GW_187

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1702 (977 + / 725 −)

genes with fdr < 0.1 = 1434 (847 + / 587 −)

genes with fdr < 0.05 = 1116 (685 + / 431 −)

genes with fdr < 0.01 = 854 (545 + / 309 −)

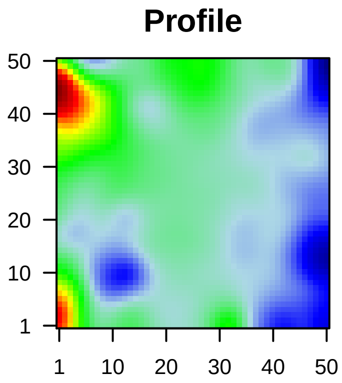
genes in genesets = 16332

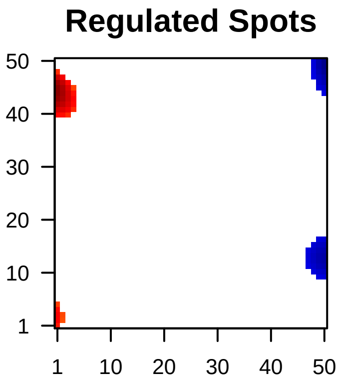
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

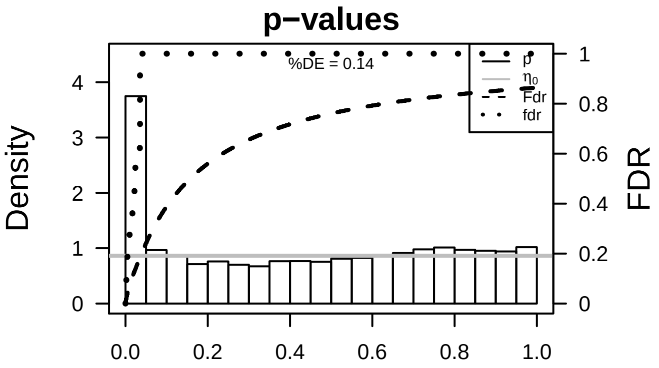
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−1.66	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	216	−1.59	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	218	−2.18	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	55107	1.53	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
5	306	1.29	2e−16	3e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
6	80117	1.63	2e−16	3e−14	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:
7	151516	1.96	2e−16	3e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
8	140851	1.31	2e−16	3e−14	1 x 5	
9	57172	−1.44	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
10	84290	1.92	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
11	857	1.77	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
12	6364	1.38	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
13	894	−1.27	2e−16	3e−14	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
14	978	1.67	2e−16	3e−14	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
15	1041	1.28	2e−16	3e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
16	1056	−1.28	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
17	22802	−1.94	2e−16	3e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
18	1366	−1.39	2e−16	3e−14	6 x 50	claudin 7 [Source:HGNC Symbol;Acc:2049]
19	84518	1.43	2e−16	3e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
20	1308	1.7	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	16.79	NULL	717	Chr	Chr 16
2	15.01	NULL	572	Disease	GUDJ_psoriasis up
3	11.33	NULL	42	BP	keratinization
4	11.08	NULL	21	CC	cornified envelope
5	8.74	NULL	242	BP	extracellular matrix organization
6	8.24	NULL	69	BP	extracellular matrix disassembly
7	8.21	NULL	12	GSEA C2	ZHU_CMV_8_HR_UP
8	7.97	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
9	7.62	NULL	64	BP	collagen catabolic process
10	7.61	NULL	76	BP	epidermis development
11	7.59	NULL	53	BP	keratinocyte differentiation
12	7.38	NULL	12	BP	hemidesmosome assembly
13	7.35	NULL	60	BP	interferon−gamma−mediated signaling pathway
14	7.11	NULL	7	MMML CGS	MACIEJ_MMML 9
15	7.02	NULL	190	CC	extracellular matrix
16	6.95	NULL	4	MMML CGS	MACIEJ_MMML 23
17	6.88	NULL	6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
18	6.86	NULL	1182	CC	extracellular region
19	6.79	NULL	16	GSEA C2	GRATIAS_RETINOBLASTOMA_16Q24
20	6.69	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−9.15	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−8.57	NULL	918	Chr	Chr 17
3	−6.16	NULL	914	Chr	Chr 3
4	−5.6	NULL	6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
5	−5.06	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
6	−4.99	NULL	1581	BP	regulation of transcription, DNA−dependent
7	−4.8	NULL	16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
8	−4.79	NULL	11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
9	−4.79	NULL	1574	BP	transcription, DNA−templated
10	−4.64	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	−4.52	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
12	−4.46	NULL	119	BP	xenobiotic metabolic process
13	−4.44	NULL	1749	MF	DNA binding
14	−4.42	NULL	15	GSEA C2	NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
15	−4.27	NULL	318	MF	chromatin binding
16	−4.21	NULL	24	TF Tissue	VAQUERIZAS_Trachea
17	−4.14	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
18	−4.1	NULL	16	CC	dystrophin−associated glycoprotein complex
19	−4.09	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
20	−4.09	NULL	18	MF	acyl−CoA dehydrogenase activity

GW_187

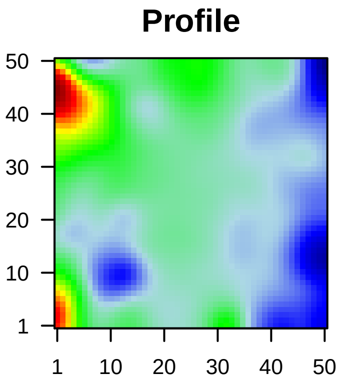
Local Summary

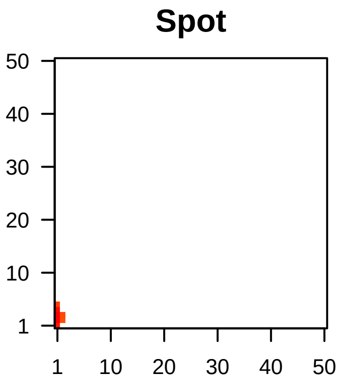
%DE = 0.95
metagenes = 7
genes = 135
genes in genesets = 133

genes with fdr < 0.1 = 116 (108 + / 8 −)
genes with fdr < 0.05 = 115 (107 + / 8 −)
genes with fdr < 0.01 = 97 (92 + / 5 −)

<r> metagenes = 0.98
<r> genes = 0.38

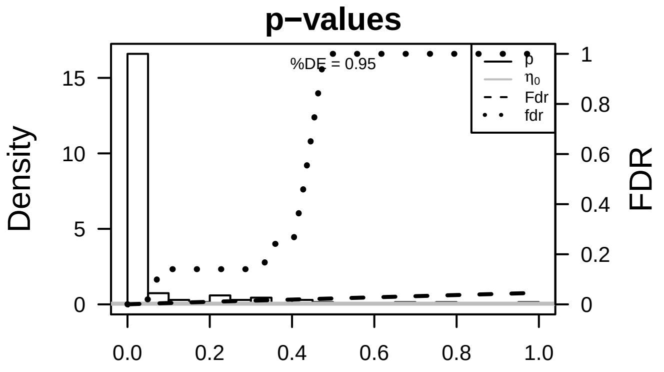
<FC> = 0.6
<shrinkage−t> = 21.11
<p−value> = 0
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	1.53	2e−16	9e−17	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	140851	1.31	2e−16	9e−17	1 x 5	
3	857	1.77	2e−16	9e−17	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
4	1437	1.69	2e−16	9e−17	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
5	1464	1.6	2e−16	9e−17	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
6	56603	1.53	2e−16	9e−17	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
7	11009	1.31	2e−16	9e−17	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
8	4312	1.67	2e−16	9e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
9	4319	1.35	2e−16	9e−17	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
10	4314	2.02	2e−16	9e−17	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
11	4502	1.29	2e−16	9e−17	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
12	10630	1.41	2e−16	9e−17	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
13	11098	1.38	2e−16	9e−17	1 x 1	protease, serine, 23 [Source:HGNC Symbol;Acc:14370]
14	5743	1.91	2e−16	9e−17	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
15	7045	1.36	2e−16	9e−17	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
16	7424	1.84	2e−16	9e−17	1 x 3	vascular endothelial growth factor C [Source:HGNC Symbol;A
17	55714	1.25	4e−16	2e−14	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
18	54541	1.21	4e−15	3e−14	1 x 4	DNA−damage−inducible transcript 4 [Source:HGNC Symbol;A
19	1012	1.19	1e−14	1e−13	1 x 5	cadherin 13 [Source:HGNC Symbol;Acc:1753]
20	3576	1.17	3e−14	1e−12	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	21.7	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	20.54	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
3	19.15	NULL	4 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
4	18.11	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
5	18.05	NULL	4 / 16	GSEA C2	LI_PROSTATE_CANCER_EPIGENETIC
6	16.99	NULL	5 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
7	16.06	NULL	3 / 10	BP	cellular response to zinc ion
8	15.91	NULL	2 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
9	15.87	NULL	28 / 242	BP	extracellular matrix organization
10	15.52	NULL	2 / 11	BP	prostaglandin metabolic process
11	14.95	NULL	4 / 16	GSEA C2	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN
12	14.92	NULL	3 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
13	13.98	NULL	9 / 64	BP	collagen catabolic process
14	13.96	NULL	3 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
15	13.88	NULL	2 / 16	BP	positive regulation of vasoconstriction
16	13.53	NULL	3 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
17	13.41	NULL	2 / 7	MMML CGS	MACIEJ_MMML 13
18	13.4	NULL	9 / 69	BP	extracellular matrix disassembly
19	13.32	NULL	2 / 12	GSEA C2	BROWNE_HCMV_INFECTION_4HR_UP
20	13.19	NULL	3 / 16	CC	lamellipodium membrane
21	13.1	NULL	7 / 68	Glio	cultured astroglia vs. in vivo astrocytes
22	13.08	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
23	12.95	NULL	2 / 16	GSEA C2	REACTOME_BASIGIN_INTERACTIONS
24	12.87	NULL	2 / 11	GSEA C2	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
25	12.76	NULL	2 / 13	GSEA C2	CHIN_BREAST_CANCER_COPY_NUMBER_UP
26	12.74	NULL	2 / 13	BP	induction of positive chemotaxis
27	12.66	NULL	3 / 15	BP	negative regulation of growth
28	12.61	NULL	22 / 250	Lymphoma	LENZ_Stromal signature 1
29	12.6	NULL	2 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
30	12.53	NULL	14 / 190	CC	extracellular matrix
31	12.53	NULL	39 / 683	CC	extracellular space
32	12.49	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
33	12.48	NULL	8 / 35	Glio	Colman_survival_associated
34	12.36	NULL	12 / 204	BP	angiogenesis
35	12.35	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
36	12.31	NULL	2 / 12	GSEA C2	GEISS_RESPONSE_TO_DSRNA_DN
37	12.26	NULL	2 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
38	12.25	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
39	12.18	NULL	4 / 15	BP	negative regulation of anoikis
40	12.14	NULL	2 / 13	GSEA C2	WANG_METHYLATED_IN_BREAST_CANCER

GW_187

Local Summary

%DE = 0.8

metagenes = 29

genes = 332

genes in genesets = 325

genes with fdr < 0.1 = 236 (223 + / 13 −)

genes with fdr < 0.05 = 224 (211 + / 13 −)

genes with fdr < 0.01 = 185 (177 + / 8 −)

<r> metagenes = 0.92

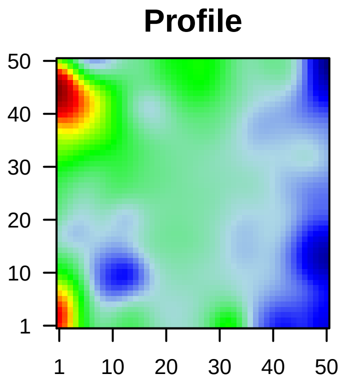
<r> genes = 0.36

<FC> = 0.59

<shrinkage−t> = 20.59

<p−value> = 0

<fdr> = 0.33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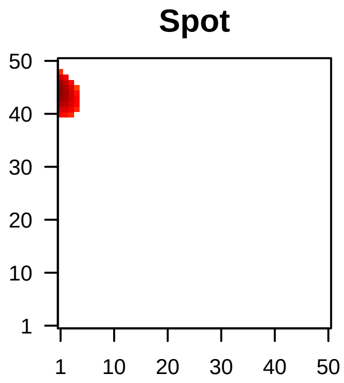
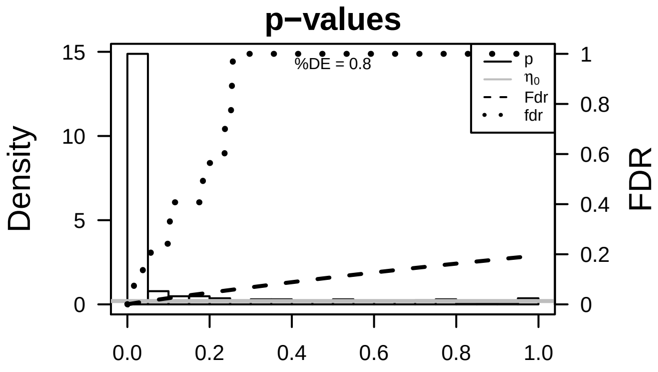

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	306	1.29	2e−16	4e−16	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
2	80117	1.63	2e−16	4e−16	2 x 40	ADP−ribosylation factor−like 14 [Source:HGNC Symbol;Acc:2
3	151516	1.96	2e−16	4e−16	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
4	978	1.67	2e−16	4e−16	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
5	1041	1.28	2e−16	4e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
6	1308	1.7	2e−16	4e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
7	1288	1.47	2e−16	4e−16	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
8	51200	1.73	2e−16	4e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
9	9547	1.45	2e−16	4e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
10	55894	2.85	2e−16	4e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	3.22	2e−16	4e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1823	1.55	2e−16	4e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
13	1828	1.46	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	2152	1.83	2e−16	4e−16	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
15	644054	1.52	2e−16	4e−16	2 x 46	family with sequence similarity 25, member C [Source:HGNC
16	100133093	1.65	2e−16	4e−16	2 x 46	family with sequence similarity 25, member C [Source:HGNC
17	9982	1.72	2e−16	4e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
18	80157	1.59	2e−16	4e−16	1 x 48	cell wall biogenesis 43 C−terminal homolog (S. cerevisiae) [S
19	2352	2.48	2e−16	4e−16	1 x 42	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
20	25818	1.3	2e−16	4e−16	1 x 47	kallikrein−related peptidase 5 [Source:HGNC Symbol;Acc:63


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.54	NULL	87 / 572	Disease	GUDJ_psoriasis up
2	15.1	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
3	13.81	NULL	19 / 82	CC	intermediate filament
4	13.8	NULL	9 / 44	CC	keratin filament
5	13.53	NULL	5 / 12	BP	hemidesmosome assembly
6	13.24	NULL	18 / 76	BP	epidermis development
7	12.83	NULL	38 / 135	H.Tiss	WIRTH_Mucosa
8	12.69	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	11.58	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
10	11.51	NULL	11 / 21	CC	desmosome
11	10.97	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
12	10.62	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
13	10.25	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
14	9.68	NULL	5 / 21	CC	gap junction
15	9.66	NULL	20 / 186	MF	structural molecule activity
16	9.14	NULL	6 / 42	BP	keratinization
17	8.96	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
18	8.76	NULL	5 / 21	CC	cornified envelope
19	8.75	NULL	3 / 15	BP	fibrinolysis
20	8.34	NULL	3 / 13	GSEA C2	HASINA_NOL7_TARGETS_UP
21	8.32	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
22	8.18	NULL	2 / 11	BP	positive regulation of positive chemotaxis
23	8.15	NULL	9 / 53	BP	keratinocyte differentiation
24	8.12	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
25	8.05	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
26	8.01	NULL	2 / 15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_DN
27	7.92	NULL	2 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
28	7.48	NULL	11 / 82	MF	structural constituent of cytoskeleton
29	7.47	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
30	7.38	NULL	4 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
31	7.38	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
32	7.33	NULL	3 / 16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
33	7.29	NULL	4 / 33	Glio	willscher_GBM_proteomics_wtOnly_SpotC
34	7.2	NULL	7 / 48	Glio	Noushmehr_Pron_GCIMP_hypermeth_DN
35	7.13	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
36	7.11	NULL	3 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
37	7.09	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
38	7.08	NULL	3 / 10	MF	gap junction channel activity
39	7.07	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
40	7.04	NULL	3 / 16	GSEA C2	HARRIS_HYPOXIA

GW_187

Local Summary

%DE = 0.76

metagenes = 26

genes = 309

genes in genesets = 305

genes with fdr < 0.1 = 196 (12 + / 184 −)

genes with fdr < 0.05 = 159 (11 + / 148 −)

genes with fdr < 0.01 = 80 (4 + / 76 −)

<r> metagenes = 0.91

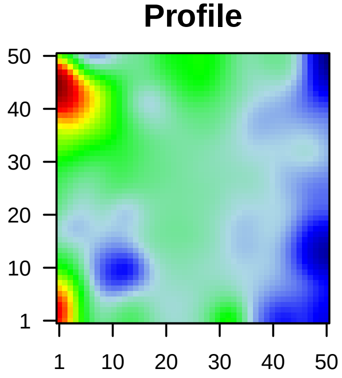
<r> genes = 0.25

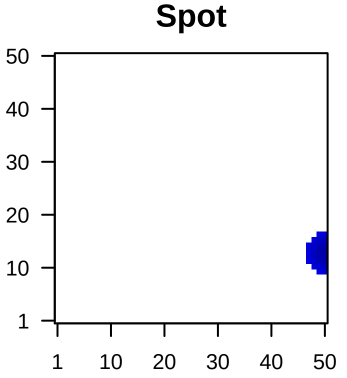
<FC> = −0.33

<shrinkage−t> = −11.56

<p−value> = 0

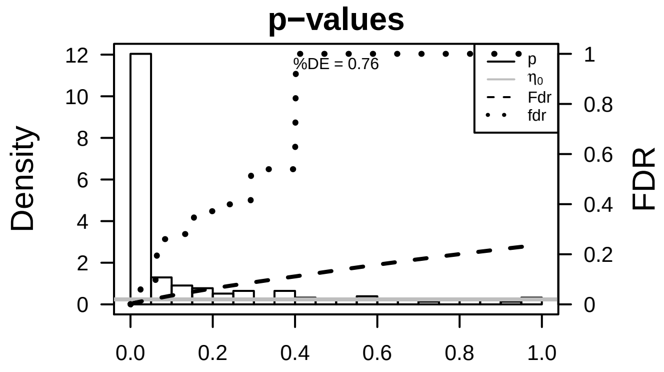
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3169	−1.39	2e−16	2e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	51316	−1.22	2e−15	2e−12	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
3	2568	−1.17	3e−14	9e−12	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
4	2139	−1.14	2e−13	8e−11	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;
5	6542	−1.09	1e−12	2e−10	50 x 16	solute carrier family 7 (cationic amino acid transporter, y+ sys
6	494470	−1.07	4e−12	2e−10	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
7	6920	−1.06	7e−12	2e−10	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
8	23171	−1.05	9e−12	6e−10	50 x 12	glycerol−3−phosphate dehydrogenase 1−like [Source:HGNC
9	260293	−1.03	2e−11	4e−08	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
10	1573	−0.95	5e−10	5e−08	50 x 11	cytochrome P450, family 2, subfamily J, polypeptide 2 [Sourc
11	9249	−0.93	2e−09	5e−08	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
12	10439	−0.92	3e−09	5e−08	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
13	63917	−0.92	3e−09	4e−07	50 x 16	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acety
14	155066	−0.89	8e−09	1e−06	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
15	83699	−0.86	2e−08	1e−06	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
16	56997	−0.84	4e−08	5e−06	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
17	1776	−0.8	2e−07	5e−06	48 x 12	deoxyribonuclease I−like 3 [Source:HGNC Symbol;Acc:2959]
18	221061	−0.79	3e−07	5e−06	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
19	7994	−0.79	3e−07	5e−06	50 x 16	K(lysine) acetyltransferase 6A [Source:HGNC Symbol;Acc:13
20	26471	−0.78	4e−07	5e−06	49 x 14	nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−14.77	NULL	5 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
2	−12.77	NULL	3 / 7	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−10.76	NULL	1 / 3	miRNA 3UTR ACGC−210
4	−10.11	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
5	−10.05	NULL	3 / 18	MF aromatase activity
6	−9.98	NULL	2 / 5	GSEA C2 SMID_BREAST_CANCER_ERBB2_DN
7	−9.62	NULL	4 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
8	−9.47	NULL	3 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
9	−8.85	NULL	1 / 7	GSEA C2 NEBEN_AML_WITH_FLT3_OR_NRAS_UP
10	−8.62	NULL	6 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
11	−8.33	NULL	3 / 13	GSEA C2 HUANG_DASATINIB_RESISTANCE_DN
12	−8.11	NULL	3 / 15	GSEA C2 SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN
13	−8.09	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
14	−7.86	NULL	3 / 10	BP epoxygenase P450 pathway
15	−7.8	NULL	4 / 9	GSEA C2 REACTOME_ETHANOL_OXIDATION
16	−7.58	NULL	2 / 11	CC photoreceptor outer segment membrane
17	−7.23	NULL	1 / 10	BP prostate gland epithelium morphogenesis
18	−7.15	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
19	−7.11	NULL	2 / 16	GSEA C2 ROY_WOUND_BLOOD_VESSEL_DN
20	−6.95	NULL	5 / 16	GSEA C2 CROMER_TUMORIGENESIS_DN
21	−6.95	NULL	2 / 15	GSEA C2 MASSARWEH_RESPONSE_TO_ESTRADIOL
22	−6.85	NULL	1 / 8	GSEA C2 HEIDENBLAD_AMPLICON_12P11_12_UP
23	−6.74	NULL	4 / 15	GSEA C2 DOANE_BREAST_CANCER_CLASSES_UP
24	−6.68	NULL	2 / 15	BP hormone metabolic process
25	−6.53	NULL	2 / 12	BP nitric oxide biosynthetic process
26	−6.45	NULL	2 / 12	BP neuron fate specification
27	−6.27	NULL	2 / 9	GSEA C2 MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
28	−6.21	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
29	−6.2	NULL	3 / 30	BP response to cold
30	−6.05	NULL	2 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_DN
31	−6.05	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
32	−6.05	NULL	3 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
33	−6.02	NULL	1 / 10	MF GABA−A receptor activity
34	−5.98	NULL	1 / 11	BP negative regulation of multicellular organism growth
35	−5.94	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition
36	−5.94	NULL	4 / 15	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
37	−5.92	NULL	5 / 63	MF oxidoreductase activity, acting on paired donors, with incorporation
38	−5.89	NULL	2 / 10	BP negative regulation of blood coagulation
39	−5.86	NULL	3 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
40	−5.82	NULL	2 / 14	GSEA C2 VANTVEER_BREAST_CANCER_ESR1_UP

GW_187

Local Summary

%DE = 0.76

metagenes = 17

genes = 234

genes in genesets = 233

genes with fdr < 0.1 = 139 (7 + / 132 −)

genes with fdr < 0.05 = 118 (4 + / 114 −)

genes with fdr < 0.01 = 89 (4 + / 85 −)

<r> metagenes = 0.96

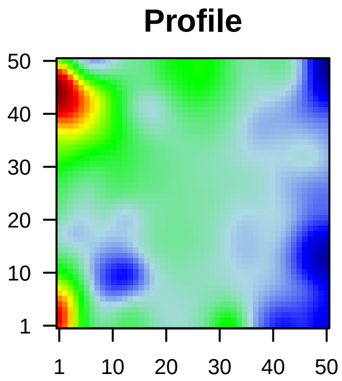
<r> genes = 0.26

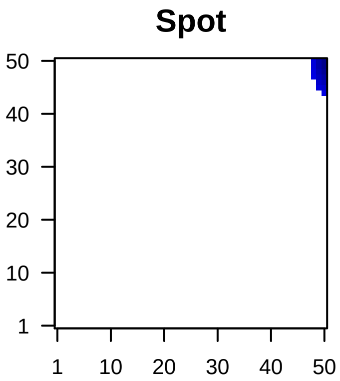
<FC> = −0.38

<shrinkage−t> = −13.36

<p−value> = 0

<fdr> = 0.54


Profile


Spot

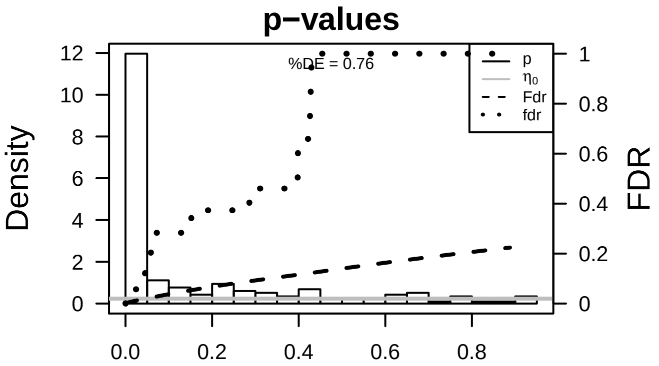
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.59	2e−16	2e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	1056	−1.28	2e−16	2e−15	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
3	3866	−2.55	2e−16	2e−15	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
4	3880	−3.95	2e−16	2e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
5	3856	−1.57	2e−16	2e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
6	11166	−1.51	2e−16	2e−15	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
7	256764	−2.89	2e−16	2e−15	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
8	84171	−1.17	3e−14	5e−12	50 x 49	lysyl oxidase−like 4 [Source:HGNC Symbol;Acc:17171]
9	56977	−1.14	1e−13	1e−09	50 x 49	storkhead box 2 [Source:HGNC Symbol;Acc:25450]
10	84707	−1.03	2e−11	1e−09	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
11	875	−1.01	4e−11	2e−09	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
12	339512	1	9e−11	2e−09	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
13	56963	−0.99	1e−10	2e−09	50 x 50	repulsive guidance molecule family member a [Source:HGNC
14	4922	−0.98	2e−10	4e−08	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
15	200810	−0.95	8e−10	2e−07	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransferas
16	4690	−0.91	4e−09	2e−07	49 x 50	NCK adaptor protein 1 [Source:HGNC Symbol;Acc:7664]
17	9076	0.88	1e−08	2e−07	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
18	139728	−0.88	1e−08	4e−06	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
19	6657	−0.82	1e−07	4e−06	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
20	54913	−0.8	2e−07	4e−06	48 x 47	ribonuclease P/MRP 25kDa subunit [Source:HGNC Symbol;

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−39.51	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−17.77	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
3	−16.19	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
4	−15.53	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
5	−14.95	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
6	−14.95	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
7	−14.42	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
8	−14.42	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
9	−13.5	NULL	1 / 18	CC	costamere
10	−13.07	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
11	−12.39	NULL	1 / 21	BP	sarcomere organization
12	−11.35	NULL	4 / 13	BP	regulation of blood vessel size
13	−11.18	NULL	4 / 82	MF	structural constituent of cytoskeleton
14	−10.85	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
15	−10.31	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
16	−9.95	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
17	−9.63	NULL	2 / 82	CC	intermediate filament
18	−9.52	NULL	1 / 15	H.Tiss	WIRTH_Cerebellum
19	−9.29	NULL	1 / 35	CC	cell periphery
20	−9.17	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
21	−9.16	NULL	2 / 12	GSEA C2	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
22	−8.54	NULL	2 / 12	BP	cellular aldehyde metabolic process
23	−8.45	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
24	−8.43	NULL	2 / 54	BP	response to estrogen
25	−8.36	NULL	2 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
26	−8.07	NULL	1 / 20	MF	scaffold protein binding
27	−8.04	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
28	−7.91	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
29	−7.87	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
30	−7.87	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
31	−7.66	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
32	−7.52	NULL	2 / 44	MF	structural constituent of muscle
33	−7.42	NULL	14 / 375	Disease	GUDJ_psoriasis down
34	−7.4	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
35	−7.4	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
36	−7.32	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
37	−7.02	NULL	9 / 34	BP	glutathione metabolic process
38	−6.91	NULL	5 / 23	BP	apoptotic mitochondrial changes
39	−6.83	NULL	1 / 2	miRNA target	miR−129
40	−6.8	NULL	2 / 16	GSEA C2	GOUYER_TATI_TARGETS_DN


p−values