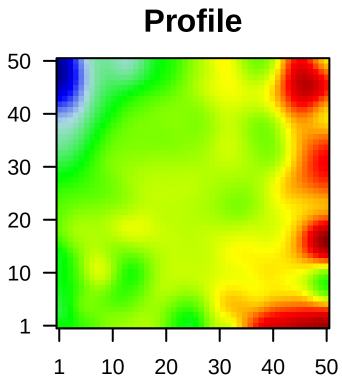
GW_021

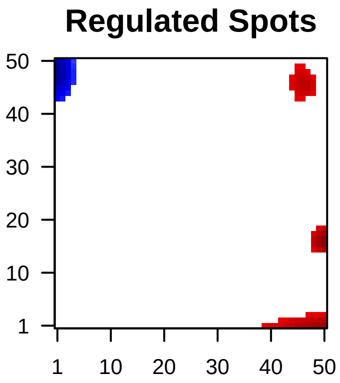
Global Summary

%DE = 0.16
genes with fdr < 0.2 = 2149 (1128 + / 1021 −)
genes with fdr < 0.1 = 1649 (873 + / 776 −)
genes with fdr < 0.05 = 1462 (777 + / 685 −)
genes with fdr < 0.01 = 979 (522 + / 457 −)

genes in genesets = 16332

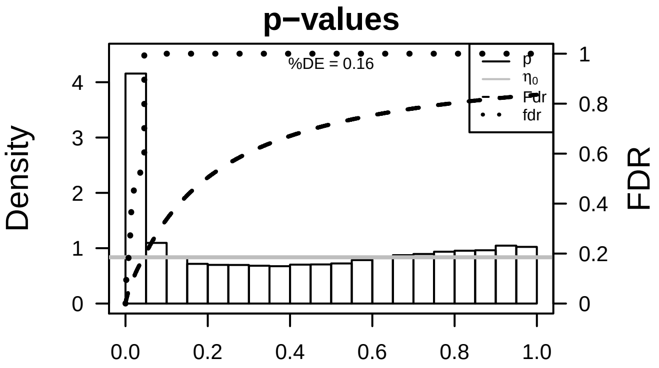
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.09
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	2.09	2e−16	4e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	57016	−1.88	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	8644	−2.27	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	−1.76	2e−16	4e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	55107	−1.82	2e−16	4e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
6	9915	1.67	2e−16	4e−14	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
7	22809	2.1	2e−16	4e−14	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
8	330	1.58	2e−16	4e−14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
9	387695	−1.69	2e−16	4e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
10	399948	1.88	2e−16	4e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
11	760	−1.57	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
12	84290	−1.68	2e−16	4e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	23580	1.55	2e−16	4e−14	47 x 45	CDC42 effector protein (Rho GTPase binding) 4 [Source:HG
14	9635	−1.81	2e−16	4e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	25999	1.83	2e−16	4e−14	50 x 4	CAP−GLY domain containing linker protein 3 [Source:HGNC
16	26047	2.62	2e−16	4e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
17	22837	−1.53	2e−16	4e−14	6 x 50	cordon−bleu WH2 repeat protein−like 1 [Source:HGNC Symb
18	169044	2.03	2e−16	4e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
19	9547	−1.89	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
20	6374	1.96	2e−16	4e−14	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;A



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.05	NULL	417	H.Tiss	WIRTH_Immune system
2	9.74	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	9.74	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	8.8	NULL	232	Chr	Chr 18
5	8.31	NULL	370	BP	mitotic cell cycle
6	8.25	NULL	15	CC	MHC class II protein complex
7	7.84	NULL	312	BP	immune response
8	7.83	NULL	949	CC	nucleoplasm
9	7.63	NULL	534	Chr	Chr 8
10	7.46	NULL	280	Chr	Chr 13
11	6.96	NULL	149	BP	DNA replication
12	6.91	NULL	4640	CC	nucleus
13	6.89	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
14	6.86	NULL	1135	Chr	Chr 19
15	6.8	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
16	6.69	NULL	5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCO
17	6.66	NULL	1749	MF	DNA binding
18	6.57	NULL	4	MMML CGS	MACIEJ_MMML 23
19	6.5	NULL	14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
20	6.44	NULL	699	Chr	Chr 5
Underexpressed					
1	−19.73	NULL	135	H.Tiss	WIRTH_Mucosa
2	−9.43	NULL	572	Disease	GUDJ_psoriasis up
3	−8.05	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−7.88	NULL	717	Chr	Chr 16
5	−7.55	NULL	21	CC	cornified envelope
6	−6.9	NULL	743	Chr	Chr 7
7	−6.82	NULL	7	MMML CGS	MACIEJ_MMML 13
8	−6.78	NULL	15	BP	negative regulation of growth
9	−6.7	NULL	190	CC	extracellular matrix
10	−6.61	NULL	10	BP	cellular response to zinc ion
11	−6.44	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	−6.35	NULL	13	BP	cellular response to cadmium ion
13	−6.08	NULL	4	MMML CGS	MACIEJ_MMML 47
14	−5.95	NULL	53	BP	keratinocyte differentiation
15	−5.94	NULL	15	GSEA C2	IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_DN
16	−5.9	NULL	13	BP	negative regulation of peptidase activity
17	−5.82	NULL	519	Chr	Chr 14
18	−5.81	NULL	19	BP	peptide cross−linking
19	−5.76	NULL	1182	CC	extracellular region
20	−5.72	NULL	957	Chr	Chr 11

GW_021

Local Summary

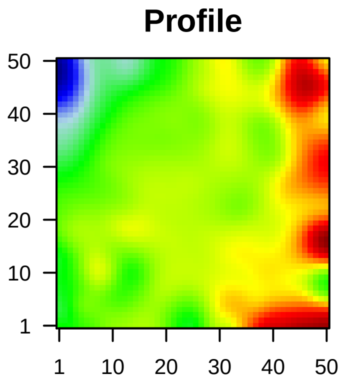
%DE = 0.66
metagenes = 25
genes = 463
genes in genesets = 438

genes with fdr < 0.1 = 218 (206 + / 12 −)
genes with fdr < 0.05 = 207 (198 + / 9 −)
genes with fdr < 0.01 = 157 (154 + / 3 −)

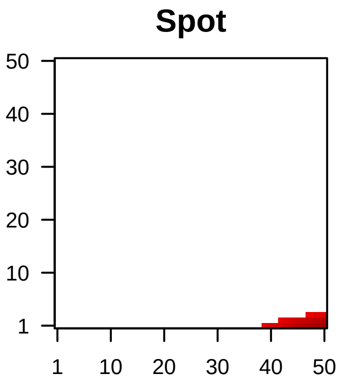
<r> metagenes = 0.88
<r> genes = 0.43

<FC> = 0.42
<shrinkage−t> = 14.9
<p−value> = 0
<fdr> = 0.51

Profile



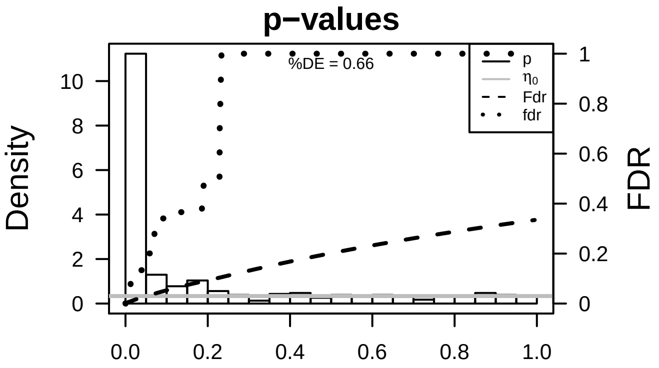
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	22809	2.1	2e−16	3e−15	44 x 1	activating transcription factor 5 [Source:HGNC Symbol;Acc:7
2	330	1.58	2e−16	3e−15	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
3	169044	2.03	2e−16	3e−15	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
4	3001	1.71	2e−16	3e−15	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
5	3120	1.77	2e−16	3e−15	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
6	3123	2.74	2e−16	3e−15	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
7	4248	1.85	2e−16	3e−15	45 x 1	mannosyl (beta−1,4−)−glycoprotein beta−1,4−N−acetylglucos
8	25849	1.97	2e−16	3e−15	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
9	57484	1.67	2e−16	3e−15	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
10	10537	2.33	2e−16	3e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
11	7412	1.9	2e−16	3e−15	50 x 1	vascular cell adhesion molecule 1 [Source:HGNC Symbol;Ac
12	2999	1.52	4e−16	1e−11	47 x 1	granzyme H (cathepsin G−like 2, protein h−CCPX) [Source:H
13	8605	1.52	4e−16	1e−11	50 x 3	phospholipase A2, group IVC (cytosolic, calcium−independen
14	3002	1.4	8e−14	1e−11	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
15	9806	1.38	1e−13	2e−11	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
16	115701	1.37	2e−13	1e−10	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
17	9466	1.33	1e−12	2e−10	45 x 1	interleukin 27 receptor, alpha [Source:HGNC Symbol;Acc:17
18	915	1.31	2e−12	3e−10	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
19	29944	1.3	4e−12	6e−10	42 x 1	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187
20	5341	1.27	1e−11	6e−10	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.53	NULL	14 / 15	CC	MHC class II protein complex
2	23.34	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
3	22.41	NULL	99 / 417	H.Tiss	WIRTH_Immune system
4	21.39	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
5	18.77	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
6	18.66	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
7	17.75	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
8	17.36	NULL	62 / 312	BP	immune response
9	17.17	NULL	16 / 47	BP	antigen processing and presentation
10	15.93	NULL	9 / 28	CC	transport vesicle membrane
11	15.35	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
12	15.14	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	15.08	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
14	14.92	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
15	14.79	NULL	9 / 32	CC	ER to Golgi transport vesicle membrane
16	14.65	NULL	20 / 60	BP	T cell costimulation
17	14.32	NULL	7 / 13	Cancer	GENTLES_modul18
18	14.07	NULL	9 / 35	CC	trans−Golgi network membrane
19	13.36	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
20	13.23	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
21	12.7	NULL	18 / 74	BP	regulation of immune response
22	12.44	NULL	6 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
23	12.05	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
24	12.05	NULL	9 / 46	CC	endocytic vesicle membrane
25	11.91	NULL	98 / 553	Cancer	Lembcke_Colonic Inflammation
26	11.67	NULL	4 / 16	BP	cytolysis
27	11.56	NULL	17 / 84	BP	T cell receptor signaling pathway
28	11.54	NULL	14 / 60	BP	interferon−gamma−mediated signaling pathway
29	11.29	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
30	11.1	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
31	11.01	NULL	16 / 87	BP	antigen processing and presentation of exogenous peptide antigen
32	10.95	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
33	10.81	NULL	4 / 12	CC	T cell receptor complex
34	10.59	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
35	10.52	NULL	3 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
36	10.32	NULL	4 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE
37	10.2	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
38	10.11	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
39	10.1	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
40	10.04	NULL	5 / 14	GSEA C2	BIOCARTA_IL12_PATHWAY

GW_021

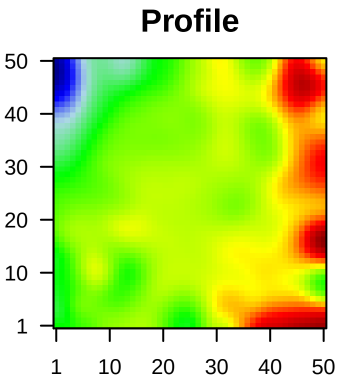
Local Summary

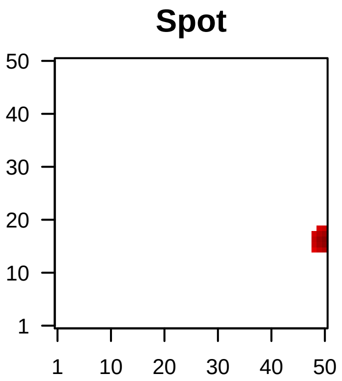
%DE = 0.79
metagenes = 14
genes = 182
genes in genesets = 181

genes with fdr < 0.1 = 121 (117 + / 4 −)
genes with fdr < 0.05 = 110 (107 + / 3 −)
genes with fdr < 0.01 = 96 (94 + / 2 −)

<r> metagenes = 0.97
<r> genes = 0.34

<FC> = 0.63
<shrinkage−t> = 22.25
<p−value> = 0
<fdr> = 0.37





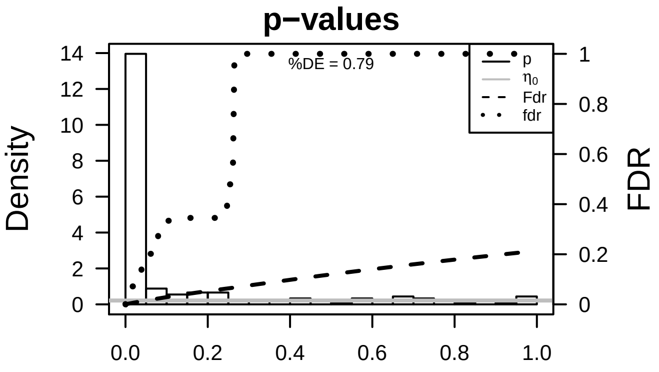
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	2.09	2e−16	7e−16	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	9915	1.67	2e−16	7e−16	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
3	399948	1.88	2e−16	7e−16	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
4	3670	1.98	2e−16	7e−16	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
5	3977	1.69	2e−16	7e−16	50 x 17	leukemia inhibitory factor receptor alpha [Source:HGNC Sym
6	728715	1.59	2e−16	7e−16	50 x 18	
7	26002	1.54	2e−16	7e−16	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
8	83988	1.78	2e−16	7e−16	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
9	9603	1.83	2e−16	7e−16	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
10	10439	2.03	2e−16	7e−16	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
11	494470	1.86	2e−16	7e−16	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
12	6263	2.22	2e−16	7e−16	50 x 18	ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
13	6542	1.86	2e−16	7e−16	50 x 16	solute carrier family 7 (cationic amino acid transporter, y+ sys
14	29091	1.43	2e−14	4e−13	50 x 17	syntaxin binding protein 6 (amisyn) [Source:HGNC Symbol;A
15	5382	1.42	3e−14	4e−13	48 x 15	postmeiotic segregation increased 2 pseudogene 4 [Source:
16	162494	1.42	3e−14	6e−13	50 x 17	rhomboid, veinlet−like 3 (Drosophila) [Source:HGNC Symbol;
17	733	1.41	5e−14	4e−12	48 x 18	complement component 8, gamma polypeptide [Source:HGN
18	153579	1.37	3e−13	4e−12	50 x 17	butyrophilin−like 9 [Source:HGNC Symbol;Acc:24176]
19	57556	1.37	3e−13	4e−11	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic
20	3792	1.32	1e−12	4e−11	50 x 17	Kell blood group, metallo−endopeptidase [Source:HGNC Sym

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	14.49	NULL	4 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.59	NULL	1 / 2	miRNA target	miR−153
3	12.13	NULL	2 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
4	11.8	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
5	11.73	NULL	1 / 6	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_UP
6	11.38	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
7	10.66	NULL	4 / 20	MF	RNA polymerase II transcription coactivator activity
8	10.35	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
9	10.22	NULL	3 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
10	10.12	NULL	2 / 15	BP	retinal ganglion cell axon guidance
11	9.03	NULL	1 / 3	miRNA target	miR−148a
12	9.01	NULL	2 / 15	BP	positive regulation vascular endothelial growth factor production
13	8.9	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_DN
14	8.73	NULL	2 / 11	MF	enhancer sequence−specific DNA binding
15	8.66	NULL	1 / 10	GSEA C2	KEGG_ALZHEIMERS_DISEASE
16	8.61	NULL	1 / 4	miRNA target	let−7c
17	8.61	NULL	1 / 4	miRNA target	miR−204
18	8.61	NULL	1 / 4	miRNA target	miR−34b
19	8.61	NULL	1 / 4	miRNA target	miR−34c
20	8.28	NULL	1 / 2	TF	MYC_Cell cycle DOWN
21	8.18	NULL	1 / 11	GSEA C2	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
22	8.18	NULL	1 / 11	GSEA C2	KEGG_CALCIUM_SIGNALING_PATHWAY
23	8.1	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
24	7.89	NULL	1 / 10	GSEA C2	BROWNE_HCMV_INFECTION_12HR_UP
25	7.89	NULL	1 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
26	7.87	NULL	1 / 8	GSEA C2	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
27	7.75	NULL	6 / 127	miRNA 3UTR	GTACT−212−−132
28	7.49	NULL	1 / 5	miRNA target	miR−15a
29	7.49	NULL	1 / 5	miRNA target	miR−320
30	7.39	NULL	1 / 8	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
31	7.26	NULL	1 / 11	BP	innervation
32	7.26	NULL	1 / 11	BP	negative regulation of intracellular estrogen receptor signaling path
33	7.22	NULL	2 / 13	Cancer	GENTLES_modul12
34	7.19	NULL	1 / 2	TF	MYC_Chromatin_modification UP
35	7.18	NULL	7 / 139	miRNA 3UTR	GTCAA−129
36	7.16	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
37	7.09	NULL	1 / 14	GSEA C2	ROSS_AML_OF_FAB_M7_TYPE
38	7.08	NULL	1 / 12	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
39	7.08	NULL	1 / 12	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_DN
40	7.08	NULL	1 / 12	GSEA C2	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION



GW_021

Local Summary

%DE = 0.79

metagenes = 26

genes = 250

genes in genesets = 249

genes with fdr < 0.1 = 149 (148 + / 1 −)

genes with fdr < 0.05 = 135 (135 + / 0 −)

genes with fdr < 0.01 = 93 (93 + / 0 −)

<r> metagenes = 0.95

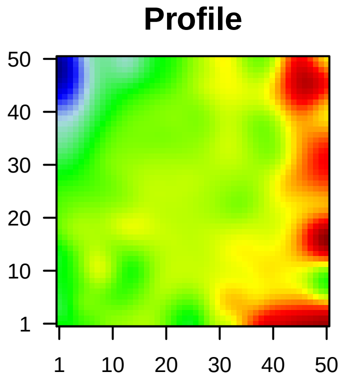
<r> genes = 0.35

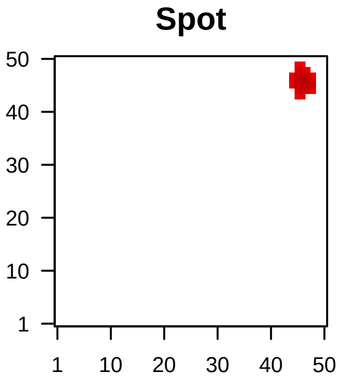
<FC> = 0.48

<shrinkage−t> = 16.89

<p−value> = 0

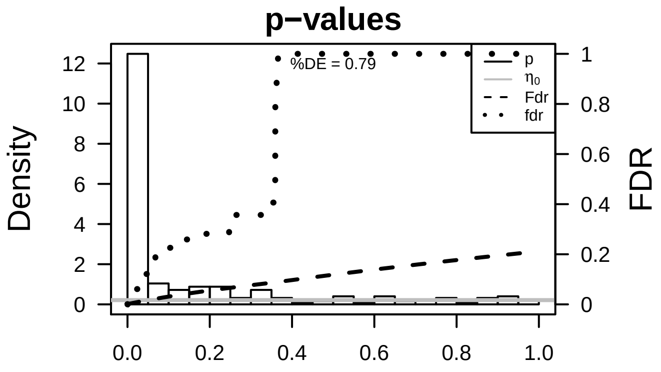
<fdr> = 0.47





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23580	1.55	2e−16	6e−15	47 x 45	CDC42 effector protein (Rho GTPase binding) 4 [Source:HGN
2	84223	1.66	2e−16	6e−15	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
3	10388	1.36	3e−13	2e−10	47 x 46	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
4	3787	1.29	6e−12	2e−10	46 x 45	potassium voltage−gated channel, delayed−rectifier, subfamil
5	55872	1.27	1e−11	2e−10	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
6	285498	1.26	2e−11	2e−10	46 x 44	ring finger protein 212 [Source:HGNC Symbol;Acc:27729]
7	128178	1.26	2e−11	1e−09	47 x 45	EDAR−associated death domain [Source:HGNC Symbol;Acc:
8	3706	1.22	6e−11	1e−09	48 x 47	inositol−trisphosphate 3−kinase A [Source:HGNC Symbol;Ac
9	79682	1.22	6e−11	1e−09	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
10	256714	1.21	9e−11	1e−09	48 x 46	MAP7 domain containing 2 [Source:HGNC Symbol;Acc:2589
11	84215	1.21	1e−10	1e−09	46 x 45	zinc finger protein 541 [Source:HGNC Symbol;Acc:25294]
12	899	1.2	1e−10	1e−08	45 x 46	cyclin F [Source:HGNC Symbol;Acc:1591]
13	4843	1.16	5e−10	1e−08	47 x 44	nitric oxide synthase 2, inducible [Source:HGNC Symbol;Acc:
14	8364	1.07	5e−10	9e−08	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
15	84303	1.11	3e−09	9e−08	47 x 45	coiled−coil−helix−coiled−coil−helix domain containing 6 [Sour
16	7913	1.1	4e−09	2e−07	45 x 49	DEK oncogene [Source:HGNC Symbol;Acc:2768]
17	3148	1.08	7e−09	4e−07	46 x 46	high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
18	5050	1.05	2e−08	4e−07	47 x 45	platelet−activating factor acetylhydrolase 1b, catalytic subunit
19	64105	1.05	2e−08	3e−06	45 x 48	centromere protein K [Source:HGNC Symbol;Acc:29479]
20	54492	1	9e−08	3e−06	47 x 44	neuralized E3 ubiquitin protein ligase 1B [Source:HGNC Sym



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	21.73	NULL	41 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	21.73	NULL	41 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	21.18	NULL	8 / 11	GSEA C2	KALMA_E2F1_TARGETS
4	19.23	NULL	10 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	17.31	NULL	35 / 149	BP	DNA replication
6	16.15	NULL	5 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
7	15.94	NULL	12 / 30	BP	DNA strand elongation involved in DNA replication
8	15.7	NULL	54 / 370	BP	mitotic cell cycle
9	13.57	NULL	6 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
10	13.55	NULL	12 / 57	Glio	developing astrocytes
11	13.09	NULL	57 / 530	Cancer	Lembcke_Normal vs Adenoma
12	13	NULL	7 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
13	12.9	NULL	7 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
14	12.5	NULL	7 / 16	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
15	12.32	NULL	4 / 16	GSEA C2	LY_AGING_PREMATURE_DN
16	12.18	NULL	4 / 20	CC	synaptonemal complex
17	11.77	NULL	6 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
18	11.6	NULL	5 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
19	11.46	NULL	8 / 15	GSEA C2	CHANG_CYCLING_GENES
20	11.42	NULL	5 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
21	11.42	NULL	5 / 14	MMML CGS	MACIEJ_MMML 4
22	11.34	NULL	35 / 298	BP	DNA repair
23	11.03	NULL	6 / 16	GSEA C2	KEGG_BASE_EXCISION_REPAIR
24	10.96	NULL	27 / 232	BP	mitosis
25	10.86	NULL	9 / 22	BP	DNA replication initiation
26	10.6	NULL	4 / 16	Cancer	WOLFER_overlap genes
27	10.52	NULL	8 / 15	GSEA C2	KEGG_DNA_REPLICATION
28	10.48	NULL	7 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
29	10.37	NULL	6 / 15	GSEA C2	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN
30	10.32	NULL	4 / 13	Pathw Act	GUSTAFSON_PI3K_UP
31	10.31	NULL	1 / 5	MMML CGS	MACIEJ_MMML 20
32	10.09	NULL	62 / 949	CC	nucleoplasm
33	10.01	NULL	2 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
34	10.01	NULL	2 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
35	9.75	NULL	5 / 15	GSEA C2	REACTOME_FANCONI_ANEMIA_PATHWAY
36	9.68	NULL	7 / 21	BP	telomere maintenance via semi−conservative replication
37	9.67	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
38	9.63	NULL	3 / 10	CC	lateral element
39	9.46	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
40	9.4	NULL	3 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN

GW_021

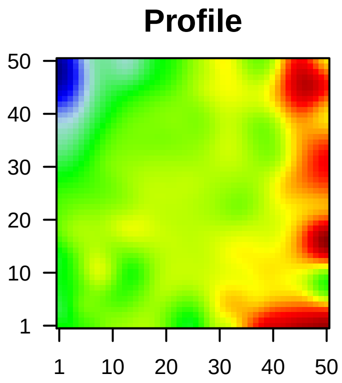
Local Summary

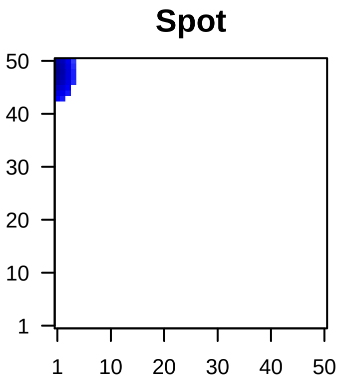
%DE = 0.88
metagenes = 28
genes = 362
genes in genesets = 353

genes with fdr < 0.1 = 287 (17 + / 270 −)
genes with fdr < 0.05 = 280 (16 + / 264 −)
genes with fdr < 0.01 = 248 (12 + / 236 −)

<r> metagenes = 0.9
<r> genes = 0.37

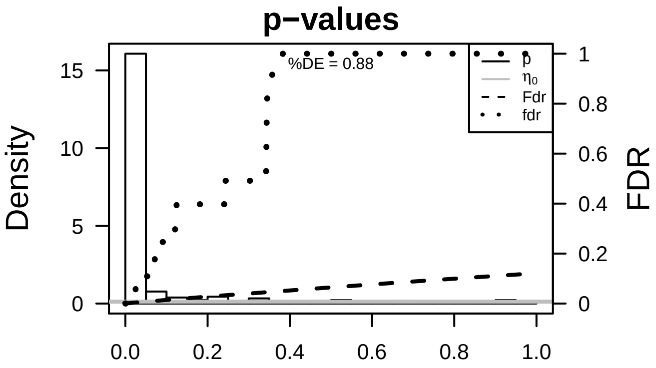
<FC> = −0.67
<shrinkage−t> = −23.44
<p−value> = 0
<fdr> = 0.25


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−1.88	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	8644	−2.27	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	387695	−1.69	2e−16	4e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
4	760	−1.57	2e−16	4e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	84290	−1.68	2e−16	4e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
6	9635	−1.81	2e−16	4e−16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
7	9547	−1.89	2e−16	4e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
8	92196	1.7	2e−16	4e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
9	1828	−1.58	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
10	1830	−1.64	2e−16	4e−16	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
11	2171	−1.68	2e−16	4e−16	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
12	9982	−1.65	2e−16	4e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
13	10804	−1.93	2e−16	4e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
14	3489	−1.68	2e−16	4e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
15	53833	−2.01	2e−16	4e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
16	3851	−2.09	2e−16	4e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
17	286887	−1.55	2e−16	4e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
18	388533	−1.61	2e−16	4e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
19	3963	−1.96	2e−16	4e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
20	653499	−1.99	2e−16	4e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−52.56	NULL	99 / 135	H.Tiss	WIRTH_Mucosa
2	−25.64	NULL	124 / 572	Disease	GUDJ_psoriasis up
3	−21.31	NULL	19 / 21	CC	cornified envelope
4	−19.67	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	−18.1	NULL	26 / 53	BP	keratinocyte differentiation
6	−16.59	NULL	9 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
7	−15.74	NULL	6 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
8	−14.45	NULL	31 / 76	BP	epidermis development
9	−13.86	NULL	12 / 21	CC	desmosome
10	−13.54	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
11	−13.15	NULL	12 / 19	BP	peptide cross−linking
12	−12.39	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
13	−12.08	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
14	−12.06	NULL	8 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
15	−12	NULL	20 / 42	BP	keratinization
16	−11.97	NULL	13 / 44	CC	keratin filament
17	−11.69	NULL	8 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	−11.55	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
19	−11.46	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
20	−11.18	NULL	6 / 13	BP	negative regulation of peptidase activity
21	−11.03	NULL	8 / 16	GSEA C2	JAEGER_METASTASIS_DN
22	−10.78	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
23	−10.35	NULL	21 / 82	CC	intermediate filament
24	−10.33	NULL	10 / 38	BP	epithelial cell differentiation
25	−10.06	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
26	−10.01	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
27	−9.82	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
28	−9.75	NULL	32 / 186	MF	structural molecule activity
29	−9.36	NULL	4 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
30	−8.79	NULL	3 / 15	CC	connexon complex
31	−8.65	NULL	5 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
32	−8.64	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
33	−8.54	NULL	2 / 13	BP	cellular response to cadmium ion
34	−8.23	NULL	75 / 1182	CC	extracellular region
35	−8.19	NULL	5 / 39	BP	retinoid metabolic process
36	−8.16	NULL	4 / 15	MF	retinol dehydrogenase activity
37	−8.13	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
38	−8.1	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
39	−7.81	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
40	−7.8	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS