GW_137

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1367 (879 + / 488 −)

genes with fdr < 0.1 = 1024 (712 + / 312 −)

genes with fdr < 0.05 = 699 (529 + / 170 −)

genes with fdr < 0.01 = 387 (314 + / 73 −)

genes in genesets = 16332

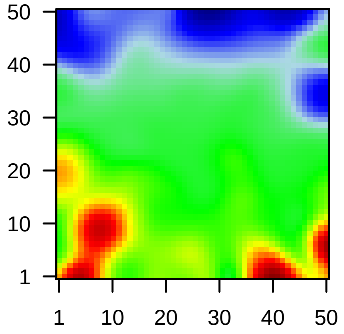
<FC> = 0

<shrinkage−t> = 0

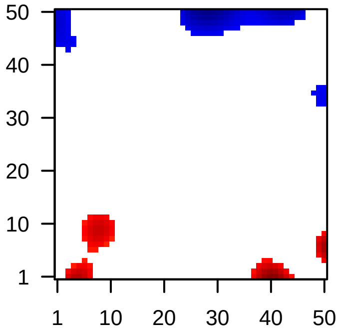
<p−value> = 0.16

<fdr> = 0.87

Profile



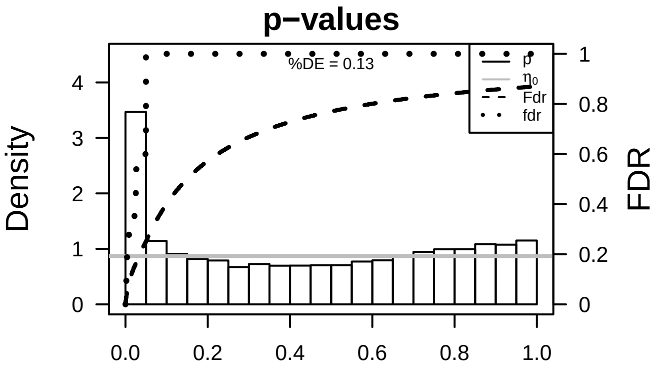
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	2.66	2e−16	2e−13	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	347	2.38	2e−16	2e−13	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
3	6358	2.04	2e−16	2e−13	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
4	1675	2.05	2e−16	2e−13	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
5	1490	2.18	2e−16	2e−13	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
6	2532	2.28	2e−16	2e−13	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
7	2354	2.13	2e−16	2e−13	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
8	3039	2.76	2e−16	2e−13	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	3040	2.95	2e−16	2e−13	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
10	3043	2.4	2e−16	2e−13	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
11	3127	2.24	2e−16	2e−13	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
12	3488	2.23	2e−16	2e−13	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
13	286887	−1.84	2e−16	2e−13	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
14	4256	2.24	2e−16	2e−13	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
15	347733	2.41	2e−16	2e−13	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
16	3866	1.95	2e−15	8e−12	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
17	25849	1.95	2e−15	8e−12	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
18	10365	1.94	2e−15	4e−11	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
19	169044	1.92	4e−15	4e−11	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
20	203569	1.9	8e−15	4e−11	16 x 13	P antigen family, member 2 (prostate associated) [Source:HG

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.92	NULL	1135	Chr	Chr 19
2	11.85	NULL	190	CC	extracellular matrix
3	10.75	NULL	375	Disease	GUDJ_psoriasis down
4	10.31	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	10.05	NULL	683	CC	extracellular space
6	8.94	NULL	59	Lymphoma	LENZ_Stromal signature 2
7	8.92	NULL	1182	CC	extracellular region
8	8.73	NULL	16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
9	8.54	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
10	8.1	NULL	112	MF	heparin binding
11	7.92	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
12	7.87	NULL	717	Chr	Chr 16
13	7.59	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
14	7.43	NULL	4	MMML CGS	MACIEJ_MMML 23
15	7.32	NULL	15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
16	7.31	NULL	8	GSEA C2	ZHAN_MULTIPLE_MYELOMA_SPIKED
17	7.23	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
18	7.19	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
19	7.14	NULL	242	BP	extracellular matrix organization
20	6.92	NULL	13	Cancer	GENTLES_modul17
Underexpressed					
1	−18.12	NULL	572	Disease	GUDJ_psoriasis up
2	−9.33	NULL	699	Chr	Chr 5
3	−8.74	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	−8.74	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	−8.68	NULL	318	miRNA target−starBase	hsa−miR−590−3p
6	−8.52	NULL	135	H.Tiss	WIRTH_Mucosa
7	−8.42	NULL	370	BP	mitotic cell cycle
8	−7.95	NULL	1233	TF	KIM_MYC targets
9	−7.84	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
10	−7.33	NULL	1318	CC	mitochondrion
11	−7.07	NULL	313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
12	−7.07	NULL	313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
13	−7.07	NULL	313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up
14	−6.96	NULL	293	miRNA target−starBase	hsa−miR−186
15	−6.84	NULL	436	miRNA target−starBase	hsa−miR−548n
16	−6.72	NULL	421	miRNA target−starBase	hsa−let−7b
17	−6.6	NULL	262	miRNA target−starBase	hsa−miR−548l
18	−6.47	NULL	321	miRNA target−starBase	hsa−miR−548a−5p
19	−6.44	NULL	324	miRNA target−starBase	hsa−miR−18a
20	−6.38	NULL	302	miRNA target−starBase	hsa−miR−548i

GW_137

Local Summary

%DE = 0.78

metagenes = 15

genes = 223

genes in genesets = 219

genes with fdr < 0.1 = 135 (132 + / 3 −)

genes with fdr < 0.05 = 111 (110 + / 1 −)

genes with fdr < 0.01 = 89 (88 + / 1 −)

<r> metagenes = 0.98

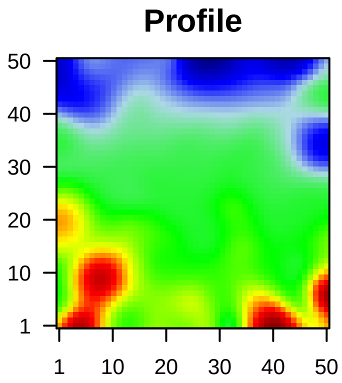
<r> genes = 0.43

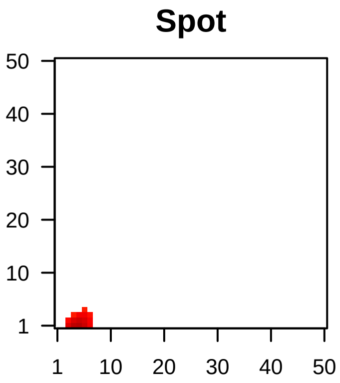
<FC> = 0.67

<shrinkage−t> = 23.34

<p−value> = 0

<fdr> = 0.47





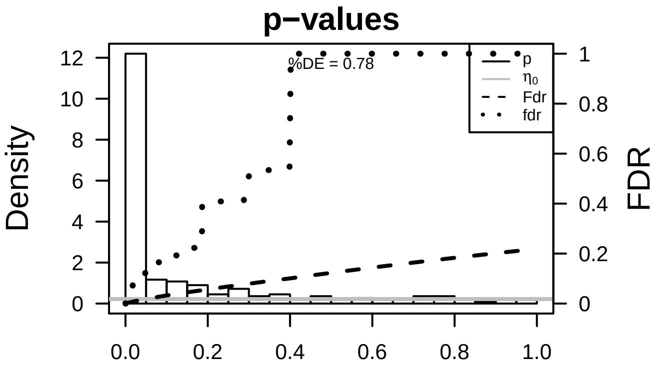
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	2.66	2e−16	2e−15	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
2	1490	2.18	2e−16	2e−15	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
3	3039	2.76	2e−16	2e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3040	2.95	2e−16	2e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
5	3043	2.4	2e−16	2e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
6	6423	1.87	2e−14	1e−12	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
7	59	1.84	5e−14	1e−12	3 x 1	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
8	64651	1.83	8e−14	1e−12	6 x 2	cysteine−serine−rich nuclear protein 1 [Source:HGNC Symbo
9	2296	1.83	8e−14	8e−12	7 x 3	forkhead box C1 [Source:HGNC Symbol;Acc:3800]
10	6876	1.79	2e−13	1e−10	3 x 1	transgelin [Source:HGNC Symbol;Acc:11553]
11	7076	1.71	3e−12	1e−10	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Ac
12	6515	1.68	6e−12	1e−10	3 x 1	solute carrier family 2 (facilitated glucose transporter), memb
13	3671	1.67	8e−12	4e−10	4 x 1	immunoglobulin superfamily containing leucine−rich repeat [S
14	4616	1.64	2e−11	4e−10	6 x 3	growth arrest and DNA−damage−inducible, beta [Source:HG
15	286133	1.63	3e−11	4e−10	6 x 1	scavenger receptor class A, member 5 (putative) [Source:HG
16	8076	1.62	3e−11	2e−09	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
17	57124	1.58	1e−10	2e−09	3 x 1	CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
18	4320	1.58	1e−10	5e−09	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
19	687	1.54	3e−10	5e−09	6 x 1	Kruppel−like factor 9 [Source:HGNC Symbol;Acc:1123]
20	5118	1.54	3e−10	3e−08	4 x 1	procollagen C−endopeptidase enhancer [Source:HGNC Sym

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.69	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
2	26.14	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
3	25.87	NULL	54 / 250	Lymphoma	LENZ_Stromal signature 1
4	21.05	NULL	37 / 190	CC	extracellular matrix
5	20.74	NULL	3 / 11	MF	oxygen transporter activity
6	19.14	NULL	3 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
7	18.96	NULL	1 / 2	miRNA target	miR−18
8	18.87	NULL	3 / 10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP
9	18.1	NULL	4 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
10	17.79	NULL	4 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
11	17.42	NULL	2 / 10	CC	hemoglobin complex
12	16.5	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
13	16.12	NULL	3 / 14	CC	endocytic vesicle lumen
14	15.68	NULL	3 / 15	Cancer	LIU_PROSTATE_CANCER_DN
15	15.26	NULL	3 / 19	MF	peroxidase activity
16	14.92	NULL	6 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
17	14.72	NULL	7 / 19	MF	extracellular matrix binding
18	14.33	NULL	4 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
19	14.27	NULL	31 / 242	BP	extracellular matrix organization
20	13.64	NULL	3 / 29	BP	positive regulation of cell death
21	13.5	NULL	2 / 8	GSEA C2	ZHAN_MULTIPLE_MYELOMA_SPIKED
22	13.34	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
23	12.86	NULL	3 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
24	12.78	NULL	3 / 26	MF	oxygen binding
25	12.1	NULL	2 / 19	BP	hydrogen peroxide catabolic process
26	12.07	NULL	4 / 20	BP	positive regulation of collagen biosynthetic process
27	12.02	NULL	4 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
28	12	NULL	2 / 13	BP	regulation of blood vessel size
29	11.95	NULL	10 / 57	MF	extracellular matrix structural constituent
30	11.79	NULL	3 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
31	11.71	NULL	3 / 13	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_2B
32	11.51	NULL	3 / 13	GSEA C2	VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP
33	11.48	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
34	11.48	NULL	1 / 7	GSEA C2	SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_
35	11.32	NULL	2 / 12	GSEA C2	RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP
36	11.14	NULL	6 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
37	11.13	NULL	2 / 22	BP	bicarbonate transport
38	11.06	NULL	6 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
39	10.94	NULL	3 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
40	10.82	NULL	3 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH



GW_137

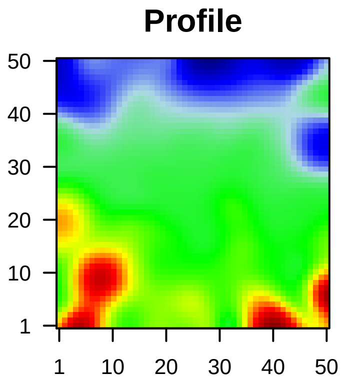
Local Summary

%DE = 0.9
metagenes = 22
genes = 320
genes in genesets = 293

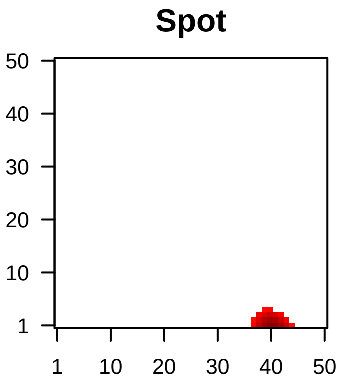
genes with fdr < 0.1 = 235 (235 + / 0 −)
genes with fdr < 0.05 = 201 (201 + / 0 −)
genes with fdr < 0.01 = 128 (128 + / 0 −)

<r> metagenes = 0.95
<r> genes = 0.43

<FC> = 0.6
<shrinkage−t> = 20.94
<p−value> = 0.01
<fdr> = 0.5



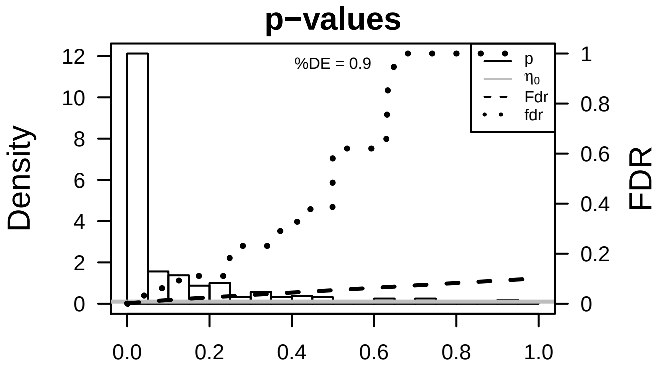
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	2.24	2e−16	7e−15	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	11067	1.79	3e−13	2e−11	44 x 1	chromosome 10 open reading frame 10 [Source:HGNC Symb
3	84446	1.74	1e−12	8e−11	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
4	80162	1.7	3e−12	1e−07	43 x 1	ATH1, acid trehalase−like 1 (yeast) [Source:HGNC Symbol;A
5	401261	1.44	4e−09	5e−07	41 x 1	
6	440157	1.37	2e−08	1e−06	39 x 1	
7	728294	1.33	5e−08	3e−06	40 x 1	D−2−hydroxyglutarate dehydrogenase [Source:HGNC Symbo
8	90639	1.25	3e−07	3e−06	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
9	57464	1.25	3e−07	3e−06	40 x 1	striatin interacting protein 2 [Source:HGNC Symbol;Acc:2220
10	115703	1.24	4e−07	6e−06	41 x 1	Rho GTPase activating protein 33 [Source:HGNC Symbol;Ac
11	440275	1.2	8e−07	6e−06	40 x 1	eukaryotic translation initiation factor 2 alpha kinase 4 [Sourc
12	202134	1.19	1e−06	6e−06	40 x 1	family with sequence similarity 153, member B [Source:HGN
13	80224	1.19	1e−06	6e−06	40 x 1	nucleotide binding protein−like [Source:HGNC Symbol;Acc:2
14	29797	1.19	1e−06	6e−06	40 x 1	
15	255031	1.18	1e−06	6e−06	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
16	126205	1.17	2e−06	6e−06	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
17	55142	1.17	2e−06	6e−06	40 x 1	HAUS augmin−like complex, subunit 2 [Source:HGNC Symbo
18	3586	1.08	2e−06	6e−06	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
19	401494	1.16	2e−06	6e−06	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [Sou
20	136051	1.16	2e−06	2e−05	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	10.91	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	9.39	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
3	7.44	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	7.14	NULL	1 / 8	GSEA C2	NIELSEN_LIPOSARCOMA_UP
5	6.69	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
6	6.61	NULL	3 / 16	BP	negative regulation of neurogenesis
7	6.26	NULL	1 / 15	CC	MHC class II protein complex
8	6.11	NULL	2 / 10	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
9	6.05	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
10	5.98	NULL	2 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
11	5.94	NULL	1 / 10	MF	hydrolase activity, acting on glycosyl bonds
12	5.84	NULL	2 / 14	BP	cellular response to estradiol stimulus
13	5.76	NULL	1 / 11	MF	tau−protein kinase activity
14	5.75	NULL	3 / 23	BP	G2 DNA damage checkpoint
15	5.49	NULL	3 / 24	BP	negative regulation of T cell proliferation
16	5.42	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
17	5.42	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
18	5.4	NULL	4 / 60	BP	T cell costimulation
19	5.38	NULL	2 / 28	CC	transport vesicle membrane
20	5.34	NULL	44 / 1135	Chr	Chr 19
21	5.09	NULL	1 / 21	CC	clathrin−coated endocytic vesicle membrane
22	5.04	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
23	5.01	NULL	2 / 14	BP	mitochondrion morphogenesis
24	4.98	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
25	4.97	NULL	1 / 14	BP	centrosome duplication
26	4.82	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
27	4.8	NULL	1 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
28	4.69	NULL	1 / 16	GSEA C2	TING_SILENCED_BY_DICER
29	4.69	NULL	1 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
30	4.69	NULL	1 / 16	GSEA C2	LEONARD_HYPOXIA
31	4.66	NULL	2 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_UP
32	4.63	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_SIZE_UP
33	4.54	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
34	4.23	NULL	1 / 18	MF	gamma−tubulin binding
35	4.18	NULL	2 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_DN
36	4.15	NULL	2 / 17	BP	negative regulation of interleukin−6 production
37	4.09	NULL	1 / 19	BP	establishment of cell polarity
38	3.99	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
39	3.96	NULL	1 / 14	Cancer	LIU_COMMON_CANCER_GENES
40	3.95	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process

GW_137

Local Summary

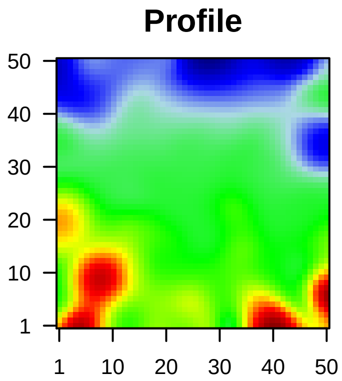
%DE = 0.91
metagenes = 10
genes = 155
genes in genesets = 155

genes with fdr < 0.1 = 122 (119 + / 3 −)
genes with fdr < 0.05 = 108 (106 + / 2 −)
genes with fdr < 0.01 = 93 (92 + / 1 −)

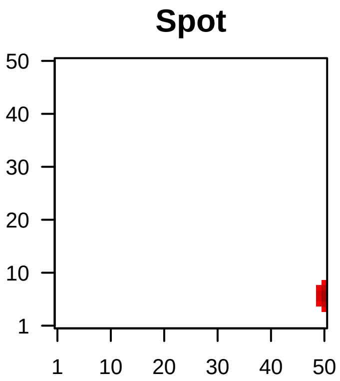
<r> metagenes = 0.93
<r> genes = 0.37

<FC> = 0.82
<shrinkage−t> = 28.69
<p−value> = 0
<fdr> = 0.35

Profile



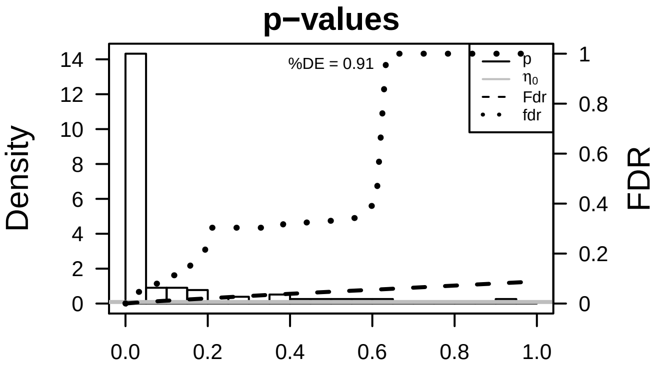
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	347	2.38	2e−16	4e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
2	6358	2.04	2e−16	4e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
3	1675	2.05	2e−16	4e−16	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
4	2532	2.28	2e−16	4e−16	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
5	3488	2.23	2e−16	4e−16	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
6	4256	2.24	2e−16	4e−16	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
7	347733	2.41	2e−16	4e−16	50 x 5	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829]
8	2	1.79	2e−13	6e−12	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
9	6347	1.74	9e−13	6e−12	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
10	1805	1.74	1e−12	4e−11	50 x 5	dermatopontin [Source:HGNC Symbol;Acc:3011]
11	5166	1.68	6e−12	4e−11	50 x 7	pyruvate dehydrogenase kinase, isozyme 4 [Source:HGNC S
12	11170	1.67	7e−12	3e−10	50 x 7	family with sequence similarity 107, member A [Source:HGN
13	8404	1.62	3e−11	6e−10	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
14	5320	1.58	1e−10	6e−10	50 x 8	phospholipase A2, group IIA (platelets, synovial fluid) [Source
15	4629	1.58	1e−10	8e−10	50 x 9	myosin, heavy chain 11, smooth muscle [Source:HGNC Sym
16	219348	1.56	2e−10	4e−09	50 x 7	placenta−specific 9 [Source:HGNC Symbol;Acc:19255]
17	4239	1.52	5e−10	6e−09	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
18	7450	1.49	1e−09	6e−09	50 x 6	von Willebrand factor [Source:HGNC Symbol;Acc:12726]
19	7049	1.47	2e−09	6e−09	50 x 9	transforming growth factor, beta receptor III [Source:HGNC S
20	730	1.46	2e−09	6e−09	49 x 7	complement component 7 [Source:HGNC Symbol;Acc:1346]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.4	NULL	4 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
2	18.86	NULL	2 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
3	17.72	NULL	4 / 13	Cancer	GENTLES_modul17
4	16.89	NULL	5 / 15	Cancer	GENTLES_modul13
5	16.11	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
6	14.34	NULL	3 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
7	13.24	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
8	13.2	NULL	4 / 10	GSEA C2	LU_TUMOR_VASCULATURE_DN
9	13.04	NULL	2 / 15	GSEA C2	ABE_INNER_EAR
10	12.9	NULL	33 / 683	CC	extracellular space
11	12.78	NULL	5 / 46	Glio	OL vs. OPC
12	12.52	NULL	2 / 12	BP	regulation of glucose metabolic process
13	12.42	NULL	3 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
14	12.4	NULL	5 / 20	BP	complement activation
15	12.28	NULL	1 / 5	miRNA target	miR−205
16	12.22	NULL	3 / 10	GSEA C2	REACTOME_INTRINSIC_PATHWAY
17	12.11	NULL	3 / 21	BP	chemokine−mediated signaling pathway
18	12.03	NULL	2 / 4	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_DN
19	11.98	NULL	4 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN
20	11.89	NULL	3 / 10	BP	germ cell migration
21	11.84	NULL	3 / 27	BP	negative regulation of smooth muscle cell proliferation
22	11.62	NULL	15 / 190	CC	extracellular matrix
23	11.61	NULL	4 / 15	GSEA C2	NAKAJIMA_MAST_CELL
24	11.55	NULL	3 / 11	BP	blood coagulation, intrinsic pathway
25	11.55	NULL	6 / 59	Lymphoma	LENZ_Stromal signature 2
26	11.4	NULL	2 / 13	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
27	11.31	NULL	21 / 375	Disease	GUDJ_psoriasis down
28	10.96	NULL	3 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
29	10.94	NULL	3 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
30	10.92	NULL	5 / 43	CC	platelet alpha granule lumen
31	10.72	NULL	1 / 4	Glio	willscher_GBM_Verhaak−PNmut_expression_A_down
32	10.67	NULL	1 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
33	10.6	NULL	3 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
34	10.58	NULL	4 / 55	Glio	OL vs. MOG− OL
35	10.47	NULL	3 / 16	GSEA C2	KORKOLA_TERATOMA_UP
36	10.37	NULL	1 / 4	GSEA C2	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM
37	10.36	NULL	4 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
38	10.29	NULL	38 / 1182	CC	extracellular region
39	10.27	NULL	2 / 14	MF	lipid transporter activity
40	10.26	NULL	2 / 14	BP	tissue regeneration

GW_137

Local Summary

%DE = 0.85

metagenes = 34

genes = 324

genes in genesets = 321

genes with fdr < 0.1 = 201 (201 + / 0 −)

genes with fdr < 0.05 = 183 (183 + / 0 −)

genes with fdr < 0.01 = 96 (96 + / 0 −)

<r> metagenes = 0.89

<r> genes = 0.27

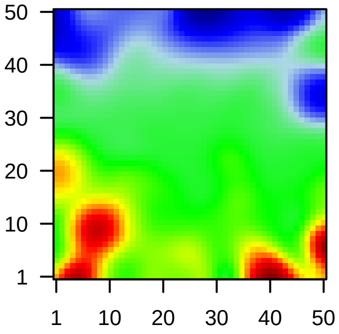
<FC> = 0.53

<shrinkage−t> = 18.44

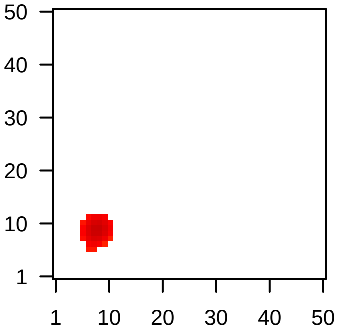
<p−value> = 0.02

<fdr> = 0.56

Profile



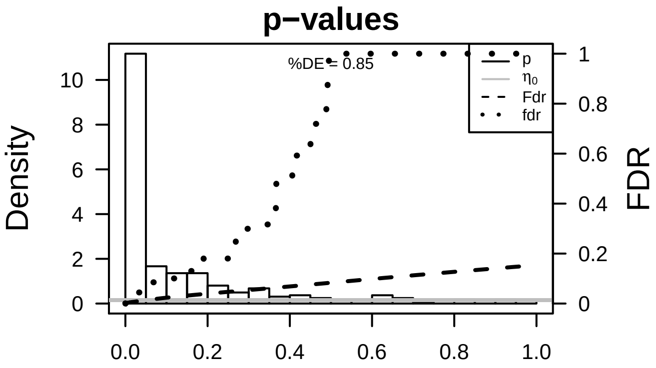
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	80728	1.6	6e−11	2e−07	10 x 11	Rho GTPase activating protein 39 [Source:HGNC Symbol;Ac
2	55291	1.44	4e−09	4e−07	6 x 11	protein phosphatase 6, regulatory subunit 3 [Source:HGNC S
3	4037	1.39	1e−08	5e−07	10 x 7	low density lipoprotein receptor−related protein 3 [Source:HG
4	404217	1.37	2e−08	5e−06	10 x 9	cortexin 1 [Source:HGNC Symbol;Acc:31108]
5	55007	1.29	1e−07	1e−05	6 x 9	family with sequence similarity 118, member A [Source:HGN
6	1465	1.23	5e−07	1e−05	7 x 7	cysteine and glycine−rich protein 1 [Source:HGNC Symbol;A
7	85495	1.22	6e−07	4e−05	8 x 7	ribonuclease P RNA component H1 [Source:HGNC Symbol;
8	3636	1.18	1e−06	1e−04	8 x 9	inositol polyphosphate phosphatase−like 1 [Source:HGNC Sy
9	4499	1.14	3e−06	1e−04	7 x 6	metallothionein 1M [Source:HGNC Symbol;Acc:14296]
10	6722	1.1	7e−06	1e−04	9 x 12	serum response factor (c−fos serum response element−bindi
11	1936	1.09	8e−06	2e−04	7 x 9	eukaryotic translation elongation factor 1 delta (guanine nucle
12	57414	1.05	2e−05	2e−04	9 x 10	rhomboid domain containing 2 [Source:HGNC Symbol;Acc:2
13	7466	1.04	2e−05	2e−04	8 x 8	Wolfram syndrome 1 (wolframin) [Source:HGNC Symbol;Acc:
14	65980	1.03	2e−05	2e−04	9 x 10	bromodomain containing 9 [Source:HGNC Symbol;Acc:2581
15	29894	1.03	2e−05	3e−04	8 x 10	cleavage and polyadenylation specific factor 1, 160kDa [Sour
16	147841	1.01	4e−05	3e−04	8 x 11	SPC24, NDC80 kinetochore complex component [Source:HG
17	55661	1.01	4e−05	3e−04	7 x 10	DEAD (Asp−Glu−Ala−Asp) box polypeptide 27 [Source:HGN
18	23644	0.99	5e−05	3e−04	8 x 11	enhancer of mRNA decapping 4 [Source:HGNC Symbol;Acc:
19	23144	0.99	5e−05	3e−04	6 x 10	zinc finger CCCH−type containing 3 [Source:HGNC Symbol;
20	84988	0.99	5e−05	3e−04	11 x 11	protein phosphatase 1, regulatory subunit 16A [Source:HGN

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	8.53	NULL	2 / 9	miRNA 3UTR	TCCG−184
2	7.83	NULL	60 / 1135	Chr	Chr 19
3	7.81	NULL	8 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
4	6.83	NULL	1 / 4	miRNA target	miR−122
5	6.6	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
6	6.57	NULL	6 / 55	miRNA 3UTR	GTGG−296
7	6.47	NULL	1 / 5	miRNA target	miR−205
8	5.91	NULL	3 / 16	GSEA C2	JIANG_HYPOXIA_CANCER
9	5.89	NULL	2 / 12	miRNA target−starBase	hsa−miR−1249
10	5.82	NULL	2 / 10	BP	eyelid development in camera−type eye
11	5.79	NULL	2 / 12	BP	long term synaptic depression
12	5.61	NULL	2 / 10	MF	K63−linked polyubiquitin binding
13	5.51	NULL	2 / 13	GSEA C2	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
14	5.38	NULL	2 / 10	GSEA C2	HELLER_HDAC_TARGETS_UP
15	5.38	NULL	2 / 10	BP	negative regulation of translational initiation
16	5.36	NULL	2 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
17	5.34	NULL	4 / 42	BP	inositol phosphate metabolic process
18	5.3	NULL	4 / 19	MF	hydrolase activity, acting on acid anhydrides, in phosphorus−contai
19	5.3	NULL	1 / 7	GSEA C2	BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2
20	5.27	NULL	2 / 14	GSEA C2	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_B
21	5.27	NULL	2 / 14	GSEA C2	REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
22	5.15	NULL	4 / 49	BP	actin filament organization
23	5.09	NULL	2 / 11	Glio	KIM amplified & overexpressed in LTS
24	5.09	NULL	1 / 7	MMML CGS	MACIEJ_MMML 13
25	5.07	NULL	2 / 14	Cancer	LIU_COMMON_CANCER_GENES
26	5.06	NULL	2 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
27	5.05	NULL	1 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
28	5.05	NULL	2 / 15	GSEA C2	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
29	4.97	NULL	2 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
30	4.94	NULL	3 / 19	MF	mitogen−activated protein kinase kinase kinase binding
31	4.87	NULL	2 / 11	GSEA C2	KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
32	4.87	NULL	2 / 12	BP	mRNA cleavage
33	4.85	NULL	2 / 16	BP	preassembly of GPI anchor in ER membrane
34	4.85	NULL	3 / 29	miRNA target−starBase	hsa−miR−296−5p
35	4.82	NULL	3 / 23	Chr	Chr HSCHR6_MHC_DBB
36	4.77	NULL	2 / 12	BP	mRNA transcription from RNA polymerase II promoter
37	4.77	NULL	4 / 26	BP	histone acetylation
38	4.62	NULL	3 / 15	GSEA C2	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROIT
39	4.6	NULL	2 / 16	MF	histone acetyl−lysine binding
40	4.53	NULL	2 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY

GW_137

Local Summary

%DE = 0.72

metagenes = 9

genes = 163

genes in genesets = 163

genes with fdr < 0.1 = 70 (1 + / 69 −)

genes with fdr < 0.05 = 61 (1 + / 60 −)

genes with fdr < 0.01 = 0 (0 + / 0 −)

<r> metagenes = 0.99

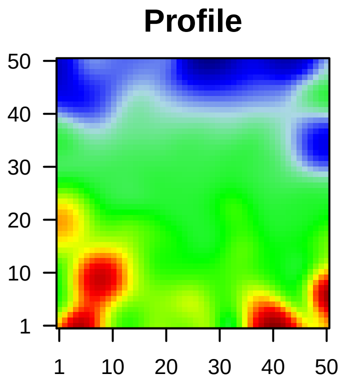
<r> genes = 0.33

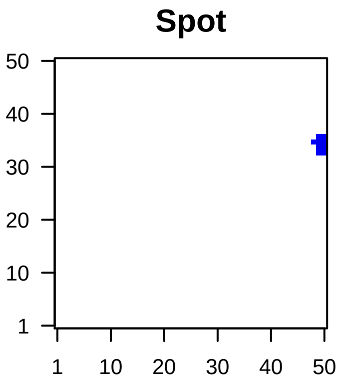
<FC> = −0.38

<shrinkage−t> = −13.3

<p−value> = 0.07

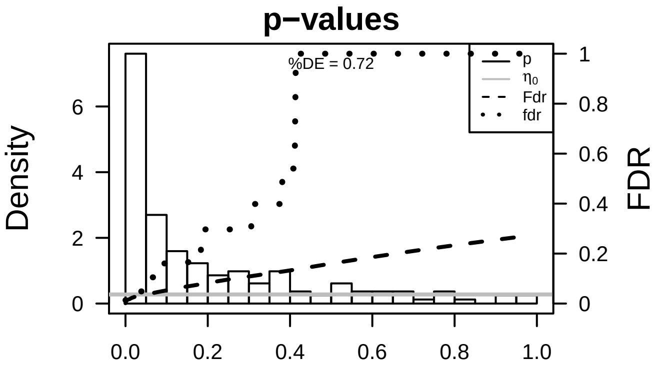
<fdr> = 0.75





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9685	−1.02	3e−05	0.01	50 x 34	clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
2	80208	−0.8	1e−03	0.01	50 x 35	spastic paraplegia 11 (autosomal recessive) [Source:HGNC S
3	84869	−0.77	2e−03	0.01	50 x 34	carbonyl reductase 4 [Source:HGNC Symbol;Acc:25891]
4	9908	−0.76	2e−03	0.01	50 x 36	GTPase activating protein (SH3 domain) binding protein 2 [Sc
5	56947	−0.76	2e−03	0.01	50 x 33	mitochondrial fission factor [Source:HGNC Symbol;Acc:2485
6	310	−0.76	2e−03	0.01	50 x 35	annexin A7 [Source:HGNC Symbol;Acc:545]
7	167153	−0.75	2e−03	0.01	50 x 34	PAP associated domain containing 4 [Source:HGNC Symbol;
8	10257	−0.75	2e−03	0.01	50 x 36	ATP−binding cassette, sub−family C (CFTR/MRP), member 4
9	54497	−0.74	2e−03	0.02	50 x 36	HEAT repeat containing 5B [Source:HGNC Symbol;Acc:2927
10	51015	−0.72	3e−03	0.02	50 x 33	isochorismatase domain containing 1 [Source:HGNC Symbol
11	57092	−0.71	4e−03	0.02	50 x 35	PEST proteolytic signal containing nuclear protein [Source:H
12	151525	−0.7	4e−03	0.02	50 x 35	WD repeat, sterile alpha motif and U−box domain containing
13	34	−0.68	6e−03	0.02	50 x 34	acyl−CoA dehydrogenase, C−4 to C−12 straight chain [Sourc
14	8539	−0.67	6e−03	0.02	50 x 35	apoptosis inhibitor 5 [Source:HGNC Symbol;Acc:594]
15	7520	−0.67	6e−03	0.02	50 x 35	X−ray repair complementing defective repair in Chinese hams
16	79893	−0.66	7e−03	0.02	48 x 35	gametogenetin binding protein 2 [Source:HGNC Symbol;Acc:
17	29110	−0.66	7e−03	0.02	48 x 35	TANK−binding kinase 1 [Source:HGNC Symbol;Acc:11584]
18	54665	−0.66	7e−03	0.02	50 x 33	round spermatid basic protein 1 [Source:HGNC Symbol;Acc:
19	51362	−0.65	8e−03	0.02	50 x 34	cell division cycle 40 [Source:HGNC Symbol;Acc:17350]
20	57763	−0.65	8e−03	0.02	50 x 34	ankyrin repeat, family A (RFXANK−like), 2 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−9.14	NULL	5 / 38	miRNA target starBase hsa−miR−1277
2	−9.09	NULL	3 / 16	GSEA C2 DAZARD_UV_RESPONSE_CLUSTER_G6
3	−9.07	NULL	2 / 11	GSEA C2 ROZANOV_MMP14_CORRELATED
4	−8.66	NULL	1 / 4	GSEA C2 LUCAS_HNF4A_TARGETS_DN
5	−8.52	NULL	2 / 16	GSEA C2 SESTO_RESPONSE_TO_UV_C5
6	−8.24	NULL	2 / 15	GSEA C2 BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
7	−8.19	NULL	1 / 8	GSEA C2 YAGI_AML_WITH_T_8_21_TRANSLOCATION
8	−7.77	NULL	17 / 325	miRNA target starBase hsa−miR−302d
9	−7.71	NULL	8 / 89	miRNA target starBase hsa−miR−505
10	−7.61	NULL	1 / 2	miRNA target miR−98
11	−7.56	NULL	11 / 153	miRNA target starBase hsa−miR−450b−5p
12	−7.31	NULL	14 / 318	miRNA target starBase hsa−miR−590−3p
13	−7.27	NULL	8 / 93	miRNA target starBase hsa−miR−10b
14	−7.21	NULL	2 / 16	GSEA C2 LAIHO_COLORECTAL_CANCER_SERRATED_UP
15	−7.07	NULL	6 / 49	miRNA 3UTR GTRT−154−−487
16	−6.98	NULL	2 / 10	MF NADPH binding
17	−6.76	NULL	2 / 19	miRNA target starBase hsa−miR−542−5p
18	−6.62	NULL	15 / 314	miRNA target starBase hsa−miR−520c−3p
19	−6.55	NULL	16 / 303	miRNA target starBase hsa−miR−302b
20	−6.54	NULL	1 / 12	GSEA C2 BROWNE_HCMV_INFECTION_14HR_UP
21	−6.5	NULL	13 / 271	miRNA target starBase hsa−miR−520b
22	−6.44	NULL	8 / 178	miRNA target starBase hsa−miR−520f
23	−6.44	NULL	3 / 42	miRNA 3UTR GTRC−486
24	−6.26	NULL	1 / 13	GSEA C2 BASAKI_YBX1_TARGETS_DN
25	−6.26	NULL	1 / 13	GSEA C2 WEST_ADRENOCORTICAL_TUMOR_UP
26	−6.18	NULL	2 / 15	GSEA C2 GENTILE_UV_RESPONSE_CLUSTER_D6
27	−6.17	NULL	7 / 90	miRNA target starBase hsa−miR−10a
28	−6.1	NULL	7 / 122	miRNA target starBase hsa−miR−105
29	−6.06	NULL	5 / 51	miRNA target starBase hsa−miR−556−3p
30	−6.05	NULL	18 / 463	miRNA target starBase hsa−miR−301a
31	−6	NULL	1 / 14	BP clathrin coat assembly
32	−6	NULL	1 / 14	GSEA C2 ZHOU_INFLAMMATORY_RESPONSE_FIMA_UP
33	−6	NULL	1 / 14	GSEA C2 PUJANA_BRCA2_PCC_NETWORK
34	−5.91	NULL	1 / 5	miRNA target starBase hsa−miR−585
35	−5.84	NULL	5 / 62	miRNA target starBase hsa−miR−627
36	−5.82	NULL	14 / 321	miRNA target starBase hsa−let−7g
37	−5.81	NULL	14 / 311	miRNA target starBase hsa−miR−302c
38	−5.79	NULL	4 / 59	miRNA target starBase hsa−miR−526b*
39	−5.77	NULL	1 / 15	GSEA C2 SCHLOSSER_SERUM_RESPONSE_DN
40	−5.77	NULL	1 / 15	GSEA C2 DACOSTA_UV_RESPONSE_VIA_ERCC3_DN

GW_137

Local Summary

%DE = 0.65

metagenes = 24

genes = 302

genes in genesets = 295

genes with fdr < 0.1 = 138 (17 + / 121 −)

genes with fdr < 0.05 = 127 (15 + / 112 −)

genes with fdr < 0.01 = 80 (10 + / 70 −)

<r> metagenes = 0.91

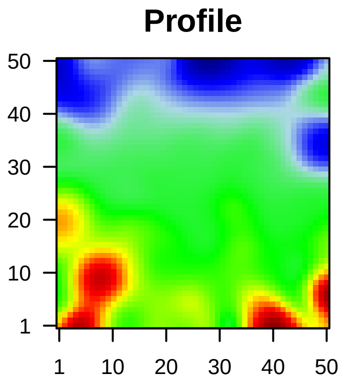
<r> genes = 0.4

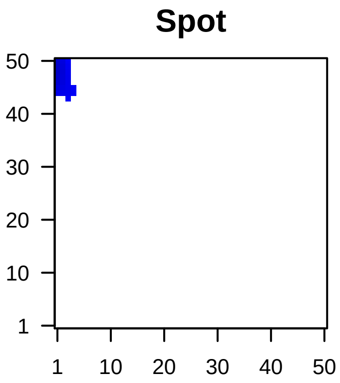
<FC> = −0.39

<shrinkage−t> = −13.67

<p−value> = 0.01

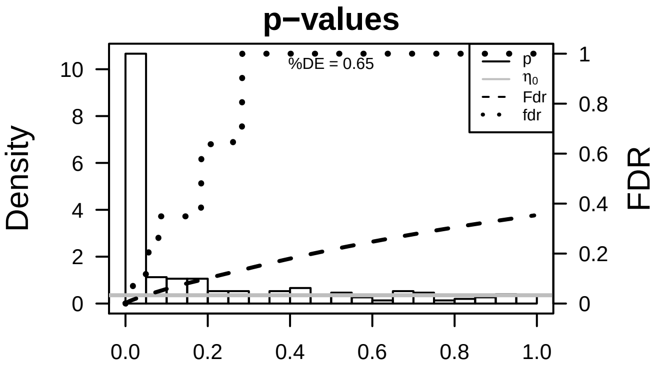
<fdr> = 0.57


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	286887	−1.84	2e−16	2e−14	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
2	6706	−1.73	1e−12	1e−09	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
3	10804	−1.65	1e−11	8e−09	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
4	53833	−1.58	9e−11	2e−08	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
5	414325	−1.53	4e−10	2e−08	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
6	1828	−1.52	5e−10	2e−08	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
7	23682	−1.51	6e−10	2e−08	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
8	6701	−1.51	7e−10	1e−06	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
9	1475	−1.4	1e−08	1e−06	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
10	6286	1.35	3e−08	1e−06	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
11	760	−1.35	3e−08	6e−06	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	387695	−1.27	2e−07	6e−06	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
13	5803	−1.27	2e−07	6e−06	1 x 45	protein tyrosine phosphatase, receptor−type, Z polypeptide 1
14	29094	1.26	2e−07	6e−06	1 x 48	lectin, galactoside−binding−like [Source:HGNC Symbol;Acc:2
15	26525	−1.25	3e−07	6e−06	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
16	9635	−1.24	4e−07	6e−06	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
17	131	−1.24	4e−07	7e−06	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
18	4753	−1.23	4e−07	2e−05	1 x 44	NEL−like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
19	2150	−1.21	8e−07	2e−05	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGNC
20	2167	1.2	9e−07	2e−05	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−30.8	NULL	89 / 135	H.Tiss	WIRTH_Mucosa
2	−25.78	NULL	18 / 21	CC	cornified envelope
3	−24.36	NULL	111 / 572	Disease	GUDJ_psoriasis up
4	−19.36	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	−18.38	NULL	19 / 42	BP	keratinization
6	−17.74	NULL	13 / 21	CC	desmosome
7	−17.13	NULL	24 / 53	BP	keratinocyte differentiation
8	−12.92	NULL	6 / 13	BP	negative regulation of peptidase activity
9	−12.45	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
10	−11.94	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
11	−11.7	NULL	7 / 29	BP	regulation of proteolysis
12	−11.67	NULL	10 / 52	BP	negative regulation of endopeptidase activity
13	−11.34	NULL	10 / 19	BP	peptide cross−linking
14	−11.21	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
15	−11.19	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
16	−11.09	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
17	−10.44	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	−10.18	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
19	−9.94	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
20	−9.82	NULL	2 / 10	BP	negative regulation of interleukin−2 production
21	−9.79	NULL	3 / 15	CC	connexon complex
22	−8.77	NULL	4 / 21	CC	gap junction
23	−8.74	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
24	−8.73	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
25	−8.65	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
26	−8.41	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
27	−8.39	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
28	−8.25	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
29	−8.13	NULL	2 / 14	BP	positive regulation of interleukin−10 production
30	−8.08	NULL	5 / 23	MF	peptidase inhibitor activity
31	−8.03	NULL	2 / 11	MF	gamma−catenin binding
32	−7.72	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
33	−7.42	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
34	−7.31	NULL	2 / 10	GSEA C2	KIM_MYCL1_AMPLIFICATION_TARGETS_UP
35	−7.19	NULL	4 / 15	MF	retinol dehydrogenase activity
36	−7.08	NULL	3 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
37	−6.98	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
38	−6.94	NULL	24 / 76	BP	epidermis development
39	−6.92	NULL	2 / 15	GSEA C2	NEWMAN_ERCC6_TARGETS_UP
40	−6.52	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN

GW_137

Local Summary

%DE = 0.81

metagenes = 83

genes = 1126

genes in genesets = 1109

genes with fdr < 0.1 = 656 (3 + / 653 −)

genes with fdr < 0.05 = 459 (2 + / 457 −)

genes with fdr < 0.01 = 99 (1 + / 98 −)

<r> metagenes = 0.71

<r> genes = 0.21

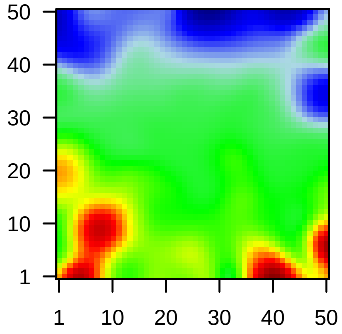
<FC> = −0.41

<shrinkage−t> = −14.54

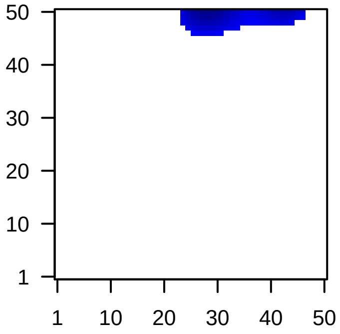
<p−value> = 0.06

<fdr> = 0.71

Profile

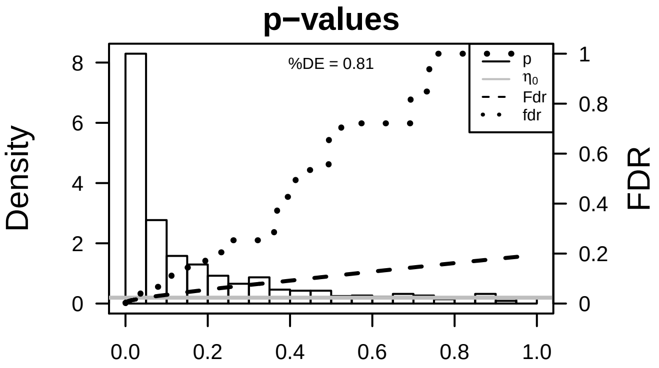


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8836	−1.06	1e−05	0.002	40 x 50	gamma−glutamyl hydrolase (conjugase, folylpolygammagluta
2	26872	−1.05	2e−05	0.002	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
3	51030	−1.03	3e−05	0.002	26 x 50	trans−golgi network vesicle protein 23 homolog B (S. cerevisi
4	9643	−1	4e−05	0.002	26 x 50	mortality factor 4 like 2 [Source:HGNC Symbol;Acc:16849]
5	6897	−0.99	5e−05	0.002	39 x 50	threonyl−tRNA synthetase [Source:HGNC Symbol;Acc:11572
6	3161	−0.98	6e−05	0.002	43 x 50	hyaluronan−mediated motility receptor (RHAMM) [Source:HG
7	3945	0.97	7e−05	0.002	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
8	23279	−0.97	7e−05	0.002	42 x 50	nucleoporin 160kDa [Source:HGNC Symbol;Acc:18017]
9	8624	−0.97	7e−05	0.002	29 x 50	proteasome (prosome, macropain) assembly chaperone 1 [S
10	136	−0.96	9e−05	0.002	41 x 50	adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
11	84365	−0.95	9e−05	0.004	40 x 50	nucleolar protein interacting with the FHA domain of MKI67 [
12	6392	−0.94	1e−04	0.004	31 x 50	succinate dehydrogenase complex, subunit D, integral memb
13	1738	−0.93	1e−04	0.004	28 x 50	dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
14	10884	−0.92	2e−04	0.004	40 x 50	mitochondrial ribosomal protein S30 [Source:HGNC Symbol;
15	10190	−0.91	2e−04	0.004	31 x 50	thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:
16	7336	−0.91	2e−04	0.004	40 x 50	ubiquitin−conjugating enzyme E2 variant 1 [Source:HGNC Sy
17	28957	−0.91	2e−04	0.004	39 x 50	mitochondrial ribosomal protein S28 [Source:HGNC Symbol;
18	3094	−0.83	2e−04	0.004	32 x 50	histidine triad nucleotide binding protein 1 [Source:HGNC Sy
19	9650	−0.89	3e−04	0.004	40 x 50	mitochondrial fission regulator 1 [Source:HGNC Symbol;Acc:
20	3251	−0.89	3e−04	0.004	42 x 50	hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−19.91	NULL	69 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−19.91	NULL	69 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−13.88	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	−13.45	NULL	89 / 370	BP	mitotic cell cycle
5	−13.19	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
6	−12.55	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
7	−10.96	NULL	11 / 18	BP	spindle organization
8	−10.69	NULL	5 / 8	MMML CGS	MACIEJ_MMML 50
9	−10.56	NULL	194 / 1318	CC	mitochondrion
10	−10.48	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	−10.18	NULL	179 / 1233	TF	KIM_MYC targets
12	−10.07	NULL	9 / 16	GSEA C2	HORIUCHI_WTAP_TARGETS_DN
13	−10.07	NULL	64 / 287	BP	viral process
14	−9.77	NULL	19 / 57	Glio	developing astrocytes
15	−9.51	NULL	10 / 14	MMML CGS	MACIEJ_MMML 4
16	−9.42	NULL	57 / 232	BP	mitosis
17	−9.14	NULL	19 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−
18	−9.02	NULL	31 / 83	BP	respiratory electron transport chain
19	−8.99	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	−8.85	NULL	106 / 649	BP	gene expression
21	−8.81	NULL	61 / 253	BP	translation
22	−8.81	NULL	35 / 148	BP	G1/S transition of mitotic cell cycle
23	−8.79	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
24	−8.72	NULL	45 / 153	MF	structural constituent of ribosome
25	−8.68	NULL	13 / 35	BP	mitotic nuclear envelope disassembly
26	−8.59	NULL	266 / 2378	CC	cytosol
27	−8.48	NULL	8 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
28	−8.46	NULL	7 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
29	−8.34	NULL	8 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
30	−8.14	NULL	41 / 167	CC	ribosome
31	−8.13	NULL	22 / 66	CC	condensed chromosome kinetochore
32	−8.01	NULL	6 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
33	−8	NULL	134 / 949	CC	nucleoplasm
34	−7.98	NULL	8 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
35	−7.92	NULL	8 / 11	BP	mitotic metaphase plate congression
36	−7.83	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
37	−7.76	NULL	54 / 318	miRNA target starBase	hsa−miR−590−3p
38	−7.75	NULL	24 / 100	Lymphoma	ROSOLOWSKI_blue total
39	−7.53	NULL	6 / 12	GSEA C2	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
40	−7.51	NULL	6 / 14	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_2