GW_228

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2104 (1185 + / 919 −)

genes with fdr < 0.1 = 1601 (952 + / 649 −)

genes with fdr < 0.05 = 1349 (817 + / 532 −)

genes with fdr < 0.01 = 999 (620 + / 379 −)

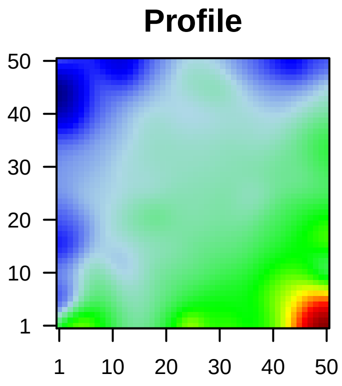
genes in genesets = 16332

<FC> = 0

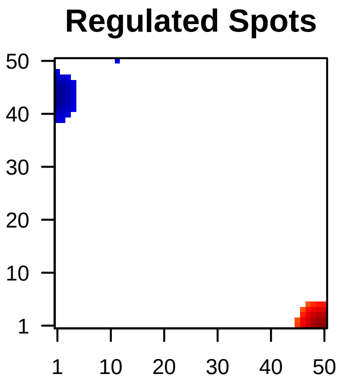
<shrinkage−t> = 0

<p−value> = 0.08

<fdr> = 0.85



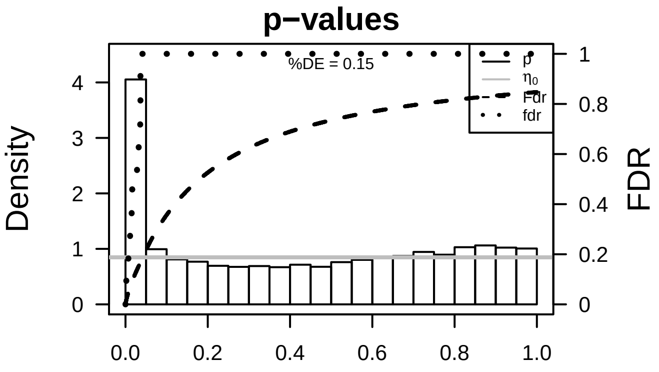
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.23	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	1.96	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1109	−1.81	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	347	1.62	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
5	348	1.7	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
6	92591	2.11	2e−16	3e−14	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
7	84446	1.6	2e−16	3e−14	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
8	713	1.64	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
9	57172	2.76	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
10	894	1.78	2e−16	3e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
11	930	2.24	2e−16	3e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
12	914	1.62	2e−16	3e−14	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
13	939	1.71	2e−16	3e−14	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
14	952	1.67	2e−16	3e−14	45 x 5	CD38 molecule [Source:HGNC Symbol;Acc:1667]
15	915	1.58	2e−16	3e−14	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
16	1158	2.12	2e−16	3e−14	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
17	9635	−1.76	2e−16	3e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
18	11151	1.55	2e−16	3e−14	50 x 1	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
19	51755	2.48	2e−16	3e−14	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
20	49860	2.23	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	23.45	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	22.7	NULL	417	H.Tiss	WIRTH_Immune system
3	14.75	NULL	312	BP	immune response
4	12.64	NULL	36	BP	muscle filament sliding
5	12.62	NULL	127	H.Tiss	WIRTH_Muscle
6	12.02	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
7	11.8	NULL	15	CC	MHC class II protein complex
8	11.59	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
9	11.01	NULL	316	Cancer	SPANG_BCL6−index2
10	10.76	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
11	10.76	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
12	10.76	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
13	10.76	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
14	10.71	NULL	16	H.Tiss	WIRTH_Hippocampus
15	10.44	NULL	74	BP	regulation of immune response
16	10.12	NULL	60	BP	T cell costimulation
17	9.7	NULL	162	CC	external side of plasma membrane
18	9.51	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
19	9.38	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
20	9.29	NULL	47	BP	antigen processing and presentation
Underexpressed					
1	−13.28	NULL	530	Cancer	Lembcke_Normal vs Adenoma
2	−13.27	NULL	135	H.Tiss	WIRTH_Mucosa
3	−12.72	NULL	572	Disease	GUDJ_psoriasis up
4	−12.25	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
5	−12.25	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
6	−8.57	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
7	−7.54	NULL	370	BP	mitotic cell cycle
8	−7.45	NULL	76	BP	epidermis development
9	−7.25	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	−7.22	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
11	−7.06	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
12	−6.74	NULL	15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_DN
13	−6.67	NULL	21	CC	desmosome
14	−6.64	NULL	12	BP	hemidesmosome assembly
15	−6.36	NULL	1233	TF	KIM_MYC targets
16	−5.97	NULL	13	H.Tiss	WIRTH_Tonsil
17	−5.9	NULL	12	BP	keratinocyte proliferation
18	−5.84	NULL	15	GSEA C2	LY_AGING_MIDDLE_DN
19	−5.67	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
20	−5.67	NULL	232	BP	mitosis

GW_228

Local Summary

%DE = 0.98

metagenes = 26

genes = 378

genes in genesets = 375

genes with fdr < 0.1 = 362 (358 + / 4 −)

genes with fdr < 0.05 = 357 (354 + / 3 −)

genes with fdr < 0.01 = 347 (344 + / 3 −)

<r> metagenes = 0.98

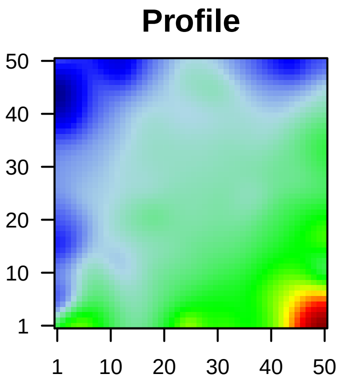
<r> genes = 0.54

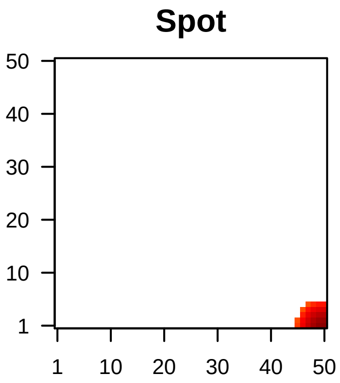
<FC> = 1.04

<shrinkage−t> = 36.48

<p−value> = 0

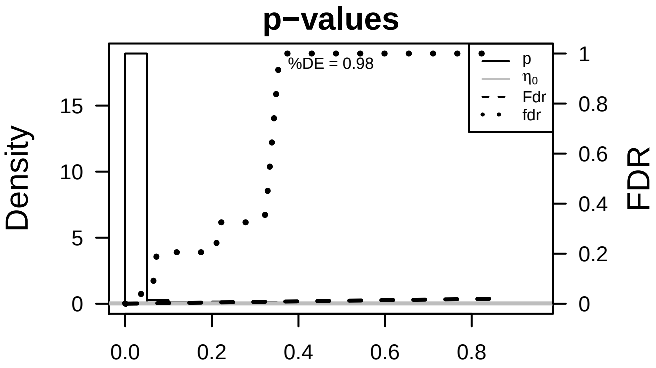
<fdr> = 0.09


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	1.7	2e−16	3e−17	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	92591	2.11	2e−16	3e−17	48 x 2	ankyrin repeat and SOCS box containing 16 [Source:HGNC
3	713	1.64	2e−16	3e−17	50 x 1	complement component 1, q subcomponent, B chain [Source
4	57172	2.76	2e−16	3e−17	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
5	894	1.78	2e−16	3e−17	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
6	930	2.24	2e−16	3e−17	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
7	914	1.62	2e−16	3e−17	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
8	939	1.71	2e−16	3e−17	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
9	915	1.58	2e−16	3e−17	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
10	11151	1.55	2e−16	3e−17	50 x 1	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
11	51755	2.48	2e−16	3e−17	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
12	10563	2.56	2e−16	3e−17	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
13	4283	2.01	2e−16	3e−17	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
14	1535	1.65	2e−16	3e−17	47 x 1	cytochrome b−245, alpha polypeptide [Source:HGNC Symbo
15	1794	1.62	2e−16	3e−17	50 x 1	dedicator of cytokinesis 2 [Source:HGNC Symbol;Acc:2988]
16	81704	1.61	2e−16	3e−17	50 x 1	dedicator of cytokinesis 8 [Source:HGNC Symbol;Acc:19191]
17	54855	2.8	2e−16	3e−17	49 x 1	family with sequence similarity 46, member C [Source:HGNC
18	84824	1.91	2e−16	3e−17	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]
19	80307	1.7	2e−16	3e−17	45 x 1	
20	51303	2.04	2e−16	3e−17	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.89	NULL	110 / 417	H.Tiss	WIRTH_Immune system
2	29.46	NULL	121 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.7	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
4	21.14	NULL	13 / 15	CC	MHC class II protein complex
5	20.91	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	20.09	NULL	68 / 312	BP	immune response
7	19.72	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
8	19.23	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
9	17.23	NULL	54 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	17.23	NULL	54 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	17.23	NULL	54 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	17.23	NULL	54 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	16.61	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
14	16.12	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
15	14.75	NULL	20 / 60	BP	T cell costimulation
16	14.43	NULL	8 / 13	Cancer	GENTLES_modul18
17	14.03	NULL	18 / 74	BP	regulation of immune response
18	13.78	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	13.75	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	13.43	NULL	12 / 28	BP	B cell receptor signaling pathway
21	13.2	NULL	16 / 47	BP	antigen processing and presentation
22	13.19	NULL	29 / 162	CC	external side of plasma membrane
23	13.13	NULL	7 / 16	Lymphoma	WRIGHT_ABC UP
24	12.71	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
25	12.35	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
26	12.34	NULL	20 / 84	BP	T cell receptor signaling pathway
27	12.33	NULL	6 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
28	12.29	NULL	8 / 16	GSEA C2	SU_THYMUS
29	12.28	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
30	11.95	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	11.71	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
32	11.7	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
33	11.69	NULL	28 / 204	BP	cell surface receptor signaling pathway
34	11.67	NULL	4 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
35	11.1	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
36	11.08	NULL	6 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
37	10.97	NULL	36 / 316	Cancer	SPANG_BCL6−index2
38	10.76	NULL	6 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
39	10.68	NULL	6 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
40	10.6	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D

GW_228

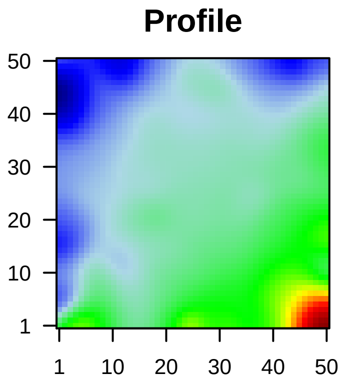
Local Summary

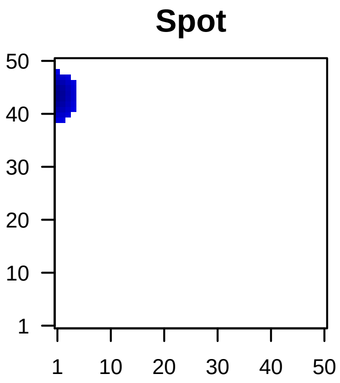
%DE = 0.94
metagenes = 33
genes = 367
genes in genesets = 360

genes with fdr < 0.1 = 316 (3 + / 313 −)
genes with fdr < 0.05 = 309 (3 + / 306 −)
genes with fdr < 0.01 = 257 (2 + / 255 −)

<r> metagenes = 0.91
<r> genes = 0.34

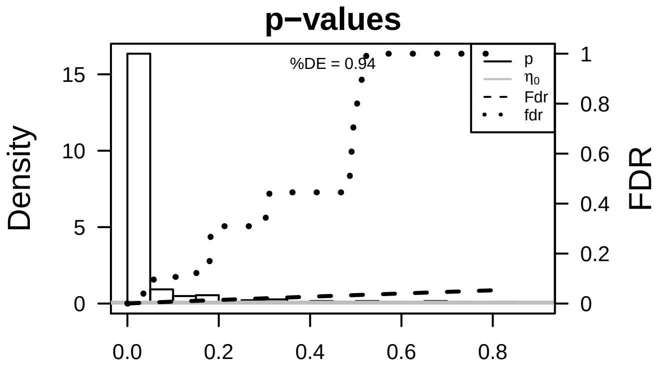
<FC> = −0.68
<shrinkage−t> = −23.96
<p−value> = 0
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9635	−1.76	2e−16	4e−16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
2	1825	−1.54	2e−16	4e−16	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
3	2167	−1.65	2e−16	4e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
4	3306	−1.99	2e−16	4e−16	1 x 42	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
5	3552	−1.67	2e−16	4e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
6	56300	−2	2e−16	4e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
7	10397	−1.68	2e−16	4e−16	1 x 42	N−myc downstream regulated 1 [Source:HGNC Symbol;Acc:
8	5317	−1.57	2e−16	4e−16	1 x 46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
9	6273	−1.71	2e−16	4e−16	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
10	2810	−1.8	2e−16	4e−16	1 x 45	stratifin [Source:HGNC Symbol;Acc:10773]
11	6513	−1.56	2e−16	4e−16	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
12	6665	−1.77	2e−16	4e−16	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Symb
13	23682	−1.54	4e−16	2e−14	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
14	116211	−1.5	2e−15	2e−14	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/
15	6318	−1.49	2e−15	2e−14	1 x 48	serpin peptidase inhibitor, clade B (ovalbumin), member 4 [So
16	6706	−1.49	3e−15	9e−14	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
17	1001	−1.46	7e−15	3e−13	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
18	1839	−1.44	2e−14	6e−13	1 x 45	heparin−binding EGF−like growth factor [Source:HGNC Symb
19	150696	−1.41	7e−14	6e−13	2 x 45	prominin 2 [Source:HGNC Symbol;Acc:20685]
20	113146	−1.4	1e−13	6e−13	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.96	NULL	40 / 135	H.Tiss	WIRTH_Mucosa
2	−21.2	NULL	93 / 572	Disease	GUDJ_psoriasis up
3	−20.9	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−19.29	NULL	11 / 21	CC	desmosome
5	−14.26	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
6	−12.26	NULL	18 / 76	BP	epidermis development
7	−12.01	NULL	5 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
8	−11.6	NULL	2 / 2	miRNA target	miR−199a*
9	−11.58	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
10	−11.57	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
11	−11.53	NULL	2 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
12	−10.78	NULL	3 / 12	BP	keratinocyte proliferation
13	−10.1	NULL	5 / 12	BP	hemidesmosome assembly
14	−10.04	NULL	6 / 32	CC	cell−cell adherens junction
15	−10.04	NULL	5 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
16	−9.49	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
17	−9.28	NULL	9 / 44	BP	skin development
18	−9.02	NULL	4 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
19	−8.91	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
20	−8.81	NULL	5 / 15	CC	connexon complex
21	−8.64	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
22	−8.61	NULL	19 / 82	CC	intermediate filament
23	−8.29	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_DENA_UP
24	−8.17	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
25	−8.06	NULL	2 / 15	MF	interleukin−1 receptor binding
26	−7.98	NULL	9 / 53	BP	keratinocyte differentiation
27	−7.98	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
28	−7.84	NULL	2 / 9	GSEA C2	KYNG_DNA_DAMAGE_UP
29	−7.84	NULL	2 / 9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
30	−7.79	NULL	6 / 21	CC	gap junction
31	−7.73	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
32	−7.61	NULL	3 / 13	GSEA C2	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_UP
33	−7.61	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
34	−7.58	NULL	2 / 11	BP	response to metal ion
35	−7.5	NULL	3 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
36	−7.49	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
37	−7.48	NULL	3 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
38	−7.48	NULL	4 / 22	MF	cadherin binding
39	−7.43	NULL	3 / 15	GSEA C2	CROMER_METASTASIS_DN
40	−7.43	NULL	1 / 5	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQ

GW_228

Local Summary

%DE = 0.92

metagenes = 1

genes = 22

genes in genesets = 22

genes with fdr < 0.1 = 18 (0 + / 18 −)

genes with fdr < 0.05 = 18 (0 + / 18 −)

genes with fdr < 0.01 = 12 (0 + / 12 −)

<r> metagenes = NA

<r> genes = 0.32

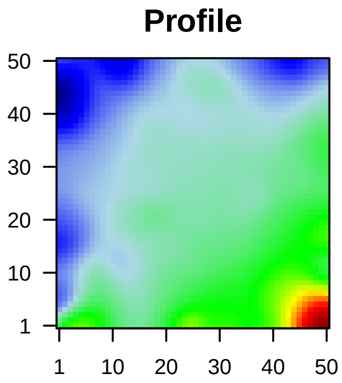
<FC> = −0.52

<shrinkage−t> = −18.59

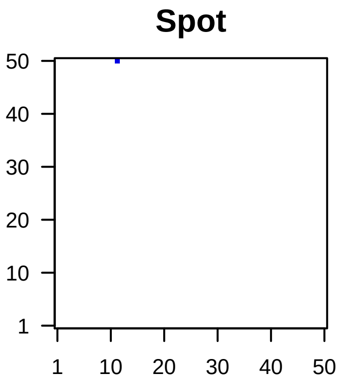
<p−value> = 0

<fdr> = 0.45

Profile

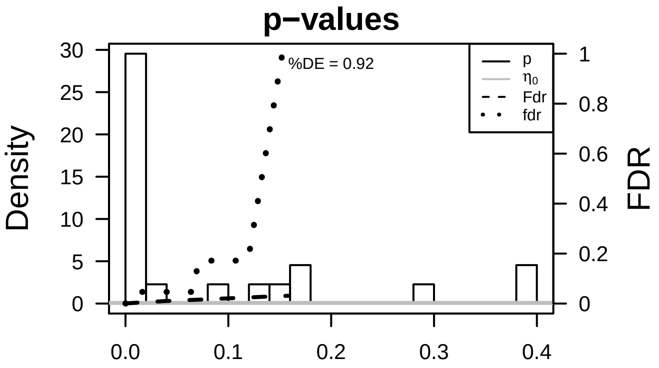


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10653	−1.04	3e−09	3e−07	12 x 50	serine peptidase inhibitor, Kunitz type, 2 [Source:HGNC Sym
2	4071	−0.89	3e−07	3e−07	12 x 50	transmembrane 4 L six family member 1 [Source:HGNC Sym
3	10610	−0.96	3e−07	2e−06	12 x 50	ST6 (alpha−N−acetyl−neuraminyl−2,3−beta−galactosyl−1,3)−
4	53637	−0.91	1e−06	2e−06	12 x 50	sphingosine−1−phosphate receptor 5 [Source:HGNC Symbol
5	2950	−0.82	2e−06	3e−04	12 x 50	glutathione S−transferase pi 1 [Source:HGNC Symbol;Acc:46
6	2049	−0.69	2e−04	3e−04	12 x 50	EPH receptor B3 [Source:HGNC Symbol;Acc:3394]
7	90407	−0.68	3e−04	8e−04	12 x 50	transmembrane protein 41A [Source:HGNC Symbol;Acc:305
8	6575	−0.61	1e−03	8e−04	12 x 50	solute carrier family 20 (phosphate transporter), member 2 [S
9	31	−0.6	1e−03	2e−03	12 x 50	acetyl−CoA carboxylase alpha [Source:HGNC Symbol;Acc:8
10	406988	−0.57	3e−03	7e−03	12 x 50	MIR205 host gene (non−protein coding) [Source:HGNC Sym
11	873	−0.48	1e−02	7e−03	12 x 50	carbonyl reductase 1 [Source:HGNC Symbol;Acc:1548]
12	7464	−0.47	1e−02	7e−03	12 x 50	coronin, actin binding protein, 2A [Source:HGNC Symbol;Acc
13	6016	−0.46	2e−02	3e−02	12 x 50	Ras−like without CAAX 1 [Source:HGNC Symbol;Acc:10023]
14	79745	−0.4	4e−02	5e−02	12 x 50	CAP−GLY domain containing linker protein family, member 4
15	6256	−0.32	9e−02	5e−02	12 x 50	retinoid X receptor, alpha [Source:HGNC Symbol;Acc:10477]
16	4051	−0.28	1e−01	5e−02	12 x 50	cytochrome P450, family 4, subfamily F, polypeptide 3 [Sourc
17	6319	−0.26	2e−01	5e−02	12 x 50	stearoyl−CoA desaturase (delta−9−desaturase) [Source:HG
18	1595	−0.26	2e−01	5e−02	12 x 50	cytochrome P450, family 51, subfamily A, polypeptide 1 [Sou
19	9817	−0.25	2e−01	2e−01	12 x 50	kelch−like ECH−associated protein 1 [Source:HGNC Symbol;
20	23200	−0.2	3e−01	2e−01	12 x 50	ATPase, class VI, type 11B [Source:HGNC Symbol;Acc:1355



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−31.27	NULL	1 / 2	miRNA target	miR−124a
2	−28.05	NULL	1 / 5	GSEA C2	OHM_EMBRYONIC_CARCINOMA_UP
3	−23.34	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
4	−20.96	NULL	1 / 8	GSEA C2	JAZAG_TGFB1_SIGNALING_VIA_SMAD4_DN
5	−20.73	NULL	1 / 10	GSEA C2	SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN
6	−20.73	NULL	1 / 10	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN
7	−19.39	NULL	1 / 8	GSEA C2	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
8	−19.27	NULL	1 / 9	GSEA C2	FURUKAWA_DUSP6_TARGETS_PCI35_UP
9	−18.33	NULL	1 / 12	GSEA C2	PENG_LEUCINE_DEPRIVATION_DN
10	−18.33	NULL	1 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP
11	−17.91	NULL	1 / 10	GSEA C2	MARTINELLI_IMMATURE_NEUTROPHIL_DN
12	−16.93	NULL	1 / 11	GSEA C2	CLAUS_PGR_POSITIVE_MENINGIOMA_DN
13	−16.58	NULL	1 / 14	GSEA C2	TAVOR_CEBPA_TARGETS_UP
14	−16.58	NULL	1 / 14	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_DN
15	−16.58	NULL	1 / 14	GSEA C2	WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2
16	−16.56	NULL	1 / 10	BP	negative regulation of JUN kinase activity
17	−16.56	NULL	1 / 10	H.Tiss	WIRTH_B−cells
18	−16.56	NULL	1 / 10	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_DN
19	−15.86	NULL	1 / 15	GSEA C2	CAFFAREL_RESPONSE_TO_THC_24HR_5_DN
20	−15.86	NULL	1 / 15	GSEA C2	LU_IL4_SIGNALING
21	−15.84	NULL	1 / 12	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_DN
22	−15.52	NULL	1 / 11	BP	regulation of ERK1 and ERK2 cascade
23	−15.52	NULL	1 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
24	−15.52	NULL	1 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
25	−15.22	NULL	1 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN
26	−14.64	NULL	1 / 12	GSEA C2	TIMOFEEVA_GROWTH_STRESS_VIA_STAT1_DN
27	−14.64	NULL	1 / 12	GSEA C2	LI_LUNG_CANCER
28	−14.64	NULL	1 / 12	GSEA C2	YAMASHITA_LIVER_CANCER_STEM_CELL_DN
29	−14.44	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
30	−14.32	NULL	1 / 14	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
31	−13.89	NULL	1 / 13	BP	negative regulation of MAPK cascade
32	−13.89	NULL	1 / 13	GSEA C2	OHM_METHYLATED_IN_ADULT_CANCERS
33	−13.89	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
34	−13.89	NULL	1 / 13	GSEA C2	HOQUE_METHYLATED_IN_CANCER
35	−13.89	NULL	1 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
36	−13.89	NULL	1 / 13	GSEA C2	KEGG_PROSTATE_CANCER
37	−13.82	NULL	1 / 15	GSEA C2	KORKOLA_TERATOMA
38	−13.7	NULL	1 / 15	GSEA C2	CROMER_METASTASIS_DN
39	−13.4	NULL	1 / 2	Cancer	GENTLES_modul8
40	−13.26	NULL	1 / 16	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE