GW_115

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1618 (851 + / 767 −)

genes with fdr < 0.1 = 1182 (643 + / 539 −)

genes with fdr < 0.05 = 928 (503 + / 425 −)

genes with fdr < 0.01 = 664 (364 + / 300 −)

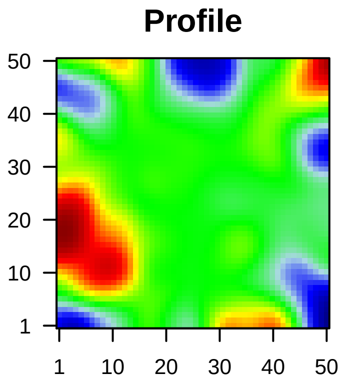
genes in genesets = 16332

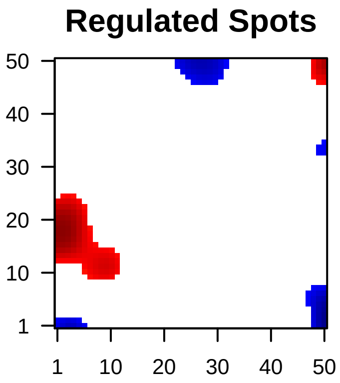
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.13

<fdr> = 0.86


Profile

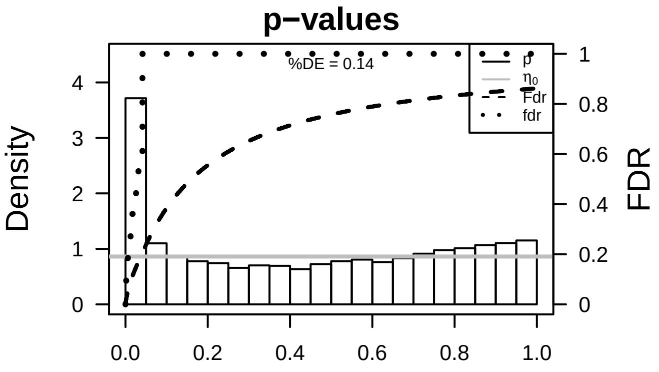

Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.44	2e−16	8e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	2.19	2e−16	8e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	216	1.87	2e−16	8e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
4	218	2.31	2e−16	8e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	501	−1.84	2e−16	8e−14	6 x 46	aldehyde dehydrogenase 7 family, member A1 [Source:HGNC
6	445	2.19	2e−16	8e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
7	655	1.72	2e−16	8e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
8	664	−1.7	2e−16	8e−14	2 x 43	BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H
9	339512	2.68	2e−16	8e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
10	260436	3.95	2e−16	8e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	760	−2.05	2e−16	8e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	1048	1.73	2e−16	8e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	1281	−1.7	2e−16	8e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
14	1577	1.81	2e−16	8e−14	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
15	414325	−1.83	2e−16	8e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1687	−1.68	2e−16	8e−14	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
17	1843	−2.23	2e−16	8e−14	22 x 50	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3
18	2353	−2.04	2e−16	8e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog [Source:
19	2354	−1.92	2e−16	8e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
20	3169	2.06	2e−16	8e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.1	NULL	918	Chr	Chr 17
2	9.15	NULL	1135	Chr	Chr 19
3	8.83	NULL	530	Cancer	Lembcke_Normal vs Adenoma
4	7.4	NULL	31	BP	negative regulation of viral genome replication
5	6.84	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
6	6.81	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
7	6.35	NULL	21	CC	cornified envelope
8	6.3	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
9	6.3	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
10	6.07	NULL	51	BP	type I interferon signaling pathway
11	6.05	NULL	15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
12	6.04	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
13	6.01	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	5.98	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
15	5.93	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
16	5.89	NULL	386	Chr	Chr 22
17	5.81	NULL	15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
18	5.74	NULL	45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
19	5.72	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
20	5.6	NULL	15	MF	interleukin−1 receptor binding
Underexpressed					
1	−15.61	NULL	699	Chr	Chr 5
2	−12.02	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	−9.48	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
4	−9.23	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
5	−8.83	NULL	534	Chr	Chr 8
6	−8.44	NULL	190	CC	extracellular matrix
7	−8.34	NULL	436	miRNA target starBase	hsa−miR−548n
8	−8.15	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	−8.01	NULL	262	miRNA target starBase	hsa−miR−548l
10	−7.87	NULL	318	miRNA target starBase	hsa−miR−590−3p
11	−7.81	NULL	155	miRNA target starBase	hsa−miR−200b
12	−7.77	NULL	151	miRNA target starBase	hsa−miR−429
13	−7.74	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
14	−7.51	NULL	1182	CC	extracellular region
15	−7.49	NULL	280	Chr	Chr 13
16	−7.4	NULL	362	miRNA 3UTR	CAGT−200B−−200C−−429
17	−7.26	NULL	150	miRNA target starBase	hsa−miR−200c
18	−7.24	NULL	336	miRNA target starBase	hsa−miR−548d−5p
19	−7.17	NULL	463	miRNA target starBase	hsa−miR−301a
20	−7.08	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP


p−values

GW_115

Local Summary

%DE = 0.69

metagenes = 115

genes = 963

genes in genesets = 951

genes with fdr < 0.1 = 363 (359 + / 4 −)

genes with fdr < 0.05 = 224 (221 + / 3 −)

genes with fdr < 0.01 = 128 (127 + / 1 −)

<r> metagenes = 0.8

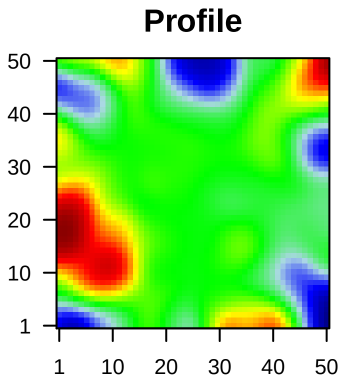
<r> genes = 0.2

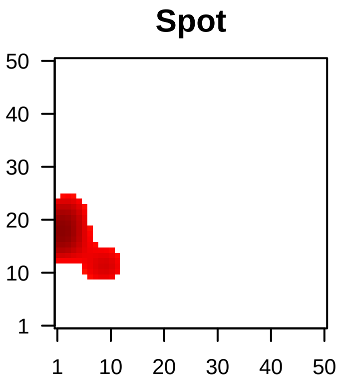
<FC> = 0.36

<shrinkage−t> = 12.58

<p−value> = 0.03

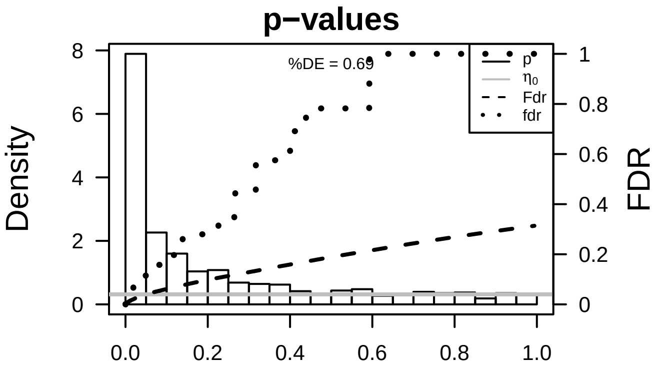
<fdr> = 0.71





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	93273	1.57	2e−14	1e−08	2 x 15	LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
2	220064	1.37	3e−11	1e−07	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
3	284085	1.29	4e−10	4e−07	3 x 18	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
4	57761	1.22	3e−09	4e−07	1 x 17	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]
5	8772	1.21	4e−09	4e−07	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
6	3303	1.19	5e−09	4e−07	11 x 12	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
7	3217	1.2	5e−09	9e−07	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
8	51069	1.18	1e−08	9e−07	2 x 18	mitochondrial ribosomal protein L2 [Source:HGNC Symbol;Ac
9	26579	1.18	1e−08	1e−06	4 x 25	myeloma overexpressed [Source:HGNC Symbol;Acc:7563]
10	3654	1.17	2e−08	6e−06	3 x 13	interleukin−1 receptor−associated kinase 1 [Source:HGNC S
11	1152	1.13	5e−08	6e−06	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
12	55290	1.12	6e−08	7e−06	1 x 16	BRF2, RNA polymerase III transcription initiation factor 50 kD
13	3326	1.09	9e−08	7e−06	1 x 14	heat shock protein 90kDa alpha (cytosolic), class B member
14	729021	1.1	1e−07	2e−05	11 x 13	
15	7205	1.07	2e−07	2e−05	2 x 16	thyroid hormone receptor interactor 6 [Source:HGNC Symbol
16	57414	1.06	2e−07	2e−05	9 x 10	rhomboid domain containing 2 [Source:HGNC Symbol;Acc:2
17	2017	1.05	3e−07	4e−05	1 x 14	cortactin [Source:HGNC Symbol;Acc:3338]
18	1978	1.04	4e−07	9e−05	1 x 17	eukaryotic translation initiation factor 4E binding protein 1 [So
19	55809	1.01	9e−07	9e−05	1 x 13	transcriptional regulating factor 1 [Source:HGNC Symbol;Acc
20	55653	0.99	1e−06	9e−05	9 x 10	breast carcinoma amplified sequence 4 [Source:HGNC Symb



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	9.44	NULL	5 / 9	GSEA C2	MOREIRA_RESPONSE_TO_TSA_UP
2	9.35	NULL	6 / 10	GSEA C2	REACTOME_HIV_LIFE_CYCLE
3	8.92	NULL	4 / 9	GSEA C2	MARZEC_IL2_SIGNALING_UP
4	8.56	NULL	5 / 11	GSEA C2	REACTOME_HIV_INFECTION
5	8.5	NULL	1 / 3	GSEA C2	WEBER_METHYLATED_LCP_IN_SPERM_DN
6	8.11	NULL	7 / 14	GSEA C2	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
7	7.59	NULL	88 / 649	BP	gene expression
8	7.38	NULL	4 / 9	GSEA C2	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE
9	7.03	NULL	143 / 1318	CC	mitochondrion
10	6.91	NULL	4 / 8	GSEA C2	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION
11	6.86	NULL	5 / 10	GSEA C2	REACTOME_TRANSCRIPTION
12	6.7	NULL	15 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
13	6.58	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
14	6.57	NULL	5 / 10	GSEA C2	REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_IN
15	6.48	NULL	41 / 253	BP	translation
16	6.45	NULL	3 / 13	GSEA C2	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
17	6.43	NULL	3 / 7	GSEA C2	PARK_HSC_MARKERS
18	6.4	NULL	70 / 530	Cancer	Lembcke_Normal vs Adenoma
19	6.35	NULL	1 / 5	GSEA C2	WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN
20	6.32	NULL	3 / 15	GSEA C2	LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
21	6.25	NULL	3 / 15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
22	6.23	NULL	3 / 8	GSEA C2	YEMELYANOV_GR_TARGETS_DN
23	6.21	NULL	5 / 12	GSEA C2	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIP
24	6.16	NULL	4 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
25	6.06	NULL	2 / 10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP
26	6.06	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
27	5.95	NULL	100 / 949	CC	nucleoplasm
28	5.94	NULL	2 / 8	GSEA C2	REACTOME_INFLUENZA_LIFE_CYCLE
29	5.9	NULL	5 / 13	GSEA C2	REACTOME_TAT_MEDIATED_HIV1_ELONGATION_ARREST_A
30	5.84	NULL	4 / 9	GSEA C2	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_CO
31	5.74	NULL	3 / 13	CC	inclusion body
32	5.74	NULL	29 / 167	CC	ribosome
33	5.72	NULL	3 / 8	GSEA C2	KEGG_PRION_DISEASES
34	5.66	NULL	3 / 12	GSEA C2	KEGG_SPLICEOSOME
35	5.62	NULL	6 / 16	GSEA C2	BIOCARTA_PTDINS_PATHWAY
36	5.59	NULL	28 / 153	MF	structural constituent of ribosome
37	5.58	NULL	2 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
38	5.53	NULL	4 / 15	GSEA C2	OZEN_MIR125B1_TARGETS
39	5.51	NULL	6 / 16	GSEA C2	REACTOME_MICRORNA_BIOGENESIS
40	5.47	NULL	2 / 9	GSEA C2	BIOCARTA_SODD_PATHWAY

GW_115

Local Summary

%DE = 0.59

metagenes = 14

genes = 196

genes in genesets = 195

genes with fdr < 0.1 = 81 (78 + / 3 −)

genes with fdr < 0.05 = 70 (68 + / 2 −)

genes with fdr < 0.01 = 64 (62 + / 2 −)

<r> metagenes = 0.97

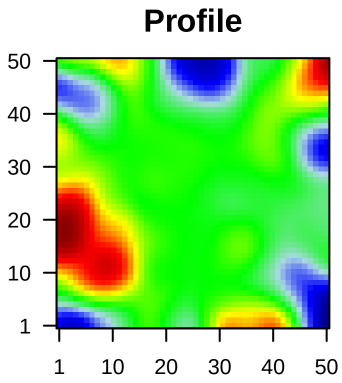
<r> genes = 0.28

<FC> = 0.47

<shrinkage−t> = 16.44

<p−value> = 0

<fdr> = 0.57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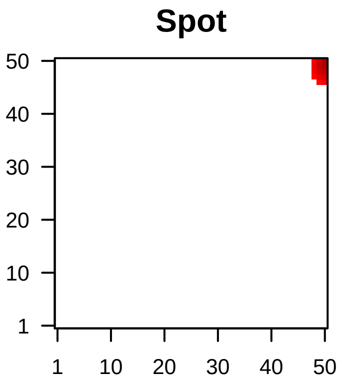
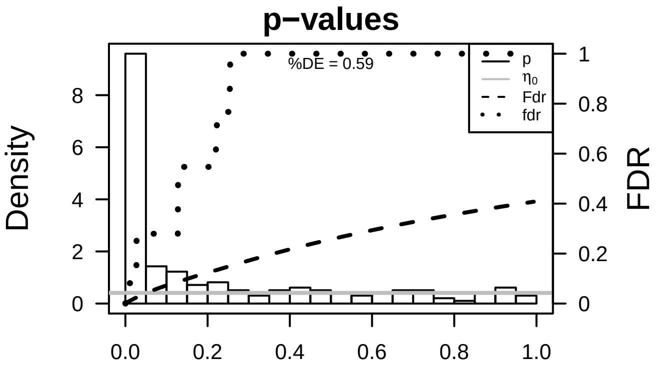

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.87	2e−16	3e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	445	2.19	2e−16	3e−15	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
3	655	1.72	2e−16	3e−15	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
4	339512	2.68	2e−16	3e−15	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
5	3866	1.77	2e−16	3e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
6	4922	2.51	2e−16	3e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
7	79679	1.67	4e−16	2e−11	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:
8	56963	1.51	3e−13	8e−11	50 x 50	repulsive guidance molecule family member a [Source:HGNC
9	3856	1.46	1e−12	1e−10	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
10	3880	1.43	4e−12	1e−10	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
11	2944	1.43	5e−12	1e−10	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
12	26227	1.42	6e−12	1e−10	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
13	200810	1.41	8e−12	3e−10	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
14	56922	1.39	1e−11	3e−10	50 x 50	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC
15	200634	1.39	1e−11	3e−09	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
16	5625	1.36	5e−11	9e−09	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
17	83959	1.32	2e−10	2e−08	50 x 50	solute carrier family 4, sodium borate transporter, member 11
18	6657	1.27	7e−10	2e−08	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
19	875	1.26	9e−10	2e−08	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
20	4915	1.25	1e−09	2e−08	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	21.5	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	19.58	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	15.57	NULL	4 / 13	BP	regulation of blood vessel size
4	15.48	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
5	15.37	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
6	15.36	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
7	13.72	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
8	13.23	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
9	13.22	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
10	13.08	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
11	12.37	NULL	3 / 11	MF	glutathione binding
12	12.37	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	12.17	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
14	10.93	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
15	10.5	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
16	10.43	NULL	1 / 5	GSEA C2	TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
17	9.94	NULL	1 / 11	Glio	neurons_glio
18	9.74	NULL	1 / 2	miRNA target	miR−127
19	9.7	NULL	3 / 19	BP	cellular amino acid biosynthetic process
20	9.57	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
21	9.45	NULL	2 / 10	GSEA C2	CERVERA_SDHB_TARGETS_1_DN
22	9.38	NULL	2 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
23	9.28	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
24	9.24	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
25	9.18	NULL	10 / 167	BP	cellular nitrogen compound metabolic process
26	9.14	NULL	1 / 10	BP	urea cycle
27	9.09	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
28	8.96	NULL	2 / 13	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
29	8.79	NULL	6 / 25	BP	glutathione derivative biosynthetic process
30	8.72	NULL	2 / 19	BP	anatomical structure formation involved in morphogenesis
31	8.7	NULL	2 / 11	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
32	8.69	NULL	2 / 15	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_DN
33	8.66	NULL	3 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
34	8.58	NULL	2 / 14	CC	membrane−bounded vesicle
35	8.48	NULL	3 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
36	8.45	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
37	8.45	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
38	8.44	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
39	8.44	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
40	8.37	NULL	2 / 16	GSEA C2	CAFFAREL_RESPONSE_TO_THC_UP

GW_115

Local Summary

%DE = 0.76

metagenes = 11

genes = 220

genes in genesets = 219

genes with fdr < 0.1 = 128 (14 + / 114 −)

genes with fdr < 0.05 = 109 (13 + / 96 −)

genes with fdr < 0.01 = 74 (9 + / 65 −)

<r> metagenes = 0.97

<r> genes = 0.44

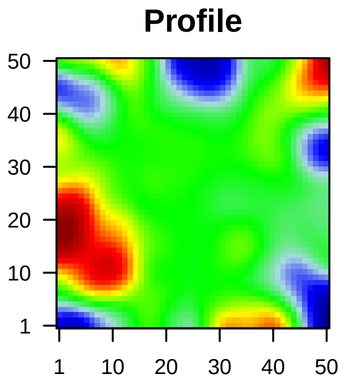
<FC> = −0.41

<shrinkage−t> = −14.46

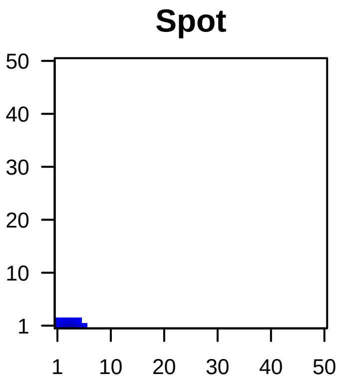
<p−value> = 0

<fdr> = 0.51

Profile



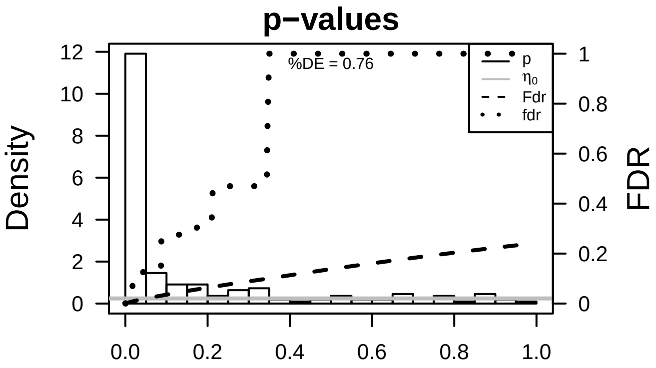
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1281	−1.7	2e−16	6e−15	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
2	7045	−1.86	2e−16	6e−15	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
3	4314	1.63	2e−15	3e−10	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
4	6423	−1.41	9e−12	3e−10	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
5	3043	−1.4	1e−11	5e−10	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
6	3553	1.38	2e−11	2e−09	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
7	1290	−1.35	7e−11	2e−09	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	115908	−1.33	1e−10	5e−09	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
9	2199	−1.31	2e−10	5e−09	4 x 1	fibulin 2 [Source:HGNC Symbol;Acc:3601]
10	6678	−1.3	3e−10	1e−08	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
11	1278	−1.28	6e−10	4e−08	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
12	10409	−1.25	1e−09	5e−08	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
13	11098	−1.23	2e−09	5e−08	1 x 1	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
14	3569	1.22	3e−09	6e−08	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
15	10631	−1.21	4e−09	2e−07	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
16	4692	−1.18	1e−08	2e−07	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
17	7431	−1.17	1e−08	3e−07	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
18	25878	−1.16	2e−08	8e−07	3 x 1	matrix−remodelling associated 5 [Source:HGNC Symbol;Acc:
19	10962	−1.13	4e−08	8e−07	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
20	22856	−1.11	7e−08	8e−07	5 x 1	chondroitin sulfate synthase 1 [Source:HGNC Symbol;Acc:17

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−41.1	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−33.09	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
3	−32.25	NULL	62 / 190	CC	extracellular matrix
4	−30.06	NULL	69 / 250	Lymphoma	LENZ_Stromal signature 1
5	−27.98	NULL	11 / 19	MF	extracellular matrix binding
6	−26.93	NULL	8 / 12	miRNA target	miR−29c
7	−26.57	NULL	8 / 11	MF	platelet−derived growth factor binding
8	−23.52	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
9	−21.83	NULL	19 / 57	MF	extracellular matrix structural constituent
10	−21.73	NULL	56 / 242	BP	extracellular matrix organization
11	−21.22	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
12	−19.09	NULL	13 / 37	BP	collagen fibril organization
13	−18.92	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
14	−18.49	NULL	30 / 69	BP	extracellular matrix disassembly
15	−18.36	NULL	26 / 64	BP	collagen catabolic process
16	−18.13	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
17	−18.13	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
18	−17.34	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
19	−16.27	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
20	−15.87	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
21	−15.72	NULL	15 / 68	CC	collagen
22	−15.67	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
23	−15.36	NULL	4 / 16	GSEA C2	COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN
24	−15.24	NULL	19 / 83	CC	basement membrane
25	−14.72	NULL	13 / 68	Glio	cultured astroglia vs. in vivo astrocytes
26	−13.8	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
27	−13.62	NULL	6 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
28	−13.6	NULL	15 / 85	MF	integrin binding
29	−13.5	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
30	−13.14	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
31	−13.07	NULL	10 / 35	Glio	Colman_survival_associated
32	−12.44	NULL	3 / 14	CC	endocytic vesicle lumen
33	−12.35	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
34	−12.23	NULL	4 / 13	GSEA C2	REACTOME_FORMATION_OF_PLATELET_PLUG
35	−12.23	NULL	4 / 13	GSEA C2	REACTOME_PLATELET_ACTIVATION
36	−12.19	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
37	−12.18	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
38	−12.17	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
39	−12	NULL	90 / 1182	CC	extracellular region
40	−11.93	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1

GW_115

Local Summary

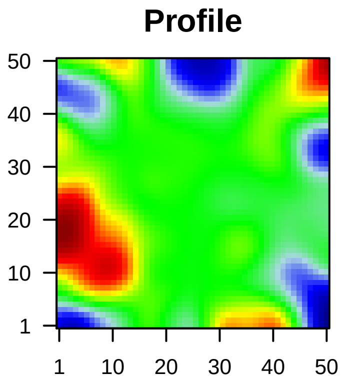
%DE = 0.84
metagenes = 27
genes = 409
genes in genesets = 407

genes with fdr < 0.1 = 258 (21 + / 237 −)
genes with fdr < 0.05 = 223 (19 + / 204 −)
genes with fdr < 0.01 = 137 (13 + / 124 −)

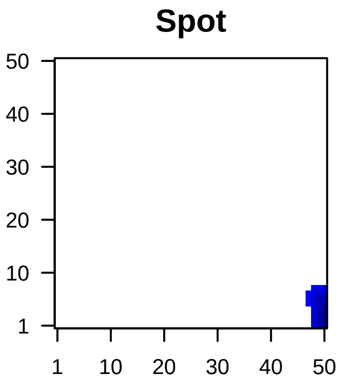
<r> metagenes = 0.93
<r> genes = 0.43

<FC> = −0.41
<shrinkage−t> = −14.36
<p−value> = 0
<fdr> = 0.52

Profile



Spot



Local Genelist

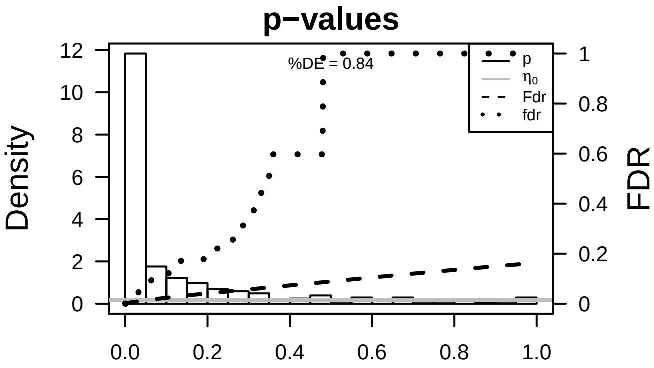
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	3.95	2e−16	5e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
2	3512	−1.81	2e−16	5e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	5996	−1.69	2e−16	5e−15	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
4	1363	−1.56	4e−14	5e−10	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
5	79901	−1.41	7e−12	1e−09	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
6	6352	1.37	3e−11	2e−09	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
7	10628	−1.33	6e−11	1e−08	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
8	6451	−1.29	3e−10	1e−08	50 x 5	SH3 domain binding glutamic acid−rich protein like [Source:H
9	348	−1.29	4e−10	2e−08	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	10537	1.27	7e−10	8e−08	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
11	2745	−1.24	2e−09	2e−07	50 x 3	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
12	347	−1.21	4e−09	2e−07	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
13	23180	−1.19	8e−09	2e−07	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
14	30061	−1.18	1e−08	3e−07	50 x 5	solute carrier family 40 (iron−regulated transporter), member
15	8404	−1.15	2e−08	3e−07	50 x 6	SPARC−like 1 (hevin) [Source:HGNC Symbol;Acc:11220]
16	9079	−1.15	3e−08	3e−07	50 x 6	LIM domain binding 2 [Source:HGNC Symbol;Acc:6533]
17	6363	−1.14	3e−08	3e−07	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
18	25849	−1.14	3e−08	4e−07	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:HC
19	55303	−1.14	4e−08	7e−07	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
20	3059	1.13	5e−08	8e−07	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.85	NULL	11 / 15	CC	MHC class II protein complex
2	−17.08	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	−16.33	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
4	−14.08	NULL	104 / 553	Cancer	Lembcke_Colonic Inflammation
5	−13.59	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−12.75	NULL	81 / 417	H.Tiss	WIRTH_Immune system
7	−12.42	NULL	52 / 312	BP	immune response
8	−12.12	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	−11.41	NULL	14 / 47	BP	antigen processing and presentation
10	−10.9	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
11	−10.49	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
12	−10.42	NULL	7 / 28	CC	transport vesicle membrane
13	−10.07	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
14	−9.8	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−9.79	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
16	−9.71	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
17	−9.71	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
18	−9.71	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
19	−9.71	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
20	−9.66	NULL	4 / 16	GSEA C2	KORKOLA_TERATOMA_UP
21	−9.46	NULL	6 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
22	−9.41	NULL	5 / 14	GSEA C2	CHEOK_RESPONSE_TO_HD_MTX_UP
23	−9.39	NULL	17 / 74	BP	regulation of immune response
24	−9.27	NULL	3 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
25	−9.18	NULL	3 / 14	MF	lipid transporter activity
26	−8.84	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
27	−8.79	NULL	13 / 60	BP	T cell costimulation
28	−8.78	NULL	4 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
29	−8.76	NULL	30 / 162	CC	external side of plasma membrane
30	−8.71	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane
31	−8.67	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
32	−8.39	NULL	3 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
33	−8.33	NULL	8 / 35	CC	trans−Golgi network membrane
34	−8.3	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
35	−8.27	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
36	−8.26	NULL	6 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
37	−8.07	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
38	−8.03	NULL	2 / 12	GSEA C2	LEE_RECENT_THYMIC_EMIGRANT
39	−7.97	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
40	−7.88	NULL	4 / 10	GSEA C2	FERRANDO_LYL1_NEIGHBORS

p−values



GW_115

Local Summary

%DE = 0.6

metagenes = 5

genes = 114

genes in genesets = 114

genes with fdr < 0.1 = 50 (0 + / 50 −)

genes with fdr < 0.05 = 49 (0 + / 49 −)

genes with fdr < 0.01 = 9 (0 + / 9 −)

<r> metagenes = 0.99

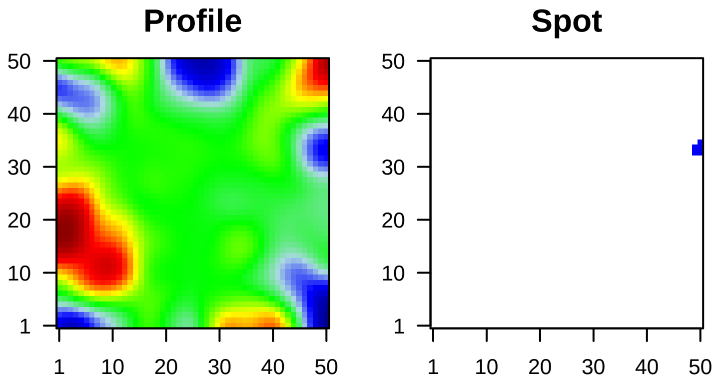
<r> genes = 0.35

<FC> = −0.38

<shrinkage−t> = −13.32

<p−value> = 0.03

<fdr> = 0.64



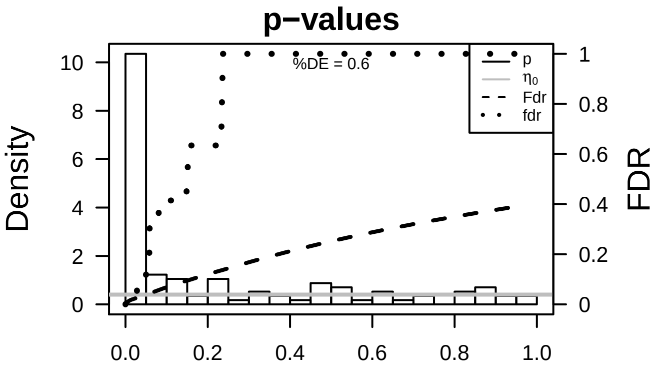
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1429	−1.22	4e−09	3e−05	50 x 34	crystallin, zeta (quinone reductase) [Source:HGNC Symbol;A
2	5612	−1.03	7e−07	2e−04	50 x 34	protein−kinase, interferon−inducible double stranded RNA de
3	3150	−0.94	5e−06	2e−04	50 x 35	high mobility group nucleosome binding domain 1 [Source:HG
4	23484	−0.92	9e−06	7e−04	50 x 33	leptin receptor overlapping transcript−like 1 [Source:HGNC S
5	55074	−0.85	4e−05	7e−04	50 x 33	oxidation resistance 1 [Source:HGNC Symbol;Acc:15822]
6	1195	−0.83	5e−05	7e−04	50 x 35	CDC−like kinase 1 [Source:HGNC Symbol;Acc:2068]
7	9685	−0.83	6e−05	6e−03	50 x 34	clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
8	7334	−0.76	2e−04	6e−03	50 x 33	ubiquitin−conjugating enzyme E2N [Source:HGNC Symbol;A
9	23588	−0.75	3e−04	6e−03	50 x 33	kelch domain containing 2 [Source:HGNC Symbol;Acc:20231
10	167153	−0.73	4e−04	1e−02	50 x 34	PAP associated domain containing 4 [Source:HGNC Symbol;
11	34	−0.69	8e−04	1e−02	50 x 34	acyl−CoA dehydrogenase, C−4 to C−12 straight chain [Sourc
12	58486	−0.68	1e−03	1e−02	50 x 34	zinc finger, BED−type containing 5 [Source:HGNC Symbol;A
13	6727	−0.67	1e−03	1e−02	50 x 33	signal recognition particle 14kDa (homologous Alu RNA bindi
14	10289	−0.64	2e−03	1e−02	50 x 35	eukaryotic translation initiation factor 1B [Source:HGNC Syml
15	58527	−0.63	2e−03	1e−02	50 x 33	ABRA C−terminal like [Source:HGNC Symbol;Acc:21230]
16	25782	−0.63	2e−03	1e−02	49 x 34	RAB3 GTPase activating protein subunit 2 (non−catalytic) [Sc
17	119504	−0.62	2e−03	1e−02	50 x 33	anaphase promoting complex subunit 16 [Source:HGNC Sym
18	221154	−0.62	3e−03	2e−02	50 x 33	mitochondrial calcium uptake 2 [Source:HGNC Symbol;Acc:3
19	51362	−0.61	3e−03	2e−02	50 x 34	cell division cycle 40 [Source:HGNC Symbol;Acc:17350]
20	10473	−0.61	3e−03	3e−02	50 x 33	high mobility group nucleosomal binding domain 4 [Source:H

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.13	NULL	2 / 10	MF	NADPH binding
2	−10.09	NULL	2 / 16	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_UP
3	−9.31	NULL	6 / 89	miRNA target starBase	hsa−miR−505
4	−8.77	NULL	1 / 14	GSEA C2	CHEOK_RESPONSE_TO_HD_MTX_DN
5	−8.7	NULL	3 / 14	GSEA C2	REACTOME_MRNA_3_END_PROCESSING
6	−8.49	NULL	2 / 10	BP	negative regulation of DNA damage response, signal transduction l
7	−8.34	NULL	6 / 45	miRNA target starBase	hsa−miR−411
8	−8.34	NULL	3 / 16	Cancer	GENTLES_modul14
9	−8.27	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C5
10	−8.09	NULL	1 / 8	GSEA C2	YAGI_AML_WITH_T_8_21_TRANSLOCATION
11	−8.05	NULL	2 / 19	miRNA target starBase	hsa−miR−542−5p
12	−7.85	NULL	2 / 20	MF	protein serine/threonine/tyrosine kinase activity
13	−7.73	NULL	1 / 11	BP	positive regulation of DNA−dependent transcription, elongation
14	−7.73	NULL	1 / 11	BP	regulation of epithelial cell proliferation
15	−7.67	NULL	2 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
16	−7.25	NULL	3 / 50	BP	protein homotetramerization
17	−7.13	NULL	2 / 21	BP	positive regulation of DNA repair
18	−7.09	NULL	2 / 15	GSEA C2	DAIRKEE_TERT_TARGETS_DN
19	−6.97	NULL	3 / 46	miRNA target starBase	hsa−miR−1322
20	−6.9	NULL	1 / 11	BP	cell wall macromolecule catabolic process
21	−6.83	NULL	4 / 80	CC	chromatin
22	−6.8	NULL	1 / 16	GSEA C2	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN
23	−6.8	NULL	1 / 16	miRNA target starBase	hsa−miR−891a
24	−6.79	NULL	5 / 101	miRNA 3'UTR	UAAG−501
25	−6.74	NULL	1 / 14	GSEA C2	ZUCCHI_METASTASIS_DN
26	−6.69	NULL	4 / 61	miRNA target starBase	hsa−miR−1200
27	−6.59	NULL	1 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
28	−6.5	NULL	3 / 39	miRNA target starBase	hsa−miR−1258
29	−6.48	NULL	1 / 15	GSEA C2	WONG_IFNA2_RESISTANCE_DN
30	−6.47	NULL	2 / 15	BP	glycogen biosynthetic process
31	−6.46	NULL	1 / 24	MF	mRNA 3'−UTR binding
32	−6.43	NULL	1 / 12	GSEA C2	BROWNE_HCMV_INFECTION_14HR_UP
33	−6.41	NULL	2 / 15	GSEA C2	ONDER_CDH1_TARGETS_1_DN
34	−6.4	NULL	4 / 49	miRNA 3'UTR	GTTT−154−−487
35	−6.24	NULL	6 / 90	miRNA target starBase	hsa−miR−362−5p
36	−6.21	NULL	1 / 10	BP	histone mRNA catabolic process
37	−6.14	NULL	1 / 13	GSEA C2	BASAKI_YBX1_TARGETS_DN
38	−6.14	NULL	1 / 13	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_UP
39	−6.13	NULL	1 / 11	BP	positive regulation of ubiquitin−protein ligase activity
40	−6.11	NULL	2 / 31	BP	peptidyl−threonine phosphorylation



GW_115

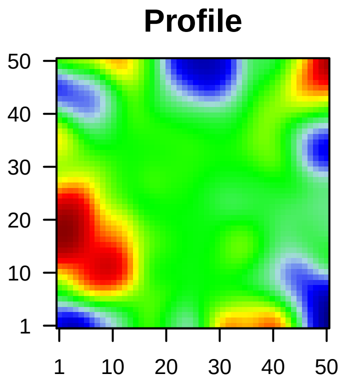
Local Summary

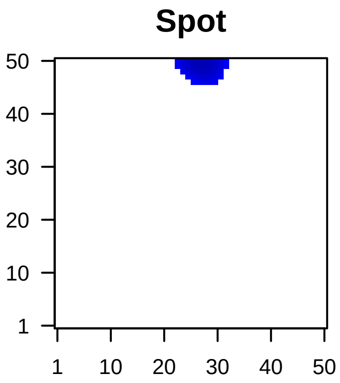
%DE = 0.73
metagenes = 40
genes = 537
genes in genesets = 530

genes with fdr < 0.1 = 229 (3 + / 226 −)
genes with fdr < 0.05 = 154 (2 + / 152 −)
genes with fdr < 0.01 = 52 (1 + / 51 −)

<r> metagenes = 0.89
<r> genes = 0.26

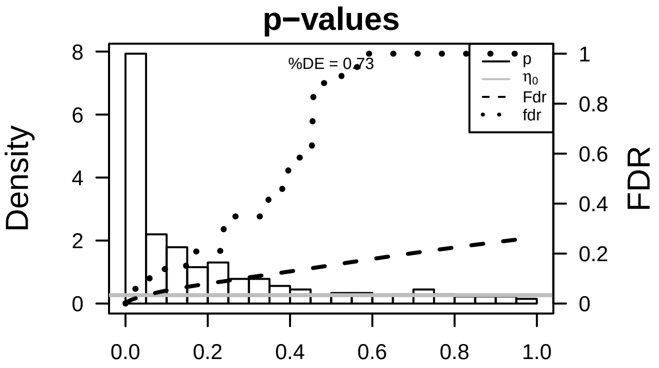
<FC> = −0.34
<shrinkage−t> = −12.02
<p−value> = 0.04
<fdr> = 0.72


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10413	−1.46	1e−12	1e−07	26 x 50	Yes−associated protein 1 [Source:HGNC Symbol;Acc:16262]
2	114908	−1.26	9e−10	4e−05	26 x 50	transmembrane protein 123 [Source:HGNC Symbol;Acc:3013
3	91612	−1.06	3e−07	8e−05	24 x 48	churchill domain containing 1 [Source:HGNC Symbol;Acc:20
4	8560	−1.01	1e−06	8e−05	27 x 50	delta(4)−desaturase, sphingolipid 1 [Source:HGNC Symbol;A
5	665	−0.99	1e−06	1e−04	24 x 50	BCL2/adenovirus E1B 19kDa interacting protein 3−like [Sour
6	64776	−0.97	3e−06	1e−04	32 x 49	chromosome 11 open reading frame 1 [Source:HGNC Symb
7	23471	−0.88	4e−06	1e−04	28 x 46	translocation associated membrane protein 1 [Source:HGNC
8	100008589	0.95	4e−06	3e−04	23 x 50	RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
9	10412	−0.93	6e−06	7e−04	31 x 49	NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:
10	85461	−0.88	2e−05	7e−04	24 x 50	tetratricopeptide repeat, ankyrin repeat and coiled−coil contai
11	80335	−0.88	2e−05	7e−04	23 x 49	WD repeat domain 82 [Source:HGNC Symbol;Acc:28826]
12	221037	−0.87	2e−05	7e−04	24 x 49	jumonji domain containing 1C [Source:HGNC Symbol;Acc:12
13	55863	−0.86	3e−05	7e−04	31 x 49	transmembrane protein 126B [Source:HGNC Symbol;Acc:30
14	1207	−0.86	3e−05	1e−03	31 x 49	chloride channel, nucleotide−sensitive, 1A [Source:HGNC Sy
15	1176	−0.85	4e−05	1e−03	26 x 50	adaptor−related protein complex 3, sigma 1 subunit [Source:
16	653566	−0.83	6e−05	1e−03	28 x 49	
17	57515	−0.83	6e−05	1e−03	25 x 49	serine incorporator 1 [Source:HGNC Symbol;Acc:13464]
18	114884	−0.81	8e−05	1e−03	25 x 50	oxysterol binding protein−like 10 [Source:HGNC Symbol;Acc:
19	51014	−0.81	8e−05	2e−03	26 x 50	transmembrane emp24 protein transport domain containing 7
20	5911	−0.8	1e−04	2e−03	26 x 49	RAP2A, member of RAS oncogene family [Source:HGNC Sy


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.85	NULL	5 / 8	MMML CGS	MACIEJ_MMML 50
2	−10.26	NULL	39 / 269	miRNA target−starBase	hsa−miR−1244
3	−10.05	NULL	55 / 436	miRNA target−starBase	hsa−miR−548n
4	−9.59	NULL	25 / 155	miRNA target−starBase	hsa−miR−802
5	−9.31	NULL	11 / 67	miRNA target−starBase	hsa−miR−1246
6	−9.01	NULL	26 / 198	miRNA target−starBase	hsa−miR−33a
7	−8.86	NULL	65 / 957	Chr	Chr 11
8	−8.81	NULL	24 / 157	miRNA target−starBase	hsa−miR−548o
9	−8.7	NULL	4 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MS_DN
10	−8.66	NULL	32 / 271	miRNA target−starBase	hsa−miR−548h
11	−8.36	NULL	37 / 313	miRNA target−starBase	hsa−miR−559
12	−8.34	NULL	38 / 324	miRNA target−starBase	hsa−miR−18a
13	−8.3	NULL	24 / 189	miRNA target−starBase	hsa−miR−513a−3p
14	−8.28	NULL	25 / 184	miRNA target−starBase	hsa−miR−586
15	−8.28	NULL	10 / 61	miRNA target−starBase	hsa−miR−659
16	−8.12	NULL	32 / 262	miRNA target−starBase	hsa−miR−548l
17	−8	NULL	34 / 280	miRNA target−starBase	hsa−miR−320a
18	−7.95	NULL	36 / 307	miRNA target−starBase	hsa−miR−548c−5p
19	−7.89	NULL	40 / 310	miRNA target−starBase	hsa−miR−340
20	−7.82	NULL	4 / 11	GSEA C2	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
21	−7.74	NULL	24 / 169	miRNA target−starBase	hsa−miR−374b
22	−7.73	NULL	5 / 11	MMML CGS	MACIEJ_MMML 49
23	−7.7	NULL	2 / 10	BP	notochord development
24	−7.7	NULL	2 / 10	BP	paraxial mesoderm development
25	−7.69	NULL	19 / 172	miRNA target−starBase	hsa−miR−607
26	−7.63	NULL	21 / 206	miRNA target−starBase	hsa−miR−148b
27	−7.58	NULL	24 / 181	miRNA target−starBase	hsa−miR−548e
28	−7.56	NULL	23 / 173	miRNA target−starBase	hsa−miR−548k
29	−7.53	NULL	3 / 10	MF	lamin binding
30	−7.52	NULL	22 / 166	miRNA target−starBase	hsa−miR−320b
31	−7.4	NULL	10 / 74	miRNA target−starBase	hsa−miR−877
32	−7.29	NULL	23 / 187	miRNA target−starBase	hsa−miR−520d−5p
33	−7.29	NULL	39 / 300	miRNA target−starBase	hsa−miR−561
34	−7.27	NULL	2 / 5	miRNA target	miR−372
35	−7.24	NULL	37 / 336	miRNA target−starBase	hsa−miR−548d−5p
36	−7.22	NULL	29 / 288	miRNA target−starBase	hsa−miR−548j
37	−7.17	NULL	33 / 328	Glio	Up
38	−7.16	NULL	21 / 130	miRNA target−starBase	hsa−miR−155
39	−7.14	NULL	32 / 315	miRNA target−starBase	hsa−miR−30e
40	−7.09	NULL	32 / 313	Glio	willscher_GBM_Verhaak−CL_expression_D_up