GW_067

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1862 (1031 + / 831 −)

genes with fdr < 0.1 = 1415 (826 + / 589 −)

genes with fdr < 0.05 = 1186 (718 + / 468 −)

genes with fdr < 0.01 = 835 (536 + / 299 −)

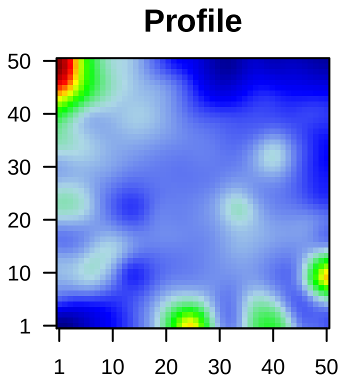
genes in genesets = 16332

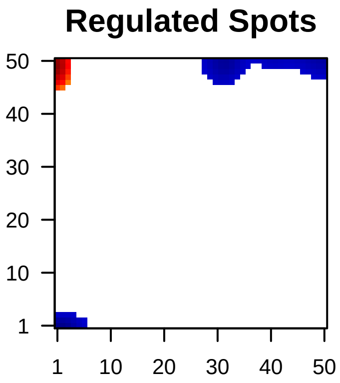
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

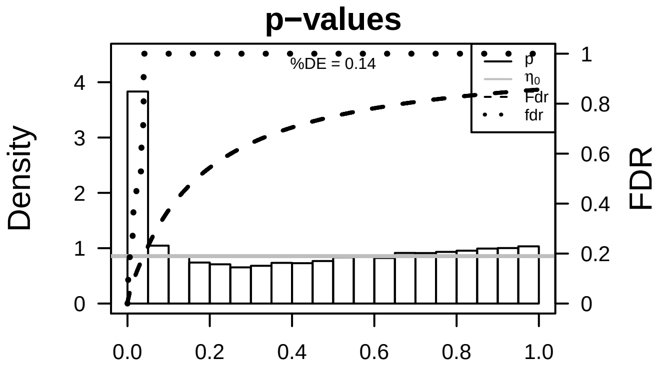
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	4.03	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.45	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10551	2.33	2e−16	2e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	220	1.61	2e−16	2e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC
5	222	1.49	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
6	242	1.28	2e−16	2e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
7	55107	1.86	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
8	51326	1.38	2e−16	2e−14	42 x 1	ADP−ribosylation factor−like 17B [Source:HGNC Symbol;Acc
9	525	1.4	2e−16	2e−14	12 x 8	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1
10	563	1.77	2e−16	2e−14	50 x 10	alpha−2−glycoprotein 1, zinc−binding [Source:HGNC Symbol
11	650	1.61	2e−16	2e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10
12	80341	3.05	2e−16	2e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
13	149563	1.76	2e−16	2e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symbo
14	92747	3.03	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
15	394263	1.29	2e−16	2e−14	3 x 50	
16	401546	1.28	2e−16	2e−14	50 x 11	chromosome 9 open reading frame 152 [Source:HGNC Symb
17	51806	−1.3	2e−16	2e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
18	57172	1.82	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
19	6358	1.32	2e−16	2e−14	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
20	6364	−1.52	2e−16	2e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	21.91	NULL	135	H.Tiss	WIRTH_Mucosa
2	19.26	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	16.99	NULL	42	BP	keratinization
4	16.63	NULL	127	H.Tiss	WIRTH_Muscle
5	15.04	NULL	16	H.Tiss	WIRTH_Hippocampus
6	15.04	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
7	14.71	NULL	21	CC	cornified envelope
8	12.69	NULL	36	BP	muscle filament sliding
9	11.99	NULL	53	BP	keratinocyte differentiation
10	11.9	NULL	572	Disease	GUDJ_psoriasis up
11	11.06	NULL	5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
12	10.4	NULL	76	BP	epidermis development
13	9.48	NULL	44	MF	structural constituent of muscle
14	9.27	NULL	449	Chr	Chr 20
15	8.62	NULL	14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
16	8.39	NULL	21	CC	desmosome
17	8.31	NULL	37	CC	sarcomere
18	8.15	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
19	7.39	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	6.89	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−9.16	NULL	534	Chr	Chr 8
2	−6.96	NULL	957	Chr	Chr 11
3	−6.72	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
4	−6.36	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
5	−6.21	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
6	−6.08	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
7	−6.01	NULL	914	Chr	Chr 3
8	−5.96	NULL	13	BP	response to vitamin D
9	−5.68	NULL	4640	CC	nucleus
10	−5.61	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_40_MCF10A
11	−5.41	NULL	16	GSEA C2	WOO_LIVER_CANCER_RECURRENCE_UP
12	−5.28	NULL	16	GSEA C2	LEONARD_HYPOXIA
13	−5.22	NULL	15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
14	−5.08	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
15	−4.99	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
16	−4.93	NULL	618	Chr	Chr 4
17	−4.9	NULL	1318	CC	mitochondrion
18	−4.87	NULL	287	BP	viral process
19	−4.84	NULL	15	GSEA C2	WU_HBX_TARGETS_1_UP
20	−4.83	NULL	153	MF	structural constituent of ribosome

GW_067

Local Summary

%DE = 0.84

metagenes = 17

genes = 233

genes in genesets = 227

genes with fdr < 0.1 = 173 (164 + / 9 −)

genes with fdr < 0.05 = 167 (158 + / 9 −)

genes with fdr < 0.01 = 152 (145 + / 7 −)

<r> metagenes = 0.95

<r> genes = 0.44

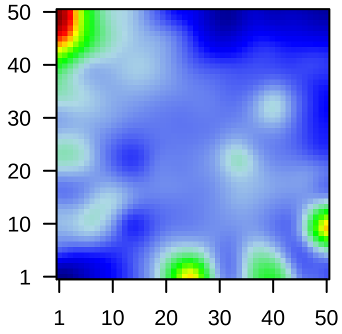
<FC> = 0.77

<shrinkage−t> = 27.21

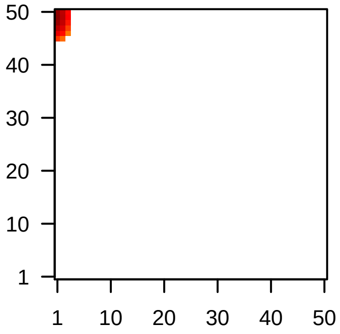
<p−value> = 0

<fdr> = 0.27

Profile



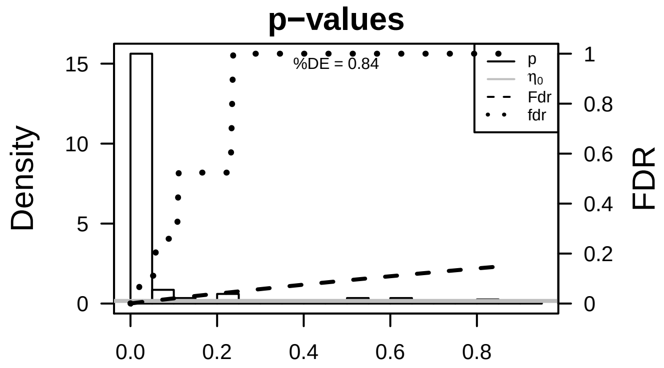
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	222	1.49	2e−16	2e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
2	242	1.28	2e−16	2e−16	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
3	394263	1.29	2e−16	2e−16	3 x 50	
4	1041	1.66	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
5	4680	1.81	2e−16	2e−16	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	22802	1.78	2e−16	2e−16	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	84518	1.7	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
8	54544	2.12	2e−16	2e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	3	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	93099	1.5	2e−16	2e−16	1 x 47	dermokine [Source:HGNC Symbol;Acc:25063]
11	1823	1.3	2e−16	2e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
12	1828	2.19	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	1832	1.32	2e−16	2e−16	1 x 46	desmoplakin [Source:HGNC Symbol;Acc:3052]
14	131177	2.36	2e−16	2e−16	3 x 50	family with sequence similarity 3, member D [Source:HGNC
15	2312	2.03	2e−16	2e−16	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
16	10804	1.47	2e−16	2e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
17	26525	1.52	2e−16	2e−16	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Ac
18	56300	1.8	2e−16	2e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
19	3860	1.89	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
20	3868	1.36	2e−16	2e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	49.95	NULL	83 / 135	H.Tiss	WIRTH_Mucosa
2	38.41	NULL	18 / 21	CC	cornified envelope
3	35.4	NULL	19 / 42	BP	keratinization
4	28.05	NULL	24 / 53	BP	keratinocyte differentiation
5	24.99	NULL	12 / 21	CC	desmosome
6	24.77	NULL	97 / 572	Disease	GUDJ_psoriasis up
7	23.87	NULL	23 / 76	BP	epidermis development
8	16.15	NULL	10 / 19	BP	peptide cross−linking
9	15.43	NULL	6 / 13	BP	negative regulation of peptidase activity
10	15.42	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	14.94	NULL	16 / 82	CC	intermediate filament
12	14.73	NULL	10 / 44	CC	keratin filament
13	14.23	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
14	14.05	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	13.32	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
16	13.24	NULL	23 / 186	MF	structural molecule activity
17	13.22	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
18	12.95	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
19	12.48	NULL	10 / 52	BP	negative regulation of endopeptidase activity
20	12.28	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
21	12.24	NULL	3 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
22	12.19	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
23	12.02	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
24	11.96	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
25	11.77	NULL	7 / 38	BP	epithelial cell differentiation
26	11.64	NULL	7 / 29	BP	regulation of proteolysis
27	11.62	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
28	11.4	NULL	5 / 23	MF	peptidase inhibitor activity
29	11.4	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
30	11.01	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
31	10.97	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
32	10.93	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
33	10.79	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
34	10.65	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
35	10.17	NULL	3 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
36	10.02	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
37	9.96	NULL	4 / 16	GSEA C2	JAEGER_METASTASIS_DN
38	9.68	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
39	9.34	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
40	8.89	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN

GW_067

Local Summary

%DE = 0.72

metagenes = 16

genes = 259

genes in genesets = 258

genes with fdr < 0.1 = 139 (23 + / 116 −)

genes with fdr < 0.05 = 118 (16 + / 102 −)

genes with fdr < 0.01 = 95 (11 + / 84 −)

<r> metagenes = 0.96

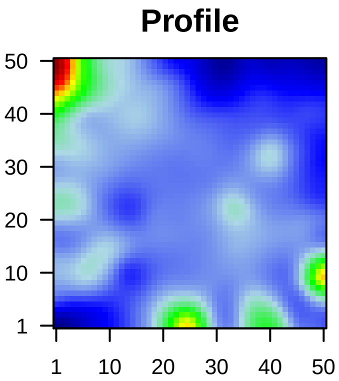
<r> genes = 0.41

<FC> = −0.31

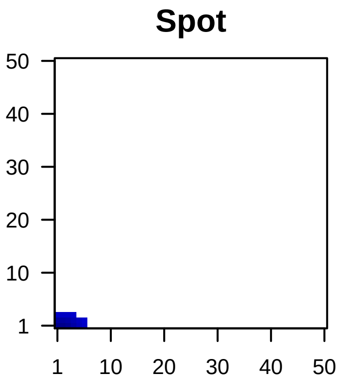
<shrinkage−t> = −10.83

<p−value> = 0

<fdr> = 0.5



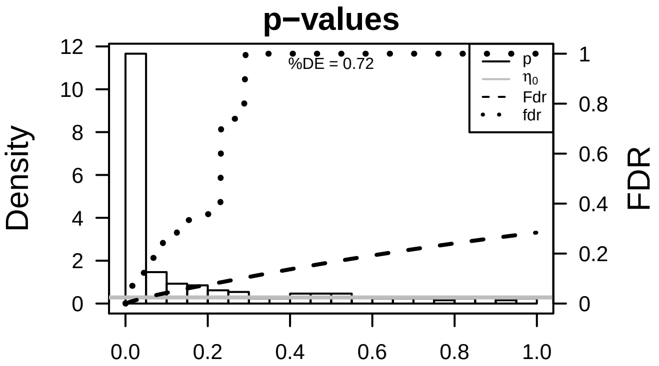
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	27122	−1.62	2e−16	2e−15	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Sy
2	8870	−1.38	2e−16	2e−15	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:5392
3	3553	−1.47	2e−16	2e−15	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
4	3576	−1.4	2e−16	2e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
5	5743	−1.51	2e−16	2e−15	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
6	5997	−1.51	2e−16	2e−15	5 x 1	regulator of G−protein signaling 2, 24kDa [Source:HGNC Syn
7	12	1.34	2e−16	2e−15	1 x 1	
8	1490	−1.26	1e−15	1e−13	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
9	3491	−1.24	3e−15	2e−13	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
10	3569	−1.22	6e−15	1e−11	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
11	414062	−1.15	2e−13	1e−11	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
12	871	−1.14	4e−13	1e−11	1 x 1	serpin peptidase inhibitor, clade H (heat shock protein 47), m
13	115908	−1.14	4e−13	1e−11	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
14	4312	−1.13	6e−13	3e−11	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
15	4319	1.12	1e−12	8e−10	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
16	83716	1.06	2e−11	8e−10	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S
17	6781	−1.05	2e−11	2e−09	1 x 3	stanniocalcin 1 [Source:HGNC Symbol;Acc:11373]
18	6515	−1.02	7e−11	2e−09	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
19	7045	0.93	9e−11	2e−09	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
20	1009	−1.01	1e−10	2e−09	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−20.99	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
2	−19.49	NULL	5 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
3	−19.34	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	−18.29	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
5	−18.1	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
6	−18	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
7	−17.43	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
8	−17.19	NULL	76 / 250	Lymphoma	LENZ_Stromal signature 1
9	−16.9	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
10	−16.77	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
11	−16.56	NULL	4 / 13	BP	response to vitamin D
12	−16.42	NULL	67 / 190	CC	extracellular matrix
13	−16.39	NULL	7 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
14	−16.27	NULL	4 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
15	−16.06	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
16	−16.03	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
17	−15.72	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
18	−15.65	NULL	3 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
19	−15.24	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
20	−15.18	NULL	2 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
21	−15.16	NULL	4 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
22	−15.14	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
23	−14.86	NULL	1 / 2	miRNA target	miR−18
24	−14.71	NULL	9 / 36	BP	embryo implantation
25	−14.36	NULL	8 / 12	miRNA target	miR−29c
26	−14.3	NULL	11 / 19	MF	extracellular matrix binding
27	−14.16	NULL	78 / 683	CC	extracellular space
28	−13.92	NULL	4 / 16	GSEA C2	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
29	−13.52	NULL	2 / 7	GSEA C2	DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_UP
30	−13.51	NULL	4 / 26	BP	positive regulation of nitric oxide biosynthetic process
31	−13.23	NULL	14 / 37	BP	collagen fibril organization
32	−13.21	NULL	3 / 10	BP	negative regulation of G−protein coupled receptor protein signaling
33	−13.19	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
34	−13.12	NULL	3 / 14	GSEA C2	HALMOS_CEBPA_TARGETS_DN
35	−12.96	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
36	−12.64	NULL	61 / 242	BP	extracellular matrix organization
37	−12.58	NULL	3 / 17	BP	positive regulation of NF−kappaB import into nucleus
38	−12.56	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
39	−12.48	NULL	3 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
40	−12.47	NULL	19 / 57	MF	extracellular matrix structural constituent

GW_067

Local Summary

%DE = 0.59

metagenes = 70

genes = 1013

genes in genesets = 995

genes with fdr < 0.1 = 319 (28 + / 291 −)

genes with fdr < 0.05 = 230 (22 + / 208 −)

genes with fdr < 0.01 = 133 (13 + / 120 −)

<r> metagenes = 0.64

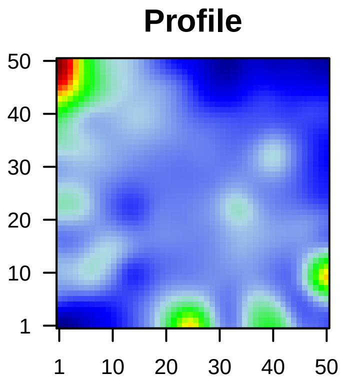
<r> genes = 0.19

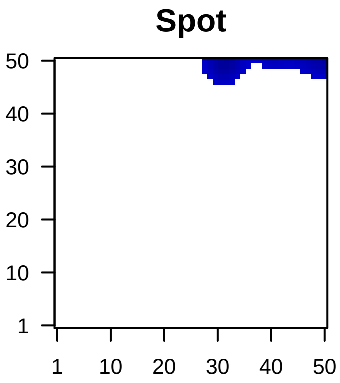
<FC> = −0.22

<shrinkage−t> = −7.57

<p−value> = 0.03

<fdr> = 0.7





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3866	−1.82	2e−16	5e−14	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
2	3945	−1.44	2e−16	5e−14	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
3	7358	−1.22	7e−15	1e−11	50 x 50	UDP−glucose 6−dehydrogenase [Source:HGNC Symbol;Acc
4	655	−1.19	4e−14	3e−10	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
5	11166	−1.11	1e−12	3e−10	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
6	4922	−1.11	1e−12	6e−09	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
7	81831	−1.05	2e−11	2e−08	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym
8	875	−1.02	6e−11	6e−07	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
9	55190	−0.95	2e−09	7e−07	47 x 50	nudix (nucleoside diphosphate linked moiety X)−type motif 11
10	154664	−0.92	5e−09	7e−07	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
11	8500	0.91	5e−09	7e−07	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (P
12	7991	−0.91	7e−09	2e−06	46 x 50	tumor suppressor candidate 3 [Source:HGNC Symbol;Acc:30
13	22974	0.89	1e−08	2e−06	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
14	139728	−0.88	2e−08	2e−06	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
15	26047	−0.88	2e−08	4e−06	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A
16	51377	−0.86	4e−08	4e−06	28 x 50	ubiquitin carboxyl−terminal hydrolase L5 [Source:HGNC Sym
17	10987	−0.85	5e−08	4e−06	33 x 50	COP9 signalosome subunit 5 [Source:HGNC Symbol;Acc:22
18	339512	−0.85	6e−08	4e−06	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
19	509	−0.85	6e−08	2e−05	31 x 50	ATP synthase, H+ transporting, mitochondrial F1 complex, ga
20	29097	−0.83	1e−07	2e−05	40 x 50	cornichon family AMPA receptor auxiliary protein 4 [Source:H

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.35	NULL	12 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
2	−10.93	NULL	11 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
3	−10.88	NULL	199 / 1318	CC	mitochondrion
4	−10.06	NULL	7 / 12	BP	oxidative phosphorylation
5	−10.04	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
6	−9.98	NULL	47 / 153	MF	structural constituent of ribosome
7	−8.89	NULL	61 / 253	BP	translation
8	−8.51	NULL	43 / 167	CC	ribosome
9	−8.45	NULL	7 / 10	CC	large ribosomal subunit
10	−8.37	NULL	64 / 534	Chr	Chr 8
11	−8.24	NULL	5 / 13	BP	regulation of blood vessel size
12	−8.12	NULL	10 / 16	GSEA C2	MOREAUX_MULTIPLE_MYELOMA_BY_TACI_DN
13	−7.98	NULL	7 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
14	−7.98	NULL	33 / 83	BP	respiratory electron transport chain
15	−7.85	NULL	39 / 152	BP	cellular metabolic process
16	−7.66	NULL	5 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
17	−7.42	NULL	4 / 16	GSEA C2	REACTOME_PYRUVATE_METABOLISM
18	−7.3	NULL	13 / 23	CC	mitochondrial ribosome
19	−7.15	NULL	27 / 128	BP	translational initiation
20	−7.12	NULL	10 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
21	−7.08	NULL	65 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
22	−7.08	NULL	65 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
23	−7.04	NULL	24 / 92	BP	viral life cycle
24	−6.88	NULL	164 / 1233	TF	KIM_MYC targets
25	−6.84	NULL	151 / 1253	BP	small molecule metabolic process
26	−6.84	NULL	24 / 92	BP	translational elongation
27	−6.83	NULL	6 / 19	BP	ATP biosynthetic process
28	−6.83	NULL	22 / 81	BP	viral transcription
29	−6.82	NULL	8 / 16	GSEA C2	MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN
30	−6.74	NULL	63 / 287	BP	viral process
31	−6.65	NULL	66 / 304	CC	mitochondrial inner membrane
32	−6.64	NULL	3 / 15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
33	−6.53	NULL	7 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
34	−6.45	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
35	−6.39	NULL	9 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
36	−6.3	NULL	243 / 2378	CC	cytosol
37	−6.26	NULL	6 / 15	GSEA C2	BARRIER_CANCER_RELAPSE_TUMOR_SAMPLE_UP
38	−6.25	NULL	29 / 109	BP	SRP−dependent cotranslational protein targeting to membrane
39	−6.14	NULL	7 / 20	TF	MYC_Metabolism UP
40	−6.08	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP