GW_154

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1627 (966 + / 661 −)

genes with fdr < 0.1 = 1316 (821 + / 495 −)

genes with fdr < 0.05 = 1097 (705 + / 392 −)

genes with fdr < 0.01 = 789 (539 + / 250 −)

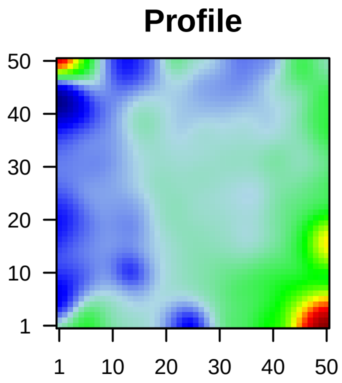
genes in genesets = 16332

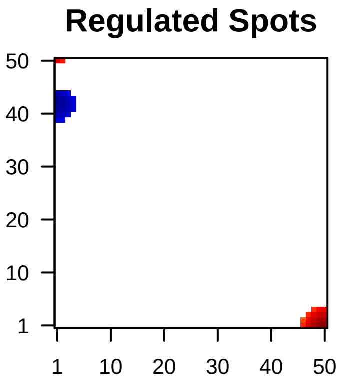
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

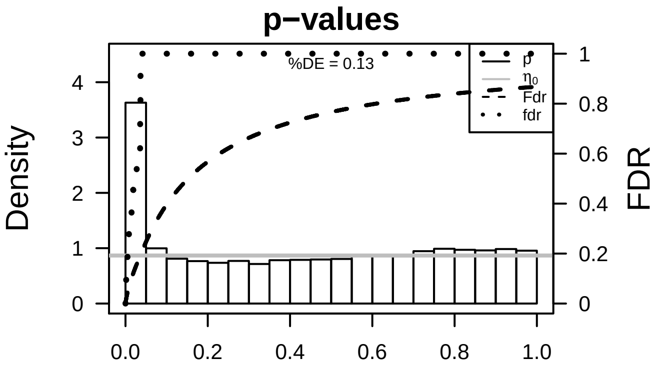
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.16	2e−16	3e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	58	−1.33	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	216	1.16	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	260436	3.3	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
5	56892	1.29	2e−16	3e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
6	375791	1.3	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
7	57172	2.12	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
8	6364	2.97	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
9	595	1.13	2e−16	3e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
10	930	1.27	2e−16	3e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
11	909	1.5	2e−16	3e−14	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
12	1048	1.31	2e−16	3e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	4680	1.28	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	1087	1.17	2e−16	3e−14	4 x 50	carcinoembryonic antigen−related cell adhesion molecule 7 [
15	1675	−1.16	2e−16	3e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
16	22802	2.12	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	9076	1.35	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
18	9071	1.64	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
19	84518	1.15	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
20	26047	1.16	2e−16	3e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	19.54	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	15.9	NULL	135	H.Tiss	WIRTH_Mucosa
3	14.62	NULL	572	Disease	GUDJ_psoriasis up
4	13.06	NULL	417	H.Tiss	WIRTH_Immune system
5	12.75	NULL	312	BP	immune response
6	11.08	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
7	10.29	NULL	21	CC	cornified envelope
8	9.74	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	8.93	NULL	111	BP	chemotaxis
10	8.87	NULL	1182	CC	extracellular region
11	8.79	NULL	274	Lymphoma	SPANG_IL21 DN
12	8.42	NULL	53	BP	keratinocyte differentiation
13	8.14	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
14	8.03	NULL	618	Chr	Chr 4
15	7.98	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
16	7.9	NULL	7	MMML CGS	MACIEJ_MMML 5
17	7.75	NULL	162	CC	external side of plasma membrane
18	7.64	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
19	7.52	NULL	43	MF	chemokine activity
20	7.52	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−7.93	NULL	633	Chr	Chr 9
2	−7.93	NULL	717	Chr	Chr 16
3	−7.08	NULL	127	H.Tiss	WIRTH_Muscle
4	−6.59	NULL	36	BP	muscle filament sliding
5	−6.46	NULL	519	Chr	Chr 14
6	−5.13	NULL	16	H.Tiss	WIRTH_Hippocampus
7	−4.94	NULL	44	MF	structural constituent of muscle
8	−4.6	NULL	16	CC	M band
9	−4.45	NULL	6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
10	−4.42	NULL	84	BP	muscle contraction
11	−4.35	NULL	12	CC	myosin filament
12	−4.11	NULL	39	BP	glycolysis
13	−3.82	NULL	1233	TF	KIM_MYC targets
14	−3.81	NULL	19	MF	L−ascorbic acid binding
15	−3.79	NULL	70	BP	cell junction assembly
16	−3.76	NULL	88	CC	Z disc
17	−3.54	NULL	15	GSEA C2	CROMER_METASTASIS_DN
18	−3.47	NULL	164	BP	cell death
19	−3.44	NULL	7	GSEA C2	YE_METASTATIC_LIVER_CANCER
20	−3.38	NULL	167	BP	cellular nitrogen compound metabolic process

GW_154

Local Summary

%DE = 0.79

metagenes = 17

genes = 276

genes in genesets = 274

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

genes with fdr < 0.05 = 184 (178 + / 6 −)

genes with fdr < 0.01 = 153 (151 + / 2 −)

<r> metagenes = 0.99

<r> genes = 0.59

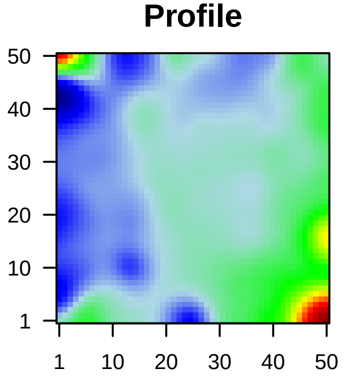
<FC> = 0.55

<shrinkage−t> = 19.31

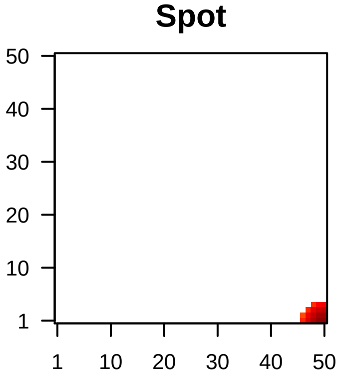
<p−value> = 0

<fdr> = 0.33

Profile



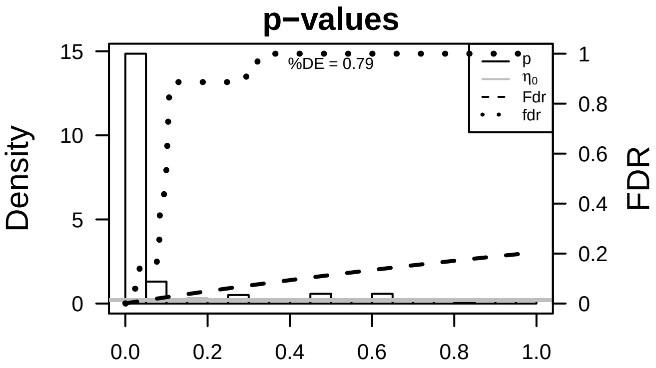
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	3.3	2e−16	5e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
2	57172	2.12	2e−16	5e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
3	6364	2.97	2e−16	5e−16	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
4	930	1.27	2e−16	5e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
5	51755	1.92	2e−16	5e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
6	1545	2.91	2e−16	5e−16	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
7	1593	1.44	2e−16	5e−16	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sour
8	54855	1.69	2e−16	5e−16	49 x 1	family with sequence similarity 46, member C [Source:HGNC
9	51303	1.22	2e−16	5e−16	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
10	3120	1.7	2e−16	5e−16	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
11	3512	2.81	2e−16	5e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	3543	1.29	2e−16	5e−16	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
13	91353	1.56	2e−16	5e−16	48 x 1	
14	10320	1.26	2e−16	5e−16	49 x 1	IKAROS family zinc finger 1 (Ikaros) [Source:HGNC Symbol;
15	4050	1.26	2e−16	5e−16	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
16	51237	1.71	2e−16	5e−16	48 x 1	marginal zone B and B1 cell−specific protein [Source:HGNC
17	25849	2.19	2e−16	5e−16	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
18	11040	1.8	2e−16	5e−16	49 x 1	pim−2 oncogene [Source:HGNC Symbol;Acc:8987]
19	5450	1.34	2e−16	5e−16	48 x 1	POU class 2 associating factor 1 [Source:HGNC Symbol;Acc
20	5996	1.33	2e−16	5e−16	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.29	NULL	92 / 417	H.Tiss	WIRTH_Immune system
2	23.58	NULL	96 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.48	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
4	20.21	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	19.17	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
6	17.57	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
7	17.01	NULL	2 / 8	GSEA C2	REACTOME_ENDOGENOUS_STEROLS
8	16.59	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	16.54	NULL	52 / 312	BP	immune response
10	16.4	NULL	3 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
11	15.51	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
12	14.39	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
13	13.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
14	13.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
15	13.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
16	13.66	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
17	13.62	NULL	12 / 15	CC	MHC class II protein complex
18	13.52	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
19	13.49	NULL	2 / 12	BP	sterol metabolic process
20	13.25	NULL	7 / 13	Cancer	GENTLES_modul18
21	13.1	NULL	3 / 13	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_DN
22	12.81	NULL	4 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
23	12.07	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
24	12.01	NULL	25 / 162	CC	external side of plasma membrane
25	11.74	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
26	11.61	NULL	9 / 28	BP	B cell receptor signaling pathway
27	11.56	NULL	6 / 16	Lymphoma	WRIGHT_ABC UP
28	11.52	NULL	17 / 84	BP	T cell receptor signaling pathway
29	11.25	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
30	11.21	NULL	3 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
31	11.15	NULL	2 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP
32	11.03	NULL	6 / 27	MF	antigen binding
33	10.86	NULL	4 / 13	BP	lymph node development
34	10.84	NULL	5 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
35	10.81	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
36	10.8	NULL	2 / 15	GSEA C2	NAKAJIMA_MAST_CELL
37	10.63	NULL	4 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
38	10.53	NULL	1 / 9	GSEA C2	BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP
39	10.45	NULL	18 / 74	BP	regulation of immune response
40	10.42	NULL	17 / 60	BP	T cell costimulation

GW_154

Local Summary

%DE = 0.94

metagenes = 2

genes = 71

genes in genesets = 70

genes with fdr < 0.1 = 63 (60 + / 3 −)

genes with fdr < 0.05 = 63 (60 + / 3 −)

genes with fdr < 0.01 = 60 (58 + / 2 −)

<r> metagenes = 1

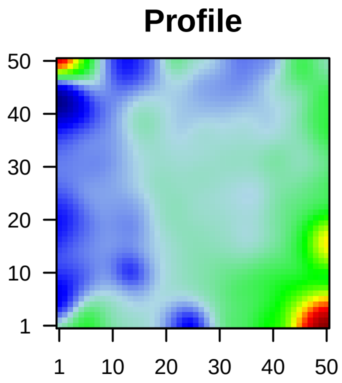
<r> genes = 0.58

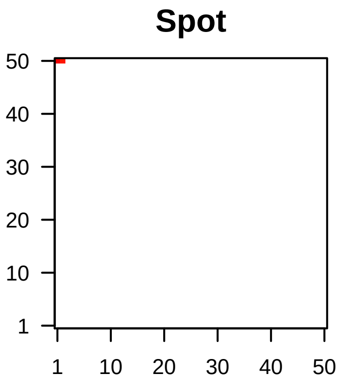
<FC> = 0.96

<shrinkage−t> = 33.83

<p−value> = 0

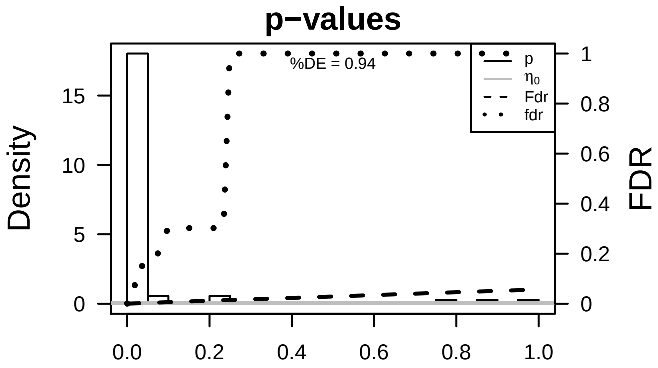
<fdr> = 0.13





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	375791	1.3	2e−16	3e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
2	1048	1.31	2e−16	3e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
3	4680	1.28	2e−16	3e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
4	22802	2.12	2e−16	3e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	84518	1.15	2e−16	3e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
6	49860	1.83	2e−16	3e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
7	26085	1.91	2e−16	3e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
8	5653	2.11	2e−16	3e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
9	3860	1.42	2e−16	3e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
10	3851	2.17	2e−16	3e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
11	196374	1.7	2e−16	3e−17	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
12	3934	1.54	2e−16	3e−17	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
13	4118	2.28	2e−16	3e−17	1 x 50	mal, T−cell differentiation protein [Source:HGNC Symbol;Acc
14	83886	1.56	2e−16	3e−17	1 x 50	protease, serine 27 [Source:HGNC Symbol;Acc:15475]
15	6286	2.01	2e−16	3e−17	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
16	57152	1.39	2e−16	3e−17	1 x 50	secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
17	11005	1.32	2e−16	3e−17	1 x 50	serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
18	6700	1.28	2e−16	3e−17	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
19	6702	1.73	2e−16	3e−17	1 x 50	
20	6704	1.85	2e−16	3e−17	1 x 50	small proline−rich protein 2E [Source:HGNC Symbol;Acc:112



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	43.97	NULL	39 / 135	H.Tiss	WIRTH_Mucosa
2	36.69	NULL	10 / 21	CC	cornified envelope
3	32.15	NULL	11 / 42	BP	keratinization
4	27.25	NULL	7 / 19	BP	peptide cross−linking
5	26.55	NULL	12 / 53	BP	keratinocyte differentiation
6	21.24	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
7	19.78	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	18.04	NULL	3 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	16.78	NULL	9 / 76	BP	epidermis development
10	15.23	NULL	29 / 572	Disease	GUDJ_psoriasis up
11	14.3	NULL	9 / 122	MF	serine−type endopeptidase activity
12	11.92	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
13	11.43	NULL	3 / 44	CC	keratin filament
14	11.26	NULL	10 / 186	MF	structural molecule activity
15	11.18	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
16	10.93	NULL	1 / 11	Glio	VERHAAK_Brain
17	10.72	NULL	2 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
18	10.72	NULL	2 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
19	10.64	NULL	2 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
20	10.59	NULL	2 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
21	10.39	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
22	10.33	NULL	1 / 12	MF	channel activity
23	10.21	NULL	3 / 38	BP	epithelial cell differentiation
24	10.2	NULL	1 / 10	MF	RAGE receptor binding
25	10.01	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
26	10.01	NULL	2 / 38	BP	myelination
27	9.81	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
28	9.81	NULL	3 / 13	BP	negative regulation of peptidase activity
29	9.5	NULL	2 / 22	BP	endothelial cell migration
30	9.49	NULL	3 / 27	BP	response to bacterium
31	9.46	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
32	9.46	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
33	9.08	NULL	1 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
34	8.96	NULL	1 / 15	BP	positive regulation of extrinsic apoptotic signaling pathway via deat
35	8.96	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
36	8.96	NULL	1 / 15	GSEA C2	BIOCARTA_MAL_PATHWAY
37	8.63	NULL	1 / 14	BP	tissue regeneration
38	8.62	NULL	2 / 16	BP	cobalamin metabolic process
39	8.61	NULL	1 / 16	Cancer	GENTLES_modul11
40	8.6	NULL	1 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS

GW_154

Local Summary

%DE = 0.82

metagenes = 20

genes = 224

genes in genesets = 221

genes with fdr < 0.1 = 150 (5 + / 145 −)

genes with fdr < 0.05 = 135 (5 + / 130 −)

genes with fdr < 0.01 = 95 (3 + / 92 −)

<r> metagenes = 0.98

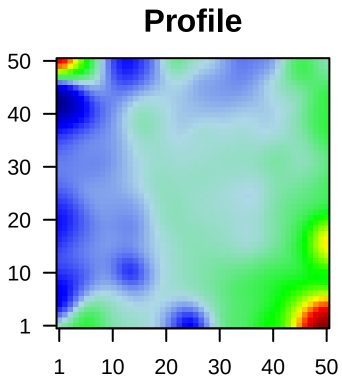
<r> genes = 0.34

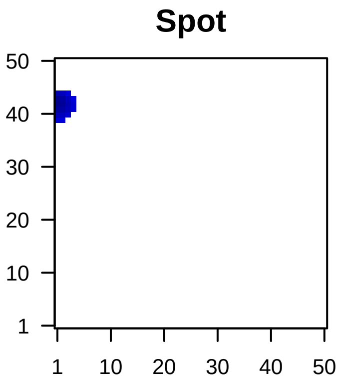
<FC> = −0.36

<shrinkage−t> = −12.6

<p−value> = 0

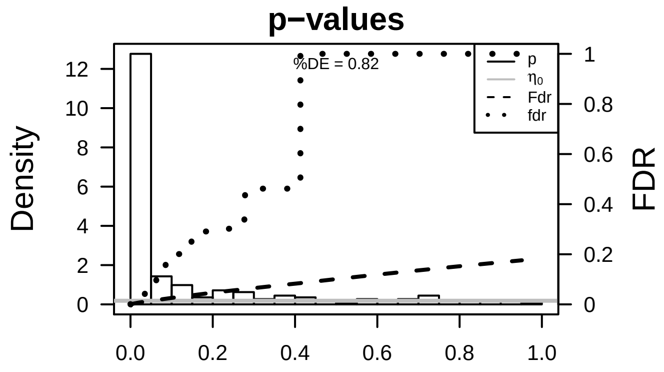
<fdr> = 0.48





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1515	−1.44	2e−16	1e−15	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
2	2167	−1.56	2e−16	1e−15	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
3	3306	−1.17	2e−16	1e−15	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
4	3489	−1.72	2e−16	1e−15	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
5	50805	−1.32	2e−16	1e−15	1 x 43	iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
6	55214	−1.46	2e−16	1e−15	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
7	6513	−1.24	2e−16	1e−15	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
8	144406	−1.33	2e−16	1e−15	1 x 42	WD repeat domain 66 [Source:HGNC Symbol;Acc:28506]
9	5744	−1.09	6e−15	1e−11	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
10	116211	−1.02	3e−13	1e−11	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
11	51200	−1.01	5e−13	4e−11	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
12	7498	0.99	1e−12	6e−11	3 x 43	xanthine dehydrogenase [Source:HGNC Symbol;Acc:12805]
13	3775	−0.98	3e−12	1e−10	1 x 43	potassium channel, subfamily K, member 1 [Source:HGNC S
14	4015	−0.97	5e−12	1e−10	1 x 41	lysyl oxidase [Source:HGNC Symbol;Acc:6664]
15	387882	−0.95	1e−11	1e−10	2 x 41	chromosome 12 open reading frame 75 [Source:HGNC Sym
16	113146	−0.95	1e−11	4e−09	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
17	80149	0.9	1e−10	2e−08	1 x 39	zinc finger CCCH−type containing 12A [Source:HGNC Symb
18	10397	−0.8	6e−10	1e−07	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
19	90102	−0.83	3e−09	2e−07	1 x 42	pleckstrin homology−like domain, family B, member 2 [Source
20	404203	−0.81	9e−09	2e−07	1 x 43	serine peptidase inhibitor, Kazal type 6 [Source:HGNC Symb



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.5	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
2	−12.36	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	−12.15	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
4	−11.94	NULL	1 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
5	−11.79	NULL	2 / 16	Glio	VERHAAK_MES subtype
6	−10.94	NULL	2 / 2	miRNA target	miR−199a*
7	−10.62	NULL	4 / 25	BP	brown fat cell differentiation
8	−10.36	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
9	−9.83	NULL	1 / 2	miRNA target	miR−346
10	−9.62	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
11	−9.52	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
12	−9.17	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
13	−9.04	NULL	4 / 12	BP	hemidesmosome assembly
14	−8.81	NULL	1 / 10	BP	white fat cell differentiation
15	−8.76	NULL	1 / 12	GSEA C2	SANCHEZ_MDM2_TARGETS
16	−8.62	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
17	−8.53	NULL	4 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
18	−8.4	NULL	1 / 8	GSEA C2	NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
19	−8.37	NULL	1 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
20	−8.37	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
21	−8.34	NULL	1 / 11	GSEA C2	REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_
22	−8.18	NULL	2 / 19	MF	L−ascorbic acid binding
23	−8.06	NULL	1 / 5	GSEA C2	ELVIDGE_HIF2A_TARGETS_UP
24	−7.93	NULL	1 / 12	MF	fatty acid binding
25	−7.87	NULL	1 / 8	GSEA C2	REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR
26	−7.7	NULL	1 / 15	GSEA C2	ZIRN_TRETINOIN_RESPONSE_WT1_UP
27	−7.66	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
28	−7.57	NULL	1 / 13	BP	cellular response to lithium ion
29	−7.5	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
30	−7.34	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
31	−7.22	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ
32	−7.13	NULL	2 / 15	BP	response to osmotic stress
33	−6.97	NULL	1 / 13	BP	nerve development
34	−6.97	NULL	1 / 15	BP	triglyceride catabolic process
35	−6.91	NULL	3 / 29	MF	oxidoreductase activity, acting on paired donors, with incorporation
36	−6.82	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
37	−6.81	NULL	9 / 76	BP	epidermis development
38	−6.7	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
39	−6.68	NULL	1 / 14	BP	multicellular organismal aging
40	−6.59	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN