GW_060

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1721 (1029 + / 692 −)

genes with fdr < 0.1 = 1315 (834 + / 481 −)

genes with fdr < 0.05 = 1084 (714 + / 370 −)

genes with fdr < 0.01 = 821 (573 + / 248 −)

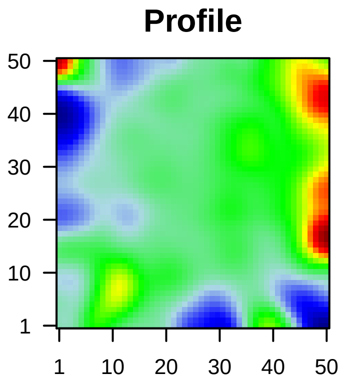
genes in genesets = 16332

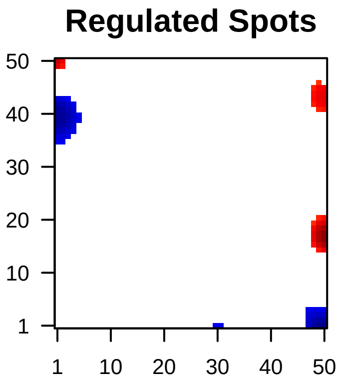
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.86


Profile

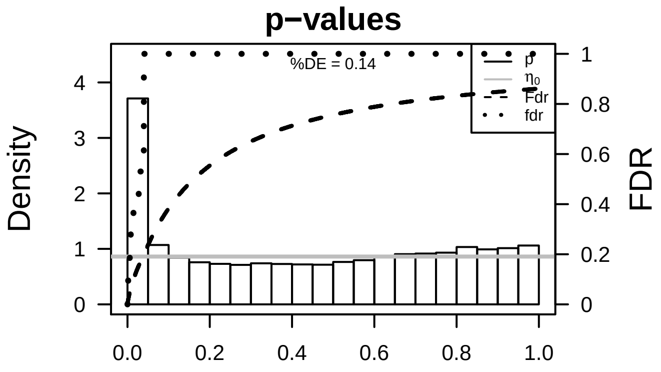

Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	1.59	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Sym
2	216	−1.49	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
3	163782	1.45	2e−16	3e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
4	347	1.6	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
5	9915	1.84	2e−16	3e−14	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
6	22809	1.88	2e−16	3e−14	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
7	23705	1.75	2e−16	3e−14	50 x 7	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
8	875	1.48	2e−16	3e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
9	84952	2.16	2e−16	3e−14	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
10	1116	1.49	2e−16	3e−14	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
11	56994	1.51	2e−16	3e−14	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
12	169044	2.09	2e−16	3e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
13	1282	1.39	2e−16	3e−14	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
14	1298	2.41	2e−16	3e−14	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
15	1363	1.41	2e−16	3e−14	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
16	49860	2.36	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
17	1464	1.94	2e−16	3e−14	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
18	92196	1.45	2e−16	3e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	55894	1.35	2e−16	3e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	414325	1.73	2e−16	3e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.28	NULL	1033	Chr	Chr 2
2	11.13	NULL	42	BP	keratinization
3	10.36	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
4	9.66	NULL	21	CC	cornified envelope
5	8.54	NULL	135	H.Tiss	WIRTH_Mucosa
6	8.36	NULL	81	BP	viral transcription
7	8.35	NULL	87	BP	translational termination
8	8.31	NULL	92	BP	viral life cycle
9	8.3	NULL	92	BP	translational elongation
10	7.76	NULL	8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
11	7.7	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
12	7.35	NULL	51	CC	cytosolic large ribosomal subunit
13	7.33	NULL	128	BP	translational initiation
14	7.18	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
15	7.18	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
16	7.06	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
17	7.06	NULL	53	BP	keratinocyte differentiation
18	6.83	NULL	10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
19	6.6	NULL	530	Cancer	Lembcke_Normal vs Adenoma
20	6.53	NULL	699	Chr	Chr 5
Underexpressed					
1	−10.03	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−9.89	NULL	717	Chr	Chr 16
3	−9.15	NULL	519	Chr	Chr 14
4	−9.1	NULL	633	Chr	Chr 9
5	−8.89	NULL	417	H.Tiss	WIRTH_Immune system
6	−8.88	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−8.88	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−8.88	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−8.88	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−8.84	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
11	−8.75	NULL	7	MMML CGS	MACIEJ_MMML 5
12	−7.2	NULL	316	Cancer	SPANG_BCL6−index2
13	−6.74	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
14	−6.49	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
15	−6.38	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
16	−6.1	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	−5.94	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
18	−5.89	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
19	−5.89	NULL	34	Chr	Chr Y
20	−5.57	NULL	51	BP	type I interferon signaling pathway


p−values

GW_060

Local Summary

%DE = 0.72

metagenes = 19

genes = 227

genes in genesets = 223

genes with fdr < 0.1 = 123 (123 + / 0 −)

genes with fdr < 0.05 = 105 (105 + / 0 −)

genes with fdr < 0.01 = 90 (90 + / 0 −)

<r> metagenes = 0.97

<r> genes = 0.33

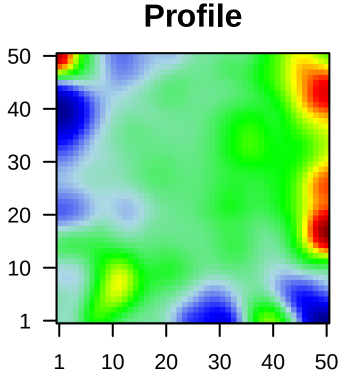
<FC> = 0.47

<shrinkage−t> = 16.54

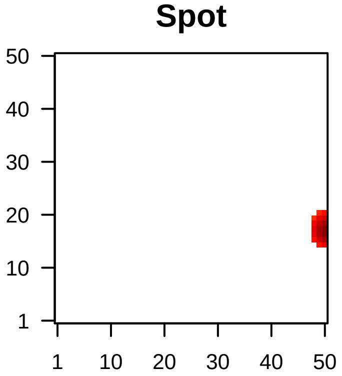
<p−value> = 0

<fdr> = 0.49

Profile



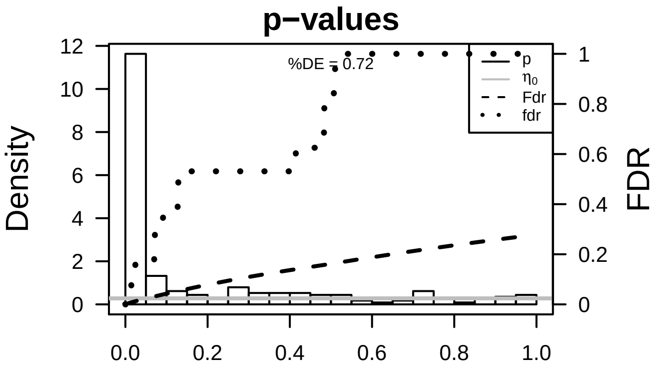
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9915	1.84	2e−16	8e−16	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
2	56994	1.51	2e−16	8e−16	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
3	1298	2.41	2e−16	8e−16	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
4	285016	1.53	2e−16	8e−16	50 x 17	family with sequence similarity 150, member B [Source:HGN
5	221061	1.63	2e−16	8e−16	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
6	112703	1.41	2e−16	8e−16	50 x 18	family with sequence similarity 71, member E1 [Source:HGN
7	2248	2.16	2e−16	8e−16	50 x 19	fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
8	728715	1.72	2e−16	8e−16	50 x 18	
9	4602	2.8	2e−16	8e−16	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
10	4613	1.42	2e−16	8e−16	50 x 17	v−myc avian myelocytomatosis viral oncogene neuroblastom
11	9603	1.6	2e−16	8e−16	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
12	162494	1.7	2e−16	8e−16	50 x 17	rhomboid, veinlet−like 3 (Drosophila) [Source:HGNC Symbol;
13	494470	1.72	2e−16	8e−16	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
14	57556	1.58	2e−16	8e−16	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic
15	30812	1.43	2e−16	8e−16	50 x 18	SRY (sex determining region Y)−box 8 [Source:HGNC Symbo
16	79805	1.5	2e−16	8e−16	50 x 18	vasohibin 2 [Source:HGNC Symbol;Acc:25723]
17	9686	1.36	2e−16	8e−16	50 x 19	vestigial like 4 (Drosophila) [Source:HGNC Symbol;Acc:2896
18	55691	1.31	7e−16	2e−14	50 x 18	FERM domain containing 4A [Source:HGNC Symbol;Acc:254
19	114801	1.3	9e−16	2e−13	50 x 19	transmembrane protein 200A [Source:HGNC Symbol;Acc:21
20	26018	1.28	4e−15	2e−13	50 x 16	leucine−rich repeats and immunoglobulin−like domains 1 [So

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.71	NULL	5 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	14.75	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
3	14.69	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
4	13.37	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
5	13.32	NULL	2 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
6	13.25	NULL	4 / 34	BP	thymus development
7	13.23	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
8	12.7	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
9	12.52	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
10	12.49	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
11	12.49	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
12	11.87	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
13	11.57	NULL	2 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
14	11.53	NULL	2 / 16	GSEA C2	WU_HBX_TARGETS_3_UP
15	11.13	NULL	1 / 11	BP	homeostasis of number of cells
16	11.13	NULL	1 / 11	Pathw Act	BENTINK_e2f3.2
17	11.13	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
18	11.13	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
19	11.08	NULL	2 / 15	BP	embryonic digestive tract development
20	10.71	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
21	10.59	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
22	10.43	NULL	4 / 42	BP	B cell differentiation
23	10.29	NULL	5 / 40	TF Tissue	VAQUERIZAS_Fetal brain
24	10.25	NULL	4 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
25	10.11	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
26	10.11	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
27	10.04	NULL	3 / 5	Lymphoma	MASCQUE_mBL UP
28	9.69	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
29	9.69	NULL	1 / 14	GSEA C2	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
30	9.69	NULL	1 / 14	GSEA C2	TENEDINI_MEGAKARYOCYTE_MARKERS
31	9.69	NULL	1 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
32	9.69	NULL	1 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
33	9.56	NULL	2 / 12	GSEA C2	KIM_WT1_TARGETS_12HR_UP
34	9.52	NULL	1 / 2	TF	MYC_Chromatin_modification UP
35	9.44	NULL	2 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
36	9.31	NULL	1 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
37	9.31	NULL	1 / 15	GSEA C2	RUGO_RESPONSE_TO_GAMMA_RADIATION
38	9.31	NULL	1 / 15	GSEA C2	WEI_MIR34A_TARGETS
39	9.31	NULL	1 / 15	GSEA C2	KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION
40	9.31	NULL	1 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP

GW_060

Local Summary

%DE = 0.65

metagenes = 15

genes = 145

genes in genesets = 143

genes with fdr < 0.1 = 62 (60 + / 2 −)

genes with fdr < 0.05 = 52 (51 + / 1 −)

genes with fdr < 0.01 = 46 (45 + / 1 −)

<r> metagenes = 0.96

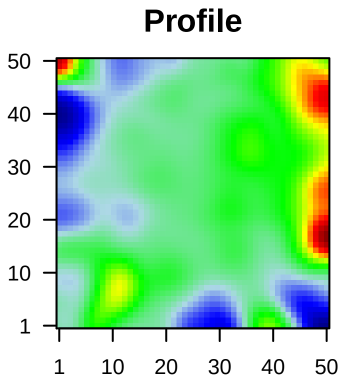
<r> genes = 0.24

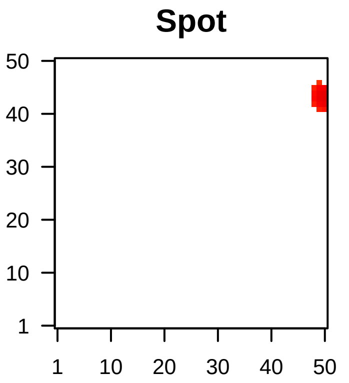
<FC> = 0.37

<shrinkage−t> = 13.08

<p−value> = 0

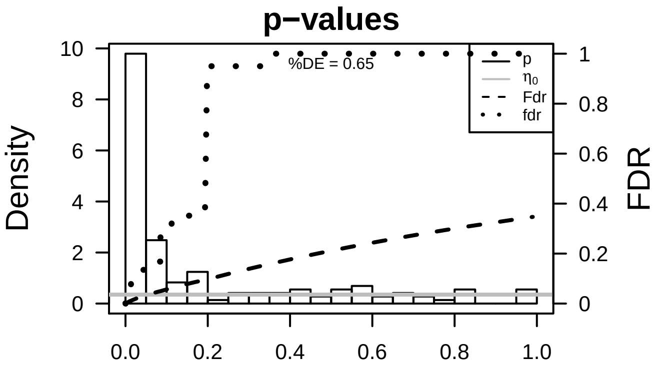
<fdr> = 0.58





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9965	1.72	2e−16	4e−15	50 x 42	fibroblast growth factor 19 [Source:HGNC Symbol;Acc:3675]
2	3205	1.81	2e−16	4e−15	49 x 45	homeobox A9 [Source:HGNC Symbol;Acc:5109]
3	157869	1.76	2e−16	4e−15	50 x 42	somatomedin B and thrombospondin, type 1 domain containi
4	2119	1.23	3e−14	2e−12	50 x 43	ets variant 5 [Source:HGNC Symbol;Acc:3494]
5	8884	1.21	1e−13	2e−12	48 x 44	solute carrier family 5 (sodium/multivitamin and iodide cotrans
6	11013	1.2	1e−13	1e−10	49 x 45	thymosin beta 15a [Source:HGNC Symbol;Acc:30744]
7	23462	1.13	3e−12	8e−10	50 x 45	hes−related family bHLH transcription factor with YRPW moti
8	5443	1.09	2e−11	1e−09	50 x 42	proopiomelanocortin [Source:HGNC Symbol;Acc:9201]
9	8324	1.07	4e−11	9e−09	50 x 42	frizzled family receptor 7 [Source:HGNC Symbol;Acc:4045]
10	80164	1.03	2e−10	2e−08	50 x 43	Protein FLJ22184 [Source:UniProtKB/TrEMBL;Acc:F5H1R7]
11	116987	1	8e−10	2e−08	50 x 41	ArfGAP with GTPase domain, ankyrin repeat and PH domain
12	6659	0.99	1e−09	2e−08	50 x 45	SRY (sex determining region Y)−box 4 [Source:HGNC Symb
13	388228	0.99	1e−09	6e−08	50 x 45	SH3 domain binding kinase 1 [Source:HGNC Symbol;Acc:17
14	91409	0.97	2e−09	1e−07	50 x 44	coiled−coil domain containing 74B [Source:HGNC Symbol;Ac
15	80731	0.95	5e−09	2e−06	50 x 41	thrombospondin, type I, domain containing 7B [Source:HGNC
16	219736	0.89	4e−08	9e−06	50 x 45	storkhead box 1 [Source:HGNC Symbol;Acc:23508]
17	6608	0.84	2e−07	9e−06	50 x 42	smoothened, frizzled family receptor [Source:HGNC Symbol;
18	201161	0.82	5e−07	9e−06	50 x 45	centromere protein V [Source:HGNC Symbol;Acc:29920]
19	729288	0.81	6e−07	9e−06	50 x 41	zinc finger protein 286B [Source:HGNC Symbol;Acc:33241]
20	4038	0.8	8e−07	1e−05	50 x 41	low density lipoprotein receptor−related protein 4 [Source:HG



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	18.31	NULL	1 / 5	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
2	18.31	NULL	1 / 5	miRNA target	miR−126
3	17.69	NULL	1 / 2	miRNA target	miR−129
4	14.21	NULL	6 / 30	miRNA target-starBase	hsa−miR−1237
5	13.05	NULL	1 / 4	GSEA C2	LUCAS_HNF4A_TARGETS_DN
6	12.99	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
7	11.69	NULL	4 / 19	MF	Wnt−activated receptor activity
8	11.38	NULL	2 / 22	BP	proximal/distal pattern formation
9	11.27	NULL	1 / 2	MMML CGS	MACIEJ_MMML 46
10	11.26	NULL	1 / 11	MF	polysaccharide binding
11	11.02	NULL	1 / 12	TF Tissue	VAQUERIZAS_Kidney
12	10.95	NULL	1 / 5	H.Tiss	WIRTH_Pituitary gland
13	10.53	NULL	1 / 13	GSEA C2	LEE_INTRATHYMIC_T_PROGENITOR
14	10.53	NULL	1 / 13	TF Tissue	VAQUERIZAS_Skin
15	10.5	NULL	4 / 23	BP	gonad development
16	10.43	NULL	1 / 12	MF	fibroblast growth factor receptor binding
17	10.43	NULL	1 / 12	GSEA C2	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION
18	10.43	NULL	1 / 12	GSEA C2	REACTOME_FRS2MEDIATED_CASCADE
19	10.43	NULL	1 / 12	GSEA C2	REACTOME_PHOSPHOLIPASE_CMEDIATED_CASCADE
20	10.23	NULL	1 / 13	GSEA C2	LIU_TARGETS_OF_VMYB_VS_CMYB_UP
21	10.11	NULL	2 / 14	BP	neuromuscular synaptic transmission
22	10.09	NULL	1 / 14	GSEA C2	GOLUB_ALL_VS_AML_DN
23	9.8	NULL	4 / 26	MF	Wnt−protein binding
24	9.7	NULL	1 / 15	BP	definitive hemopoiesis
25	9.55	NULL	1 / 14	GSEA C2	REACTOME_PI3K_CASCADE
26	9.35	NULL	1 / 16	TF Tissue	VAQUERIZAS_Pancreas
27	9.32	NULL	2 / 30	BP	neural crest cell migration
28	9.11	NULL	2 / 37	TF Tissue	VAQUERIZAS_Prostate
29	8.96	NULL	1 / 7	GSEA C2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
30	8.94	NULL	2 / 23	BP	ventricular septum morphogenesis
31	8.77	NULL	2 / 21	Glio	Martinez_Glio_hypermeth
32	8.74	NULL	1 / 18	BP	negative regulation of myeloid cell differentiation
33	8.48	NULL	3 / 47	miRNA target-starBase	hsa−miR−346
34	8.42	NULL	6 / 70	BP	canonical Wnt signaling pathway
35	8.35	NULL	2 / 43	TF Tissue	VAQUERIZAS_Uterus
36	8.29	NULL	1 / 8	GSEA C2	REACTOME_HORMONE_BIOSYNTHESIS
37	8.22	NULL	2 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
38	8.16	NULL	2 / 13	GSEA C2	SILIGAN_BOUND_BY_EWS_FLT1_FUSION
39	8.08	NULL	1 / 10	BP	biotin metabolic process
40	8.08	NULL	1 / 10	BP	pantothenate metabolic process

GW_060

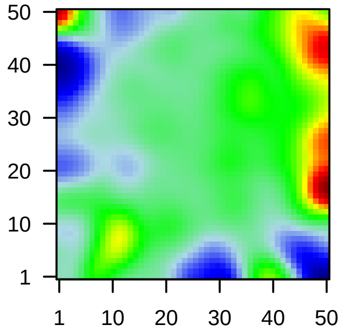
Local Summary

%DE = 0.76
metagenes = 4
genes = 95
genes in genesets = 93

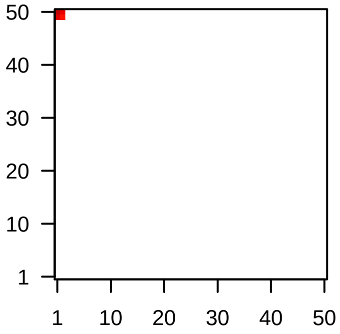
genes with fdr < 0.1 = 64 (61 + / 3 −)
genes with fdr < 0.05 = 64 (61 + / 3 −)
genes with fdr < 0.01 = 52 (50 + / 2 −)

<r> metagenes = 1
<r> genes = 0.56

<FC> = 0.65
<shrinkage−t> = 22.81
<p−value> = 0
<fdr> = 0.32



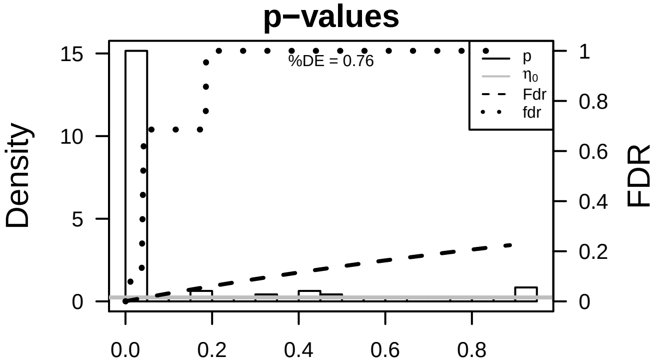
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	49860	2.36	2e−16	4e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
2	1673	1.77	2e−16	4e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
3	26085	1.37	2e−16	4e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
4	3860	1.22	2e−16	4e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
5	192666	1.6	2e−16	4e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
6	388533	1.57	2e−16	4e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
7	4118	1.47	2e−16	4e−16	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
8	5646	1.43	2e−16	4e−16	1 x 50	protease, serine, 3 [Source:HGNC Symbol;Acc:9486]
9	84651	2.17	2e−16	4e−16	1 x 50	serine peptidase inhibitor, Kazal type 7 (putative) [Source:HG
10	6701	1.57	2e−16	4e−16	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
11	6702	2.03	2e−16	4e−16	1 x 50	
12	6704	1.67	2e−16	4e−16	1 x 50	small proline−rich protein 2E [Source:HGNC Symbol;Acc:112
13	7053	2	2e−16	4e−16	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
14	391123	1.92	2e−16	4e−16	1 x 49	V−set and immunoglobulin domain containing 8 [Source:HGN
15	374897	1.32	4e−16	1e−12	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
16	84518	1.2	6e−14	8e−12	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	5653	1.18	4e−13	2e−10	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
18	54544	1.1	1e−11	7e−10	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
19	6707	0.97	6e−11	7e−10	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
20	196374	1.06	7e−11	1e−09	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	40.48	NULL	12 / 21	CC	cornified envelope
2	38.07	NULL	47 / 135	H.Tiss	WIRTH_Mucosa
3	33.06	NULL	13 / 42	BP	keratinization
4	28.47	NULL	16 / 53	BP	keratinocyte differentiation
5	26.38	NULL	7 / 19	BP	peptide cross−linking
6	19.36	NULL	13 / 76	BP	epidermis development
7	19.34	NULL	44 / 572	Disease	GUDJ_psoriasis up
8	14.6	NULL	4 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	14.52	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
10	13.17	NULL	5 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	12.9	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
12	12.79	NULL	4 / 13	BP	negative regulation of peptidase activity
13	12.09	NULL	2 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
14	11.83	NULL	10 / 122	MF	serine−type endopeptidase activity
15	11.38	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
16	11.37	NULL	2 / 17	Disease	BCHETNIA_EBM up
17	10.8	NULL	9 / 79	MF	serine−type endopeptidase inhibitor activity
18	10.74	NULL	12 / 186	MF	structural molecule activity
19	10.64	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
20	10.38	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
21	10.09	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
22	10.09	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
23	10.01	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
24	9.97	NULL	4 / 10	MF	RAGE receptor binding
25	9.71	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
26	9.16	NULL	34 / 1182	CC	extracellular region
27	9.04	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
28	8.64	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
29	8.3	NULL	3 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
30	8.2	NULL	4 / 23	MF	peptidase inhibitor activity
31	8.13	NULL	1 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_UP
32	8.09	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
33	7.79	NULL	1 / 11	Glio	VERHAAK_Brain
34	7.51	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
35	7.49	NULL	6 / 82	CC	intermediate filament
36	7.47	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
37	7.47	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
38	7.38	NULL	1 / 12	MF	channel activity
39	7.25	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
40	7.18	NULL	1 / 12	GSEA C2	GENTILE_UV_HIGH_DOSE_UP

GW_060

Local Summary

%DE = 0.84

metagenes = 2

genes = 10

genes in genesets = 10

genes with fdr < 0.1 = 8 (0 + / 8 −)

genes with fdr < 0.05 = 8 (0 + / 8 −)

genes with fdr < 0.01 = 2 (0 + / 2 −)

<r> metagenes = 0.99

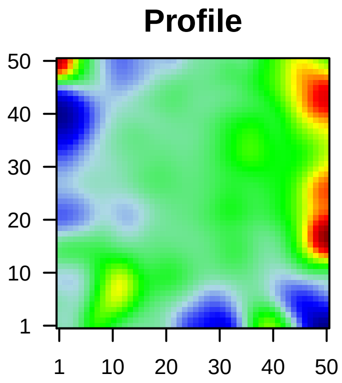
<r> genes = 0.37

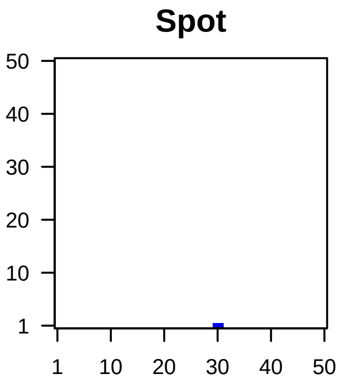
<FC> = −0.43

<shrinkage−t> = −14.88

<p−value> = 0

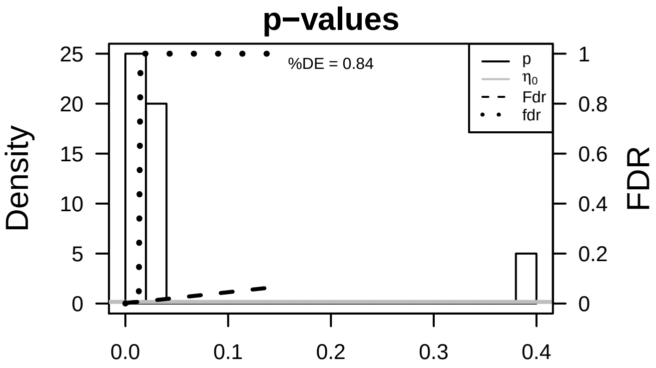
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	54922	−0.88	6e−08	2e−05	30 x 1	Ras interacting protein 1 [Source:HGNC Symbol;Acc:24716]
2	51246	−0.72	9e−06	1e−03	30 x 1	shisa family member 5 [Source:HGNC Symbol;Acc:30376]
3	100	−0.56	6e−04	1e−02	30 x 1	adenosine deaminase [Source:HGNC Symbol;Acc:186]
4	341405	−0.44	7e−03	1e−02	30 x 1	ankyrin repeat domain 33 [Source:HGNC Symbol;Acc:13788]
5	710	−0.38	2e−02	1e−02	30 x 1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [
6	197259	−0.38	2e−02	1e−02	31 x 1	mixed lineage kinase domain−like [Source:HGNC Symbol;Ac
7	55281	−0.36	3e−02	1e−02	31 x 1	transmembrane protein 140 [Source:HGNC Symbol;Acc:218
8	83982	−0.35	3e−02	2e−02	30 x 1	interferon, alpha−inducible protein 27−like 2 [Source:HGNC
9	79156	−0.34	4e−02	1e+00	31 x 1	pleckstrin homology domain containing, family F (with FYVE
10	6288	0.14	4e−01	1e+00	31 x 1	serum amyloid A1 [Source:HGNC Symbol;Acc:10513]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−29.45	NULL	1 / 13	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_UP
2	−26.32	NULL	1 / 15	BP	negative regulation of autophagy
3	−26.32	NULL	1 / 15	GSEA C2	EHLERS_ANEUPLOIDY_UP
4	−26.06	NULL	1 / 8	GSEA C2	KEGG_PRIMARY_IMMUNODEFICIENCY
5	−24.56	NULL	1 / 9	GSEA C2	SCHLOSSER_SERUM_RESPONSE_UP
6	−24.56	NULL	1 / 9	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
7	−21.39	NULL	1 / 11	CC	dendrite cytoplasm
8	−21.39	NULL	1 / 11	BP	positive regulation of T cell differentiation
9	−21.39	NULL	1 / 11	GSEA C2	DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN
10	−21.39	NULL	1 / 11	GSEA C2	REACTOME_PURINE_SALVAGE_REACTIONS
11	−19.86	NULL	1 / 12	BP	purine−containing compound salvage
12	−19.86	NULL	1 / 12	BP	response to vitamin E
13	−19.86	NULL	1 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
14	−19.86	NULL	1 / 12	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_DN
15	−19.86	NULL	1 / 12	GSEA C2	BROWNE_HCMV_INFECTION_14HR_DN
16	−19.86	NULL	1 / 12	GSEA C2	KEGG_PURINE_METABOLISM
17	−18.59	NULL	1 / 13	BP	positive regulation of heart rate
18	−18.59	NULL	1 / 13	BP	positive regulation of smooth muscle contraction
19	−18.59	NULL	1 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
20	−18.59	NULL	1 / 13	GSEA C2	NAGY_TFTC_COMPONENTS_HUMAN
21	−18.59	NULL	1 / 13	GSEA C2	ROZANOV_MMP14_TARGETS_UP
22	−18.59	NULL	1 / 13	GSEA C2	DOUGLAS_BMI1_TARGETS_UP
23	−18.59	NULL	1 / 13	GSEA C2	HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENES
24	−17.53	NULL	1 / 14	BP	purine ribonucleoside monophosphate biosynthetic process
25	−17.53	NULL	1 / 14	GSEA C2	VECCHI_GASTRIC_CANCER_EARLY_DN
26	−17.53	NULL	1 / 14	GSEA C2	RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
27	−17.53	NULL	1 / 14	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
28	−17.53	NULL	1 / 14	GSEA C2	BALDWIN_PRKCI_TARGETS_UP
29	−17.53	NULL	1 / 14	GSEA C2	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY
30	−17.53	NULL	1 / 14	GSEA C2	REACTOME_METABLISM_OF_NUCLEOTIDES
31	−17.53	NULL	1 / 14	GSEA C2	REACTOME_PURINE_METABOLISM
32	−17.4	NULL	1 / 20	MF	WW domain binding
33	−16.98	NULL	1 / 28	BP	branching morphogenesis of an epithelial tube
34	−16.98	NULL	1 / 28	CC	Golgi stack
35	−16.62	NULL	1 / 15	BP	embryonic digestive tract development
36	−16.62	NULL	1 / 15	GSEA C2	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
37	−16.62	NULL	1 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
38	−16.62	NULL	1 / 15	GSEA C2	YAGI_AML_WITH_11Q23_REARRANGED
39	−15.97	NULL	1 / 10	GSEA C2	REACTOME_INTRINSIC_PATHWAY
40	−15.82	NULL	1 / 16	BP	positive regulation of calcium−mediated signaling

GW_060

Local Summary

%DE = 0.81

metagenes = 16

genes = 272

genes in genesets = 270

genes with fdr < 0.1 = 176 (22 + / 154 −)

genes with fdr < 0.05 = 168 (20 + / 148 −)

genes with fdr < 0.01 = 120 (17 + / 103 −)

<r> metagenes = 0.99

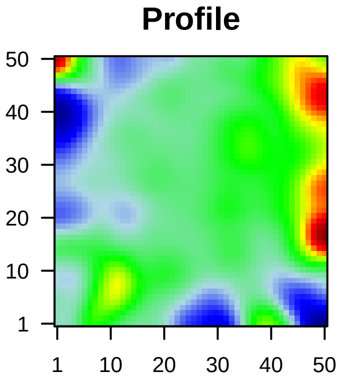
<r> genes = 0.59

<FC> = −0.27

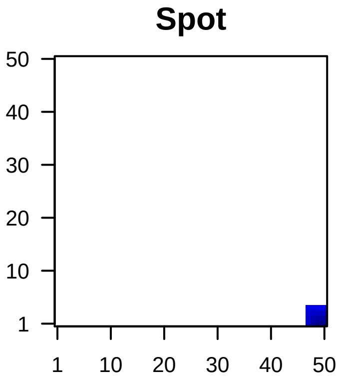
<shrinkage−t> = −9.41

<p−value> = 0

<fdr> = 0.46



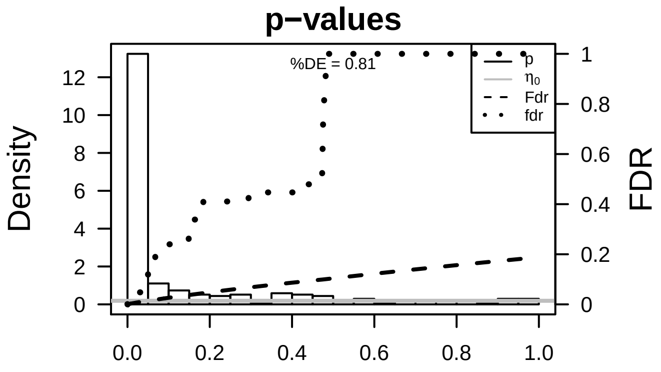
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1116	1.49	2e−16	3e−15	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
2	25849	1.97	2e−16	3e−15	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:HG
3	6578	1.56	2e−16	3e−15	50 x 4	solute carrier organic anion transporter family, member 2A1 [S
4	9806	1.79	2e−16	3e−15	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglycar
5	3119	−1.19	2e−13	2e−10	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
6	57484	1.11	6e−12	2e−10	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
7	2995	1.11	9e−12	5e−09	50 x 3	glycophorin C (Gerbich blood group) [Source:HGNC Symbol;
8	23643	−1.05	1e−10	4e−08	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
9	1117	1	8e−10	5e−08	48 x 4	chitinase 3−like 2 [Source:HGNC Symbol;Acc:1933]
10	8728	−0.98	2e−09	2e−07	50 x 3	ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
11	5996	−0.93	9e−09	2e−07	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Acc
12	4069	−0.93	1e−08	5e−07	50 x 2	lysozyme [Source:HGNC Symbol;Acc:6740]
13	5730	−0.9	3e−08	5e−07	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
14	10365	−0.9	3e−08	7e−07	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
15	5142	0.89	4e−08	8e−07	50 x 4	phosphodiesterase 4B, cAMP−specific [Source:HGNC Symbo
16	7852	0.88	6e−08	8e−07	48 x 3	chemokine (C−X−C motif) receptor 4 [Source:HGNC Symbol;
17	64759	0.87	7e−08	1e−06	50 x 4	tensin 3 [Source:HGNC Symbol;Acc:21616]
18	3620	−0.86	1e−07	1e−06	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
19	3669	−0.86	1e−07	1e−05	48 x 1	interferon stimulated exonuclease gene 20kDa [Source:HGN
20	894	0.8	8e−07	1e−05	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.05	NULL	92 / 417	H.Tiss	WIRTH_Immune system
2	−20.57	NULL	99 / 553	Cancer	Lembcke_Colonic Inflammation
3	−17.93	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
4	−14.87	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
5	−14.72	NULL	12 / 15	CC	MHC class II protein complex
6	−12.5	NULL	47 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−12.5	NULL	47 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−12.5	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−12.5	NULL	47 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−12	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
11	−11.86	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	−11.49	NULL	8 / 16	GSEA C2	SU_THYMUS
13	−11.11	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
14	−11.07	NULL	17 / 74	BP	regulation of immune response
15	−10.65	NULL	49 / 312	BP	immune response
16	−10.33	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
17	−10.01	NULL	7 / 28	Lymphoma	DAVE_Immune response 1
18	−9.84	NULL	9 / 28	BP	B cell receptor signaling pathway
19	−9.51	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
20	−9.48	NULL	15 / 47	BP	antigen processing and presentation
21	−9.16	NULL	5 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
22	−9.15	NULL	6 / 13	Cancer	GENTLES_modul18
23	−9.14	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
24	−8.98	NULL	14 / 60	BP	T cell costimulation
25	−8.92	NULL	7 / 45	BP	cellular defense response
26	−8.89	NULL	5 / 11	BP	positive regulation of B cell differentiation
27	−8.59	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
28	−8.53	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
29	−8.49	NULL	3 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
30	−8.43	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	−8.41	NULL	3 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
32	−8.35	NULL	8 / 45	BP	T cell activation
33	−8.21	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
34	−8.13	NULL	3 / 12	GSEA C2	BIOCARTA_CTLA4_PATHWAY
35	−8.02	NULL	2 / 8	GSEA C2	BOQUEST_STEM_CELL_DN
36	−7.85	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
37	−7.81	NULL	5 / 12	BP	immunoglobulin mediated immune response
38	−7.81	NULL	2 / 8	GSEA C2	HELLER_SILENCED_BY_METHYLATION_UP
39	−7.77	NULL	4 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
40	−7.64	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP

GW_060

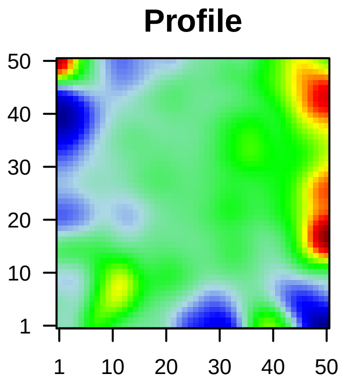
Local Summary

%DE = 0.68
metagenes = 34
genes = 351
genes in genesets = 343

genes with fdr < 0.1 = 145 (6 + / 139 −)
genes with fdr < 0.05 = 100 (6 + / 94 −)
genes with fdr < 0.01 = 66 (5 + / 61 −)

<r> metagenes = 0.96
<r> genes = 0.27

<FC> = −0.27
<shrinkage−t> = −9.31
<p−value> = 0.01
<fdr> = 0.66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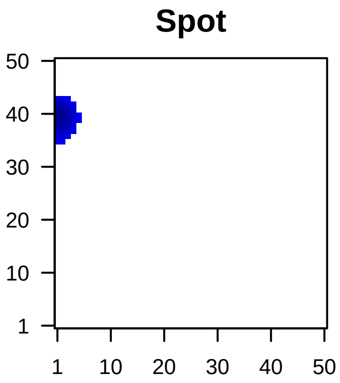

Spot

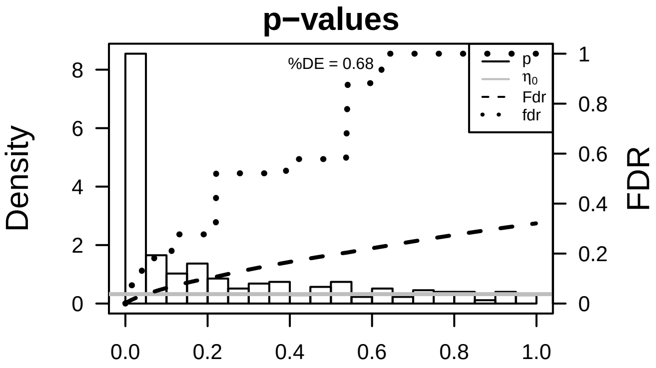
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	50805	1.94	2e−16	1e−14	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
2	55214	−1.33	2e−16	1e−14	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
3	780851	−1.29	2e−15	4e−13	2 x 39	small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
4	780853	−1.26	6e−15	4e−13	2 x 39	small nucleolar RNA, C/D box 3C [Source:HGNC Symbol;Acc
5	10397	−1.15	9e−15	3e−12	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
6	81706	1.22	4e−14	3e−12	1 x 43	protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou
7	780854	−1.22	5e−14	4e−11	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
8	80326	1.18	4e−13	2e−09	1 x 40	wingless−type MMTV integration site family, member 10A [So
9	116211	−1.09	2e−11	4e−08	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
10	133	−0.92	6e−10	4e−08	1 x 42	adrenomedullin [Source:HGNC Symbol;Acc:259]
11	25976	−1	7e−10	4e−07	3 x 43	TCDD−inducible poly(ADP−ribose) polymerase [Source:HGN
12	5744	−0.95	4e−09	1e−06	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
13	3306	−0.92	2e−08	5e−06	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
14	723790	−0.88	6e−08	7e−06	2 x 38	histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
15	9124	−0.86	1e−07	1e−05	1 x 40	PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:2067]
16	80115	−0.84	2e−07	1e−05	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
17	51734	−0.83	3e−07	2e−05	1 x 39	methionine sulfoxide reductase B1 [Source:HGNC Symbol;Ac
18	6513	−0.81	6e−07	2e−05	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
19	1308	−0.8	7e−07	2e−05	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
20	81671	−0.8	8e−07	5e−05	4 x 39	vacuole membrane protein 1 [Source:HGNC Symbol;Acc:295

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−10.77	NULL	2 / 2	miRNA target miR−199a*
2	−10.42	NULL	3 / 7	MMML CGS MACIEJ_MMML 9
3	−9.59	NULL	1 / 5	GSEA C2 KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
4	−9.54	NULL	2 / 12	BP androgen metabolic process
5	−9.5	NULL	3 / 13	GSEA C2 HASINA_NOL7_TARGETS_UP
6	−9.08	NULL	3 / 15	GSEA C2 FARMER_BREAST_CANCER_CLUSTER_3
7	−8.76	NULL	3 / 16	GSEA C2 FARMER_BREAST_CANCER_CLUSTER_4
8	−8.67	NULL	1 / 6	GSEA C2 KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_
9	−8.63	NULL	2 / 12	GSEA C2 ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN
10	−8.37	NULL	3 / 15	GSEA C2 LEE_LIVER_CANCER_DENA_UP
11	−8.25	NULL	3 / 16	GSEA C2 UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
12	−8.14	NULL	1 / 2	miRNA target miR−659
13	−8.02	NULL	2 / 8	GSEA C2 WILLIAMS_ESR2_TARGETS_DN
14	−7.37	NULL	2 / 19	MF L−ascorbic acid binding
15	−7.36	NULL	1 / 4	GSEA C2 TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIND
16	−7.32	NULL	4 / 15	GSEA C2 NAGASHIMA_NRG1_SIGNALING_UP
17	−7.24	NULL	3 / 22	MF cadherin binding
18	−7.1	NULL	1 / 2	miRNA target miR−346
19	−6.99	NULL	3 / 15	GSEA C2 GEORGANTAS_HSC_MARKERS
20	−6.93	NULL	2 / 15	GSEA C2 TAKAO_RESPONSE_TO_UVB_RADIATION_DN
21	−6.91	NULL	1 / 9	GSEA C2 KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
22	−6.91	NULL	1 / 9	GSEA C2 KYNG_DNA_DAMAGE_UP
23	−6.91	NULL	1 / 9	GSEA C2 KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
24	−6.68	NULL	2 / 16	GSEA C2 LEE_LIVER_CANCER_MYC_TGFA_UP
25	−6.68	NULL	2 / 16	GSEA C2 LEE_LIVER_CANCER_ACOX1_UP
26	−6.67	NULL	2 / 13	GSEA C2 REACTOME_PACKAGING_OF_TELOMERE_ENDS
27	−6.65	NULL	3 / 10	GSEA C2 XU_RESPONSE_TO_TRETINOIN_DN
28	−6.58	NULL	2 / 11	MMML CGS MACIEJ_MMML 3
29	−6.55	NULL	3 / 15	GSEA C2 SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B
30	−6.54	NULL	3 / 15	MF cytoskeletal adaptor activity
31	−6.53	NULL	2 / 14	GSEA C2 STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA
32	−6.53	NULL	2 / 12	GSEA C2 MIZUKAMI_HYPOXIA_UP
33	−6.51	NULL	1 / 10	GSEA C2 RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
34	−6.51	NULL	1 / 10	GSEA C2 KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
35	−6.51	NULL	1 / 10	GSEA C2 PARK_TRETINOIN_RESPONSE
36	−6.5	NULL	2 / 10	BP surfactant homeostasis
37	−6.48	NULL	2 / 16	GSEA C2 SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP
38	−6.41	NULL	2 / 11	BP response to metal ion
39	−6.32	NULL	2 / 15	GSEA C2 AMIT_EGF_RESPONSE_240_MCF10A
40	−6.3	NULL	1 / 7	GSEA C2 REACTOME_CALCITONIN_LIKE_LIGAND_RECEPTORS


p−values