GW_153

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1561 (989 + / 572 −)

genes with fdr < 0.1 = 1313 (870 + / 443 −)

genes with fdr < 0.05 = 1096 (776 + / 320 −)

genes with fdr < 0.01 = 828 (614 + / 214 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

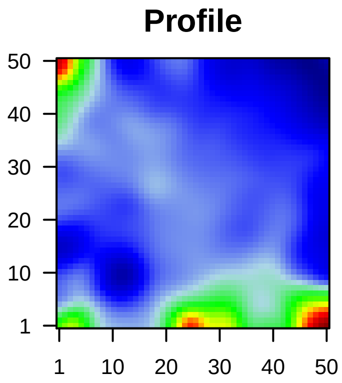
<fdr> = 0.87

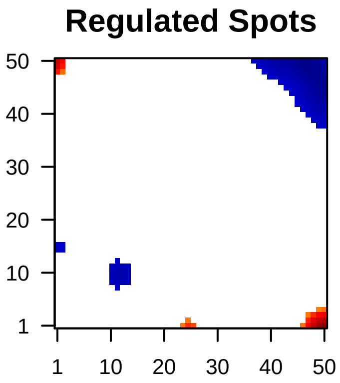
Global Genelist

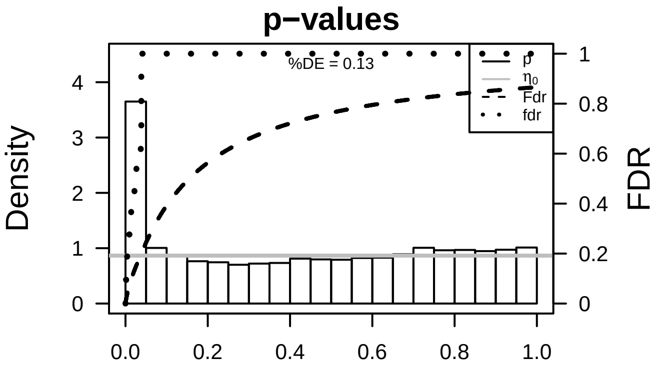
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.98	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.74	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	242	1.8	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
4	144193	1.53	2e−16	3e−14	15 x 50	amidohydrolase domain containing 1 [Source:HGNC Symbol;
5	200315	1.35	2e−16	3e−14	1 x 40	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
6	341	1.88	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
7	348	1.45	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
8	360	1.69	2e−16	3e−14	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
9	140458	1.35	2e−16	3e−14	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
10	84419	1.37	2e−16	3e−14	5 x 50	chromosome 15 open reading frame 48 [Source:HGNC Symb
11	339512	1.61	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
12	713	1.43	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
13	714	1.37	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
14	260436	−1.39	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
15	29113	1.51	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
16	375791	1.68	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
17	51806	2.18	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
18	6363	1.71	2e−16	3e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
19	1048	1.96	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
20	4680	1.42	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	21.85	NULL	572	Disease	GUDJ_psoriasis up
2	20.17	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	18.2	NULL	135	H.Tiss	WIRTH_Mucosa
4	17.07	NULL	36	BP	muscle filament sliding
5	16.69	NULL	127	H.Tiss	WIRTH_Muscle
6	16.26	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	16.26	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	16.26	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	16.26	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	14.24	NULL	312	BP	immune response
11	13.53	NULL	417	H.Tiss	WIRTH_Immune system
12	13.3	NULL	1182	CC	extracellular region
13	13.15	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
14	12.92	NULL	250	Lymphoma	LENZ_Stromal signature 1
15	12.19	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
16	11.76	NULL	16	H.Tiss	WIRTH_Hippocampus
17	10.34	NULL	2659	CC	plasma membrane
18	10.32	NULL	76	BP	epidermis development
19	10.24	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
20	10	NULL	316	Cancer	SPANG_BCL6−index2
Underexpressed					
1	−8.96	NULL	618	Chr	Chr 4
2	−7.98	NULL	4640	CC	nucleus
3	−7.68	NULL	914	Chr	Chr 3
4	−7.08	NULL	1749	MF	DNA binding
5	−6.53	NULL	949	CC	nucleoplasm
6	−6.49	NULL	940	MF	nucleic acid binding
7	−6.08	NULL	1233	TF	KIM_MYC targets
8	−5.83	NULL	1574	BP	transcription, DNA−templated
9	−5.76	NULL	595	MF	RNA binding
10	−5.46	NULL	1581	BP	regulation of transcription, DNA−dependent
11	−5.36	NULL	649	BP	gene expression
12	−5.29	NULL	298	BP	DNA repair
13	−5.28	NULL	714	Chr	Chr 6
14	−5.27	NULL	229	BP	RNA splicing
15	−5.03	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
16	−5.03	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
17	−4.85	NULL	1318	CC	mitochondrion
18	−4.78	NULL	370	BP	mitotic cell cycle
19	−4.71	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
20	−4.63	NULL	253	BP	translation







GW_153

Local Summary

%DE = 0.93

metagenes = 4

genes = 83

genes in genesets = 83

genes with fdr < 0.1 = 70 (70 + / 0 −)

genes with fdr < 0.05 = 70 (70 + / 0 −)

genes with fdr < 0.01 = 63 (63 + / 0 −)

<r> metagenes = 1

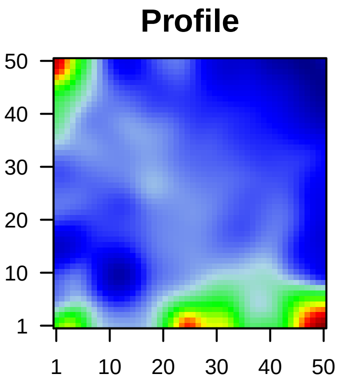
<r> genes = 0.67

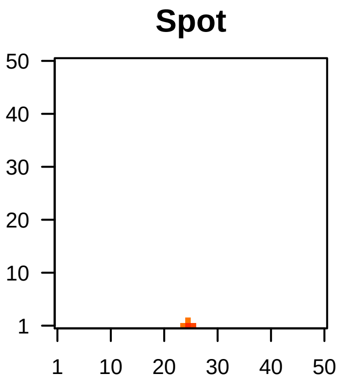
<FC> = 0.95

<shrinkage−t> = 33.29

<p−value> = 0

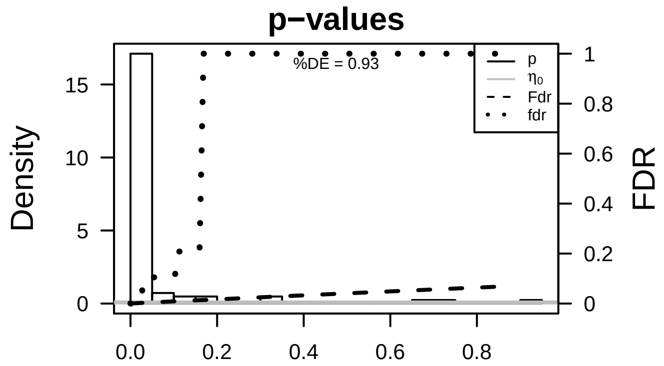
<fdr> = 0.19


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.98	2e−16	7e−17	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.74	2e−16	7e−17	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	140458	1.35	2e−16	7e−17	25 x 1	ankyrin repeat and SOCS box containing 5 [Source:HGNC Sy
4	1114	1.83	2e−16	7e−17	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Ac
5	1158	1.97	2e−16	7e−17	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
6	202333	1.32	2e−16	7e−17	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14
7	2318	1.95	2e−16	7e−17	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
8	10324	2.23	2e−16	7e−17	25 x 1	kelch−like family member 41 [Source:HGNC Symbol;Acc:169
9	4151	1.41	2e−16	7e−17	25 x 1	myoglobin [Source:HGNC Symbol;Acc:6915]
10	4608	2.03	2e−16	7e−17	25 x 1	myosin binding protein H [Source:HGNC Symbol;Acc:7552]
11	4620	1.32	2e−16	7e−17	25 x 1	myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
12	4625	1.4	2e−16	7e−17	25 x 1	myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
13	4633	1.96	2e−16	7e−17	25 x 1	myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
14	9499	1.81	2e−16	7e−17	25 x 1	myotilin [Source:HGNC Symbol;Acc:12399]
15	4703	2.12	2e−16	7e−17	25 x 1	nebulin [Source:HGNC Symbol;Acc:7720]
16	6588	1.94	2e−16	7e−17	25 x 1	sarcolipin [Source:HGNC Symbol;Acc:11089]
17	8557	1.53	2e−16	7e−17	25 x 1	titin−cap [Source:HGNC Symbol;Acc:11610]
18	7134	2.18	2e−16	7e−17	25 x 1	troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
19	7140	1.4	2e−16	7e−17	25 x 1	troponin T type 3 (skeletal, fast) [Source:HGNC Symbol;Acc:
20	845	1.31	4e−16	4e−15	25 x 1	calsequestrin 2 (cardiac muscle) [Source:HGNC Symbol;Acc:



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	62.17	NULL	21 / 36	BP	muscle filament sliding
2	54.45	NULL	46 / 127	H.Tiss	WIRTH_Muscle
3	53.74	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
4	46.31	NULL	9 / 16	H.Tiss	WIRTH_Hippocampus
5	44.5	NULL	19 / 44	MF	structural constituent of muscle
6	40.73	NULL	8 / 12	CC	myosin filament
7	35.92	NULL	7 / 14	CC	contractile fiber
8	32.49	NULL	11 / 37	CC	sarcomere
9	28.84	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
10	27.74	NULL	19 / 84	BP	muscle contraction
11	27.63	NULL	9 / 37	BP	cardiac muscle contraction
12	27.21	NULL	6 / 13	CC	muscle myosin complex
13	24.94	NULL	7 / 16	CC	M band
14	24.68	NULL	9 / 20	CC	I band
15	24.58	NULL	6 / 12	BP	skeletal muscle contraction
16	23.97	NULL	17 / 88	CC	Z disc
17	23.75	NULL	11 / 34	CC	myofibril
18	22.46	NULL	3 / 15	Cancer	BEN−PORATH_UP
19	22.05	NULL	2 / 10	BP	heart contraction
20	20.93	NULL	2 / 6	GSEA C2	BIOCARTA_HSP27_PATHWAY
21	20.31	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
22	20.1	NULL	5 / 12	MF	titin binding
23	19.78	NULL	6 / 18	BP	regulation of muscle contraction
24	19.6	NULL	4 / 15	BP	striated muscle contraction
25	17.68	NULL	2 / 20	MF	myosin binding
26	16.93	NULL	4 / 11	CC	A band
27	16.33	NULL	2 / 12	BP	muscle fiber development
28	16.25	NULL	4 / 26	BP	ventricular cardiac muscle tissue morphogenesis
29	15.73	NULL	6 / 42	CC	myosin complex
30	14.88	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_UP
31	14.88	NULL	1 / 9	GSEA C2	PENG_GLUCOSE_DEPRIVATION_DN
32	14.6	NULL	5 / 15	GSEA C2	REACTOME_STRIATED_MUSCLE_CONTRACTION
33	14.55	NULL	3 / 18	CC	costamere
34	14.54	NULL	3 / 13	CC	pseudopodium
35	14.4	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_GONADOTROPHINS_DN
36	14.4	NULL	2 / 16	GSEA C2	SASSON_RESPONSE_TO_FORSKOLIN_DN
37	14.36	NULL	2 / 15	BP	actin filament−based movement
38	14.3	NULL	3 / 15	GSEA C2	EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
39	14.12	NULL	21 / 297	MF	actin binding
40	14	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO

GW_153

Local Summary

%DE = 0.85

metagenes = 15

genes = 264

genes in genesets = 262

genes with fdr < 0.1 = 203 (195 + / 8 −)

genes with fdr < 0.05 = 203 (195 + / 8 −)

genes with fdr < 0.01 = 179 (173 + / 6 −)

<r> metagenes = 0.99

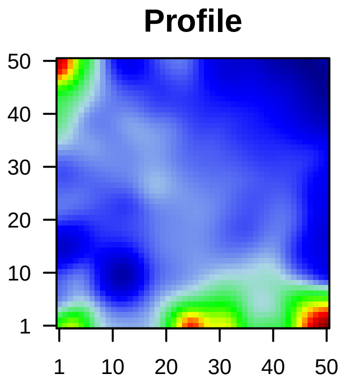
<r> genes = 0.6

<FC> = 0.58

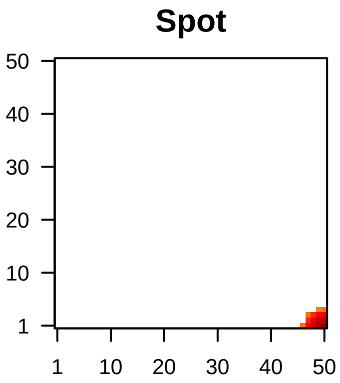
<shrinkage−t> = 20.23

<p−value> = 0

<fdr> = 0.28



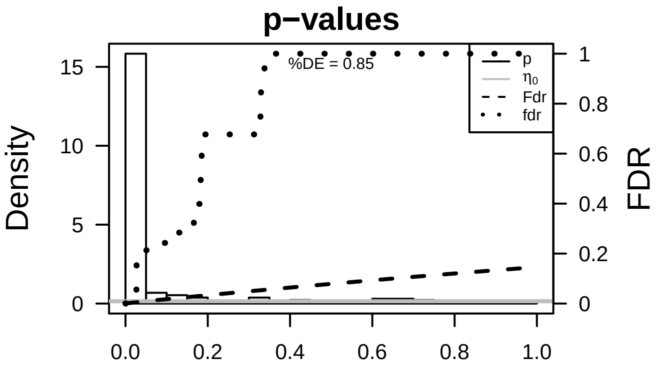
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	1.88	2e−16	7e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	348	1.45	2e−16	7e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	713	1.43	2e−16	7e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
4	714	1.37	2e−16	7e−16	50 x 1	complement component 1, q subcomponent, C chain [Source
5	260436	−1.39	2e−16	7e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
6	6363	1.71	2e−16	7e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
7	4283	1.9	2e−16	7e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
8	115361	1.33	2e−16	7e−16	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
9	3113	1.6	2e−16	7e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
10	3119	1.73	2e−16	7e−16	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
11	3126	1.8	2e−16	7e−16	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
12	3620	2.55	2e−16	7e−16	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:
13	5996	1.41	2e−16	7e−16	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
14	972	1.3	4e−16	6e−15	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
15	8320	1.3	7e−16	2e−14	48 x 1	eomesodermin [Source:HGNC Symbol;Acc:3372]
16	7351	1.3	7e−16	2e−14	50 x 1	uncoupling protein 2 (mitochondrial, proton carrier) [Source:H
17	3394	1.29	1e−15	4e−14	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
18	7305	1.27	2e−15	8e−14	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
19	3109	1.26	4e−15	5e−13	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
20	3003	1.23	2e−14	6e−13	49 x 1	granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.48	NULL	12 / 15	CC	MHC class II protein complex
2	27.62	NULL	90 / 417	H.Tiss	WIRTH_Immune system
3	23.29	NULL	15 / 47	BP	antigen processing and presentation
4	23.13	NULL	52 / 312	BP	immune response
5	22.25	NULL	94 / 553	Cancer	Lembcke_Colonic Inflammation
6	19.23	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
7	18.45	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
8	18.29	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
9	18.25	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
10	17.55	NULL	14 / 60	BP	T cell costimulation
11	17.01	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	16.93	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
13	16.71	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	16.71	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	16.71	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	16.71	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	16.63	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
18	16.38	NULL	7 / 28	CC	transport vesicle membrane
19	16.3	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
20	15.2	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
21	15.16	NULL	8 / 35	CC	trans−Golgi network membrane
22	15.04	NULL	4 / 22	BP	positive regulation of interleukin−12 production
23	14.89	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
24	14.66	NULL	6 / 13	Cancer	GENTLES_modul18
25	14.64	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
26	14.63	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
27	14.53	NULL	5 / 12	BP	immunoglobulin mediated immune response
28	14.53	NULL	17 / 74	BP	regulation of immune response
29	14.47	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
30	14.4	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
31	14.37	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
32	14.18	NULL	15 / 84	BP	T cell receptor signaling pathway
33	13.96	NULL	8 / 16	GSEA C2	SU_THYMUS
34	13.83	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
35	13.82	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
36	13.69	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
37	13.66	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
38	13.65	NULL	8 / 46	CC	endocytic vesicle membrane
39	13.56	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
40	13.36	NULL	5 / 12	BP	dendritic cell chemotaxis

GW_153

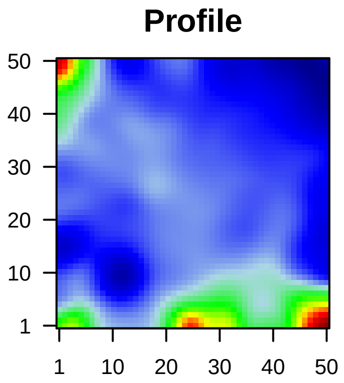
Local Summary

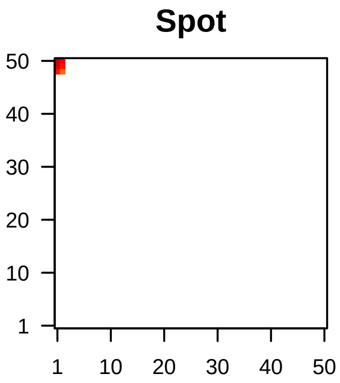
%DE = 0.92
metagenes = 6
genes = 119
genes in genesets = 117

genes with fdr < 0.1 = 101 (92 + / 9 −)
genes with fdr < 0.05 = 97 (89 + / 8 −)
genes with fdr < 0.01 = 84 (80 + / 4 −)

<r> metagenes = 0.99
<r> genes = 0.53

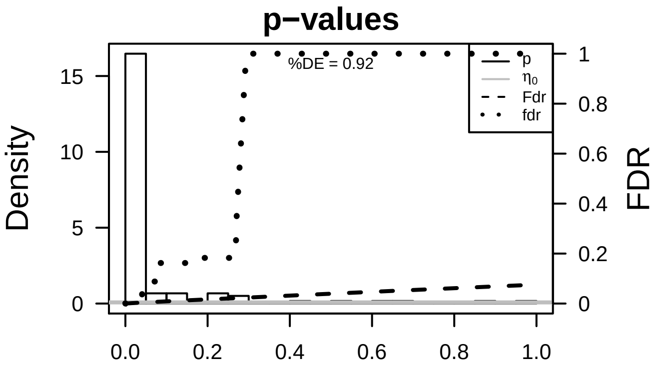
<FC> = 0.82
<shrinkage−t> = 28.86
<p−value> = 0
<fdr> = 0.24





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	242	1.8	2e−16	6e−17	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Syn
2	360	1.69	2e−16	6e−17	1 x 50	aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
3	375791	1.68	2e−16	6e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	1048	1.96	2e−16	6e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
5	4680	1.42	2e−16	6e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	84518	1.57	2e−16	6e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	414325	1.63	2e−16	6e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
8	1673	1.99	2e−16	6e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
9	43849	1.75	2e−16	6e−17	1 x 50	kallikrein−related peptidase 12 [Source:HGNC Symbol;Acc:6
10	26085	1.77	2e−16	6e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
11	5653	2.23	2e−16	6e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
12	5650	2.5	2e−16	6e−17	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
13	3860	1.38	2e−16	6e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
14	192666	1.65	2e−16	6e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
15	388533	2.34	2e−16	6e−17	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
16	66004	1.5	2e−16	6e−17	1 x 50	Ly6/neurotoxin 1 [Source:HGNC Symbol;Acc:29604]
17	137797	2.13	2e−16	6e−17	1 x 50	LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
18	27076	1.55	2e−16	6e−17	1 x 50	LY6/PLAUR domain containing 3 [Source:HGNC Symbol;Acc
19	342897	1.36	2e−16	6e−17	1 x 50	non−specific cytotoxic cell receptor protein 1 homolog (zebra
20	5266	1.23	2e−16	6e−17	1 x 49	peptidase inhibitor 3, skin−derived [Source:HGNC Symbol;Ac



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	46.88	NULL	57 / 135	H.Tiss	WIRTH_Mucosa
2	27.18	NULL	59 / 572	Disease	GUDJ_psoriasis up
3	25.1	NULL	14 / 21	CC	cornified envelope
4	21.87	NULL	16 / 42	BP	keratinization
5	21.38	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
6	21.17	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
7	20.6	NULL	15 / 76	BP	epidermis development
8	17.47	NULL	19 / 53	BP	keratinocyte differentiation
9	17.23	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
10	15.51	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
11	14.54	NULL	5 / 13	BP	negative regulation of peptidase activity
12	14.35	NULL	2 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
13	13.63	NULL	4 / 10	MF	RAGE receptor binding
14	13.52	NULL	8 / 52	BP	negative regulation of endopeptidase activity
15	13.19	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
16	12.94	NULL	5 / 29	BP	regulation of proteolysis
17	12.88	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
18	12.29	NULL	8 / 19	BP	peptide cross−linking
19	12.26	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
20	12.24	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
21	12.07	NULL	10 / 122	MF	serine−type endopeptidase activity
22	11.77	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
23	11.58	NULL	37 / 1182	CC	extracellular region
24	11.12	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
25	10.83	NULL	4 / 23	MF	peptidase inhibitor activity
26	10.83	NULL	6 / 83	CC	anchored to membrane
27	10.61	NULL	2 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
28	10.33	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
29	10.17	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
30	9.68	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
31	9.45	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
32	9.13	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
33	9.08	NULL	6 / 73	BP	defense response to bacterium
34	8.99	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
35	8.96	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
36	8.94	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
37	8.47	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
38	8.41	NULL	2 / 17	Disease	BCHETNIA_EBM up
39	8.3	NULL	1 / 7	GSEA C2	KOBAYASHI_EGFR_SIGNALING_6HR_UP
40	8.24	NULL	2 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN

GW_153

Local Summary

%DE = 0.88

metagenes = 18

genes = 102

genes in genesets = 86

genes with fdr < 0.1 = 68 (2 + / 66 −)

genes with fdr < 0.05 = 68 (2 + / 66 −)

genes with fdr < 0.01 = 41 (0 + / 41 −)

<r> metagenes = 0.94

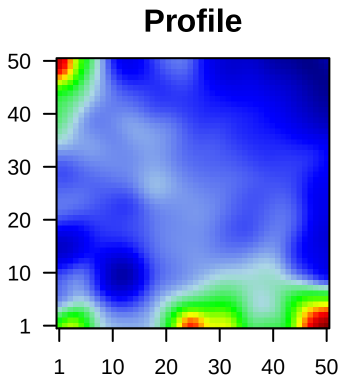
<r> genes = 0.25

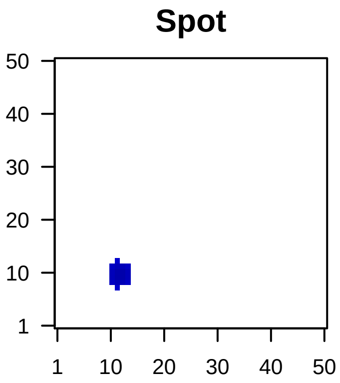
<FC> = −0.34

<shrinkage−t> = −12.01

<p−value> = 0.01

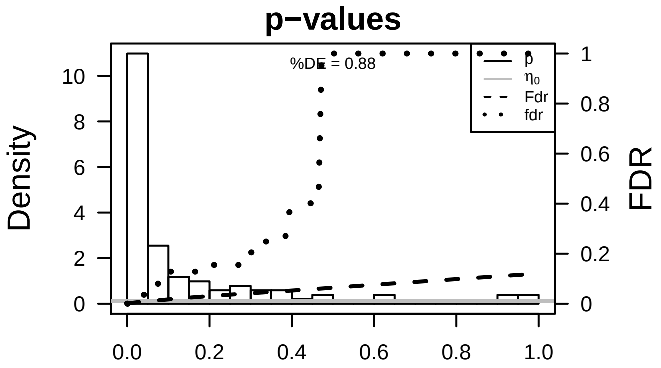
<fdr> = 0.57





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25894	−0.97	1e−09	1e−06	12 x 11	pleckstrin homology domain containing, family G (with RhoGe
2	4485	−0.86	1e−07	2e−05	12 x 12	macrophage stimulating 1 (hepatocyte growth factor−like) [So
3	441520	−0.74	4e−06	2e−05	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
4	645037	−0.74	5e−06	2e−05	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
5	729422	−0.73	6e−06	2e−05	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	525	−0.72	8e−06	2e−04	12 x 8	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1
7	3911	−0.64	4e−05	2e−04	12 x 11	laminin, alpha 5 [Source:HGNC Symbol;Acc:6485]
8	23532	−0.64	8e−05	2e−04	13 x 10	preferentially expressed antigen in melanoma [Source:HGNC
9	645073	−0.63	8e−05	2e−04	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	26748	−0.63	1e−04	2e−04	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
11	729428	−0.62	1e−04	2e−04	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
12	4041	−0.62	1e−04	2e−04	12 x 9	low density lipoprotein receptor−related protein 5 [Source:HG
13	2576	−0.62	1e−04	2e−04	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	729442	−0.62	1e−04	3e−04	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2577	−0.61	2e−04	3e−04	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
16	51481	−0.6	2e−04	1e−03	13 x 11	variable charge, X−linked 3A [Source:HGNC Symbol;Acc:181
17	83986	−0.57	3e−04	1e−03	11 x 10	integrin alpha FG−GAP repeat containing 3 [Source:HGNC S
18	2579	−0.56	4e−04	1e−03	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
19	729447	−0.56	5e−04	1e−03	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
20	100008586	−0.55	6e−04	2e−03	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.26	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
2	−12.47	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
3	−12.42	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
4	−12.14	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
5	−10.09	NULL	1 / 2	miRNA target	miR−107
6	−9.85	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
7	−9.02	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
8	−8.98	NULL	2 / 17	BP	calcium ion homeostasis
9	−8.92	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
10	−8.87	NULL	2 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
11	−8.81	NULL	2 / 14	GSEA C2	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
12	−8.75	NULL	2 / 16	GSEA C2	LIU_SOX4_TARGETS_DN
13	−8.6	NULL	2 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
14	−8.26	NULL	19 / 630	Chr	Chr X
15	−7.7	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
16	−7.65	NULL	1 / 10	BP	branching involved in salivary gland morphogenesis
17	−7.49	NULL	1 / 2	miRNA target	miR−661
18	−7.19	NULL	1 / 5	miRNA target	miR−196a
19	−6.93	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
20	−6.93	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
21	−6.91	NULL	1 / 14	MF	hydrolase activity, acting on acid anhydrides, catalyzing transmemb
22	−6.9	NULL	1 / 12	BP	regulation of embryonic development
23	−6.82	NULL	1 / 11	BP	bone remodeling
24	−6.78	NULL	1 / 20	BP	sperm motility
25	−6.6	NULL	1 / 13	BP	morphogenesis of embryonic epithelium
26	−6.5	NULL	1 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
27	−6.37	NULL	2 / 13	GSEA C2	ENK_UV_RESPONSE_KERATINOCYTE_UP
28	−6.35	NULL	1 / 13	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_DN
29	−6.35	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
30	−6.35	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
31	−6.3	NULL	1 / 11	GSEA C2	GARCIA_TARGETS_OF_FLI1_AND_DAX1_UP
32	−6.21	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
33	−6.21	NULL	1 / 13	BP	branching involved in mammary gland duct morphogenesis
34	−6.21	NULL	1 / 13	GSEA C2	ROZANOV_MMP14_TARGETS_UP
35	−6.09	NULL	1 / 14	BP	negative regulation of retinoic acid receptor signaling pathway
36	−6.09	NULL	1 / 14	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN
37	−5.95	NULL	1 / 14	GSEA C2	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_
38	−5.95	NULL	1 / 14	GSEA C2	WEST_ADRENOCORTICAL_TUMOR_DN
39	−5.89	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_UP
40	−5.88	NULL	1 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN

GW_153

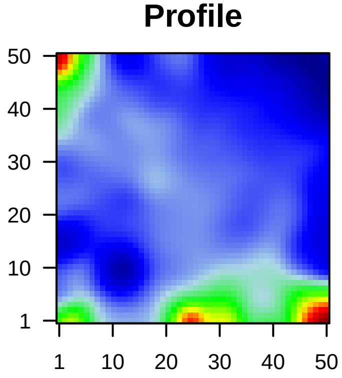
Local Summary

%DE = 0.52
metagenes = 4
genes = 64
genes in genesets = 64

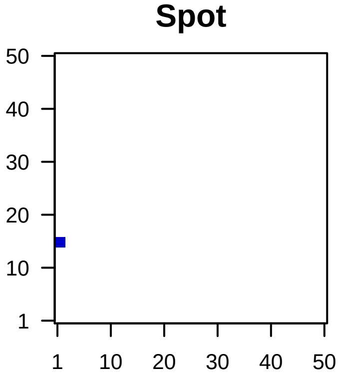
genes with fdr < 0.1 = 10 (0 + / 10 −)
genes with fdr < 0.05 = 4 (0 + / 4 −)
genes with fdr < 0.01 = 2 (0 + / 2 −)

<r> metagenes = 1
<r> genes = 0.35

<FC> = −0.21
<shrinkage−t> = −7.32
<p−value> = 0.08
<fdr> = 0.84



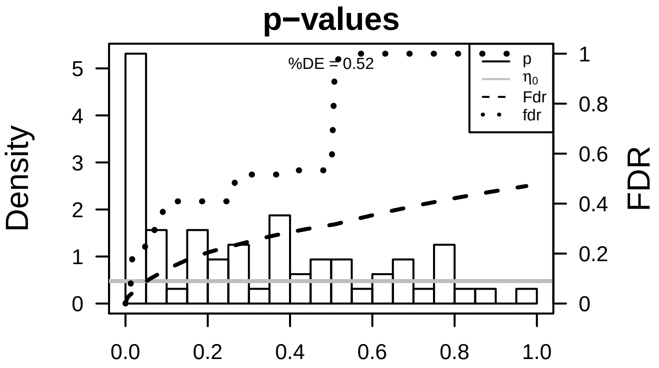
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4495	−0.93	6e−09	3e−05	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
2	79929	−0.79	8e−07	4e−04	1 x 16	MAP6 domain containing 1 [Source:HGNC Symbol;Acc:2575
3	51083	−0.7	1e−05	2e−02	1 x 15	galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41
4	219927	−0.56	5e−04	3e−02	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
5	55039	−0.51	2e−03	6e−02	1 x 16	tRNA methyltransferase 12 homolog (S. cerevisiae) [Source:
6	84948	−0.46	4e−03	6e−02	1 x 16	tigger transposable element derived 5 [Source:HGNC Symbo
7	65265	−0.43	7e−03	6e−02	1 x 16	chromosome 8 open reading frame 33 [Source:HGNC Symb
8	64979	−0.42	9e−03	6e−02	1 x 16	mitochondrial ribosomal protein L36 [Source:HGNC Symbol;
9	7205	−0.4	1e−02	6e−02	2 x 16	thyroid hormone receptor interactor 6 [Source:HGNC Symbol
10	8345	−0.4	1e−02	6e−02	1 x 15	histone cluster 1, H2bh [Source:HGNC Symbol;Acc:4755]
11	10202	−0.4	1e−02	1e−01	1 x 15	dehydrogenase/reductase (SDR family) member 2 [Source:H
12	55630	−0.38	2e−02	2e−01	1 x 16	solute carrier family 39 (zinc transporter), member 4 [Source:
13	6535	−0.34	3e−02	2e−01	1 x 16	solute carrier family 6 (neurotransmitter transporter), member
14	5439	−0.34	3e−02	2e−01	1 x 16	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa [
15	93273	−0.33	4e−02	2e−01	2 x 15	LEM domain containing 1 [Source:HGNC Symbol;Acc:18725]
16	11004	−0.32	5e−02	2e−01	2 x 16	kinesin family member 2C [Source:HGNC Symbol;Acc:6393]
17	705	−0.32	5e−02	2e−01	1 x 16	bystin−like [Source:HGNC Symbol;Acc:1157]
18	54512	−0.3	6e−02	2e−01	1 x 16	exosome component 4 [Source:HGNC Symbol;Acc:18189]
19	11047	−0.29	7e−02	2e−01	2 x 15	adhesion regulating molecule 1 [Source:HGNC Symbol;Acc:1
20	388581	−0.29	7e−02	3e−01	1 x 15	family with sequence similarity 132, member A [Source:HGN



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.69	NULL	1 / 7	MMML CGS	MACIEJ_MMML 13
2	−16.03	NULL	2 / 10	GSEA C2	ZHU_CMV_24_HR_UP
3	−16.03	NULL	2 / 10	GSEA C2	ZHU_CMV_ALL_UP
4	−15.64	NULL	1 / 10	BP	cellular response to zinc ion
5	−15.1	NULL	1 / 6	GSEA C2	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
6	−15.1	NULL	1 / 6	GSEA C2	REACTOME_GPCR_LIGAND_BINDING
7	−14.03	NULL	2 / 16	BP	monocyte differentiation
8	−13.99	NULL	1 / 7	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
9	−13.99	NULL	1 / 7	GSEA C2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
10	−13.71	NULL	1 / 13	BP	cellular response to cadmium ion
11	−13.08	NULL	1 / 8	GSEA C2	SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
12	−13.08	NULL	1 / 8	GSEA C2	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
13	−12.75	NULL	1 / 15	BP	negative regulation of growth
14	−12.6	NULL	1 / 11	CC	Golgi−associated vesicle
15	−11.96	NULL	1 / 17	BP	cellular response to vascular endothelial growth factor stimulus
16	−11.69	NULL	1 / 10	GSEA C2	WELCSH_BRCA1_TARGETS_1_DN
17	−11.69	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
18	−11.14	NULL	1 / 11	GSEA C2	SCIBETTA_KDM5B_TARGETS_DN
19	−11.14	NULL	1 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
20	−11.14	NULL	1 / 11	GSEA C2	PARK_APL_PATHOGENESIS_DN
21	−10.77	NULL	1 / 15	BP	negative regulation of microtubule depolymerization
22	−10.66	NULL	1 / 12	GSEA C2	BHATTACHARYA_EMBRYONIC_STEM_CELL
23	−10.42	NULL	1 / 16	GSEA C2	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_UP
24	−10.24	NULL	1 / 13	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_C
25	−10.24	NULL	1 / 13	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
26	−10.01	NULL	1 / 3	GSEA C2	WEBER_METHYLATED_LCP_IN_SPERM_DN
27	−9.86	NULL	1 / 14	GSEA C2	FARMER_BREAST_CANCER_BASAL_VS_LULMINAL
28	−9.86	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP
29	−9.86	NULL	1 / 14	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_DN
30	−9.52	NULL	1 / 15	MF	neuropeptide hormone activity
31	−9.52	NULL	1 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
32	−9.52	NULL	1 / 15	GSEA C2	FERNANDEZ_BOUND_BY_MYC
33	−9.21	NULL	1 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
34	−9.21	NULL	1 / 16	GSEA C2	TAVOR_CEBPA_TARGETS_DN
35	−9.21	NULL	1 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
36	−9.21	NULL	1 / 16	GSEA C2	BROWNE_HCMV_INFECTION_24HR_UP
37	−8.93	NULL	1 / 17	Disease	BCHETNIA_EBM up
38	−8.67	NULL	1 / 18	BP	smooth muscle contraction
39	−8.34	NULL	3 / 15	GSEA C2	LY_AGING_MIDDLE_DN
40	−8.25	NULL	2 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN

GW_153

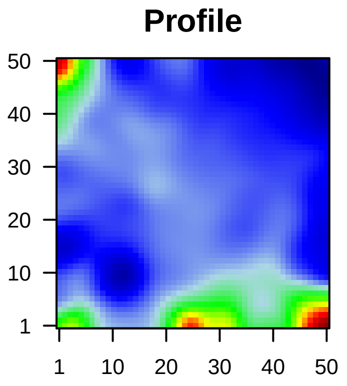
Local Summary

%DE = 0.54
metagenes = 100
genes = 1211
genes in genesets = 1197

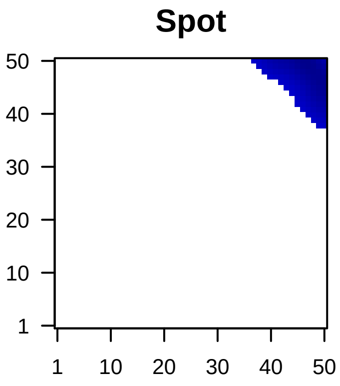
genes with fdr < 0.1 = 255 (24 + / 231 −)
genes with fdr < 0.05 = 148 (17 + / 131 −)
genes with fdr < 0.01 = 65 (12 + / 53 −)

<r> metagenes = 0.77
<r> genes = 0.19

<FC> = −0.19
<shrinkage−t> = −6.58
<p−value> = 0.06
<fdr> = 0.8



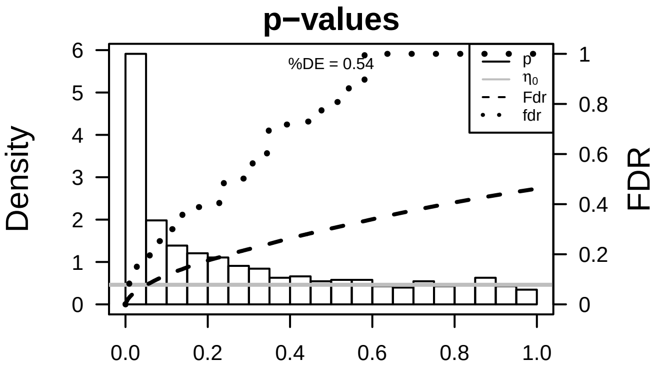
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	339512	1.61	2e−16	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
2	3866	1.82	2e−16	2e−14	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
3	3880	−3.45	2e−16	2e−14	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
4	4922	1.9	2e−16	2e−14	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
5	26227	−1.38	2e−16	2e−14	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
6	4072	−1.25	7e−15	3e−11	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
7	84223	1.2	7e−14	2e−08	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
8	154664	1.07	3e−11	2e−08	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
9	56977	−1.05	7e−11	7e−08	50 x 49	storkhead box 2 [Source:HGNC Symbol;Acc:25450]
10	83959	1.01	3e−10	7e−08	50 x 50	solute carrier family 4, sodium borate transporter, member 11
11	84707	−1.01	3e−10	2e−06	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
12	55353	−0.94	5e−09	2e−06	42 x 50	lysosomal protein transmembrane 4 beta [Source:HGNC Sym
13	57291	−0.92	1e−08	2e−06	50 x 50	differentiation antagonizing non−protein coding RNA [Source:
14	11166	0.91	1e−08	2e−06	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
15	50810	−0.91	2e−08	2e−06	46 x 50	Hepatoma−derived growth factor−related protein 3 [Source:U
16	10606	−0.9	2e−08	1e−05	43 x 50	phosphoribosylaminoimidazole carboxylase, phosphoribosyla
17	8500	−0.88	4e−08	4e−05	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
18	79682	−0.85	1e−07	4e−05	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
19	2944	−0.84	2e−07	4e−05	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
20	116832	−0.83	2e−07	7e−05	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.51	NULL	11 / 16	Cancer	WOLFER_overlap genes
2	−13.46	NULL	98 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	−13.46	NULL	98 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	−11.24	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	−11.05	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
6	−10.21	NULL	134 / 370	BP	mitotic cell cycle
7	−10.08	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
8	−9.67	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
9	−9.51	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
10	−9.49	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
11	−9.3	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
12	−9.3	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
13	−9.22	NULL	140 / 530	Cancer	Lembcke_Normal vs Adenoma
14	−9.07	NULL	20 / 30	BP	DNA strand elongation involved in DNA replication
15	−9.05	NULL	15 / 22	BP	DNA replication initiation
16	−8.97	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
17	−8.97	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
18	−8.96	NULL	2 / 18	CC	costamere
19	−8.63	NULL	4 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
20	−8.47	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
21	−8.37	NULL	12 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
22	−8.17	NULL	181 / 949	CC	nucleoplasm
23	−8.1	NULL	58 / 149	BP	DNA replication
24	−8.05	NULL	6 / 8	GSEA C2	REACTOME_DNA_REPLICATION_PRE_INITIATION
25	−8.02	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
26	−8.01	NULL	11 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
27	−7.77	NULL	4 / 4	MMML CGS	MACIEJ_MMML 41
28	−7.66	NULL	1 / 21	BP	sarcomere organization
29	−7.59	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
30	−7.5	NULL	8 / 12	BP	mitotic chromosome condensation
31	−7.35	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
32	−7.18	NULL	9 / 15	GSEA C2	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
33	−7.15	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
34	−7.1	NULL	9 / 15	GSEA C2	MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_DN
35	−7.06	NULL	7 / 15	Cancer	BEN−PORATH_UP
36	−7	NULL	5 / 8	GSEA C2	REACTOME_SYNTHESIS_OF_DNA
37	−6.95	NULL	3 / 11	MF	glutathione binding
38	−6.95	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
39	−6.94	NULL	118 / 914	Chr	Chr 3
40	−6.85	NULL	6 / 13	Pathw Act	GUSTAFSON_PI3K_UP