GW_263

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1503 (800 + / 703 −)

genes with fdr < 0.1 = 1257 (669 + / 588 −)

genes with fdr < 0.05 = 1085 (575 + / 510 −)

genes with fdr < 0.01 = 775 (424 + / 351 −)

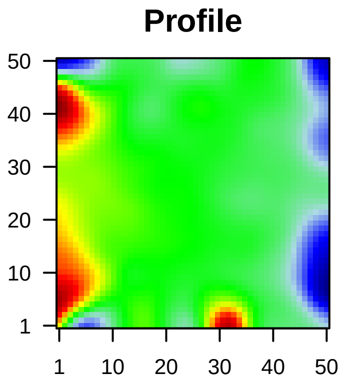
genes in genesets = 16332

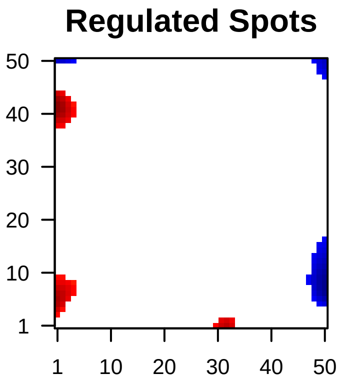
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

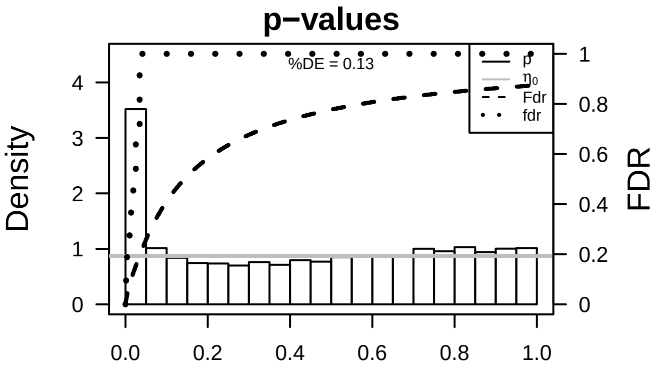
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.56	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	−1.42	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	216	−1.62	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	218	−1.9	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	163782	1.63	2e−16	4e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
6	440712	1.55	2e−16	4e−14	1 x 39	chromosome 1 open reading frame 186 [Source:HGNC Sym
7	148304	1.54	2e−16	4e−14	1 x 41	chromosome 1 open reading frame 74 [Source:HGNC Symb
8	135398	1.36	2e−16	4e−14	1 x 40	chromosome 6 open reading frame 141 [Source:HGNC Sym
9	768	2.03	2e−16	4e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
10	51806	1.85	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
11	414062	1.35	2e−16	4e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
12	595	1.35	2e−16	4e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
13	25819	1.34	2e−16	4e−14	1 x 41	CCR4 carbon catabolite repression 4−like (S. cerevisiae) [So
14	1001	1.34	2e−16	4e−14	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
15	22802	−1.67	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
16	1258	1.53	2e−16	4e−14	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symb
17	1308	1.51	2e−16	4e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	1278	−1.5	2e−16	4e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
19	1291	−1.34	2e−16	4e−14	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
20	1293	−1.71	2e−16	4e−14	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	12.35	NULL	51	BP	type I interferon signaling pathway
2	11.81	NULL	123	BP	defense response to virus
3	11.47	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
4	11.27	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	10.56	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	9.92	NULL	31	BP	negative regulation of viral genome replication
7	9.65	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	9.09	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
9	8.66	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
10	8.63	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
11	8.56	NULL	12	BP	hemidesmosome assembly
12	8.22	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	8.14	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
14	7.85	NULL	109	BP	response to virus
15	7.76	NULL	572	Disease	GUDJ_psoriasis up
16	7.62	NULL	204	BP	cytokine−mediated signaling pathway
17	7.59	NULL	449	Chr	Chr 20
18	7.18	NULL	312	BP	immune response
19	7.1	NULL	12	GSEA C2	ZHU_CMV_8_HR_UP
20	7.07	NULL	6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−11.84	NULL	914	Chr	Chr 3
2	−9.39	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−9.1	NULL	16	MMML CGS	MACIEJ_MMML 1
4	−8.75	NULL	11	MF	platelet−derived growth factor binding
5	−8.62	NULL	19	BP	peptide cross−linking
6	−7.96	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
7	−7.91	NULL	375	Disease	GUDJ_psoriasis down
8	−7.19	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	−7.13	NULL	190	CC	extracellular matrix
10	−7.1	NULL	250	Lymphoma	LENZ_Stromal signature 1
11	−6.74	NULL	135	H.Tiss	WIRTH_Mucosa
12	−6.74	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
13	−6.67	NULL	57	MF	extracellular matrix structural constituent
14	−6.32	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
15	−6.29	NULL	53	BP	keratinocyte differentiation
16	−5.95	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
17	−5.87	NULL	12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
18	−5.87	NULL	24	TF Tissue	VAQUERIZAS_Trachea
19	−5.82	NULL	42	BP	keratinization
20	−5.73	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D

GW_263

Local Summary

%DE = 0.97

metagenes = 7

genes = 120

genes in genesets = 118

genes with fdr < 0.1 = 113 (112 + / 1 −)

genes with fdr < 0.05 = 107 (106 + / 1 −)

genes with fdr < 0.01 = 97 (96 + / 1 −)

<r> metagenes = 0.99

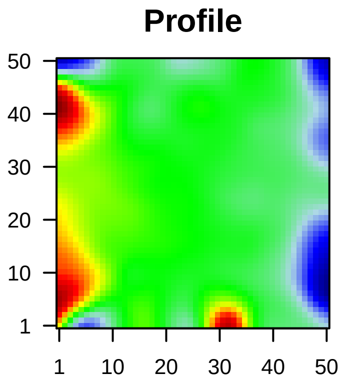
<r> genes = 0.45

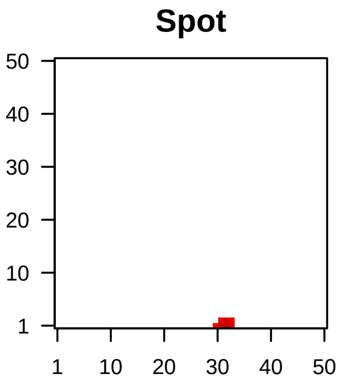
<FC> = 0.68

<shrinkage−t> = 23.83

<p−value> = 0

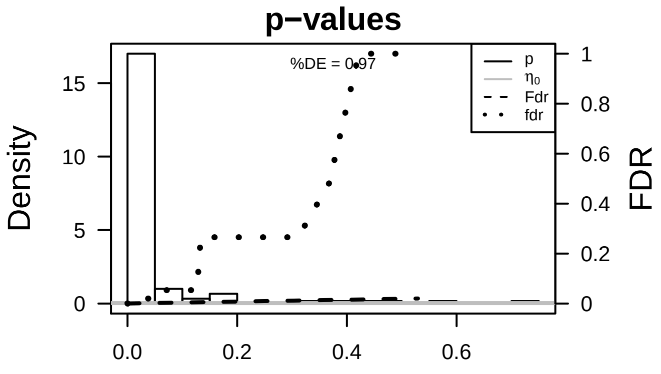
<fdr> = 0.24





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3627	2.43	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
2	6373	1.67	2e−16	2e−16	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
3	3433	1.46	2e−16	2e−16	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [S
4	10410	1.27	2e−16	2e−16	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
5	9636	1.72	2e−16	2e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:40
6	6355	1.31	2e−15	1e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
7	2537	1.31	2e−15	1e−14	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
8	91543	1.28	6e−15	3e−14	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:
9	115362	1.26	1e−14	5e−14	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
10	10581	1.14	4e−14	5e−14	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC
11	684	1.24	5e−14	1e−12	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
12	7453	1.19	4e−13	1e−12	32 x 1	tryptophanyl−tRNA synthetase [Source:HGNC Symbol;Acc:1
13	2633	1.18	7e−13	9e−12	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HG
14	51296	1.14	3e−12	4e−11	32 x 1	solute carrier family 15 (oligopeptide transporter), member 3
15	9560	1.11	1e−11	6e−11	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
16	94240	1.09	4e−11	6e−11	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
17	4599	0.99	5e−11	2e−10	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
18	8519	1.05	2e−10	2e−10	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
19	85441	1.04	2e−10	2e−10	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
20	6890	1.04	3e−10	2e−10	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	52.01	NULL	29 / 51	BP	type I interferon signaling pathway
2	51.36	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
3	46.68	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	44.04	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
5	42.26	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	42.13	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
7	40.45	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
8	38.85	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
9	37.29	NULL	31 / 123	BP	defense response to virus
10	35.8	NULL	13 / 31	BP	negative regulation of viral genome replication
11	35.25	NULL	27 / 109	BP	response to virus
12	34.4	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
13	33.83	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
14	32.57	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
15	31.55	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
16	31.39	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
17	31.36	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
18	30.49	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
19	29	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
20	27.99	NULL	34 / 204	BP	cytokine−mediated signaling pathway
21	26.71	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
22	25.77	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
23	25.5	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
24	25.26	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
25	24.94	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
26	24.22	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
27	23.84	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
28	23.15	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
29	22.6	NULL	46 / 572	Disease	GUDJ_psoriasis up
30	22.48	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
31	22.48	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
32	22	NULL	2 / 10	BP	positive regulation of cAMP−mediated signaling
33	21.72	NULL	3 / 5	GSEA C2	BROWNE_INTERFERON_RESPONSIVE_GENES
34	21.59	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
35	21.49	NULL	7 / 10	CC	MHC class I protein complex
36	20.73	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
37	20.65	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
38	19.93	NULL	5 / 18	BP	response to interferon−gamma
39	19.76	NULL	2 / 12	BP	positive regulation of leukocyte chemotaxis
40	19.51	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP

GW_263

Local Summary

%DE = 0.81

metagenes = 22

genes = 302

genes in genesets = 299

genes with fdr < 0.1 = 190 (185 + / 5 −)

genes with fdr < 0.05 = 189 (184 + / 5 −)

genes with fdr < 0.01 = 132 (128 + / 4 −)

<r> metagenes = 0.94

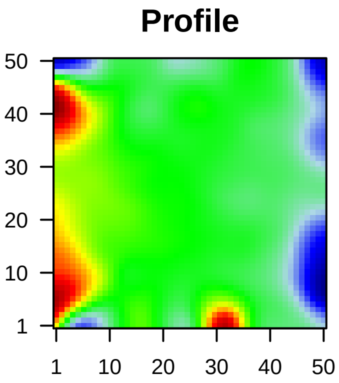
<r> genes = 0.31

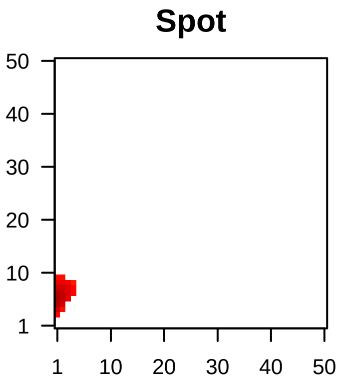
<FC> = 0.45

<shrinkage−t> = 15.82

<p−value> = 0

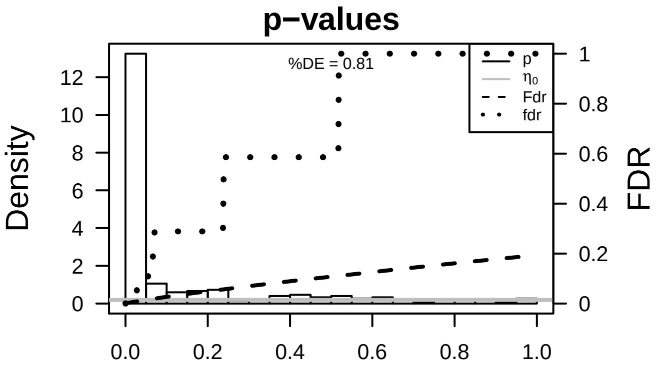
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	768	2.03	2e−16	2e−15	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
2	595	1.35	2e−16	2e−15	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
3	1258	1.53	2e−16	2e−15	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
4	1464	1.7	2e−16	2e−15	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
5	285761	1.38	2e−16	2e−15	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
6	1687	1.43	2e−16	2e−15	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
7	27122	1.38	2e−16	2e−15	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
8	7424	1.63	2e−16	2e−15	1 x 3	vascular endothelial growth factor C [Source:HGNC Symbol;
9	3918	1.34	4e−16	1e−14	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
10	857	1.32	7e−16	1e−12	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
11	55450	1.24	4e−14	1e−12	1 x 4	calcium/calmodulin−dependent protein kinase II inhibitor 1 [S
12	25914	1.24	5e−14	1e−11	1 x 8	rotatin [Source:HGNC Symbol;Acc:18654]
13	5228	1.2	3e−13	3e−10	1 x 6	placental growth factor [Source:HGNC Symbol;Acc:8893]
14	23768	1.13	6e−12	2e−09	1 x 4	fibronectin leucine rich transmembrane protein 2 [Source:HG
15	3371	1.08	4e−11	3e−09	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
16	90853	1.06	1e−10	3e−09	2 x 5	SPOC domain containing 1 [Source:HGNC Symbol;Acc:2633
17	10381	1.05	1e−10	5e−09	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
18	10897	1.04	2e−10	8e−09	3 x 8	Yip1 interacting factor homolog A (S. cerevisiae) [Source:HG
19	375790	1.02	4e−10	8e−09	1 x 7	agrin [Source:HGNC Symbol;Acc:329]
20	650	1.02	5e−10	8e−09	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.89	NULL	6 / 12	BP	hemidesmosome assembly
2	15.66	NULL	3 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
3	15.09	NULL	1 / 2	miRNA target	miR−16−1
4	14.38	NULL	2 / 4	miRNA target	miR−195
5	12.51	NULL	14 / 70	BP	cell junction assembly
6	11.83	NULL	3 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
7	11.78	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
8	11.63	NULL	4 / 12	BP	heparan sulfate proteoglycan biosynthetic process
9	11.36	NULL	2 / 6	miRNA target	let−7b
10	11.15	NULL	3 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
11	11.04	NULL	33 / 242	BP	extracellular matrix organization
12	10.92	NULL	6 / 16	MF	fibronectin binding
13	10.89	NULL	4 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
14	10.74	NULL	4 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
15	10.34	NULL	37 / 403	BP	cell adhesion
16	10.23	NULL	7 / 45	BP	chondroitin sulfate metabolic process
17	10.15	NULL	5 / 16	GSEA C2	REACTOME_CELLEXTRACELLULAR_MATRIX_INTERACTIONS
18	10.1	NULL	3 / 15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
19	10.09	NULL	2 / 11	BP	dermatan sulfate biosynthetic process
20	9.93	NULL	1 / 4	miRNA target	miR−20a
21	9.85	NULL	3 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_32HR_DN
22	9.85	NULL	3 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_48HR_DN
23	9.73	NULL	3 / 16	CC	lamellipodium membrane
24	9.67	NULL	4 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
25	9.63	NULL	5 / 25	BP	chondroitin sulfate biosynthetic process
26	9.57	NULL	2 / 10	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_DN
27	9.51	NULL	4 / 16	GSEA C2	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
28	9.37	NULL	4 / 10	GSEA C2	BIOCARTA_CELL2CELL_PATHWAY
29	9.3	NULL	11 / 104	BP	glycosaminoglycan metabolic process
30	9.25	NULL	3 / 14	GSEA C2	CLIMENT_BREAST_CANCER_COPY_NUMBER_UP
31	9.24	NULL	3 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC
32	9.12	NULL	4 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
33	9.04	NULL	3 / 20	BP	vascular endothelial growth factor receptor signaling pathway
34	9	NULL	4 / 16	GSEA C2	SWEET_KRAS_TARGETS_UP
35	8.96	NULL	2 / 16	CC	microvillus membrane
36	8.8	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
37	8.74	NULL	3 / 11	BP	positive regulation of cartilage development
38	8.71	NULL	3 / 12	GSEA C2	GNATENKO_PLATELET_SIGNATURE
39	8.71	NULL	4 / 17	BP	negative regulation of signal transduction
40	8.7	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP

GW_263

Local Summary

%DE = 0.82

metagenes = 22

genes = 240

genes in genesets = 235

genes with fdr < 0.1 = 161 (151 + / 10 −)

genes with fdr < 0.05 = 157 (148 + / 9 −)

genes with fdr < 0.01 = 130 (123 + / 7 −)

<r> metagenes = 0.98

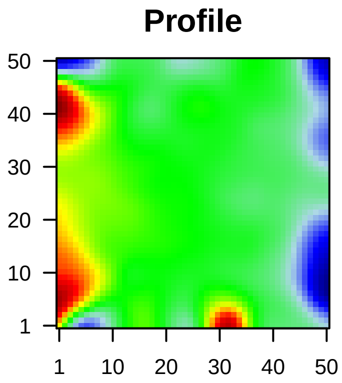
<r> genes = 0.32

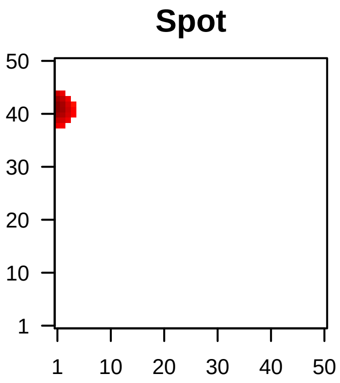
<FC> = 0.48

<shrinkage−t> = 16.86

<p−value> = 0

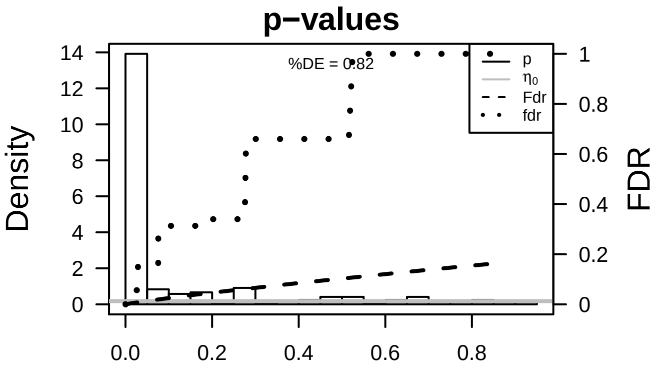
<fdr> = 0.39





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	440712	1.55	2e−16	9e−16	1 x 39	chromosome 1 open reading frame 186 [Source:HGNC Symb
2	148304	1.54	2e−16	9e−16	1 x 41	chromosome 1 open reading frame 74 [Source:HGNC Symbo
3	135398	1.36	2e−16	9e−16	1 x 40	chromosome 6 open reading frame 141 [Source:HGNC Symb
4	25819	1.34	2e−16	9e−16	1 x 41	CCR4 carbon catabolite repression 4−like (S. cerevisiae) [Sou
5	1001	1.34	2e−16	9e−16	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
6	1308	1.51	2e−16	9e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
7	55214	1.57	2e−16	9e−16	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
8	4015	1.59	2e−16	9e−16	1 x 41	lysyl oxidase [Source:HGNC Symbol;Acc:6664]
9	56901	1.47	2e−16	9e−16	1 x 44	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4−li
10	5744	2.05	2e−16	9e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
11	404203	1.46	2e−16	9e−16	1 x 43	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb
12	54626	1.31	2e−15	2e−13	1 x 44	hes family bHLH transcription factor 2 [Source:HGNC Symbol
13	28234	1.28	6e−15	6e−13	2 x 41	solute carrier organic anion transporter family, member 1B3 [S
14	3552	1.25	2e−14	7e−12	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
15	83882	1.21	2e−13	3e−11	1 x 43	tetraspanin 10 [Source:HGNC Symbol;Acc:29942]
16	51706	1.16	1e−12	3e−11	1 x 40	cytochrome b5 reductase 1 [Source:HGNC Symbol;Acc:1339
17	79148	1.16	2e−12	3e−11	1 x 39	matrix metallopeptidase 28 [Source:HGNC Symbol;Acc:1436
18	4747	1.15	2e−12	1e−10	1 x 43	
19	760	1.13	5e−12	2e−10	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
20	9610	1.12	9e−12	1e−09	1 x 39	Ras and Rab interactor 1 [Source:HGNC Symbol;Acc:18749]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	13.44	NULL	4 / 12	BP	hemidesmosome assembly
2	12.69	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
3	12.32	NULL	2 / 2	miRNA target	miR−199a*
4	11.06	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
5	10.64	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
6	10.43	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
7	10.05	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	10.04	NULL	1 / 5	GSEA C2	ELVIDGE_HIF2A_TARGETS_UP
9	9.13	NULL	42 / 572	Disease	GUDJ_psoriasis up
10	8.99	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
11	8.91	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
12	8.89	NULL	2 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
13	8.84	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
14	8.79	NULL	4 / 32	CC	cell−cell adherens junction
15	8.76	NULL	3 / 15	Pathw Act	GUSTAFSON_PI3K_DN
16	8.73	NULL	8 / 76	BP	epidermis development
17	8.64	NULL	1 / 10	BP	surfactant homeostasis
18	8.63	NULL	2 / 16	Glio	VERHAAK_MES subtype
19	8.49	NULL	2 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
20	8.45	NULL	4 / 16	BP	cellular response to extracellular stimulus
21	8.43	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
22	8.32	NULL	3 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
23	7.82	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
24	7.68	NULL	1 / 4	MMML CGS	MACIEJ_MMML 47
25	7.56	NULL	3 / 16	GSEA C2	ELVIDGE_HYPOXIA_BY_DMOG_UP
26	7.53	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
27	7.45	NULL	2 / 14	GSEA C2	LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_UP
28	7.41	NULL	1 / 13	H.Tiss	WIRTH_Thalamus
29	7.1	NULL	1 / 14	BP	negative regulation of chondrocyte differentiation
30	7.05	NULL	2 / 13	H.Tiss	WIRTH_Thymus
31	7.04	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
32	6.9	NULL	2 / 13	BP	response to copper ion
33	6.89	NULL	2 / 14	GSEA C2	LU_AGING_BRAIN_DN
34	6.84	NULL	6 / 83	CC	basement membrane
35	6.78	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
36	6.66	NULL	1 / 10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
37	6.65	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
38	6.55	NULL	9 / 82	CC	intermediate filament
39	6.46	NULL	2 / 15	BP	positive regulation vascular endothelial growth factor production
40	6.44	NULL	8 / 112	Glio	Christensen_hypermethylated_in_grade2_oligoastrocytoma

GW_263

Local Summary

%DE = 0.76

metagenes = 36

genes = 444

genes in genesets = 440

genes with fdr < 0.1 = 274 (13 + / 261 −)

genes with fdr < 0.05 = 236 (11 + / 225 −)

genes with fdr < 0.01 = 152 (4 + / 148 −)

<r> metagenes = 0.83

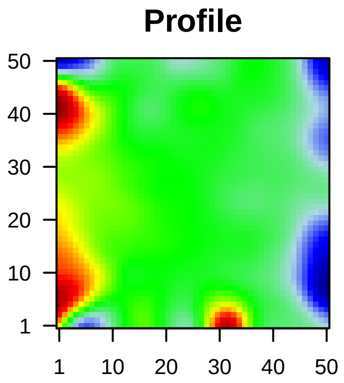
<r> genes = 0.23

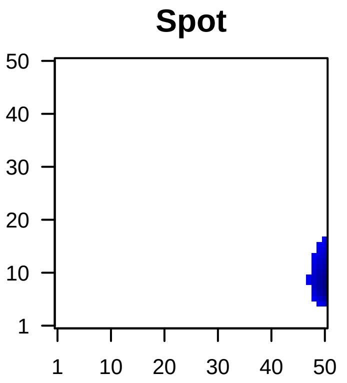
<FC> = −0.39

<shrinkage−t> = −13.73

<p−value> = 0

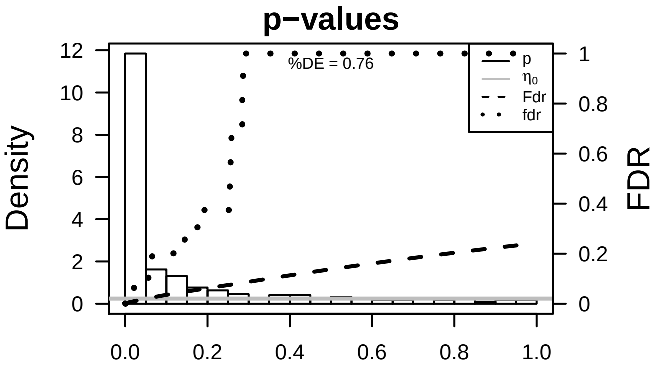
<fdr> = 0.52





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1396	1.53	2e−16	1e−14	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
2	6422	1.88	2e−16	1e−14	50 x 8	secreted frizzled−related protein 1 [Source:HGNC Symbol;Ac
3	347	−1.34	4e−16	1e−13	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
4	6192	−1.31	2e−15	3e−13	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
5	4239	−1.29	4e−15	2e−12	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
6	1675	−1.24	4e−14	3e−12	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
7	7033	−1.24	4e−14	3e−12	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
8	6414	−1.23	8e−14	3e−12	48 x 11	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:10751
9	25840	−1.22	1e−13	7e−12	50 x 11	methyltransferase like 7A [Source:HGNC Symbol;Acc:24550]
10	1363	−1.21	2e−13	7e−12	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
11	83699	−1.2	2e−13	4e−11	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
12	3488	−1.18	6e−13	4e−11	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
13	2878	−1.17	1e−12	3e−10	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
14	10439	−1.14	4e−12	3e−10	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
15	8404	−1.13	7e−12	3e−10	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
16	84952	−1.12	1e−11	5e−10	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
17	56271	−1.11	1e−11	3e−09	50 x 12	brain expressed, X−linked 4 [Source:HGNC Symbol;Acc:2547
18	2139	−1.08	4e−11	7e−09	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;/
19	4256	−1.06	1e−10	7e−09	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
20	7049	−1.05	2e−10	1e−08	50 x 9	transforming growth factor, beta receptor III [Source:HGNC S



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.44	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−11.24	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
3	−10.71	NULL	4 / 13	Cancer	GENTLES_modul17
4	−10.42	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
5	−10.31	NULL	4 / 14	MF	selenium binding
6	−9.99	NULL	6 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
7	−9.69	NULL	2 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
8	−9.61	NULL	6 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
9	−9.59	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	−9.26	NULL	4 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
11	−9.21	NULL	5 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
12	−8.93	NULL	4 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
13	−8.82	NULL	51 / 375	Disease	GUDJ_psoriasis down
14	−8.77	NULL	4 / 17	MF	metallocarboxypeptidase activity
15	−8.69	NULL	5 / 21	BP	drug metabolic process
16	−8.5	NULL	3 / 12	GSEA C2	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
17	−8.34	NULL	3 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
18	−8.33	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
19	−8.11	NULL	3 / 17	MF	carboxypeptidase activity
20	−8.04	NULL	3 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
21	−7.97	NULL	3 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
22	−7.92	NULL	3 / 9	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
23	−7.86	NULL	3 / 10	GSEA C2	REACTOME_INTRINSIC_PATHWAY
24	−7.82	NULL	6 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
25	−7.61	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
26	−7.53	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
27	−7.51	NULL	3 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
28	−7.43	NULL	3 / 11	BP	blood coagulation, intrinsic pathway
29	−7.4	NULL	6 / 15	GSEA C2	NAKAJIMA_MAST_CELL
30	−7.39	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
31	−7.39	NULL	51 / 683	CC	extracellular space
32	−7.31	NULL	4 / 19	BP	positive regulation of epithelial to mesenchymal transition
33	−7.31	NULL	3 / 14	BP	regulation of Wnt signaling pathway
34	−7.31	NULL	7 / 55	Glio	OL vs. MOG− OL
35	−7.14	NULL	3 / 14	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
36	−7.09	NULL	4 / 11	GSEA C2	RIGGI_EWING_SARCOMA_PROGENITOR_DN
37	−7	NULL	3 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN
38	−6.88	NULL	2 / 15	GSEA C2	ABE_INNER_EAR
39	−6.86	NULL	1 / 2	MMML CGS	MACIEJ_MMML 32
40	−6.84	NULL	3 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN

GW_263

Local Summary

%DE = 0.74

metagenes = 8

genes = 155

genes in genesets = 154

genes with fdr < 0.1 = 80 (2 + / 78 −)

genes with fdr < 0.05 = 80 (2 + / 78 −)

genes with fdr < 0.01 = 47 (2 + / 45 −)

<r> metagenes = 0.98

<r> genes = 0.29

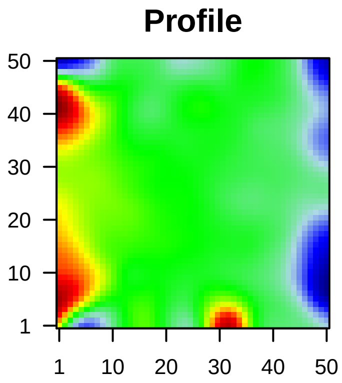
<FC> = −0.39

<shrinkage−t> = −13.68

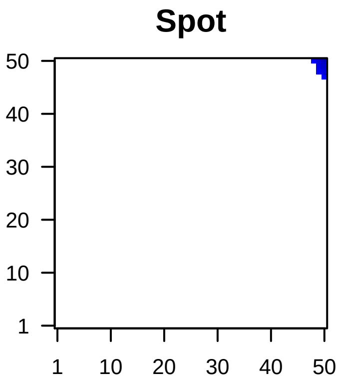
<p−value> = 0

<fdr> = 0.54

Profile



Spot



Local Genelist

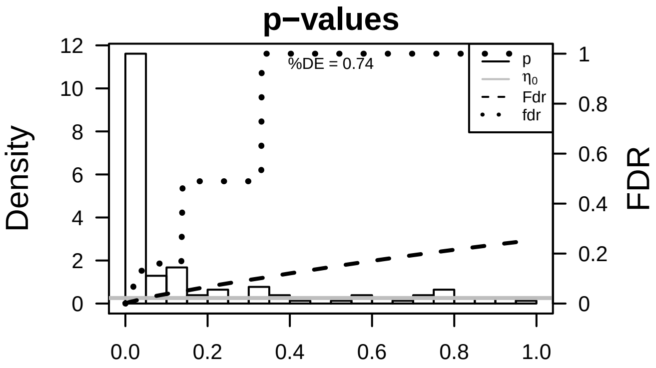
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.62	2e−16	3e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	11166	−1.36	2e−16	3e−15	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
3	256764	−1.96	2e−16	3e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
4	4922	−1.3	2e−15	4e−11	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
5	84707	−1.16	2e−12	4e−11	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
6	84171	−1.16	2e−12	5e−10	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
7	56650	−1.11	1e−11	1e−09	49 x 50	claudin domain containing 1 [Source:HGNC Symbol;Acc:132
8	120	−1.08	5e−11	1e−09	50 x 50	adducin 3 (gamma) [Source:HGNC Symbol;Acc:245]
9	4953	−1.07	8e−11	1e−09	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
10	655	1.06	1e−10	7e−08	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
11	6657	−0.99	2e−09	1e−07	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
12	123811	−0.96	5e−09	7e−07	48 x 50	FGFR1OP N−terminal like [Source:HGNC Symbol;Acc:2643
13	286676	−0.92	2e−08	2e−06	50 x 49	immunoglobulin−like domain containing receptor 1 [Source:H
14	29968	−0.88	7e−08	4e−06	49 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
15	339512	−0.86	2e−07	1e−05	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
16	8544	−0.82	5e−07	1e−05	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;A
17	8702	−0.8	1e−06	1e−05	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
18	604	−0.8	1e−06	4e−05	50 x 50	B−cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:1001]
19	85476	−0.78	2e−06	6e−05	48 x 50	G elongation factor, mitochondrial 1 [Source:HGNC Symbol;
20	56256	−0.76	4e−06	6e−05	50 x 50	SERTA domain containing 4 [Source:HGNC Symbol;Acc:252

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.48	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	−15.41	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
3	−14.29	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
4	−14.29	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
5	−13.76	NULL	1 / 2	miRNA target	miR−127
6	−13.63	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
7	−13.62	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
8	−13.58	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
9	−12.28	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
10	−11.79	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
11	−11.29	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
12	−11.29	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
13	−10.62	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
14	−10.62	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
15	−10.33	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_BASAL_UP
16	−10.25	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
17	−10.02	NULL	2 / 12	BP	cellular aldehyde metabolic process
18	−9.77	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
19	−9.64	NULL	2 / 23	BP	stem cell differentiation
20	−9.59	NULL	3 / 13	BP	regulation of blood vessel size
21	−8.79	NULL	2 / 15	GSEA C2	YANG_BREAST_CANCER_ESR1_LASER_DN
22	−8.75	NULL	1 / 14	MF	Ras GTPase activator activity
23	−8.75	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
24	−8.75	NULL	1 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
25	−8.59	NULL	8 / 34	BP	glutathione metabolic process
26	−8.52	NULL	1 / 7	GSEA C2	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLAS
27	−8.41	NULL	1 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
28	−8	NULL	1 / 11	Glio	neurons_glio
29	−7.94	NULL	5 / 20	MF	glutathione transferase activity
30	−7.94	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
31	−7.93	NULL	2 / 15	GSEA C2	KEGG_ARGININE_AND_PROLINE_METABOLISM
32	−7.88	NULL	1 / 8	GSEA C2	PUJANA_CHEK2_PCC_NETWORK
33	−7.86	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
34	−7.86	NULL	1 / 7	miRNA target	miR−145
35	−7.8	NULL	11 / 119	BP	xenobiotic metabolic process
36	−7.71	NULL	34 / 914	Chr	Chr 3
37	−7.7	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
38	−7.69	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
39	−7.6	NULL	6 / 25	BP	glutathione derivative biosynthetic process
40	−7.57	NULL	1 / 18	BP	positive regulation of Ras GTPase activity

p−values



GW_263

Local Summary

%DE = 0.84

metagenes = 4

genes = 110

genes in genesets = 108

genes with fdr < 0.1 = 80 (7 + / 73 −)

genes with fdr < 0.05 = 76 (6 + / 70 −)

genes with fdr < 0.01 = 71 (4 + / 67 −)

<r> metagenes = 0.99

<r> genes = 0.53

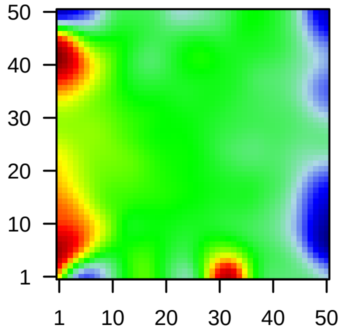
<FC> = −0.64

<shrinkage−t> = −22.73

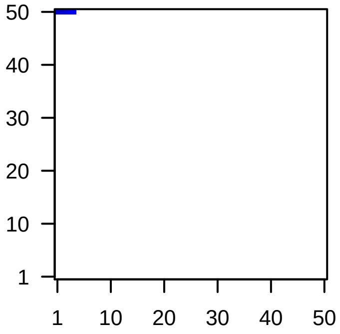
<p−value> = 0

<fdr> = 0.3

Profile



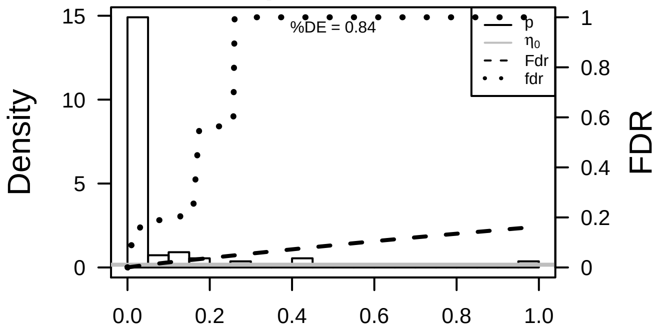
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.56	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	−1.42	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	218	−1.9	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	51806	1.85	2e−16	2e−16	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
5	22802	−1.67	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
6	49860	−1.89	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
7	2877	−2.13	2e−16	2e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
8	26085	−1.45	2e−16	2e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
9	5653	−1.6	2e−16	2e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
10	3860	−2.74	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
11	192666	−1.37	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
12	3851	−1.84	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
13	3934	−1.79	2e−16	2e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
14	4118	−1.71	2e−16	2e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
15	6337	−1.98	2e−16	2e−16	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
16	6707	−3.04	2e−16	2e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
17	7053	−2.11	2e−16	2e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
18	92196	−1.32	7e−16	1e−13	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	6699	−1.28	6e−15	7e−13	1 x 50	small proline−rich protein 1B [Source:HGNC Symbol;Acc:112
20	51458	1.24	5e−14	6e−12	1 x 50	Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−39.37	NULL	49 / 135	H.Tiss	WIRTH_Mucosa
2	−26.78	NULL	7 / 19	BP	peptide cross−linking
3	−20.22	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	−19.07	NULL	12 / 53	BP	keratinocyte differentiation
5	−18.48	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
6	−17.12	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
7	−17.05	NULL	3 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
8	−16.97	NULL	11 / 42	BP	keratinization
9	−13.42	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
10	−12.84	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
11	−12.67	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
12	−12.34	NULL	10 / 186	MF	structural molecule activity
13	−12.24	NULL	39 / 572	Disease	GUDJ_psoriasis up
14	−12.06	NULL	10 / 21	CC	cornified envelope
15	−11.52	NULL	3 / 15	MF	retinol dehydrogenase activity
16	−11.5	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−10.88	NULL	3 / 44	CC	keratin filament
18	−10.05	NULL	3 / 27	BP	response to bacterium
19	−9.75	NULL	2 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	−9.75	NULL	2 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
21	−9.7	NULL	2 / 15	GSEA C2	LUI_THYROID_CANCER_CLUSTER_2
22	−9.6	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
23	−9.54	NULL	4 / 82	CC	intermediate filament
24	−9.33	NULL	2 / 12	BP	cellular aldehyde metabolic process
25	−9.14	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
26	−9.05	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
27	−8.84	NULL	2 / 11	GSEA C2	REACTOME_XENOBIOTICS
28	−8.77	NULL	2 / 15	GSEA C2	KORKOLA_TERATOMA
29	−8.63	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
30	−8.5	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
31	−8.49	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
32	−8.44	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
33	−8.44	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
34	−8.12	NULL	1 / 13	BP	temperature homeostasis
35	−8.11	NULL	2 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
36	−7.95	NULL	1 / 10	Glio	willscher_ GBM_LTSwt_proteomics−G_UP
37	−7.9	NULL	1 / 12	MF	sodium channel activity
38	−7.86	NULL	9 / 122	MF	serine−type endopeptidase activity
39	−7.77	NULL	1 / 14	MF	glutathione peroxidase activity
40	−7.75	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP