GW_218

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1965 (1090 + / 875 −)

genes with fdr < 0.1 = 1650 (949 + / 701 −)

genes with fdr < 0.05 = 1318 (803 + / 515 −)

genes with fdr < 0.01 = 980 (641 + / 339 −)

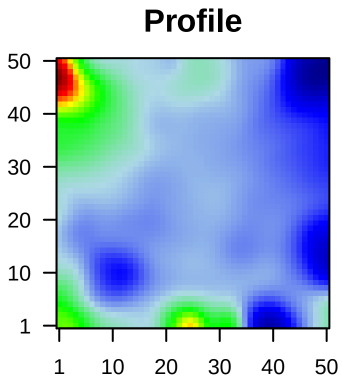
genes in genesets = 16332

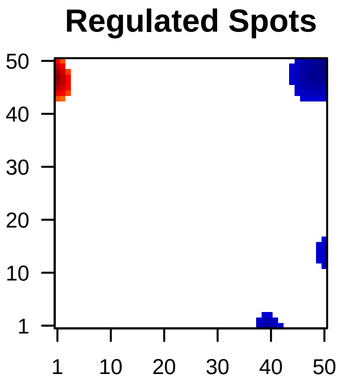
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

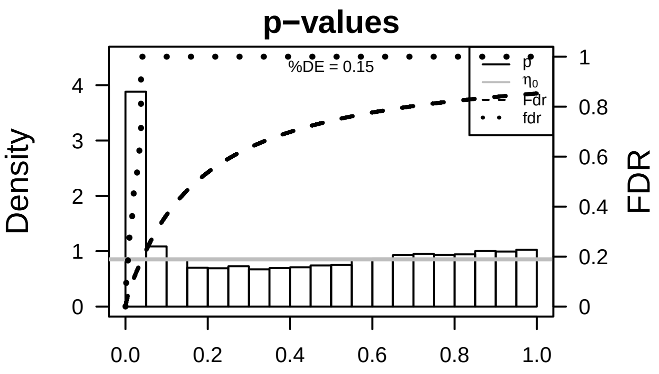
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.26	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	218	−1.76	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	230	−1.33	2e−16	2e−14	2 x 17	aldolase C, fructose−bisphosphate [Source:HGNC Symbol;Ac
5	242	1.55	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	147495	1.36	2e−16	2e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
7	151516	2.97	2e−16	2e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
8	8424	1.76	2e−16	2e−14	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamma
9	84707	−1.36	2e−16	2e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
10	387695	2.04	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
11	260436	−1.73	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
12	29113	2.2	2e−16	2e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
13	375791	1.33	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
14	55848	1.34	2e−16	2e−14	31 x 50	plasminogen receptor, C−terminal lysine transmembrane prot
15	760	2.04	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
16	59082	1.43	2e−16	2e−14	6 x 44	caspase recruitment domain family, member 18 [Source:HGN
17	845	1.35	2e−16	2e−14	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:
18	857	1.42	2e−16	2e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
19	948	1.42	2e−16	2e−14	6 x 44	CD36 molecule (thrombospondin receptor) [Source:HGNC Sy
20	970	1.31	2e−16	2e−14	33 x 2	CD70 molecule [Source:HGNC Symbol;Acc:11937]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	19.4	NULL	135	H.Tiss	WIRTH_Mucosa
2	18.71	NULL	42	BP	keratinization
3	17.01	NULL	21	CC	cornified envelope
4	16.72	NULL	127	H.Tiss	WIRTH_Muscle
5	15.51	NULL	572	Disease	GUDJ_psoriasis up
6	15.21	NULL	36	BP	muscle filament sliding
7	14.57	NULL	76	BP	epidermis development
8	14.44	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
9	13.52	NULL	53	BP	keratinocyte differentiation
10	12.88	NULL	16	H.Tiss	WIRTH_Hippocampus
11	11.63	NULL	190	CC	extracellular matrix
12	11.58	NULL	250	Lymphoma	LENZ_Stromal signature 1
13	11.45	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
14	10.82	NULL	242	BP	extracellular matrix organization
15	10.57	NULL	21	CC	desmosome
16	10.53	NULL	44	MF	structural constituent of muscle
17	10.17	NULL	12	CC	myosin filament
18	10.13	NULL	64	BP	collagen catabolic process
19	9.93	NULL	19	BP	peptide cross−linking
20	9.84	NULL	84	BP	muscle contraction
Underexpressed					
1	−10.57	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−10.57	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−8.51	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
4	−8.12	NULL	7	MMML CGS	MACIEJ_MMML 5
5	−6.9	NULL	6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
6	−6.38	NULL	914	Chr	Chr 3
7	−6.25	NULL	4	MMML CGS	MACIEJ_MMML 23
8	−5.96	NULL	370	BP	mitotic cell cycle
9	−5.94	NULL	11	GSEA C2	AMIT_EGF_RESPONSE_20_HELA
10	−5.92	NULL	1749	MF	DNA binding
11	−5.88	NULL	34	Chr	Chr Y
12	−5.71	NULL	149	BP	DNA replication
13	−5.64	NULL	1095	TF	HEBENSTREIT_high expression TF
14	−5.63	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
15	−5.6	NULL	20	Lymphoma	ROSOLOWSKI_red UP
16	−5.56	NULL	4640	CC	nucleus
17	−5.36	NULL	949	CC	nucleoplasm
18	−5.02	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
19	−4.84	NULL	918	Chr	Chr 17
20	−4.69	NULL	298	BP	DNA repair

GW_218

Local Summary

%DE = 0.9

metagenes = 21

genes = 294

genes in genesets = 287

genes with fdr < 0.1 = 246 (233 + / 13 −)

genes with fdr < 0.05 = 246 (233 + / 13 −)

genes with fdr < 0.01 = 229 (218 + / 11 −)

<r> metagenes = 0.91

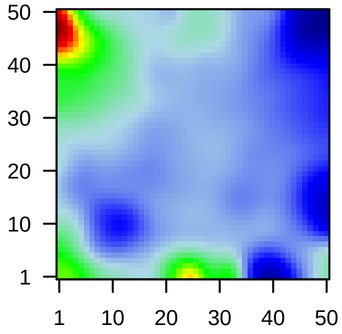
<r> genes = 0.39

<FC> = 0.91

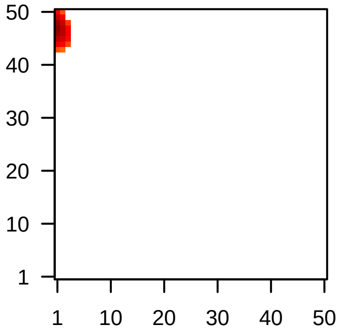
<shrinkage−t> = 31.89

<p−value> = 0

<fdr> = 0.19



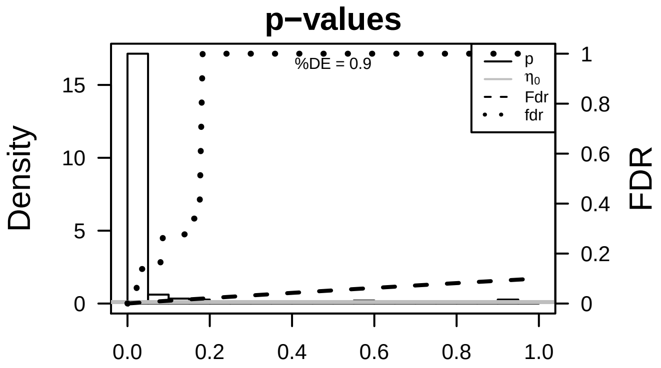
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−1.76	2e−16	8e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	242	1.55	2e−16	8e−17	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sy
3	147495	1.36	2e−16	8e−17	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
4	151516	2.97	2e−16	8e−17	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
5	8424	1.76	2e−16	8e−17	3 x 48	butyrobetaine (gamma), 2−oxoglutarate dioxygenase (gamm
6	387695	2.04	2e−16	8e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
7	29113	2.2	2e−16	8e−17	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symb
8	375791	1.33	2e−16	8e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
9	760	2.04	2e−16	8e−17	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
10	1041	1.9	2e−16	8e−17	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
11	84518	1.78	2e−16	8e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
12	51200	1.88	2e−16	8e−17	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
13	54544	2.03	2e−16	8e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
14	49860	1.42	2e−16	8e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	1474	1.95	2e−16	8e−17	1 x 47	cystatin E/M [Source:HGNC Symbol;Acc:2478]
16	1515	1.92	2e−16	8e−17	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
17	9547	2	2e−16	8e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
18	27065	2.04	2e−16	8e−17	1 x 46	Homo sapiens neuron specific gene family member 1 (NSG1
19	55894	1.33	2e−16	8e−17	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	414325	1.7	2e−16	8e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	35.57	NULL	18 / 21	CC	cornified envelope
2	35.03	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
3	28.39	NULL	20 / 42	BP	keratinization
4	26.11	NULL	24 / 53	BP	keratinocyte differentiation
5	25.34	NULL	26 / 76	BP	epidermis development
6	21.9	NULL	107 / 572	Disease	GUDJ_psoriasis up
7	20.97	NULL	12 / 21	CC	desmosome
8	17.8	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	16.78	NULL	13 / 44	CC	keratin filament
10	16.29	NULL	21 / 82	CC	intermediate filament
11	15.63	NULL	30 / 186	MF	structural molecule activity
12	15.56	NULL	10 / 19	BP	peptide cross−linking
13	15.43	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	14.74	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	14.4	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
16	14.02	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
17	13.19	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
18	12.59	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
19	12.04	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
20	10.91	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
21	10.77	NULL	6 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
22	10.7	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
23	9.79	NULL	5 / 10	MF	RAGE receptor binding
24	9.69	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
25	9.39	NULL	11 / 82	MF	structural constituent of cytoskeleton
26	9.38	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
27	9.32	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
28	9.31	NULL	4 / 21	CC	gap junction
29	9.27	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
30	9.16	NULL	7 / 38	BP	epithelial cell differentiation
31	8.58	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
32	8.55	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
33	8.42	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
34	8.41	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
35	8.34	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
36	8.32	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
37	8.27	NULL	5 / 25	BP	response to zinc ion
38	8.25	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
39	8.24	NULL	2 / 11	MF	gamma−catenin binding
40	8.24	NULL	65 / 1182	CC	extracellular region

GW_218

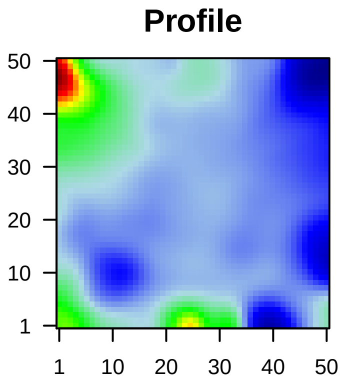
Local Summary

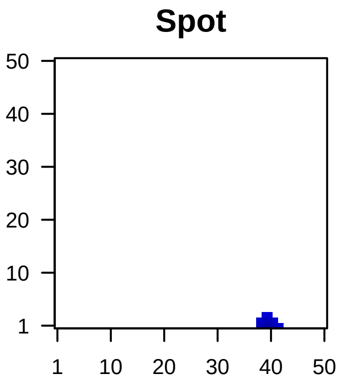
%DE = 0.87
metagenes = 11
genes = 215
genes in genesets = 190

genes with fdr < 0.1 = 170 (6 + / 164 −)
genes with fdr < 0.05 = 143 (4 + / 139 −)
genes with fdr < 0.01 = 105 (2 + / 103 −)

<r> metagenes = 0.99
<r> genes = 0.51

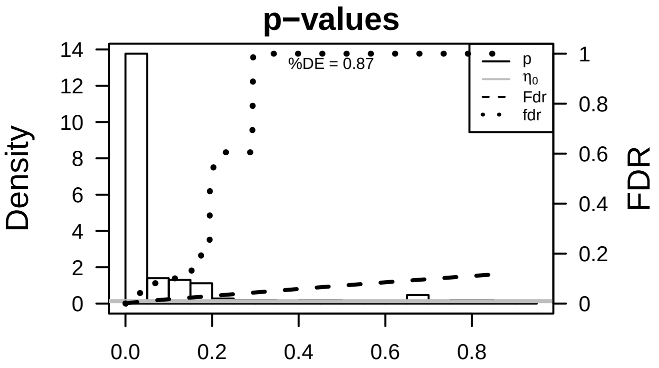
<FC> = −0.38
<shrinkage−t> = −13.52
<p−value> = 0
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	641737	−0.93	2e−10	1e−07	40 x 1	
2	440157	−0.92	4e−09	9e−07	39 x 1	
3	90639	−0.86	4e−08	1e−06	40 x 1	cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [
4	25862	−0.84	9e−08	3e−06	40 x 1	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:2
5	5256	−0.82	2e−07	3e−06	40 x 1	phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
6	84061	−0.79	5e−07	3e−06	39 x 1	magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
7	250	−0.79	5e−07	3e−06	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
8	3586	−0.73	6e−07	3e−06	40 x 1	interleukin 10 [Source:HGNC Symbol;Acc:5962]
9	100190938	−0.72	6e−07	8e−06	39 x 1	RAMP2 antisense RNA 1 [Source:HGNC Symbol;Acc:44358]
10	7766	−0.77	9e−07	2e−05	40 x 1	Zinc finger protein 223 [Source:UniProtKB/TrEMBL;Acc:K7E
11	136051	−0.76	2e−06	2e−05	40 x 1	zinc finger protein 786 [Source:HGNC Symbol;Acc:21806]
12	126205	−0.73	4e−06	2e−05	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
13	255031	−0.73	4e−06	2e−05	40 x 1	long intergenic non−protein coding RNA 957 [Source:HGNC
14	374860	−0.72	4e−06	8e−05	40 x 1	ankyrin repeat domain 30B [Source:HGNC Symbol;Acc:2416
15	727956	−0.7	9e−06	8e−05	40 x 1	succinate dehydrogenase complex, subunit A, flavoprotein ps
16	399900	−0.64	1e−05	9e−05	39 x 1	
17	8548	−0.68	1e−05	9e−05	39 x 1	basic leucine zipper nuclear factor 1 [Source:HGNC Symbol;
18	401494	−0.67	2e−05	9e−05	40 x 1	protein tyrosine phosphatase−like A domain containing 2 [Sou
19	125050	−0.67	2e−05	9e−05	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
20	642947	−0.61	2e−05	9e−05	39 x 1	



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−12.86	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
2	−9.92	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
3	−9.89	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
4	−8.26	NULL	3 / 16	GSEA C2	HAMAI_APOPTOSIS_VIA_TRAIL_UP
5	−7.73	NULL	1 / 5	GSEA C2	BIOCARTA_INFLAM_PATHWAY
6	−7.46	NULL	2 / 14	BP	cellular response to estradiol stimulus
7	−6.97	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
8	−6.97	NULL	1 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
9	−6.9	NULL	3 / 24	BP	negative regulation of T cell proliferation
10	−6.8	NULL	2 / 15	GSEA C2	THUM_SYSTOLIC_HEART_FAILURE_DN
11	−6.09	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
12	−6.01	NULL	2 / 13	GSEA C2	ST_GAQ_PATHWAY
13	−6.01	NULL	2 / 13	GSEA C2	ST_GA13_PATHWAY
14	−5.9	NULL	1 / 8	GSEA C2	BIOCARTA_ASBCELL_PATHWAY
15	−5.72	NULL	2 / 14	BP	mitochondrion morphogenesis
16	−5.67	NULL	2 / 15	BP	female gamete generation
17	−5.52	NULL	2 / 17	BP	gamete generation
18	−5.3	NULL	2 / 16	BP	cognition
19	−5.28	NULL	2 / 16	TF Tissue	VAQUERIZAS_Fetal thyroid
20	−5.23	NULL	1 / 10	CC	oligosaccharyltransferase complex
21	−5.18	NULL	1 / 10	BP	negative regulation of nitric oxide biosynthetic process
22	−5.18	NULL	1 / 10	GSEA C2	BIOCARTA_IL10_PATHWAY
23	−4.93	NULL	1 / 11	GSEA C2	KEGG_FOLATE_BIOSYNTHESIS
24	−4.9	NULL	1 / 11	BP	negative regulation of interleukin−12 production
25	−4.9	NULL	1 / 11	GSEA C2	SU_PANCREAS
26	−4.85	NULL	2 / 22	BP	negative regulation of interferon−gamma production
27	−4.84	NULL	2 / 15	GSEA C2	WANG_CLIM2_TARGETS_UP
28	−4.73	NULL	1 / 8	GSEA C2	WILLIAMS_ESR2_TARGETS_DN
29	−4.73	NULL	2 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
30	−4.65	NULL	1 / 12	BP	negative regulation of growth of symbiont in host
31	−4.64	NULL	1 / 13	GSEA C2	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS
32	−4.58	NULL	2 / 15	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN
33	−4.58	NULL	2 / 15	GSEA C2	ZHOU_INFLAMMATORY_RESPONSE_LPS_DN
34	−4.52	NULL	2 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
35	−4.51	NULL	2 / 11	GSEA C2	STEIN_ESRRA_TARGETS_DN
36	−4.47	NULL	1 / 13	MF	magnesium ion transmembrane transporter activity
37	−4.44	NULL	3 / 38	MF	methylated histone residue binding
38	−4.44	NULL	2 / 19	MF	3',5'−cyclic−nucleotide phosphodiesterase activity
39	−4.44	NULL	1 / 13	BP	negative regulation of B cell proliferation
40	−4.44	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON

GW_218

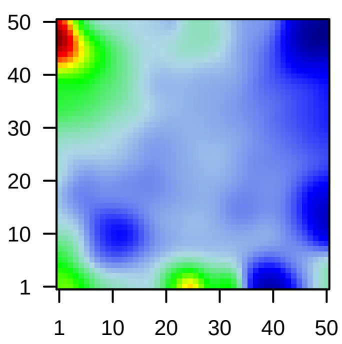
Local Summary

%DE = 0.81
metagenes = 10
genes = 165
genes in genesets = 164

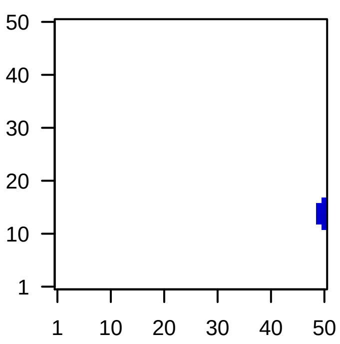
genes with fdr < 0.1 = 89 (2 + / 87 −)
genes with fdr < 0.05 = 79 (2 + / 77 −)
genes with fdr < 0.01 = 51 (0 + / 51 −)

<r> metagenes = 0.94
<r> genes = 0.32

<FC> = −0.36
<shrinkage−t> = −12.56
<p−value> = 0
<fdr> = 0.55



Profile



Spot

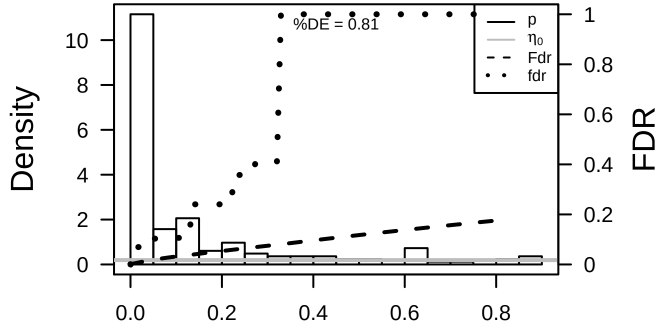
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3169	−1.52	2e−16	7e−15	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	10439	−1.18	5e−14	2e−11	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
3	55268	−1.13	7e−13	8e−11	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy
4	9071	−1.1	3e−12	4e−10	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
5	2139	−1.06	2e−11	9e−10	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;
6	260293	−1.04	4e−11	2e−08	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
7	494470	−0.98	5e−10	2e−08	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
8	6920	−0.96	1e−09	7e−07	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
9	3033	−0.86	4e−08	7e−07	50 x 14	hydroxyacyl−CoA dehydrogenase [Source:HGNC Symbol;Ac
10	8543	−0.85	6e−08	7e−07	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
11	66002	−0.85	7e−08	1e−05	50 x 13	cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
12	135112	−0.77	9e−07	1e−05	50 x 13	nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21
13	55930	−0.77	1e−06	1e−05	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
14	63917	−0.76	1e−06	5e−05	50 x 16	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acet
15	79695	−0.72	5e−06	5e−05	50 x 12	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acet
16	51101	−0.72	5e−06	5e−05	50 x 16	zinc finger, C2HC−type containing 1A [Source:HGNC Symbol
17	56994	−0.71	6e−06	3e−04	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
18	51316	−0.67	2e−05	3e−04	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
19	54097	−0.66	3e−05	4e−04	50 x 12	family with sequence similarity 3, member B [Source:HGNC
20	634	−0.64	5e−05	4e−04	50 x 12	carcinoembryonic antigen−related cell adhesion molecule 1 (

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−15.61	NULL	3 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
2	−13.9	NULL	2 / 12	BP neuron fate specification
3	−13.4	NULL	1 / 4	GSEA C2 NICK_RESPONSE_TO_PROC_TREATMENT_UP
4	−13.24	NULL	1 / 7	GSEA C2 NEBEN_AML_WITH_FLT3_OR_NRAS_UP
5	−12.69	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
6	−11.79	NULL	5 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
7	−11.19	NULL	2 / 10	GSEA C2 YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
8	−11.03	NULL	2 / 15	BP hormone metabolic process
9	−10.85	NULL	1 / 10	BP prostate gland epithelium morphogenesis
10	−10.32	NULL	3 / 15	GSEA C2 DOANE_BREAST_CANCER_CLASSES_UP
11	−10.09	NULL	2 / 15	GSEA C2 MASSARWEH_RESPONSE_TO_ESTRADIOL
12	−9.95	NULL	2 / 11	MF enhancer sequence−specific DNA binding
13	−9.75	NULL	2 / 18	MF aromatase activity
14	−9.73	NULL	3 / 15	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
15	−9.37	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
16	−9.37	NULL	1 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
17	−9.31	NULL	2 / 15	GSEA C2 ZHAN_MULTIPLE_MYELOMA_CD1_DN
18	−8.99	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition
19	−8.92	NULL	2 / 15	GSEA C2 CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
20	−8.67	NULL	2 / 14	GSEA C2 MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
21	−8.44	NULL	3 / 11	BP DNA integration
22	−8.38	NULL	1 / 10	GSEA C2 BROWNE_HCMV_INFECTION_12HR_UP
23	−8.38	NULL	1 / 10	GSEA C2 XU_GH1_AUTOCRINE_TARGETS_DN
24	−8.33	NULL	1 / 16	GSEA C2 GU_PDEF_TARGETS_DN
25	−8.32	NULL	2 / 12	MF NAD+ binding
26	−8.14	NULL	2 / 14	GSEA C2 NUYTTEN_NIPP1_TARGETS_UP
27	−8.08	NULL	2 / 19	BP calcium−independent cell−cell adhesion
28	−8.05	NULL	1 / 17	BP dorsal/ventral neural tube patterning
29	−7.95	NULL	3 / 15	GSEA C2 NAKAJIMA_MAST_CELL
30	−7.94	NULL	2 / 14	GSEA C2 LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
31	−7.94	NULL	2 / 14	GSEA C2 VANTVEER_BREAST_CANCER_ESR1_UP
32	−7.86	NULL	2 / 16	GSEA C2 RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
33	−7.56	NULL	1 / 19	BP anatomical structure formation involved in morphogenesis
34	−7.56	NULL	1 / 19	BP positive regulation of smoothened signaling pathway
35	−7.56	NULL	1 / 12	GSEA C2 CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
36	−7.56	NULL	1 / 12	GSEA C2 RIZKI_TUMOR_INVASIVENESS_3D_DN
37	−7.56	NULL	1 / 12	GSEA C2 ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
38	−7.56	NULL	1 / 11	GSEA C2 LAIHO_COLORECTAL_CANCER_SERRATED_DN
39	−7.44	NULL	3 / 16	GSEA C2 CROMER_TUMORIGENESIS_DN
40	−7.4	NULL	2 / 35	miRNA target hsa−miR−769−5p



p−values

GW_218

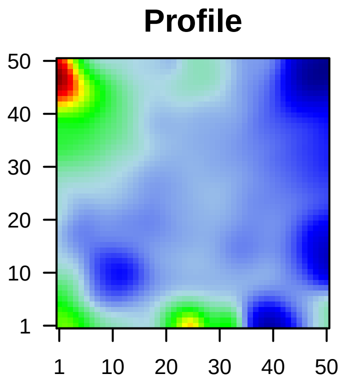
Local Summary

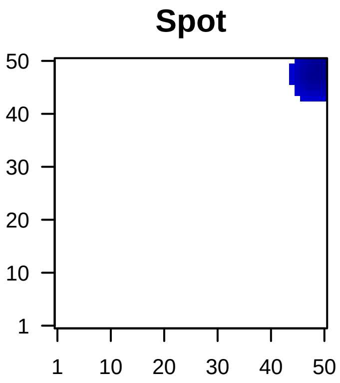
%DE = 0.82
metagenes = 51
genes = 565
genes in genesets = 560

genes with fdr < 0.1 = 336 (10 + / 326 −)
genes with fdr < 0.05 = 291 (8 + / 283 −)
genes with fdr < 0.01 = 180 (5 + / 175 −)

<r> metagenes = 0.89
<r> genes = 0.24

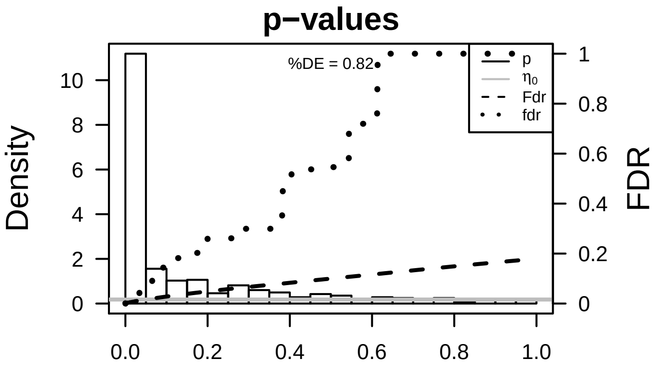
<FC> = −0.35
<shrinkage−t> = −12.33
<p−value> = 0
<fdr> = 0.57


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	84707	−1.36	2e−16	3e−15	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
2	9076	−1.35	2e−16	3e−15	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
3	3880	−1.93	2e−16	3e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
4	3856	−1.65	2e−16	3e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
5	26227	−1.9	2e−16	3e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
6	116832	−1.59	2e−16	3e−15	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
7	256764	−1.82	2e−16	3e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
8	59342	−1.28	4e−16	2e−13	50 x 47	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
9	1056	−1.24	2e−15	5e−13	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
10	4953	−1.22	8e−15	2e−12	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
11	4922	−1.2	3e−14	5e−12	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
12	200634	−1.18	7e−14	4e−11	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
13	57291	−1.14	4e−13	4e−11	50 x 50	differentiation antagonizing non−protein coding RNA [Source:
14	154664	−1.12	9e−13	4e−10	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
15	8364	−1	4e−12	3e−09	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
16	139728	−1.03	5e−11	3e−09	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
17	1528	−1.03	7e−11	6e−09	50 x 50	cytochrome b5 type A (microsomal) [Source:HGNC Symbol;
18	84223	−1.01	1e−10	6e−09	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
19	55872	−1	2e−10	9e−09	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
20	216	−0.99	3e−10	1e−07	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.96	NULL	56 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−22.96	NULL	56 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−18.22	NULL	13 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	−15.4	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
5	−12.99	NULL	40 / 149	BP	DNA replication
6	−12.57	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
7	−12.52	NULL	16 / 57	Glio	developing astrocytes
8	−12.05	NULL	72 / 370	BP	mitotic cell cycle
9	−11.64	NULL	74 / 530	Cancer	Lembcke_Normal vs Adenoma
10	−11.58	NULL	6 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
11	−11.42	NULL	15 / 30	BP	DNA strand elongation involved in DNA replication
12	−11.32	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
13	−10.6	NULL	5 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
14	−9.71	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
15	−9.66	NULL	6 / 14	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
16	−9.59	NULL	11 / 22	BP	DNA replication initiation
17	−9.57	NULL	6 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
18	−9.52	NULL	6 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
19	−9.45	NULL	4 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
20	−9.29	NULL	7 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
21	−9.19	NULL	10 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
22	−9.16	NULL	3 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
23	−8.97	NULL	10 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
24	−8.81	NULL	2 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
25	−8.81	NULL	2 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
26	−8.78	NULL	7 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
27	−8.74	NULL	6 / 15	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
28	−8.67	NULL	5 / 14	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_2
29	−8.51	NULL	6 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
30	−8.51	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
31	−8.34	NULL	86 / 914	Chr	Chr 3
32	−8.29	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
33	−8.27	NULL	8 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
34	−8.23	NULL	6 / 14	MMML CGS	MACIEJ_MMML 4
35	−8.2	NULL	6 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
36	−8.14	NULL	42 / 298	BP	DNA repair
37	−8.13	NULL	9 / 34	BP	glutathione metabolic process
38	−8.1	NULL	5 / 16	Cancer	WOLFER_overlap genes
39	−8.1	NULL	10 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
40	−8.07	NULL	9 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN