e−14	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
10	29113	1.4	2e−16	4e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
11	26256	1.33	2e−16	4e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
12	51806	−1.8	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
13	6364	1.37	2e−16	4e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
14	1066	1.87	2e−16	4e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
15	9073	1.68	2e−16	4e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
16	26047	1.32	2e−16	4e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
17	1278	1.43	2e−16	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
18	1281	1.86	2e−16	4e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
19	1290	1.45	2e−16	4e−14	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
20	441520	1.9	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.88	NULL	190	CC	extracellular matrix
2	13.61	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	13.5	NULL	242	BP	extracellular matrix organization
4	12.32	NULL	16	MMML CGS	MACIEJ_MMML 1
5	11.29	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	11.17	NULL	69	BP	extracellular matrix disassembly
7	10.55	NULL	64	BP	collagen catabolic process
8	10.14	NULL	436	miRNA target−starBase	hsa−miR−548n
9	9.81	NULL	1033	Chr	Chr 2
10	9.73	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
11	9.35	NULL	57	MF	extracellular matrix structural constituent
12	9.25	NULL	368	miRNA target−starBase	hsa−miR−144
13	8.96	NULL	280	Chr	Chr 13
14	8.93	NULL	12	miRNA target	miR−29c
15	8.87	NULL	183	CC	proteinaceous extracellular matrix
16	8.79	NULL	456	miRNA target−starBase	hsa−miR−130a
17	8.74	NULL	37	BP	collagen fibril organization
18	8.7	NULL	11	MF	platelet−derived growth factor binding
19	8.64	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
20	8.54	NULL	463	miRNA target−starBase	hsa−miR−301a
Underexpressed					
1	−14.07	NULL	1135	Chr	Chr 19
2	−11.13	NULL	51	BP	type I interferon signaling pathway
3	−10.73	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
4	−9.69	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
5	−9.15	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−8.88	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	−8.86	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	−8.54	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	−8.51	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
10	−7.97	NULL	31	BP	negative regulation of viral genome replication
11	−7.67	NULL	123	BP	defense response to virus
12	−7.49	NULL	1720	Chr	Chr 1
13	−7.37	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
14	−7.37	NULL	4	MMML CGS	MACIEJ_MMML 47
15	−7.11	NULL	4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
16	−6.72	NULL	14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
17	−6.49	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
18	−6.13	NULL	417	H.Tiss	WIRTH_Immune system
19	−6.08	NULL	11	GSEA C2	FUJII_YBX1_TARGETS_UP
20	−5.85	NULL	109	BP	response to virus



GW_102

Local Summary

%DE = 0.75

metagenes = 14

genes = 248

genes in genesets = 247

genes with fdr < 0.1 = 152 (145 + / 7 −)

genes with fdr < 0.05 = 150 (143 + / 7 −)

genes with fdr < 0.01 = 120 (117 + / 3 −)

<r> metagenes = 0.96

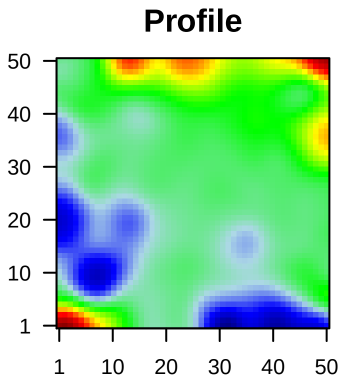
<r> genes = 0.42

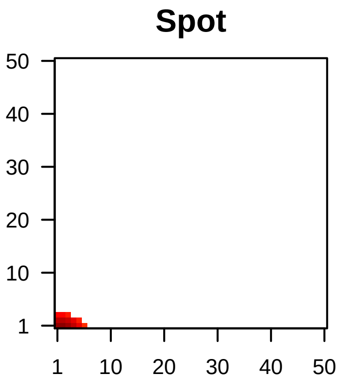
<FC> = 0.53

<shrinkage−t> = 18.67

<p−value> = 0

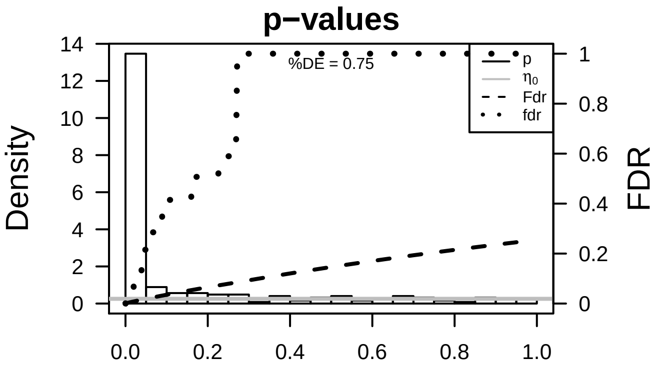
<fdr> = 0.39





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1278	1.43	2e−16	7e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
2	1281	1.86	2e−16	7e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
3	1290	1.45	2e−16	7e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
4	1490	1.36	2e−16	7e−16	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
5	6374	2.21	2e−16	7e−16	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
6	6372	2	2e−16	7e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
7	54749	1.57	2e−16	7e−16	5 x 1	ependymin related 1 [Source:HGNC Symbol;Acc:17572]
8	2619	1.43	2e−16	7e−16	2 x 1	growth arrest−specific 1 [Source:HGNC Symbol;Acc:4165]
9	3569	2.11	2e−16	7e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
10	3576	1.72	2e−16	7e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	4060	1.49	2e−16	7e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
12	4312	1.91	2e−16	7e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
13	4322	1.95	2e−16	7e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
14	4314	2.35	2e−16	7e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
15	4885	1.71	2e−16	7e−16	5 x 1	neuronal pentraxin II [Source:HGNC Symbol;Acc:7953]
16	10631	1.59	2e−16	7e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
17	5743	1.36	2e−16	7e−16	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
18	6423	1.45	2e−16	7e−16	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
19	6696	1.89	2e−16	7e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
20	7130	1.78	2e−16	7e−16	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	36.55	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
2	35.66	NULL	66 / 190	CC	extracellular matrix
3	34.47	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
4	32.23	NULL	31 / 69	BP	extracellular matrix disassembly
5	31.92	NULL	27 / 64	BP	collagen catabolic process
6	29.25	NULL	8 / 12	miRNA target	miR−29c
7	28.59	NULL	8 / 11	MF	platelet−derived growth factor binding
8	27.9	NULL	75 / 250	Lymphoma	LENZ_Stromal signature 1
9	27.45	NULL	60 / 242	BP	extracellular matrix organization
10	24.47	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
11	24.2	NULL	77 / 683	CC	extracellular space
12	22.67	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
13	22.49	NULL	13 / 37	BP	collagen fibril organization
14	22.35	NULL	19 / 57	MF	extracellular matrix structural constituent
15	22.31	NULL	11 / 19	MF	extracellular matrix binding
16	21.09	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
17	20.8	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
18	20.51	NULL	102 / 1182	CC	extracellular region
19	20.45	NULL	35 / 183	CC	proteinaceous extracellular matrix
20	19.72	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
21	19.17	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
22	18.3	NULL	6 / 12	GSEA C2	LY_AGING_MIDDLE_UP
23	18.08	NULL	10 / 40	BP	cellular response to amino acid stimulus
24	17.84	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
25	17.66	NULL	4 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
26	17.31	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
27	17.23	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
28	16.64	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
29	16.61	NULL	64 / 553	Cancer	Lembcke_Colonic Inflammation
30	16.6	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
31	16.49	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
32	16.27	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
33	16.25	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
34	16.24	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
35	15.91	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
36	15.41	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
37	15.39	NULL	5 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
38	15.36	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
39	15.32	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
40	15.31	NULL	5 / 10	BP	negative regulation of fibroblast growth factor receptor signaling pa

GW_102

Local Summary

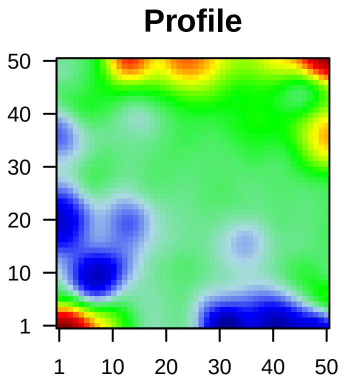
%DE = 0.78
metagenes = 9
genes = 168
genes in genesets = 167

genes with fdr < 0.1 = 124 (115 + / 9 −)
genes with fdr < 0.05 = 112 (105 + / 7 −)
genes with fdr < 0.01 = 99 (94 + / 5 −)

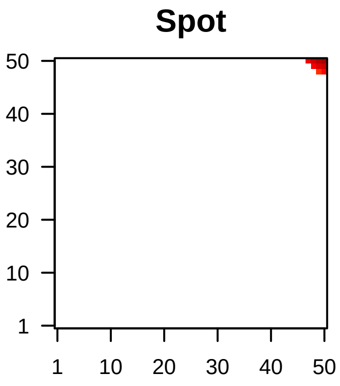
<r> metagenes = 0.97
<r> genes = 0.29

<FC> = 0.5
<shrinkage−t> = 17.61
<p−value> = 0
<fdr> = 0.32

Profile



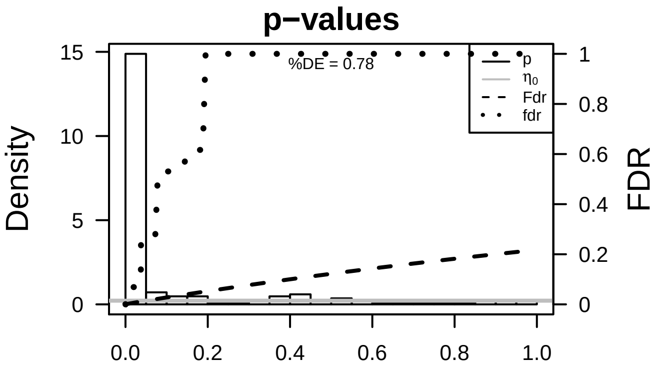
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	205428	1.45	2e−16	8e−16	50 x 50	chromosome 3 open reading frame 58 [Source:HGNC Symbo
2	26256	1.33	2e−16	8e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
3	26047	1.32	2e−16	8e−16	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
4	2944	1.82	2e−16	8e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
5	3880	1.4	2e−16	8e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
6	84171	1.53	2e−16	8e−16	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
7	4922	1.79	2e−16	8e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
8	11166	1.42	2e−16	8e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
9	54578	1.41	2e−16	8e−16	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
10	7348	2.18	2e−16	8e−16	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
11	154664	1.29	2e−15	5e−13	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
12	4072	1.24	2e−14	5e−13	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
13	216	1.23	3e−14	1e−12	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
14	10643	1.22	7e−14	4e−11	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:H
15	79679	1.15	1e−12	3e−10	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:H
16	8745	1.1	1e−11	3e−10	50 x 50	ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
17	159371	1.09	2e−11	3e−10	49 x 50	solute carrier family 35, member G1 [Source:HGNC Symbol;A
18	1780	1.08	2e−11	7e−10	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
19	6657	1.06	5e−11	7e−10	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
20	55190	1.06	6e−11	5e−09	47 x 50	nudix (nucleoside diphosphate linked moiety X)−type motif 11

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.04	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
2	17.87	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
3	17.18	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
4	15.08	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
5	13.49	NULL	3 / 13	BP	regulation of blood vessel size
6	13.18	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
7	11.7	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
8	11.44	NULL	2 / 9	GSEA C2	REACTOME_GLUCURONIDATION
9	10.95	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
10	10.95	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
11	10.9	NULL	3 / 11	MF	glutathione binding
12	10.9	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	10.27	NULL	6 / 25	BP	glutathione derivative biosynthetic process
14	9.9	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
15	9.89	NULL	8 / 34	BP	glutathione metabolic process
16	9.59	NULL	11 / 119	BP	xenobiotic metabolic process
17	9.5	NULL	1 / 12	GSEA C2	DAZARD_RESPONSE_TO_UV_SCC_UP
18	9.38	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
19	9.37	NULL	2 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
20	9.04	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
21	9.04	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
22	8.75	NULL	45 / 914	Chr	Chr 3
23	8.68	NULL	1 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
24	8.68	NULL	1 / 14	GSEA C2	LOPEZ_EPITHELIOID_MESOTHELIOMA
25	8.48	NULL	3 / 16	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
26	8.39	NULL	1 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_D
27	8.29	NULL	4 / 15	GSEA C2	MMS_MOUSE_LYMPH_HIGH_4HRS_UP
28	8.17	NULL	1 / 11	Glio	neurons_glio
29	8.06	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
30	8.01	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
31	8.01	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
32	7.61	NULL	2 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_Y
33	7.6	NULL	3 / 16	GSEA C2	RODWELL_AGING_KIDNEY_DN
34	7.52	NULL	2 / 11	BP	planar cell polarity pathway involved in neural tube closure
35	7.46	NULL	2 / 23	BP	stem cell differentiation
36	7.43	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
37	7.4	NULL	2 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_U
38	7.26	NULL	2 / 16	GSEA C2	TCGA_GLIOBLASTOMA_COPY_NUMBER_UP
39	7.24	NULL	3 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
40	7.24	NULL	3 / 16	GSEA C2	SANA_RESPONSE_TO_IFNG_DN

GW_102

Local Summary

%DE = 0.77

metagenes = 53

genes = 649

genes in genesets = 617

genes with fdr < 0.1 = 350 (8 + / 342 −)

genes with fdr < 0.05 = 311 (8 + / 303 −)

genes with fdr < 0.01 = 208 (5 + / 203 −)

<r> metagenes = 0.74

<r> genes = 0.27

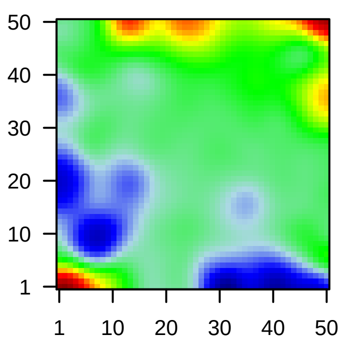
<FC> = −0.36

<shrinkage−t> = −12.51

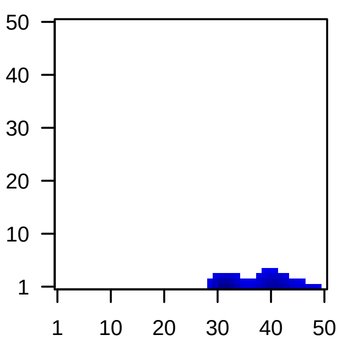
<p−value> = 0.01

<fdr> = 0.54

Profile



Spot



Local Genelist

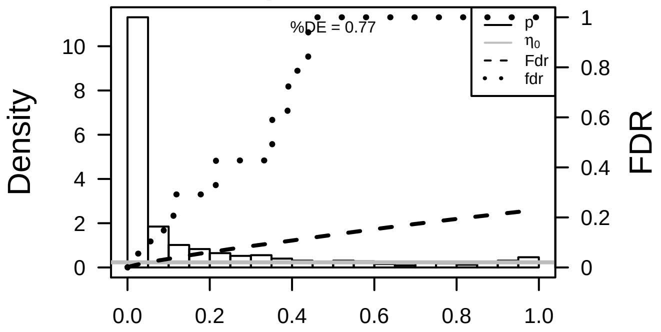
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6364	1.37	2e−16	3e−15	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
2	3627	−1.46	2e−16	3e−15	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
3	55008	−1.57	2e−16	3e−15	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
4	3127	1.74	2e−16	3e−15	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
5	10561	−1.51	2e−16	3e−15	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
6	10964	−1.58	2e−16	3e−15	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
7	2537	−1.65	2e−16	3e−15	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
8	9636	−1.97	2e−16	3e−15	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
9	5920	−1.52	2e−16	3e−15	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
10	7453	−1.54	2e−16	3e−15	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
11	684	−1.25	1e−14	1e−12	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	4599	−1.14	2e−14	3e−11	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
13	51191	−1.19	2e−13	5e−10	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
14	94240	−1.12	4e−12	5e−10	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
15	3123	1.11	7e−12	8e−10	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
16	4283	−1.1	1e−11	1e−08	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
17	6772	−1.05	8e−11	3e−07	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
18	4600	−0.97	2e−09	3e−07	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
19	8519	−0.95	4e−09	3e−07	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S
20	51326	−0.95	5e−09	3e−07	42 x 1	ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−33.61	NULL	33 / 51	BP	type I interferon signaling pathway
2	−32.53	NULL	14 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
3	−31.38	NULL	14 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
4	−30.29	NULL	11 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	−30.26	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
6	−28.67	NULL	10 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	−28.39	NULL	14 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	−26	NULL	10 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	−25.79	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
10	−25.06	NULL	43 / 123	BP	defense response to virus
11	−24.55	NULL	19 / 31	BP	negative regulation of viral genome replication
12	−23.18	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
13	−22	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
14	−21.52	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
15	−21.03	NULL	5 / 12	GSEA C2	ZHU_CMV_8_HR_UP
16	−20.74	NULL	32 / 109	BP	response to virus
17	−20.42	NULL	8 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
18	−19.91	NULL	5 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
19	−16.96	NULL	7 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
20	−16.85	NULL	7 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
21	−16.48	NULL	48 / 204	BP	cytokine−mediated signaling pathway
22	−15	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
23	−14.94	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
24	−14.81	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
25	−14.63	NULL	7 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
26	−14.63	NULL	42 / 274	Lymphoma	SPANG_IL21 DN
27	−14.52	NULL	4 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
28	−14.45	NULL	73 / 417	H.Tiss	WIRTH_Immune system
29	−14.17	NULL	8 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
30	−14.02	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
31	−13.61	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
32	−13.13	NULL	63 / 572	Disease	GUDJ_psoriasis up
33	−13.13	NULL	4 / 11	GSEA C2	FUJII_YBX1_TARGETS_UP
34	−12.78	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	−12.49	NULL	5 / 16	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
36	−12.42	NULL	7 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_LB_DN
37	−11.64	NULL	9 / 32	BP	negative regulation of type I interferon production
38	−11.6	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
39	−11.6	NULL	4 / 9	GSEA C2	FURUKAWA_DUSP6_TARGETS_PCI35_UP
40	−11.59	NULL	20 / 74	BP	regulation of immune response

p−values



GW_102

Local Summary

%DE = 0.95

metagenes = 24

genes = 262

genes in genesets = 260

genes with fdr < 0.1 = 222 (2 + / 220 −)

genes with fdr < 0.05 = 217 (2 + / 215 −)

genes with fdr < 0.01 = 117 (0 + / 117 −)

<r> metagenes = 0.94

<r> genes = 0.31

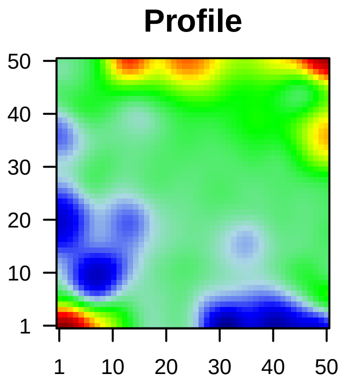
<FC> = −0.33

<shrinkage−t> = −11.68

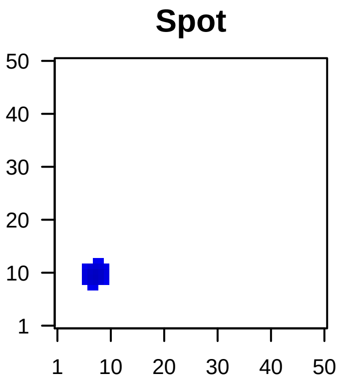
<p−value> = 0.02

<fdr> = 0.6

Profile



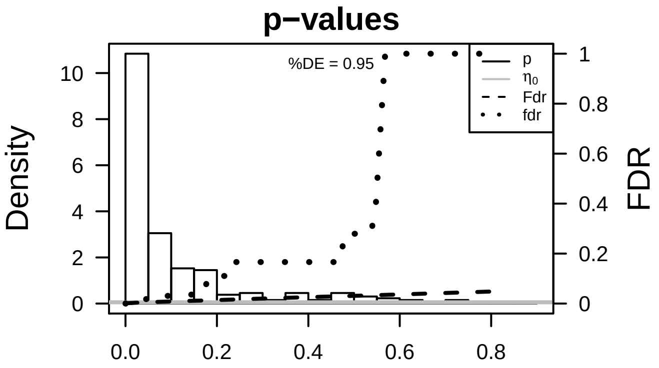
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	65980	−0.85	1e−07	1e−06	9 x 10	bromodomain containing 9 [Source:HGNC Symbol;Acc:2581
2	29894	−0.85	2e−07	5e−06	8 x 10	cleavage and polyadenylation specific factor 1, 160kDa [Sour
3	80728	−0.81	5e−07	2e−05	10 x 11	Rho GTPase activating protein 39 [Source:HGNC Symbol;Ac
4	55661	−0.77	2e−06	2e−04	7 x 10	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
5	402	−0.7	2e−05	3e−04	8 x 10	ADP−ribosylation factor−like 2 [Source:HGNC Symbol;Acc:6
6	10227	−0.64	7e−05	3e−04	6 x 9	major facilitator superfamily domain containing 10 [Source:H
7	93109	−0.64	8e−05	3e−04	10 x 12	transmembrane protein 44 [Source:HGNC Symbol;Acc:2512
8	404217	−0.62	1e−04	3e−04	10 x 9	cortexin 1 [Source:HGNC Symbol;Acc:31108]
9	1951	−0.62	1e−04	3e−04	9 x 13	cadherin, EGF LAG seven−pass G−type receptor 3 [Source:
10	55653	−0.61	2e−04	3e−04	9 x 10	breast carcinoma amplified sequence 4 [Source:HGNC Sym
11	7389	−0.61	2e−04	4e−04	7 x 9	uroporphyrinogen decarboxylase [Source:HGNC Symbol;Acc
12	11140	−0.55	2e−04	4e−04	7 x 10	cell division cycle 37 [Source:HGNC Symbol;Acc:1735]
13	116138	−0.59	2e−04	4e−04	9 x 11	kelch domain containing 3 [Source:HGNC Symbol;Acc:20704
14	55624	−0.59	3e−04	4e−04	10 x 9	protein O−linked mannose N−acetylglucosaminyltransferase
15	55643	−0.59	3e−04	4e−04	9 x 12	BTB (POZ) domain containing 2 [Source:HGNC Symbol;Acc:
16	30000	−0.58	3e−04	4e−04	9 x 11	transportin 2 [Source:HGNC Symbol;Acc:19998]
17	10726	−0.58	4e−04	4e−04	7 x 11	nudC nuclear distribution protein [Source:HGNC Symbol;Acc:
18	10519	−0.54	4e−04	4e−04	8 x 11	calcium and integrin binding 1 (calmyrin) [Source:HGNC Sym
19	537	−0.58	4e−04	4e−04	8 x 9	ATPase, H+ transporting, lysosomal accessory protein 1 [Sou
20	140465	−0.57	4e−04	4e−04	9 x 9	myosin, light chain 6B, alkali, smooth muscle and non−muscl

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.5	NULL	60 / 1135	Chr	Chr 19
2	−7.18	NULL	2 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
3	−7.08	NULL	4 / 15	GSEA C2	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROIT
4	−6.94	NULL	2 / 12	miRNA target−starBase	hsa−miR−1249
5	−6.44	NULL	2 / 16	MF	histone acetyl−lysine binding
6	−6.42	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
7	−6.41	NULL	3 / 12	BP	heparan sulfate proteoglycan biosynthetic process
8	−6.41	NULL	3 / 29	miRNA target−starBase	hsa−miR−296−5p
9	−6.33	NULL	2 / 12	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
10	−6.04	NULL	2 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
11	−6.01	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
12	−5.96	NULL	1 / 4	miRNA target	miR−122
13	−5.92	NULL	2 / 11	BP	maintenance of protein location in nucleus
14	−5.86	NULL	3 / 19	MF	mitogen−activated protein kinase kinase kinase binding
15	−5.81	NULL	2 / 11	BP	positive regulation of protein dephosphorylation
16	−5.73	NULL	2 / 14	Cancer	LIU_COMMON_CANCER_GENES
17	−5.72	NULL	2 / 12	BP	porphyrin−containing compound biosynthetic process
18	−5.41	NULL	2 / 16	GSEA C2	JIANG_HYPOXIA_CANCER
19	−5.31	NULL	3 / 16	BP	intracellular steroid hormone receptor signaling pathway
20	−5.29	NULL	3 / 14	GSEA C2	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_S
21	−5.28	NULL	3 / 22	MF	polyubiquitin binding
22	−5.2	NULL	2 / 12	BP	long term synaptic depression
23	−5.19	NULL	7 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
24	−5.06	NULL	3 / 28	MF	ribosome binding
25	−5.03	NULL	2 / 10	BP	mitotic nuclear envelope reassembly
26	−5.03	NULL	2 / 16	GSEA C2	SCHEIDEREIT_IKK_INTERACTING_PROTEINS
27	−5.01	NULL	2 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
28	−4.99	NULL	3 / 24	BP	centrosome organization
29	−4.93	NULL	2 / 12	GSEA C2	KAAB_FAILED_HEART_ATRIUM_UP
30	−4.93	NULL	2 / 15	MF	acetylglucosaminyltransferase activity
31	−4.92	NULL	5 / 50	miRNA target−starBase	hsa−miR−571
32	−4.83	NULL	36 / 940	MF	nucleic acid binding
33	−4.79	NULL	2 / 12	BP	mRNA cleavage
34	−4.72	NULL	3 / 24	miRNA target−starBase	hsa−miR−602
35	−4.65	NULL	3 / 24	MF	translation factor activity, nucleic acid binding
36	−4.65	NULL	2 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
37	−4.64	NULL	3 / 19	MF	hydrolase activity, acting on acid anhydrides, in phosphorus−conta
38	−4.6	NULL	2 / 11	GSEA C2	REACTOME_ERKS_ARE_INACTIVATED
39	−4.59	NULL	2 / 13	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_UP
40	−4.58	NULL	1 / 6	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_3_UP

GW_102

Local Summary

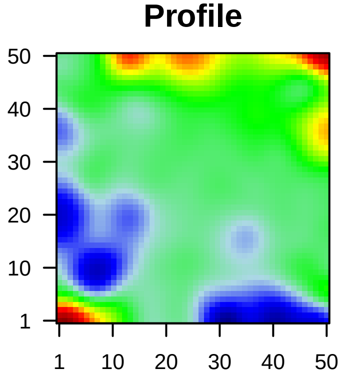
%DE = 0.71
metagenes = 15
genes = 197
genes in genesets = 192

genes with fdr < 0.1 = 103 (0 + / 103 −)
genes with fdr < 0.05 = 77 (0 + / 77 −)
genes with fdr < 0.01 = 24 (0 + / 24 −)

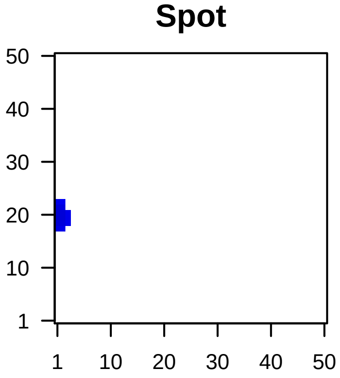
<r> metagenes = 0.97
<r> genes = 0.31

<FC> = −0.3
<shrinkage−t> = −10.66
<p−value> = 0.03
<fdr> = 0.63

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	113655	−0.86	1e−07	3e−04	1 x 18	major facilitator superfamily domain containing 3 [Source:HGI
2	51042	−0.72	9e−06	3e−04	1 x 19	zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
3	79703	−0.7	2e−05	3e−04	1 x 23	chromosome 11 open reading frame 80 [Source:HGNC Symb
4	127262	−0.68	3e−05	3e−04	1 x 23	tumor protein p63 regulated 1−like [Source:HGNC Symbol;Ac
5	88745	−0.67	3e−05	3e−04	1 x 19	ribosomal RNA processing 36 homolog (S. cerevisiae) [Sourc
6	51693	−0.66	4e−05	3e−04	1 x 21	trafficking protein particle complex 2−like [Source:HGNC Sym
7	5639	−0.66	4e−05	3e−04	1 x 22	proline rich Gla (G−carboxyglutamic acid) 2 [Source:HGNC S
8	92856	−0.66	4e−05	3e−04	1 x 18	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
9	90990	−0.66	4e−05	5e−04	1 x 23	kinesin family member C2 [Source:HGNC Symbol;Acc:29530
10	55210	−0.65	5e−05	6e−04	1 x 18	ATPase family, AAA domain containing 3A [Source:HGNC Sy
11	6884	−0.65	7e−05	6e−04	1 x 22	TAF13 RNA polymerase II, TATA box binding protein (TBP)−a
12	10682	−0.64	8e−05	2e−03	3 x 20	emopamil binding protein (sterol isomerase) [Source:HGNC S
13	27237	−0.62	1e−04	2e−03	2 x 20	Rho guanine nucleotide exchange factor (GEF) 16 [Source:H
14	54936	−0.61	2e−04	2e−03	1 x 23	ADP−ribosylhydrolase like 2 [Source:HGNC Symbol;Acc:213
15	51253	−0.6	2e−04	5e−03	1 x 19	mitochondrial ribosomal protein L37 [Source:HGNC Symbol;
16	8045	−0.58	4e−04	5e−03	2 x 22	Ras association (RalGDS/AF−6) domain family (N−terminal)
17	57109	−0.57	4e−04	5e−03	1 x 20	REX4, RNA exonuclease 4 homolog (S. cerevisiae) [Source:
18	286016	−0.56	6e−04	5e−03	1 x 19	
19	164091	−0.55	6e−04	5e−03	1 x 23	progestin and adipoQ receptor family member VII [Source:HG
20	54998	−0.54	7e−04	9e−03	1 x 20	aurora kinase A interacting protein 1 [Source:HGNC Symbol;

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.3	NULL	1 / 5	GSEA C2	NIELSEN_LIPOSARCOMA_DN
2	−9.82	NULL	3 / 10	MF	NADH dehydrogenase activity
3	−9.31	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
4	−8.84	NULL	3 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
5	−8.55	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
6	−8.55	NULL	1 / 7	GSEA C2	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP
7	−8.11	NULL	3 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
8	−7.57	NULL	2 / 9	GSEA C2	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE
9	−7.39	NULL	2 / 13	BP	ribosomal small subunit biogenesis
10	−7.23	NULL	3 / 12	BP	apoptotic nuclear changes
11	−7.13	NULL	2 / 10	GSEA C2	REACTOME_HIV_LIFE_CYCLE
12	−7.11	NULL	3 / 16	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
13	−6.93	NULL	3 / 15	GSEA C2	WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
14	−6.73	NULL	2 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
15	−6.57	NULL	2 / 12	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
16	−6.36	NULL	1 / 8	GSEA C2	CHANDRAN_METASTASIS_UP
17	−6.3	NULL	3 / 15	GSEA C2	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
18	−6.11	NULL	50 / 1318	CC	mitochondrion
19	−5.94	NULL	1 / 5	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE
20	−5.88	NULL	1 / 6	MMML CGS	MACIEJ_MMML 29
21	−5.84	NULL	1 / 8	GSEA C2	YEMELYANOV_GR_TARGETS_DN
22	−5.81	NULL	2 / 10	H.Tiss	WIRTH_B−cells
23	−5.75	NULL	2 / 13	GSEA C2	AMIT_EGF_RESPONSE_480_HELA
24	−5.7	NULL	14 / 153	MF	structural constituent of ribosome
25	−5.66	NULL	3 / 16	GSEA C2	MOOTHA_FFA_OXYDATION
26	−5.6	NULL	1 / 10	GSEA C2	BORCZUK_MALIGNANT_MESOTHELIOMA_DN
27	−5.48	NULL	7 / 96	BP	rRNA processing
28	−5.45	NULL	4 / 36	MF	coenzyme binding
29	−5.45	NULL	2 / 4	TF	MYC_Cell growth and proliferation UP
30	−5.41	NULL	1 / 5	GSEA C2	GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
31	−5.39	NULL	2 / 10	MF	3−beta−hydroxy−delta5−steroid dehydrogenase activity
32	−5.17	NULL	1 / 10	GSEA C2	REACTOME_HIV1_TRANSCRIPTION_INITIATION
33	−5.14	NULL	1 / 10	BP	drug transmembrane transport
34	−5.14	NULL	1 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
35	−5.1	NULL	4 / 34	MF	NADH dehydrogenase (ubiquinone) activity
36	−5.1	NULL	2 / 14	GSEA C2	ELVIDGE_HYPOXIA_DN
37	−5.07	NULL	2 / 10	MF	monosaccharide binding
38	−5.07	NULL	2 / 14	GSEA C2	CHANG_CORE_SERUM_RESPONSE_UP
39	−5.02	NULL	3 / 16	GSEA C2	GRATIAS_RETINOBLASTOMA_16Q24
40	−4.98	NULL	2 / 7	GSEA C2	REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE

p−values