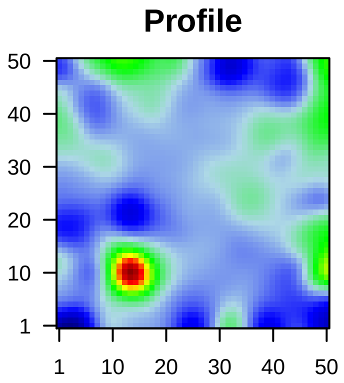
GW_293

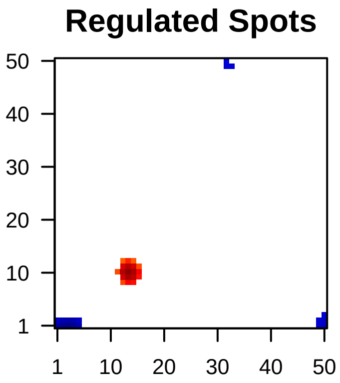
Global Summary

%DE = 0.16
genes with fdr < 0.2 = 1995 (1102 + / 893 −)
genes with fdr < 0.1 = 1514 (848 + / 666 −)
genes with fdr < 0.05 = 1299 (741 + / 558 −)
genes with fdr < 0.01 = 864 (514 + / 350 −)

genes in genesets = 16332

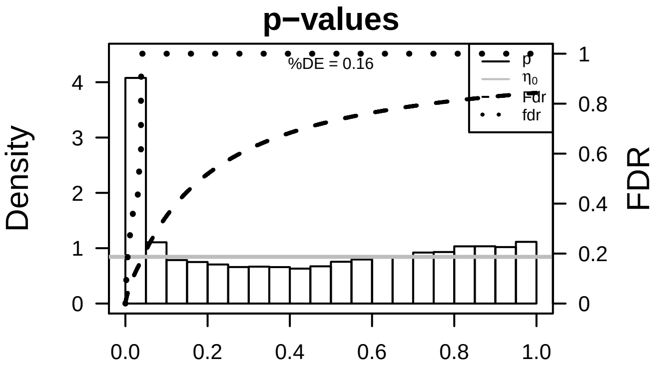
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.1
<fdr> = 0.84


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	−1.78	2e−16	4e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	126	1.57	2e−16	4e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	220	1.77	2e−16	4e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
4	218	2.19	2e−16	4e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	445328	−2.47	2e−16	4e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
6	92747	3.38	2e−16	4e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
7	375791	−1.67	2e−16	4e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
8	57172	−2.09	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
9	55832	1.61	2e−16	4e−14	47 x 50	cullin−associated and neddylation−dissociated 1 [Source:HG
10	92291	1.6	2e−16	4e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
11	629	1.79	2e−16	4e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
12	137075	1.75	2e−16	4e−14	49 x 12	claudin 23 [Source:HGNC Symbol;Acc:17591]
13	9073	1.7	2e−16	4e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
14	169044	2.69	2e−16	4e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
15	51755	−1.77	2e−16	4e−14	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
16	441520	3.26	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
17	9249	1.59	2e−16	4e−14	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
18	2167	4.22	2e−16	4e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
19	2327	1.77	2e−16	4e−14	50 x 11	flavin containing monooxygenase 2 (non−functional) [Source:
20	2354	1.65	2e−16	4e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	8.9	NULL	504	Chr	Chr 15
2	8.08	NULL	534	Chr	Chr 8
3	7.33	NULL	16	TF Tissue	VAQUERIZAS_Pancreas
4	6.87	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
5	6.68	NULL	500	MF	sequence−specific DNA binding
6	6.49	NULL	24	TF Tissue	VAQUERIZAS_Trachea
7	6.41	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
8	6.03	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
9	5.96	NULL	823	MF	sequence−specific DNA binding transcription factor activity
10	5.87	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	5.87	NULL	14	GSEA C2	TIAN_TNF_SIGNALING_NOT_VIA_NFKB
12	5.78	NULL	15	GSEA C2	KORKOLA_TERATOMA
13	5.7	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
14	5.46	NULL	8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
15	5.43	NULL	12	GSEA C2	SESTO_RESPONSE_TO_UV_C3
16	5.41	NULL	37	TF Tissue	VAQUERIZAS_Prostate
17	5.26	NULL	7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
18	5.12	NULL	62	TF Tissue	VAQUERIZAS_Lung
19	5.05	NULL	16	GSEA C2	AMIT_DELAYED_EARLY_GENES
20	5.03	NULL	7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
Underexpressed					
1	−8.74	NULL	253	BP	translation
2	−8.64	NULL	19	BP	peptide cross−linking
3	−8.03	NULL	153	MF	structural constituent of ribosome
4	−7.99	NULL	92	BP	viral life cycle
5	−7.77	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
6	−7.56	NULL	81	BP	viral transcription
7	−7.53	NULL	167	CC	ribosome
8	−7.38	NULL	87	BP	translational termination
9	−7.32	NULL	128	BP	translational initiation
10	−7.29	NULL	92	BP	translational elongation
11	−7.25	NULL	4	MMML CGS	MACIEJ_MMML 23
12	−6.49	NULL	11	MF	platelet−derived growth factor binding
13	−6.25	NULL	957	Chr	Chr 11
14	−6.19	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
15	−6.1	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
16	−6.07	NULL	11	MF	oxygen transporter activity
17	−5.85	NULL	14	GSEA C2	WILCOX_PRESPONSE_TO_ROGESTERONE_DN
18	−5.56	NULL	51	CC	cytosolic large ribosomal subunit
19	−5.53	NULL	12	miRNA target	miR−29c
20	−5.52	NULL	96	BP	rRNA processing

GW_293

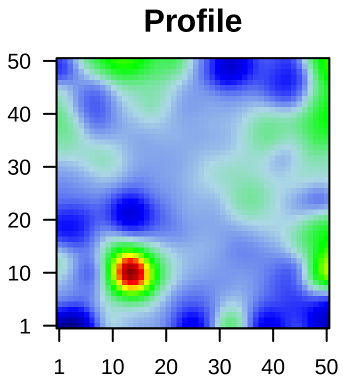
Local Summary

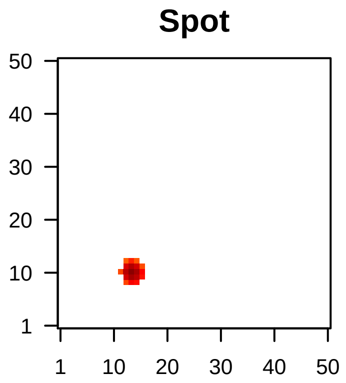
%DE = 0.74
metagenes = 19
genes = 88
genes in genesets = 64

genes with fdr < 0.1 = 64 (63 + / 1 −)
genes with fdr < 0.05 = 63 (62 + / 1 −)
genes with fdr < 0.01 = 56 (56 + / 0 −)

<r> metagenes = 0.97
<r> genes = 0.32

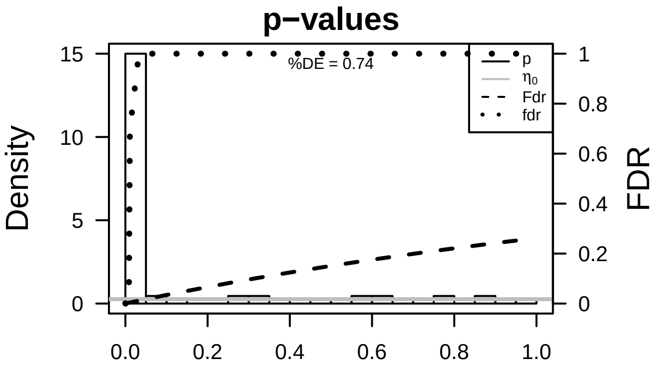
<FC> = 1.13
<shrinkage−t> = 39.63
<p−value> = 0
<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	441520	3.26	2e−16	3e−16	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
2	729428	3.51	2e−16	3e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
3	729422	4.02	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	3.49	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	3.55	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.82	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	3.77	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	2.66	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.91	2e−16	3e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	4.19	2e−16	3e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.87	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	3.79	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	3.87	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2578	2.02	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	3.24	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	100101629	2.08	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	4109	2.8	2e−16	3e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
18	9627	1.56	2e−16	3e−16	13 x 9	synuclein, alpha interacting protein [Source:HGNC Symbol;A
19	64591	1.83	2e−16	3e−16	15 x 11	testis specific protein, Y−linked 2 [Source:HGNC Symbol;Acc
20	100132399	1.51	3e−15	6e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.31	NULL	1 / 2	miRNA target	miR−107
2	17.51	NULL	30 / 630	Chr	Chr X
3	15.55	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
4	13.09	NULL	1 / 11	GSEA C2	SU_PLACENTA
5	11.23	NULL	1 / 14	GSEA C2	NIELSEN_GIST
6	10.75	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
7	9.17	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
8	9.07	NULL	1 / 10	GSEA C2	CONRAD_GERMLINE_STEM_CELL
9	8.05	NULL	1 / 12	GSEA C2	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
10	7.55	NULL	1 / 5	miRNA target	miR−181a
11	7.24	NULL	1 / 11	BP	dopamine metabolic process
12	7.24	NULL	1 / 11	BP	regulation of neurotransmitter secretion
13	7.24	NULL	1 / 11	GSEA C2	BIOCARTA_PARKIN_PATHWAY
14	7.06	NULL	2 / 34	Chr	Chr Y
15	6.66	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
16	6.57	NULL	1 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16
17	6.57	NULL	1 / 6	miRNA target	miR−181b
18	5.95	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
19	5.87	NULL	1 / 7	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9
20	5.87	NULL	9 / 120	H.Tiss	WIRTH_Testis
21	5.42	NULL	1 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
22	5.06	NULL	3 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP
23	4.94	NULL	1 / 10	BP	leukocyte tethering or rolling
24	4.58	NULL	1 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_DN
25	4.58	NULL	1 / 10	miRNA target−starBase	hsa−miR−933
26	4.44	NULL	1 / 11	Glio	willscher_GBM_Verhaak−CL_expression_M_down
27	4.44	NULL	1 / 11	Glio	willscher_GBM_Verhaak−MES_expression_M_down
28	4.44	NULL	1 / 11	Glio	willscher_GBM_Verhaak−PNmut_expression_M_up
29	4.43	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
30	4.07	NULL	7 / 259	BP	spermatogenesis
31	4.06	NULL	1 / 10	GSEA C2	WEBER_METHYLATED_HCP_IN_SPERM_DN
32	4.05	NULL	1 / 12	BP	organ growth
33	4	NULL	2 / 86	BP	nucleosome assembly
34	3.9	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
35	3.9	NULL	1 / 13	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_DN
36	3.9	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
37	3.86	NULL	1 / 10	BP	branching involved in salivary gland morphogenesis
38	3.81	NULL	1 / 11	GSEA C2	WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN
39	3.71	NULL	1 / 14	BP	negative regulation of retinoic acid receptor signaling pathway
40	3.71	NULL	1 / 14	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN

GW_293

Local Summary

%DE = 0.78

metagenes = 10

genes = 186

genes in genesets = 185

genes with fdr < 0.1 = 125 (19 + / 106 −)

genes with fdr < 0.05 = 111 (16 + / 95 −)

genes with fdr < 0.01 = 89 (12 + / 77 −)

<r> metagenes = 0.98

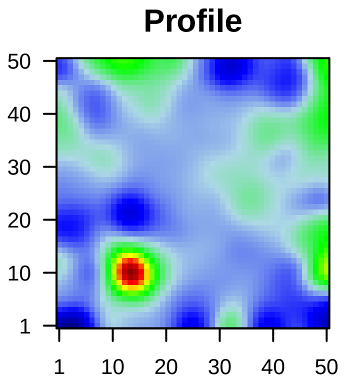
<r> genes = 0.45

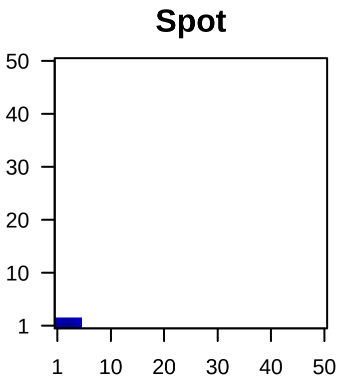
<FC> = −0.41

<shrinkage−t> = −14.35

<p−value> = 0

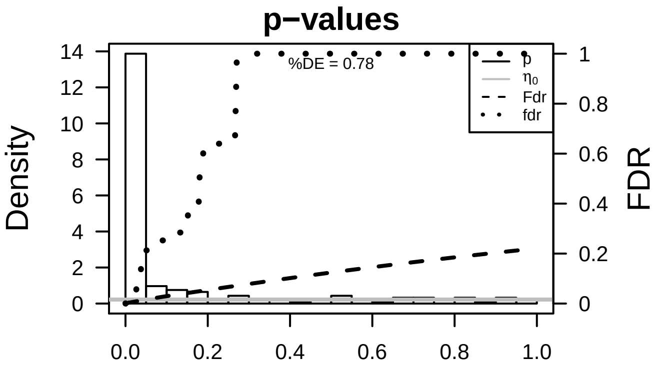
<fdr> = 0.38


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3039	−1.75	2e−16	2e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	3040	−2.65	2e−16	2e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
3	3043	−2.59	2e−16	2e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
4	4316	2.78	2e−16	2e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
5	4692	−1.81	2e−16	2e−15	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
6	12	1.82	2e−16	2e−15	1 x 1	
7	7070	−1.56	4e−16	2e−13	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801
8	4312	−1.49	6e−15	5e−12	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
9	4318	−1.41	1e−13	5e−12	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
10	1293	−1.4	2e−13	1e−11	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
11	91663	1.38	5e−13	4e−10	2 x 1	myeloid−associated differentiation marker [Source:HGNC Sy
12	6372	−1.3	1e−11	3e−09	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
13	7057	−1.24	8e−11	9e−09	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
14	27253	−1.19	4e−10	9e−09	4 x 1	protocadherin 17 [Source:HGNC Symbol;Acc:14267]
15	7130	−1.19	5e−10	2e−08	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN
16	7058	−1.17	1e−09	2e−08	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
17	23452	−1.15	2e−09	2e−08	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
18	7078	1.15	2e−09	2e−08	2 x 1	TIMP metallopeptidase inhibitor 3 [Source:HGNC Symbol;Ac
19	6423	−1.15	2e−09	4e−08	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
20	1009	−1.12	4e−09	4e−08	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGN


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−34.39	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
2	−29.74	NULL	8 / 11	MF	platelet−derived growth factor binding
3	−25.58	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
4	−25.13	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
5	−23.61	NULL	8 / 12	miRNA target	miR−29c
6	−23.46	NULL	3 / 11	MF	oxygen transporter activity
7	−22.83	NULL	60 / 250	Lymphoma	LENZ_Stromal signature 1
8	−20.42	NULL	57 / 190	CC	extracellular matrix
9	−20.2	NULL	2 / 10	CC	hemoglobin complex
10	−20.2	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
11	−20.14	NULL	3 / 14	CC	endocytic vesicle lumen
12	−19.77	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
13	−19.14	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
14	−18.7	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
15	−18.41	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
16	−18.04	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
17	−17.4	NULL	26 / 64	BP	collagen catabolic process
18	−17.15	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
19	−17.03	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
20	−16.77	NULL	29 / 69	BP	extracellular matrix disassembly
21	−15.98	NULL	4 / 26	MF	oxygen binding
22	−15.77	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
23	−15.24	NULL	5 / 19	MF	peroxidase activity
24	−15.16	NULL	55 / 242	BP	extracellular matrix organization
25	−14.77	NULL	13 / 37	BP	collagen fibril organization
26	−14.44	NULL	3 / 19	BP	hydrogen peroxide catabolic process
27	−14.44	NULL	3 / 10	BP	positive regulation of chemotaxis
28	−14.22	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
29	−13.85	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
30	−13.84	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
31	−13.69	NULL	3 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
32	−13.51	NULL	5 / 43	BP	response to hydrogen peroxide
33	−13.45	NULL	19 / 57	MF	extracellular matrix structural constituent
34	−13.42	NULL	3 / 16	GSEA C2	KEGG_BLADDER_CANCER
35	−13.15	NULL	4 / 10	BP	protein heterotrimerization
36	−13.01	NULL	2 / 22	BP	bicarbonate transport
37	−12.87	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
38	−12.7	NULL	10 / 40	BP	cellular response to amino acid stimulus
39	−12.64	NULL	15 / 68	CC	collagen
40	−12.63	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4

GW_293

Local Summary

%DE = 0.64

metagenes = 5

genes = 153

genes in genesets = 152

genes with fdr < 0.1 = 58 (15 + / 43 −)

genes with fdr < 0.05 = 45 (14 + / 31 −)

genes with fdr < 0.01 = 40 (14 + / 26 −)

<r> metagenes = 1

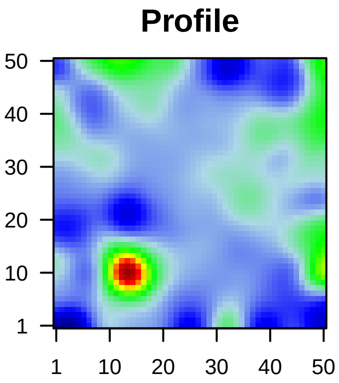
<r> genes = 0.65

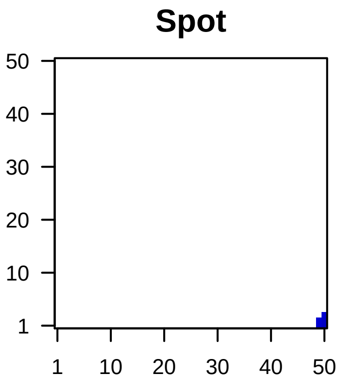
<FC> = −0.23

<shrinkage−t> = −8.03

<p−value> = 0

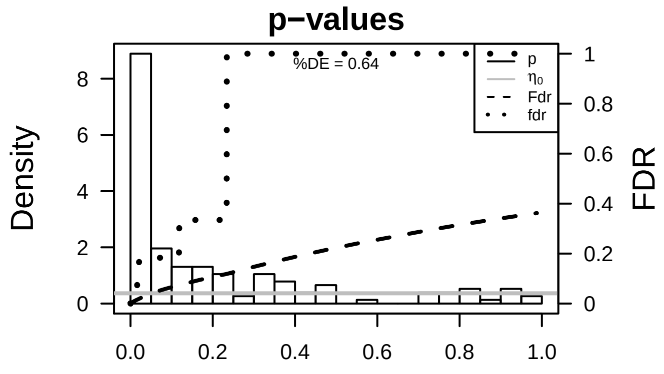
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	−2.09	2e−16	3e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	51755	−1.77	2e−16	3e−15	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
3	3512	−2.51	2e−16	3e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
4	3543	−3.81	2e−16	3e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
5	260436	1.49	5e−15	2e−11	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
6	3122	1.3	3e−13	3e−09	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
7	5730	−1.25	5e−11	3e−08	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
8	25849	1.17	1e−09	3e−08	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
9	3936	1.16	1e−09	3e−08	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
10	341	−1.15	2e−09	3e−08	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
11	126306	−1.15	2e−09	4e−08	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
12	3575	−1.14	3e−09	3e−07	50 x 2	interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
13	3125	1.09	1e−08	3e−07	50 x 1	major histocompatibility complex, class II, DR beta 3 [Source:
14	348	−1.08	1e−08	1e−06	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
15	10537	1.04	5e−08	1e−06	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	10563	1.01	1e−07	1e−06	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
17	11040	−1.01	1e−07	1e−06	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
18	54855	−1.01	1e−07	1e−06	49 x 1	family with sequence similarity 46, member C [Source:HGNC
19	972	1.01	1e−07	8e−06	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
20	5341	−0.97	4e−07	8e−06	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.65	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
2	−26.78	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	−20.58	NULL	2 / 12	GSEA C2	MCCABE_HOXC6_TARGETS_CANCER_UP
4	−18.02	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
5	−13.99	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
6	−13.16	NULL	2 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
7	−12.7	NULL	3 / 27	MF	antigen binding
8	−12.67	NULL	3 / 12	BP	dendritic cell chemotaxis
9	−12.13	NULL	1 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
10	−11.8	NULL	4 / 14	BP	ruffle organization
11	−11.45	NULL	2 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
12	−11.39	NULL	7 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
13	−11.14	NULL	2 / 12	MF	fatty acid binding
14	−11.12	NULL	58 / 417	H.Tiss	WIRTH_Immune system
15	−11.08	NULL	1 / 13	GSEA C2	LEE_INTRATHYMIC_T_PROGENITOR
16	−10.86	NULL	2 / 11	BP	high−density lipoprotein particle remodeling
17	−10.86	NULL	2 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
18	−10.43	NULL	56 / 553	Cancer	Lembcke_Colonic Inflammation
19	−10.12	NULL	1 / 11	GSEA C2	BIOCARTA_CACAM_PATHWAY
20	−9.87	NULL	1 / 16	GSEA C2	HASLINGER_B_CLL_WITH_CHROMOSOME_12_TRISOMY
21	−9.79	NULL	2 / 10	BP	positive regulation of chemotaxis
22	−9.76	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
23	−9.63	NULL	1 / 12	GSEA C2	BIOCARTA_HDAC_PATHWAY
24	−9.63	NULL	1 / 12	GSEA C2	BIOCARTA_PGC1A_PATHWAY
25	−9.49	NULL	2 / 14	CC	very−low−density lipoprotein particle
26	−9.41	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
27	−9.29	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
28	−9.21	NULL	1 / 13	GSEA C2	BIOCARTA_NFAT_PATHWAY
29	−9.2	NULL	2 / 16	GSEA C2	BROWNE_HCMV_INFECTION_2HR_UP
30	−9.13	NULL	2 / 15	BP	cholesterol efflux
31	−9.13	NULL	2 / 15	CC	high−density lipoprotein particle
32	−9.05	NULL	3 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
33	−8.83	NULL	1 / 14	MF	calmodulin−dependent protein kinase activity
34	−8.83	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
35	−8.56	NULL	2 / 11	BP	activation of Rho GTPase activity
36	−8.5	NULL	1 / 15	GSEA C2	BIOCARTA_FMLP_PATHWAY
37	−8.08	NULL	3 / 27	BP	release of sequestered calcium ion into cytosol
38	−7.96	NULL	2 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
39	−7.54	NULL	1 / 26	Disease	BCHETNIA_EBM−DM up
40	−7.49	NULL	2 / 11	BP	negative regulation of lipid catabolic process

GW_293

Local Summary

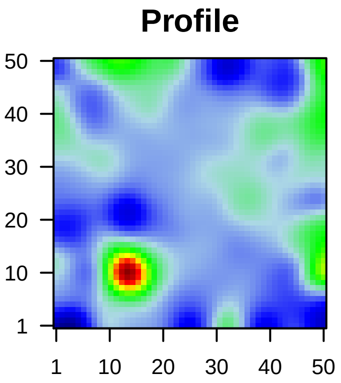
%DE = 0.66
metagenes = 3
genes = 43
genes in genesets = 42

genes with fdr < 0.1 = 23 (2 + / 21 −)
genes with fdr < 0.05 = 15 (1 + / 14 −)
genes with fdr < 0.01 = 7 (0 + / 7 −)

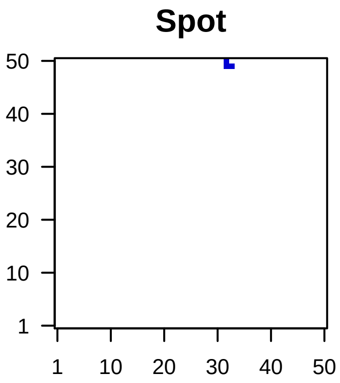
<r> metagenes = 1
<r> genes = 0.37

<FC> = −0.31
<shrinkage−t> = −10.7
<p−value> = 0.02
<fdr> = 0.68

Profile

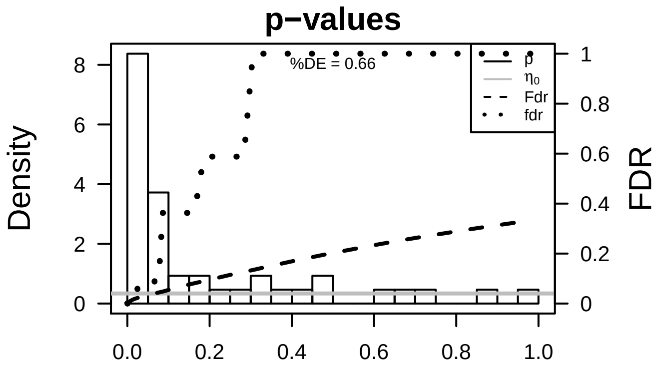


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6742	−0.99	2e−07	1e−04	32 x 50	single−stranded DNA binding protein 1, mitochondrial [Source
2	65008	−0.82	2e−05	1e−04	32 x 50	mitochondrial ribosomal protein L1 [Source:HGNC Symbol;Ac
3	6164	−0.82	2e−05	1e−04	32 x 50	ribosomal protein L34 [Source:HGNC Symbol;Acc:10340]
4	6147	−0.81	2e−05	7e−04	33 x 49	ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
5	6160	−0.76	7e−05	9e−04	32 x 49	ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]
6	6154	−0.72	2e−04	9e−04	32 x 49	ribosomal protein L26 [Source:HGNC Symbol;Acc:10327]
7	27258	−0.71	2e−04	6e−03	32 x 50	LSM3 homolog, U6 small nuclear RNA associated (S. cerevis
8	64776	−0.65	6e−04	4e−02	32 x 49	chromosome 11 open reading frame 1 [Source:HGNC Symbo
9	5828	0.55	4e−03	4e−02	32 x 50	peroxisomal biogenesis factor 2 [Source:HGNC Symbol;Acc:
10	28985	−0.51	8e−03	4e−02	33 x 49	malignant T cell amplified sequence 1 [Source:HGNC Symbo
11	51639	−0.49	1e−02	4e−02	32 x 50	Pre−mRNA branch site protein p14 [Source:UniProtKB/Swis
12	84273	−0.46	2e−02	4e−02	32 x 49	nitric oxide associated 1 [Source:HGNC Symbol;Acc:28473]
13	219844	−0.46	2e−02	4e−02	32 x 49	hydrolethalus syndrome 1 [Source:HGNC Symbol;Acc:26558
14	80746	−0.44	2e−02	4e−02	32 x 50	TSEN2 tRNA splicing endonuclease subunit pseudogene 1 [
15	6152	−0.43	2e−02	4e−02	32 x 49	ribosomal protein L24 [Source:HGNC Symbol;Acc:10325]
16	80135	0.43	2e−02	8e−02	32 x 50	ribosome production factor 1 homolog (S. cerevisiae) [Source
17	6210	−0.4	3e−02	8e−02	32 x 49	ribosomal protein S15a [Source:HGNC Symbol;Acc:10389]
18	6165	−0.38	5e−02	8e−02	33 x 49	ribosomal protein L35a [Source:HGNC Symbol;Acc:10345]
19	81853	−0.37	5e−02	8e−02	32 x 50	transmembrane protein 14B [Source:HGNC Symbol;Acc:213
20	404672	−0.37	5e−02	8e−02	32 x 50	general transcription factor IIH, polypeptide 5 [Source:HGNC



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.6	NULL	6 / 51	CC	cytosolic large ribosomal subunit
2	−23.17	NULL	2 / 10	CC	large ribosomal subunit
3	−21.52	NULL	8 / 92	BP	translational elongation
4	−21.27	NULL	7 / 81	BP	viral transcription
5	−20.48	NULL	7 / 87	BP	translational termination
6	−19.88	NULL	7 / 92	BP	viral life cycle
7	−18.86	NULL	9 / 153	MF	structural constituent of ribosome
8	−18.17	NULL	7 / 109	BP	SRP−dependent cotranslational protein targeting to membrane
9	−17.74	NULL	8 / 128	BP	translational initiation
10	−17.66	NULL	7 / 115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
11	−15.65	NULL	2 / 11	BP	ribosomal large subunit biogenesis
12	−15.39	NULL	10 / 253	BP	translation
13	−14.64	NULL	8 / 219	BP	mRNA metabolic process
14	−13.87	NULL	8 / 242	BP	RNA metabolic process
15	−12.68	NULL	7 / 167	CC	ribosome
16	−12.27	NULL	1 / 14	BP	mitochondrion morphogenesis
17	−11.81	NULL	1 / 15	GSEA C2	KEGG_DNA_REPLICATION
18	−11.73	NULL	2 / 39	Cancer	ZHANG_MM up
19	−11.42	NULL	3 / 13	GSEA C2	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
20	−11.39	NULL	1 / 16	GSEA C2	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN
21	−11.39	NULL	1 / 16	GSEA C2	GRADE_METASTASIS_DN
22	−11.39	NULL	1 / 16	GSEA C2	KEGG_MISMATCH_REPAIR
23	−11.39	NULL	1 / 16	GSEA C2	KEGG_HOMOLOGOUS_RECOMBINATION
24	−10.99	NULL	1 / 12	Glio	willscher_ GBM_LTSwt_proteomics−C_UP
25	−10.96	NULL	3 / 14	BP	mitochondrial ATP synthesis coupled proton transport
26	−10.76	NULL	7 / 287	BP	viral process
27	−10.54	NULL	3 / 15	BP	ATP synthesis coupled proton transport
28	−10.13	NULL	1 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G1
29	−10.09	NULL	1 / 11	GSEA C2	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE
30	−9.81	NULL	1 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
31	−9.41	NULL	1 / 14	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_UP
32	−9.41	NULL	10 / 649	BP	gene expression
33	−9.25	NULL	3 / 19	CC	mitochondrial proton−transporting ATP synthase complex
34	−8.71	NULL	8 / 482	BP	cellular protein metabolic process
35	−8.71	NULL	10 / 595	MF	RNA binding
36	−8.18	NULL	1 / 16	GSEA C2	CHOW_RASSF1_TARGETS_UP
37	−8.18	NULL	1 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
38	−7.17	NULL	1 / 37	CC	mitochondrial nucleoid
39	−6.64	NULL	6 / 83	BP	respiratory electron transport chain
40	−6.36	NULL	1 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA