GW_030

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1726 (947 + / 779 −)

genes with fdr < 0.1 = 1273 (738 + / 535 −)

genes with fdr < 0.05 = 1002 (595 + / 407 −)

genes with fdr < 0.01 = 681 (428 + / 253 −)

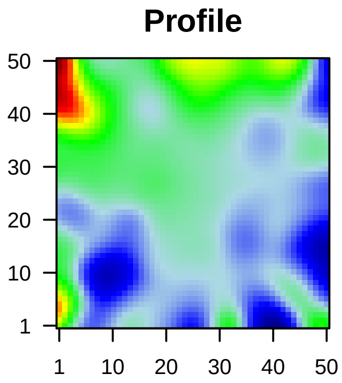
genes in genesets = 16332

<FC> = 0

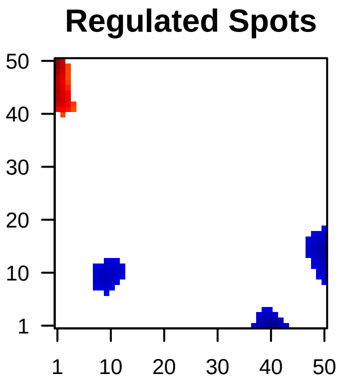
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.86



Profile



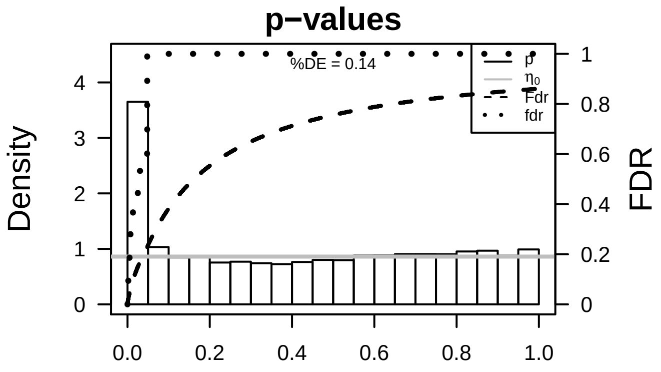
Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	80115	1.16	2e−16	4e−14	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
2	84707	−1.09	2e−16	4e−14	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
3	79783	1.38	2e−16	4e−14	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
4	760	1.44	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	51806	−1.56	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
6	857	1.27	2e−16	4e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
7	84518	1.34	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	49860	2.22	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	3627	1.66	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
10	6373	2.55	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
11	4283	1.28	2e−16	4e−14	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
12	55894	1.19	2e−16	4e−14	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	414325	1.58	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1673	2.51	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
15	1687	1.24	2e−16	4e−14	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
16	27122	1.14	2e−16	4e−14	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
17	1776	1.5	2e−16	4e−14	48 x 12	deoxyribonuclease I−like 3 [Source:HGNC Symbol;Acc:2959]
18	1848	1.1	2e−16	4e−14	1 x 4	dual specificity phosphatase 6 [Source:HGNC Symbol;Acc:3
19	4072	−1.23	2e−16	4e−14	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc
20	2201	1.85	2e−16	4e−14	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	25.98	NULL	572	Disease	GUDJ_psoriasis up
2	20.3	NULL	135	H.Tiss	WIRTH_Mucosa
3	11.89	NULL	21	CC	cornified envelope
4	11.33	NULL	76	BP	epidermis development
5	10.56	NULL	53	BP	keratinocyte differentiation
6	9.96	NULL	42	BP	keratinization
7	9.88	NULL	534	Chr	Chr 8
8	9.77	NULL	553	Cancer	Lembcke_Colonic Inflammation
9	8.42	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
10	8.25	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
11	7.94	NULL	12	BP	hemidesmosome assembly
12	7.89	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	7.83	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	7.78	NULL	14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
15	7.61	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
16	7.52	NULL	312	BP	immune response
17	7.29	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
18	7.08	NULL	10	BP	positive regulation of cAMP−mediated signaling
19	7.02	NULL	19	BP	peptide cross−linking
20	6.8	NULL	530	Cancer	Lembcke_Normal vs Adenoma
Underexpressed					
1	−9.67	NULL	918	Chr	Chr 17
2	−6.84	NULL	1033	Chr	Chr 2
3	−5.68	NULL	375	Disease	GUDJ_psoriasis down
4	−5.62	NULL	127	H.Tiss	WIRTH_Muscle
5	−5.53	NULL	11	MF	glutathione binding
6	−5.15	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
7	−5.13	NULL	717	Chr	Chr 16
8	−5.11	NULL	1581	BP	regulation of transcription, DNA−dependent
9	−4.87	NULL	1135	Chr	Chr 19
10	−4.84	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
11	−4.58	NULL	3	MMML CGS	MACIEJ_MMML 7
12	−4.56	NULL	16	H.Tiss	WIRTH_Hippocampus
13	−4.53	NULL	1749	MF	DNA binding
14	−4.21	NULL	630	Chr	Chr X
15	−4.19	NULL	36	BP	muscle filament sliding
16	−4.15	NULL	12	CC	myosin filament
17	−4.12	NULL	44	MF	structural constituent of muscle
18	−4.1	NULL	34	BP	glutathione metabolic process
19	−4.08	NULL	15	GSEA C2	WONG_ENDMETRIUM_CANCER_DN
20	−4.05	NULL	1820	MF	metal ion binding



p−values

GW_030

Local Summary

%DE = 0.84

metagenes = 32

genes = 388

genes in genesets = 380

genes with fdr < 0.1 = 259 (241 + / 18 −)

genes with fdr < 0.05 = 229 (214 + / 15 −)

genes with fdr < 0.01 = 217 (204 + / 13 −)

<r> metagenes = 0.85

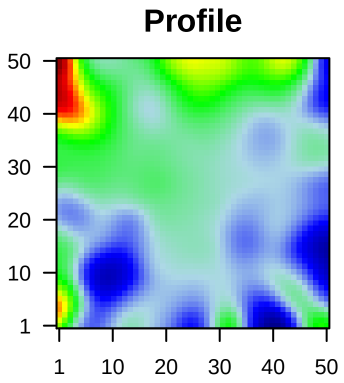
<r> genes = 0.34

<FC> = 0.45

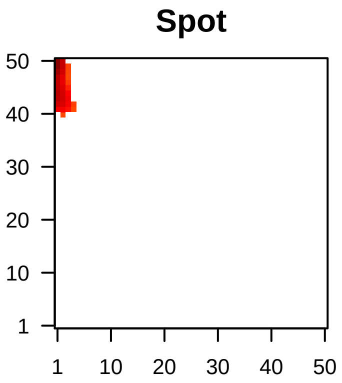
<shrinkage−t> = 16.05

<p−value> = 0

<fdr> = 0.37



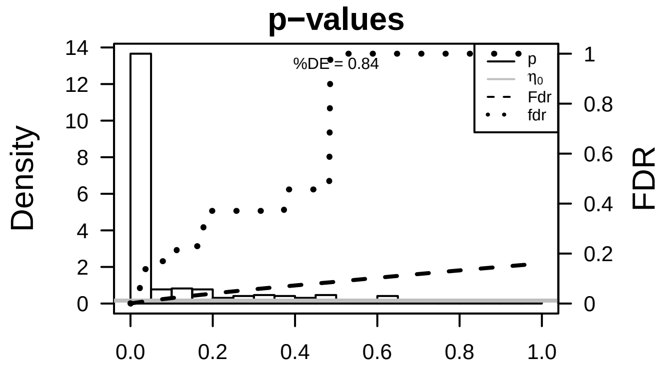
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	80115	1.16	2e−16	3e−16	1 x 43	BAI1−associated protein 2−like 2 [Source:HGNC Symbol;Acc
2	760	1.44	2e−16	3e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	84518	1.34	2e−16	3e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
4	49860	2.22	2e−16	3e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
5	55894	1.19	2e−16	3e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
6	414325	1.58	2e−16	3e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
7	1673	2.51	2e−16	3e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	9982	1.24	2e−16	3e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Syml
9	2706	1.23	2e−16	3e−16	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
10	10804	1.29	2e−16	3e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
11	1839	1.23	2e−16	3e−16	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Symb
12	3489	1.18	2e−16	3e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
13	3552	1.17	2e−16	3e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
14	50805	−1.12	2e−16	3e−16	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
15	26085	1.19	2e−16	3e−16	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
16	5653	1.62	2e−16	3e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
17	3861	1.26	2e−16	3e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
18	3868	1.33	2e−16	3e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
19	192666	2.02	2e−16	3e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
20	3851	2.4	2e−16	3e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	44.96	NULL	86 / 135	H.Tiss	WIRTH_Mucosa
2	30.99	NULL	128 / 572	Disease	GUDJ_psoriasis up
3	27.2	NULL	18 / 21	CC	cornified envelope
4	26.37	NULL	29 / 76	BP	epidermis development
5	26.1	NULL	20 / 42	BP	keratinization
6	21.51	NULL	25 / 53	BP	keratinocyte differentiation
7	18.44	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	14.56	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
9	14.04	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	14.03	NULL	10 / 19	BP	peptide cross−linking
11	13.78	NULL	11 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	13.63	NULL	25 / 82	CC	intermediate filament
13	13.04	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	11.97	NULL	13 / 44	CC	keratin filament
15	11.89	NULL	5 / 10	MF	RAGE receptor binding
16	10.93	NULL	7 / 29	BP	regulation of proteolysis
17	10.91	NULL	7 / 38	BP	epithelial cell differentiation
18	10.8	NULL	5 / 13	BP	negative regulation of peptidase activity
19	10.45	NULL	32 / 186	MF	structural molecule activity
20	10.12	NULL	10 / 52	BP	negative regulation of endopeptidase activity
21	9.95	NULL	5 / 25	BP	response to zinc ion
22	9.76	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
23	9.73	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
24	9.69	NULL	5 / 12	BP	hemidesmosome assembly
25	9.64	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
26	9.26	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
27	8.98	NULL	15 / 79	MF	serine−type endopeptidase inhibitor activity
28	8.91	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
29	8.91	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
30	8.89	NULL	2 / 2	miRNA target	miR−199a*
31	8.82	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
32	8.78	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
33	8.58	NULL	73 / 1182	CC	extracellular region
34	8.44	NULL	4 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
35	7.97	NULL	1 / 6	Glio	Martinez_Glio_hypometh
36	7.95	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
37	7.82	NULL	6 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
38	7.78	NULL	3 / 17	BP	morphogenesis of an epithelium
39	7.75	NULL	3 / 15	CC	connexon complex
40	7.71	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING

GW_030

Local Summary

%DE = 0.78

metagenes = 18

genes = 281

genes in genesets = 255

genes with fdr < 0.1 = 135 (1 + / 134 −)

genes with fdr < 0.05 = 108 (1 + / 107 −)

genes with fdr < 0.01 = 69 (1 + / 68 −)

<r> metagenes = 0.97

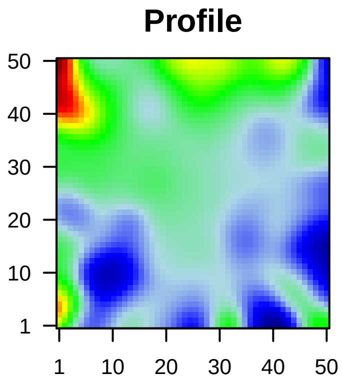
<r> genes = 0.45

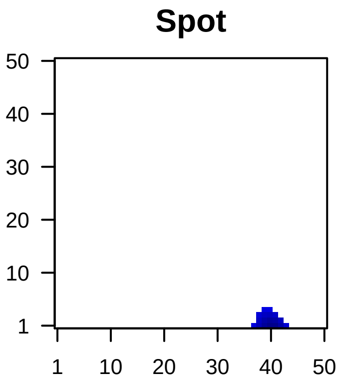
<FC> = −0.27

<shrinkage−t> = −9.44

<p−value> = 0.02

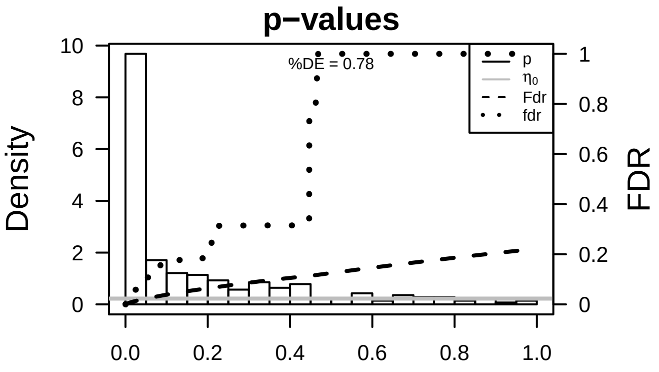
<fdr> = 0.62





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	−0.88	4e−11	1e−07	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	22834	−0.78	5e−09	1e−07	40 x 1	zinc finger protein 652 [Source:HGNC Symbol;Acc:29147]
3	8722	−0.78	5e−09	5e−07	42 x 1	cathepsin F [Source:HGNC Symbol;Acc:2531]
4	400818	−0.75	2e−08	5e−07	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
5	56834	−0.75	2e−08	3e−06	43 x 1	G protein−coupled receptor 137 [Source:HGNC Symbol;Acc:
6	23646	−0.72	7e−08	4e−06	42 x 1	phospholipase D family, member 3 [Source:HGNC Symbol;A
7	79058	−0.7	1e−07	6e−06	41 x 1	alveolar soft part sarcoma chromosome region, candidate 1 [
8	729603	−0.62	3e−07	6e−06	40 x 1	
9	51281	−0.68	4e−07	6e−06	42 x 1	ankyrin repeat and MYND domain containing 1 [Source:HGN
10	79090	−0.67	4e−07	6e−05	43 x 1	trafficking protein particle complex 6A [Source:HGNC Symbol
11	23466	−0.64	1e−06	1e−04	41 x 1	chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
12	80162	−0.62	3e−06	1e−04	43 x 1	ATH1, acid trehalase−like 1 (yeast) [Source:HGNC Symbol;A
13	755	−0.6	6e−06	1e−04	43 x 1	chromosome 21 open reading frame 2 [Source:HGNC Symbo
14	32	−0.6	6e−06	1e−04	43 x 1	acetyl−CoA carboxylase beta [Source:HGNC Symbol;Acc:85]
15	29797	−0.59	9e−06	1e−04	40 x 1	
16	250	−0.59	1e−05	1e−04	40 x 1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:
17	126205	−0.59	1e−05	3e−04	40 x 1	NLR family, pyrin domain containing 8 [Source:HGNC Symbo
18	23637	−0.57	2e−05	3e−04	38 x 1	RAB GTPase activating protein 1 [Source:HGNC Symbol;Acc
19	152485	−0.57	2e−05	3e−04	41 x 1	zinc finger protein 827 [Source:HGNC Symbol;Acc:27193]
20	27148	−0.56	2e−05	3e−04	41 x 1	serine/threonine kinase 36 [Source:HGNC Symbol;Acc:1720



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.16	NULL	2 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
2	−9.58	NULL	2 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
3	−9.02	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
4	−8.05	NULL	3 / 14	MMML CGS	MACIEJ_MMML 8
5	−7.98	NULL	3 / 13	GSEA C2	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
6	−7.77	NULL	2 / 13	GSEA C2	ST_GAQ_PATHWAY
7	−7.77	NULL	2 / 13	GSEA C2	ST_GA13_PATHWAY
8	−6.91	NULL	2 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_CLASSES_DN
9	−6.79	NULL	1 / 8	GSEA C2	CHANG_CORE_SERUM_RESPONSE_DN
10	−6.72	NULL	3 / 13	GSEA C2	SPIRA_SMOKERS_LUNG_CANCER_DN
11	−6.07	NULL	1 / 4	MMML CGS	MACIEJ_MMML 44
12	−5.77	NULL	2 / 15	GSEA C2	CAIRO_HEPATOBLASTOMA_UP
13	−5.55	NULL	2 / 18	MF	adenyl nucleotide binding
14	−5.4	NULL	1 / 11	GSEA C2	GALE_APL_WITH_FLT3_MUTATED_DN
15	−5.37	NULL	1 / 12	GSEA C2	KEGG_LYSOSOME
16	−5.35	NULL	1 / 15	CC	MHC class II protein complex
17	−5.34	NULL	1 / 10	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_12
18	−5.19	NULL	1 / 8	GSEA C2	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN
19	−5.14	NULL	3 / 44	BP	regulation of Rab GTPase activity
20	−5.12	NULL	1 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP
21	−5.06	NULL	1 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
22	−5.06	NULL	2 / 14	BP	mitochondrion morphogenesis
23	−4.99	NULL	3 / 46	MF	Rab GTPase activator activity
24	−4.9	NULL	3 / 39	miRNA target−starBase	hsa−miR−1258
25	−4.89	NULL	1 / 14	GSEA C2	WANG_RECURRENT_LIVER_CANCER_UP
26	−4.89	NULL	1 / 14	GSEA C2	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
27	−4.89	NULL	1 / 14	GSEA C2	KAAB_HEART_ATRIUM_VS_VENTRICLE_UP
28	−4.7	NULL	1 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC
29	−4.69	NULL	1 / 10	MF	hydrolase activity, acting on glycosyl bonds
30	−4.57	NULL	1 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
31	−4.56	NULL	2 / 28	CC	transport vesicle membrane
32	−4.54	NULL	1 / 10	BP	biotin metabolic process
33	−4.54	NULL	1 / 10	BP	positive regulation of cellular metabolic process
34	−4.48	NULL	1 / 7	GSEA C2	LIU_CMYB_TARGETS_DN
35	−4.47	NULL	1 / 14	GSEA C2	ROSS_AML_WITH_MLL_FUSIONS
36	−4.46	NULL	2 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
37	−4.38	NULL	4 / 69	miRNA target−starBase	hsa−miR−578
38	−4.36	NULL	1 / 21	CC	clathrin−coated endocytic vesicle membrane
39	−4.3	NULL	2 / 12	GSEA C2	BARRIER_COLON_CANCER_RECURRENCE_DN
40	−4.29	NULL	1 / 15	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP

GW_030

Local Summary

%DE = 0.65

metagenes = 31

genes = 249

genes in genesets = 245

genes with fdr < 0.1 = 115 (2 + / 113 −)

genes with fdr < 0.05 = 81 (1 + / 80 −)

genes with fdr < 0.01 = 44 (1 + / 43 −)

<r> metagenes = 0.89

<r> genes = 0.26

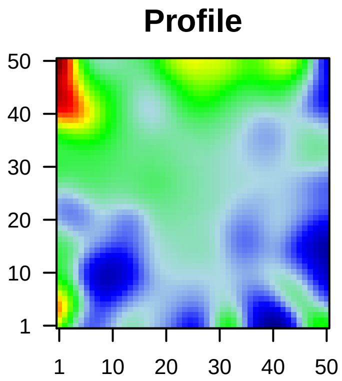
<FC> = −0.25

<shrinkage−t> = −8.59

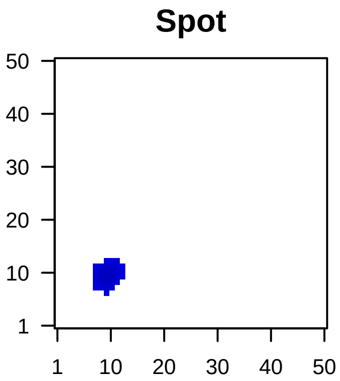
<p−value> = 0.02

<fdr> = 0.62

Profile



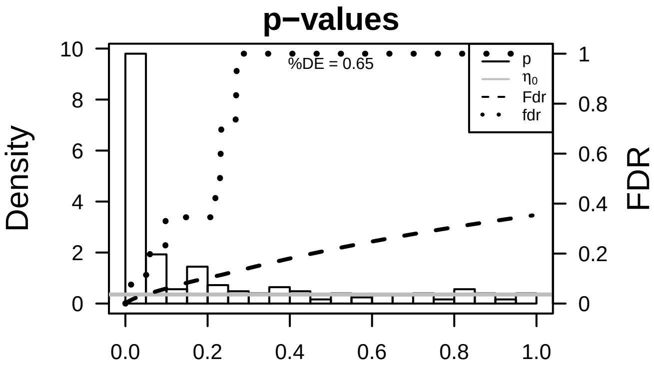
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4037	−0.84	4e−10	5e−07	10 x 7	low density lipoprotein receptor−related protein 3 [Source:HG
2	404217	0.77	6e−09	6e−07	10 x 9	cortexin 1 [Source:HGNC Symbol;Acc:31108]
3	84939	−0.76	1e−08	1e−05	10 x 11	melanoma associated antigen (mutated) 1 [Source:HGNC Sy
4	55506	−0.67	5e−07	1e−05	12 x 9	H2A histone family, member Y2 [Source:HGNC Symbol;Acc:1
5	3303	−0.66	5e−07	1e−05	11 x 12	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
6	55258	−0.67	5e−07	1e−05	11 x 9	threonine synthase−like 2 (S. cerevisiae) [Source:HGNC Sym
7	64847	−0.66	6e−07	2e−05	10 x 9	spermatogenesis associated 20 [Source:HGNC Symbol;Acc:
8	4832	−0.66	9e−07	8e−05	9 x 11	NME/NM23 nucleoside diphosphate kinase 3 [Source:HGNC
9	100128927	−0.64	2e−06	8e−05	11 x 11	zinc finger and BTB domain containing 42 [Source:HGNC Sy
10	537	−0.63	3e−06	8e−05	8 x 9	ATPase, H+ transporting, lysosomal accessory protein 1 [Sou
11	64132	−0.62	4e−06	8e−05	10 x 9	xylosyltransferase II [Source:HGNC Symbol;Acc:15517]
12	9130	−0.61	4e−06	1e−04	8 x 9	family with sequence similarity 50, member A [Source:HGNC
13	64710	−0.61	5e−06	1e−04	9 x 11	nuclear casein kinase and cyclin−dependent kinase substrate
14	26470	−0.6	7e−06	3e−04	10 x 9	seizure related 6 homolog (mouse)−like 2 [Source:HGNC Syr
15	55653	−0.57	2e−05	3e−04	9 x 10	breast carcinoma amplified sequence 4 [Source:HGNC Symb
16	57799	−0.57	2e−05	3e−04	11 x 13	RAB40C, member RAS oncogene family [Source:HGNC Sym
17	256281	−0.57	2e−05	3e−04	11 x 9	nudix (nucleoside diphosphate linked moiety X)−type motif 14
18	79894	−0.56	2e−05	3e−04	9 x 12	zinc finger protein 672 [Source:HGNC Symbol;Acc:26179]
19	11267	−0.56	3e−05	7e−04	9 x 10	SNF8, ESCRT−II complex subunit [Source:HGNC Symbol;Ac
20	25844	−0.55	3e−05	1e−03	9 x 8	Yip1 domain family, member 3 [Source:HGNC Symbol;Acc:21

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.19	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
2	−8.08	NULL	3 / 21	BP	chromatin organization
3	−7.95	NULL	2 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
4	−7.9	NULL	2 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
5	−7.89	NULL	2 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
6	−7.06	NULL	2 / 11	BP	cerebellar Purkinje cell layer development
7	−6.97	NULL	2 / 12	GSEA C2	KIM_WT1_TARGETS_12HR_UP
8	−6.96	NULL	2 / 11	BP	bone remodeling
9	−6.78	NULL	2 / 15	GSEA C2	OLSSON_E2F3_TARGETS_DN
10	−6.54	NULL	2 / 5	GSEA C2	NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
11	−6.53	NULL	7 / 45	Glio	willscher_GBM_Verhaak−PNwt_expression_J_up
12	−6.16	NULL	2 / 13	GSEA C2	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATIO
13	−6.05	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
14	−5.9	NULL	2 / 14	GSEA C2	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BI
15	−5.9	NULL	2 / 14	GSEA C2	REACTOME_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS
16	−5.88	NULL	2 / 13	GSEA C2	WALLACE_JAK2_TARGETS_UP
17	−5.85	NULL	2 / 9	miRNA 3UTR	TCCG−184
18	−5.83	NULL	2 / 14	GSEA C2	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
19	−5.67	NULL	2 / 10	MF	K63−linked polyubiquitin binding
20	−5.67	NULL	2 / 15	GSEA C2	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOS
21	−5.65	NULL	2 / 13	CC	STAGA complex
22	−5.63	NULL	2 / 15	GSEA C2	KEGG_MTOR_SIGNALING_PATHWAY
23	−5.61	NULL	2 / 15	GSEA C2	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_U
24	−5.56	NULL	2 / 14	GSEA C2	RIZKI_TUMOR_INVASIVENESS_2D_DN
25	−5.49	NULL	2 / 15	MF	acetylglucosaminyltransferase activity
26	−5.46	NULL	2 / 16	BP	preassembly of GPI anchor in ER membrane
27	−5.45	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
28	−5.45	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
29	−5.45	NULL	2 / 10	GSEA C2	BORCZUK_MALIGNANT_MESOTHELIOMA_DN
30	−5.43	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
31	−5.37	NULL	3 / 24	miRNA target−starBase	hsa−miR−892
32	−5.28	NULL	4 / 26	BP	histone acetylation
33	−5.26	NULL	1 / 10	BP	GTP biosynthetic process
34	−5.09	NULL	1 / 5	GSEA C2	NAGY_PCAF_COMPONENTS_HUMAN
35	−4.99	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
36	−4.98	NULL	1 / 11	BP	CTP biosynthetic process
37	−4.98	NULL	1 / 11	BP	UTP biosynthetic process
38	−4.89	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
39	−4.86	NULL	1 / 12	Glio	willscher_GBM_LTSmut_proteomics−B_UP
40	−4.86	NULL	1 / 12	Glio	willscher_GBM_STSwt_proteomics−B_DOWN

GW_030

Local Summary

%DE = 0.71

metagenes = 31

genes = 387

genes in genesets = 383

genes with fdr < 0.1 = 168 (9 + / 159 −)

genes with fdr < 0.05 = 132 (7 + / 125 −)

genes with fdr < 0.01 = 82 (4 + / 78 −)

<r> metagenes = 0.88

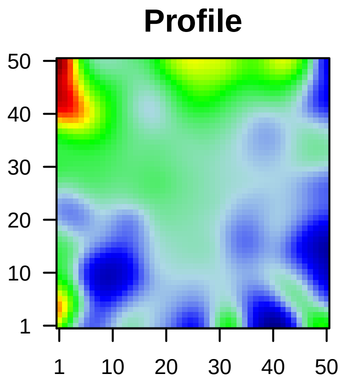
<r> genes = 0.23

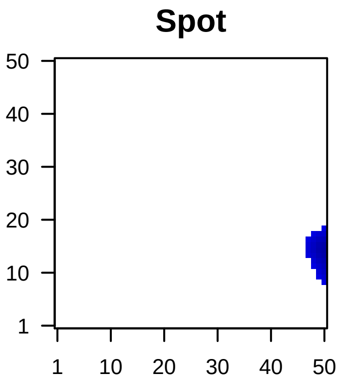
<FC> = −0.24

<shrinkage−t> = −8.31

<p−value> = 0.01

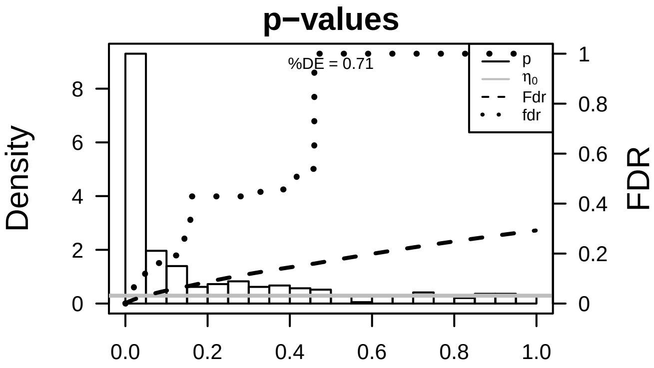
<fdr> = 0.63





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1776	1.5	2e−16	3e−14	48 x 12	deoxyribonuclease I−like 3 [Source:HGNC Symbol;Acc:2959]
2	10439	−1.06	1e−15	8e−13	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
3	10232	−1.03	9e−15	2e−12	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
4	6542	−1.02	2e−14	3e−11	50 x 16	solute carrier family 7 (cationic amino acid transporter, y+ sys
5	83988	−0.96	6e−13	3e−11	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
6	7033	−0.96	6e−13	4e−10	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
7	8842	−0.92	4e−12	2e−09	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
8	92747	−0.89	2e−11	2e−08	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
9	2568	−0.85	2e−10	3e−08	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
10	92304	−0.82	6e−10	3e−08	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
11	634	0.82	6e−10	7e−08	50 x 12	carcinoembryonic antigen−related cell adhesion molecule 1 (
12	10551	−0.81	1e−09	2e−07	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
13	7018	−0.79	3e−09	2e−07	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
14	56997	−0.77	7e−09	2e−07	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
15	155066	−0.77	8e−09	2e−07	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
16	260293	−0.77	9e−09	2e−06	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
17	7100	−0.74	3e−08	3e−06	50 x 14	toll−like receptor 5 [Source:HGNC Symbol;Acc:11851]
18	29116	−0.72	6e−08	4e−06	50 x 14	myosin regulatory light chain interacting protein [Source:HGN
19	124220	−0.7	2e−07	4e−06	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
20	10983	−0.64	2e−07	4e−06	50 x 17	cyclin I [Source:HGNC Symbol;Acc:1595]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−23.27	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
2	−14.05	NULL	5 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
3	−13.2	NULL	4 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
4	−12.04	NULL	6 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
5	−11.1	NULL	3 / 16	GSEA C2 DOANE_BREAST_CANCER_ESR1_DN
6	−9	NULL	5 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
7	−8.98	NULL	2 / 11	CC photoreceptor outer segment membrane
8	−8.63	NULL	2 / 5	GSEA C2 SMID_BREAST_CANCER_ERBB2_DN
9	−8.52	NULL	4 / 9	GSEA C2 REACTOME_ETHANOL_OXIDATION
10	−8.49	NULL	4 / 13	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN
11	−8.41	NULL	3 / 7	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_DN
12	−8.3	NULL	3 / 15	GSEA C2 MASSARWEH_RESPONSE_TO_ESTRADIOL
13	−8.2	NULL	5 / 16	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
14	−8.12	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
15	−7.99	NULL	2 / 16	GSEA C2 ROY_WOUND_BLOOD_VESSEL_DN
16	−7.89	NULL	3 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
17	−7.86	NULL	2 / 14	GSEA C2 WANG_BARRETTS_ESOPHAGUS_UP
18	−7.8	NULL	4 / 12	GSEA C2 PROVENZANI_METASTASIS_UP
19	−7.24	NULL	3 / 15	GSEA C2 SABATES_COLORECTAL_ADENOMA_UP
20	−7.18	NULL	3 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
21	−7.14	NULL	2 / 14	GSEA C2 NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
22	−6.92	NULL	4 / 15	GSEA C2 DOANE_BREAST_CANCER_CLASSES_UP
23	−6.9	NULL	4 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
24	−6.72	NULL	2 / 10	GSEA C2 LUI_THYROID_CANCER_CLUSTER_5
25	−6.59	NULL	3 / 14	GSEA C2 VANTVEER_BREAST_CANCER_METASTASIS_UP
26	−6.46	NULL	1 / 7	GSEA C2 GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
27	−6.3	NULL	2 / 12	BP nitric oxide biosynthetic process
28	−6.28	NULL	33 / 375	Disease GUDJ_psoriasis down
29	−6.22	NULL	1 / 8	GSEA C2 REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
30	−6.21	NULL	1 / 5	GSEA C2 ZIRN_TRETINOIN_RESPONSE_WT1_DN
31	−6.2	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_DN
32	−6.12	NULL	3 / 12	BP urogenital system development
33	−6.1	NULL	1 / 10	GSEA C2 BROWNE_HCMV_INFECTION_12HR_UP
34	−6.1	NULL	1 / 10	GSEA C2 XU_GH1_AUTOCRINE_TARGETS_DN
35	−6.08	NULL	2 / 7	GSEA C2 LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
36	−6.03	NULL	3 / 4	miRNA target miR−204
37	−5.97	NULL	2 / 16	GSEA C2 VALK_AML_CLUSTER_9
38	−5.95	NULL	3 / 15	GSEA C2 FAELT_B_CLL_WITH_VH3_21_DN
39	−5.87	NULL	2 / 12	GSEA C2 BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
40	−5.81	NULL	3 / 11	BP DNA integration