GW_190

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1967 (1104 + / 863 −)

genes with fdr < 0.1 = 1658 (925 + / 733 −)

genes with fdr < 0.05 = 1365 (768 + / 597 −)

genes with fdr < 0.01 = 983 (547 + / 436 −)

genes in genesets = 16332

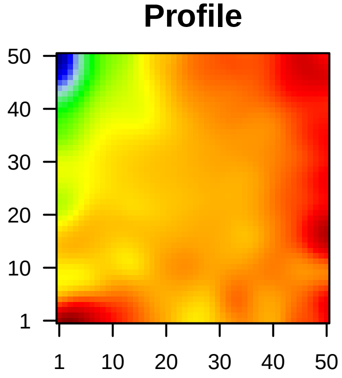
<FC> = 0

<shrinkage−t> = 0

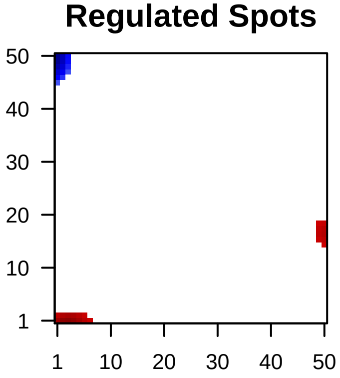
<p−value> = 0.08

<fdr> = 0.85

Profile



Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.59	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	21	2.05	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
3	131	−2.51	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	165	1.58	2e−16	2e−14	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
5	57016	−2.56	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	441282	−2.04	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
7	1646	−1.66	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
8	8644	−2.01	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
9	1109	−1.66	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
10	115701	1.85	2e−16	2e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
11	65124	−1.54	2e−16	2e−14	1 x 45	sosondowah ankyrin repeat domain family member C [Source
12	301	−1.63	2e−16	2e−14	4 x 48	annexin A1 [Source:HGNC Symbol;Acc:533]
13	9915	1.47	2e−16	2e−14	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
14	590	1.61	2e−16	2e−14	16 x 50	butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
15	121551	−1.59	2e−16	2e−14	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
16	387695	−2.55	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
17	399948	1.98	2e−16	2e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
18	64073	−2.45	2e−16	2e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
19	260436	4.21	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
20	56892	1.9	2e−16	2e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol

Global Geneset Analysis

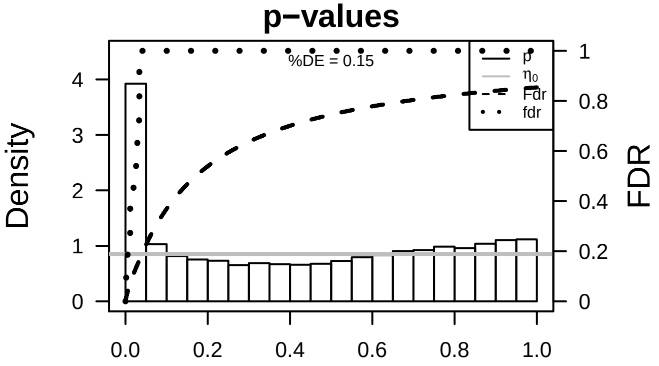
Overexpressed

Rank	GSZ	p−value	#all		Geneset
1	16.18	NULL	250	Lymphoma	LENZ_Stromal signature 1
2	14.2	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	13.09	NULL	190	CC	extracellular matrix
4	12.18	NULL	866	Chr	Chr 12
5	11.76	NULL	69	BP	extracellular matrix disassembly
6	11.51	NULL	16	MMML CGS	MACIEJ_MMML 1
7	10.93	NULL	64	BP	collagen catabolic process
8	10.92	NULL	242	BP	extracellular matrix organization
9	9.38	NULL	37	BP	collagen fibril organization
10	9.35	NULL	11	MF	platelet−derived growth factor binding
11	8.91	NULL	183	CC	proteinaceous extracellular matrix
12	8.85	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	8.7	NULL	57	MF	extracellular matrix structural constituent
14	8.54	NULL	16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
15	8.36	NULL	19	MF	extracellular matrix binding
16	8.08	NULL	68	CC	collagen
17	7.89	NULL	119	Lymphoma	ROSOLOWSKI_green total
18	7.88	NULL	12	miRNA target	miR−29c
19	7.67	NULL	16	GSEA C2	KORKOLA_SEMINOMA_UP
20	7.62	NULL	16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN

Underexpressed

Rank	GSZ	p−value	#all		Geneset
1	−35.61	NULL	135	H.Tiss	WIRTH_Mucosa
2	−21.44	NULL	21	CC	cornified envelope
3	−21.01	NULL	572	Disease	GUDJ_psoriasis up
4	−19.01	NULL	53	BP	keratinocyte differentiation
5	−17.76	NULL	42	BP	keratinization
6	−16.49	NULL	76	BP	epidermis development
7	−12.07	NULL	19	BP	peptide cross−linking
8	−11.11	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
9	−9.9	NULL	38	BP	epithelial cell differentiation
10	−9.87	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	−9.13	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	−8.21	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
13	−8.09	NULL	10	MF	RAGE receptor binding
14	−7.79	NULL	186	MF	structural molecule activity
15	−7.16	NULL	13	BP	negative regulation of peptidase activity
16	−7.09	NULL	15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
17	−7.09	NULL	14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
18	−7.01	NULL	16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
19	−6.99	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	−6.97	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN

p−values



GW_190

Local Summary

%DE = 0.74

metagenes = 13

genes = 259

genes in genesets = 258

genes with fdr < 0.1 = 146 (142 + / 4 −)

genes with fdr < 0.05 = 146 (142 + / 4 −)

genes with fdr < 0.01 = 121 (118 + / 3 −)

<r> metagenes = 0.96

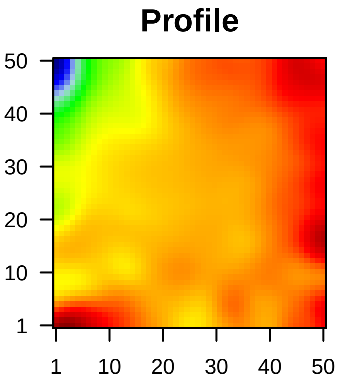
<r> genes = 0.43

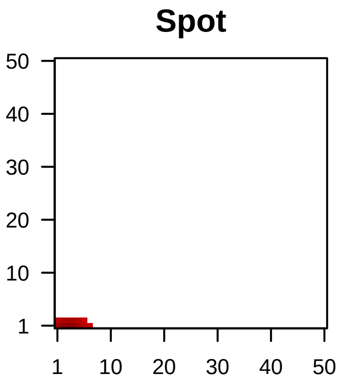
<FC> = 0.61

<shrinkage−t> = 21.54

<p−value> = 0

<fdr> = 0.44





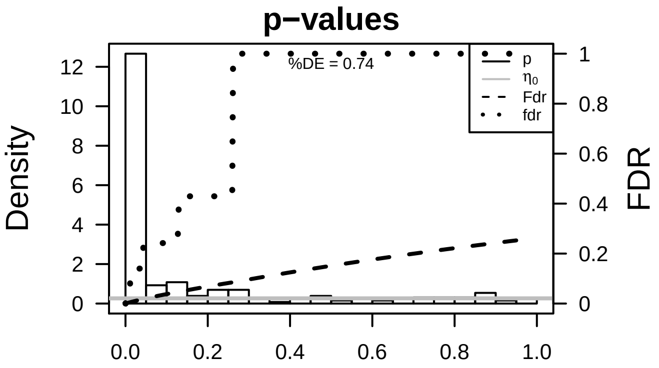
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	165	1.58	2e−16	7e−16	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
2	1300	1.59	2e−16	7e−16	3 x 1	collagen, type X, alpha 1 [Source:HGNC Symbol;Acc:2185]
3	1277	1.85	2e−16	7e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1278	2.33	2e−16	7e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
5	1281	2.11	2e−16	7e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
6	1289	1.53	2e−16	7e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1290	1.7	2e−16	7e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	1291	1.52	2e−16	7e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
9	1293	1.8	2e−16	7e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
10	115908	1.72	2e−16	7e−16	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
11	1513	2.07	2e−16	7e−16	4 x 1	cathepsin K [Source:HGNC Symbol;Acc:2536]
12	4060	1.53	2e−16	7e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
13	4320	2.08	2e−16	7e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
14	4316	3.37	2e−16	7e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
15	4318	2.5	2e−16	7e−16	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
16	10631	1.99	2e−16	7e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
17	6423	1.82	2e−16	7e−16	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
18	387914	2.8	2e−16	7e−16	6 x 1	shisa family member 2 [Source:HGNC Symbol;Acc:20366]
19	6678	1.86	2e−16	7e−16	3 x 1	secreted protein, acidic, cysteine−rich (osteonectin) [Source:
20	6696	2.76	2e−16	7e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	47.6	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	42.29	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
3	39.64	NULL	64 / 190	CC	extracellular matrix
4	38.99	NULL	30 / 69	BP	extracellular matrix disassembly
5	38.56	NULL	26 / 64	BP	collagen catabolic process
6	37.87	NULL	74 / 250	Lymphoma	LENZ_Stromal signature 1
7	36.12	NULL	8 / 11	MF	platelet−derived growth factor binding
8	31.97	NULL	59 / 242	BP	extracellular matrix organization
9	29.65	NULL	8 / 12	miRNA target	miR−29c
10	28.83	NULL	13 / 37	BP	collagen fibril organization
11	28.37	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
12	27.27	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
13	26.65	NULL	11 / 19	MF	extracellular matrix binding
14	25.17	NULL	4 / 6	GSEA C2	AGARWAL_AKT_PATHWAY_TARGETS
15	24.65	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
16	24.01	NULL	21 / 57	MF	extracellular matrix structural constituent
17	22.7	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
18	22.16	NULL	34 / 183	CC	proteinaceous extracellular matrix
19	21.67	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
20	21.04	NULL	4 / 16	GSEA C2	LU_TUMOR_VASCULATURE_UP
21	19.18	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
22	19.12	NULL	15 / 68	CC	collagen
23	18.98	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
24	18.77	NULL	10 / 40	BP	cellular response to amino acid stimulus
25	18.66	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
26	18.64	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
27	18.64	NULL	4 / 10	BP	protein heterotrimerization
28	18.6	NULL	69 / 683	CC	extracellular space
29	18.56	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
30	18.5	NULL	21 / 119	Lymphoma	ROSOLOWSKI_green total
31	18.07	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
32	17.78	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
33	17.58	NULL	98 / 1182	CC	extracellular region
34	17.4	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
35	16.09	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
36	15.75	NULL	4 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
37	15.75	NULL	4 / 16	GSEA C2	LU_TUMOR_ENDOTHELIAL_MARKERS_UP
38	15.71	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
39	15.7	NULL	64 / 553	Cancer	Lembcke_Colonic Inflammation
40	15.47	NULL	1 / 5	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_NIMUSTINE



GW_190

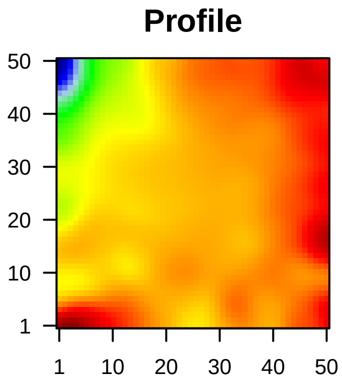
Local Summary

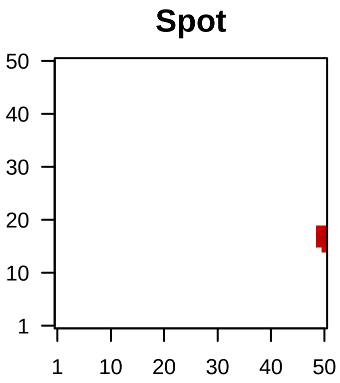
%DE = 0.74
metagenes = 9
genes = 163
genes in genesets = 162

genes with fdr < 0.1 = 109 (107 + / 2 −)
genes with fdr < 0.05 = 87 (86 + / 1 −)
genes with fdr < 0.01 = 71 (71 + / 0 −)

<r> metagenes = 0.98
<r> genes = 0.35

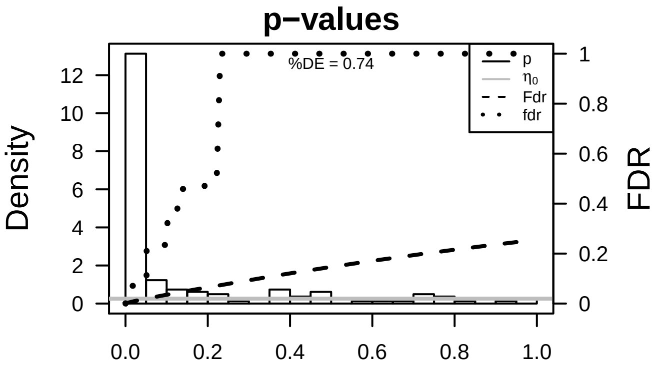
<FC> = 0.57
<shrinkage−t> = 20.02
<p−value> = 0
<fdr> = 0.46





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	2.05	2e−16	1e−15	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	9915	1.47	2e−16	1e−15	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
3	399948	1.98	2e−16	1e−15	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
4	221061	1.56	2e−16	1e−15	50 x 16	family with sequence similarity 171, member A1 [Source:HG
5	728715	2.58	2e−16	1e−15	50 x 18	
6	54959	2.94	2e−16	1e−15	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
7	10439	1.61	2e−16	1e−15	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
8	494470	1.47	2e−16	1e−15	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
9	6263	2.04	2e−16	1e−15	50 x 18	ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
10	51768	1.45	9e−16	1e−13	50 x 16	transmembrane 7 superfamily member 3 [Source:HGNC Sym
11	1365	1.41	4e−15	4e−13	50 x 15	claudin 3 [Source:HGNC Symbol;Acc:2045]
12	909	1.38	2e−14	4e−13	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
13	114801	1.37	2e−14	1e−11	50 x 19	transmembrane protein 200A [Source:HGNC Symbol;Acc:21
14	217	1.31	3e−13	2e−10	50 x 15	aldehyde dehydrogenase 2 family (mitochondrial) [Source:HG
15	55846	1.24	6e−12	6e−10	50 x 18	integrin alpha FG−GAP repeat containing 2 [Source:HGNC S
16	9603	1.21	2e−11	6e−10	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
17	79899	1.19	4e−11	6e−10	50 x 19	proline rich 5 like [Source:HGNC Symbol;Acc:25878]
18	9847	1.18	5e−11	9e−10	50 x 16	C2 calcium−dependent domain containing 5 [Source:HGNC
19	79805	1.17	7e−11	7e−08	50 x 18	vasohibin 2 [Source:HGNC Symbol;Acc:25723]
20	55608	1.07	2e−09	7e−08	50 x 19	ankyrin repeat domain 10 [Source:HGNC Symbol;Acc:20265]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	12.79	NULL	4 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	12.16	NULL	1 / 6	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_UP
3	11.26	NULL	1 / 13	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN
4	10.79	NULL	1 / 14	BP	biomineral tissue development
5	9.67	NULL	2 / 16	GSEA C2	DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP
6	9.55	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
7	9.48	NULL	1 / 2	TF	MYC_Cell cycle DOWN
8	9.43	NULL	1 / 2	TF	MYC_Chromatin_modification UP
9	9.43	NULL	1 / 2	miRNA target	miR−153
10	9.38	NULL	1 / 4	GSEA C2	IGARASHI_ATF4_TARGETS_UP
11	9	NULL	1 / 10	GSEA C2	KEGG_ALZHEIMERS_DISEASE
12	8.88	NULL	1 / 3	miRNA target	miR−148a
13	8.52	NULL	1 / 11	GSEA C2	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
14	8.52	NULL	1 / 11	GSEA C2	KEGG_CALCIUM_SIGNALING_PATHWAY
15	8.16	NULL	2 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
16	7.86	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30
17	7.8	NULL	2 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_POOR_SURVIVAL
18	7.76	NULL	2 / 16	GSEA C2	KORKOLA_TERATOMA_UP
19	7.59	NULL	4 / 40	TF Tissue	VAQUERIZAS_Fetal brain
20	7.51	NULL	2 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
21	7.42	NULL	2 / 16	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_UP
22	7.39	NULL	1 / 14	GSEA C2	ROSS_AML_OF_FAB_M7_TYPE
23	7.37	NULL	1 / 8	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN
24	7.19	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
25	7.1	NULL	1 / 15	BP	striated muscle contraction
26	7.08	NULL	1 / 10	GSEA C2	BROWNE_HCMV_INFECTION_12HR_UP
27	7.08	NULL	1 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
28	7.07	NULL	1 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
29	6.84	NULL	1 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
30	6.79	NULL	2 / 13	BP	developmental pigmentation
31	6.35	NULL	1 / 12	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
32	6.35	NULL	1 / 12	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_DN
33	6.35	NULL	1 / 12	GSEA C2	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
34	6.27	NULL	2 / 13	Cancer	GENTLES_modul12
35	6.15	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MF_DN
36	6.1	NULL	3 / 15	GSEA C2	GOLUB_ALL_VS_AML_UP
37	6.06	NULL	1 / 13	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_UP
38	6.06	NULL	1 / 13	GSEA C2	STEIN_ESR1_TARGETS
39	6.02	NULL	2 / 13	miRNA target	miR−34a
40	5.98	NULL	1 / 4	miRNA target	let−7c

GW_190

Local Summary

%DE = 0.98

metagenes = 15

genes = 222

genes in genesets = 216

genes with fdr < 0.1 = 215 (5 + / 210 −)

genes with fdr < 0.05 = 209 (4 + / 205 −)

genes with fdr < 0.01 = 205 (2 + / 203 −)

<r> metagenes = 0.95

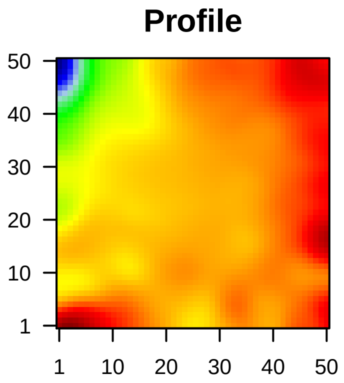
<r> genes = 0.45

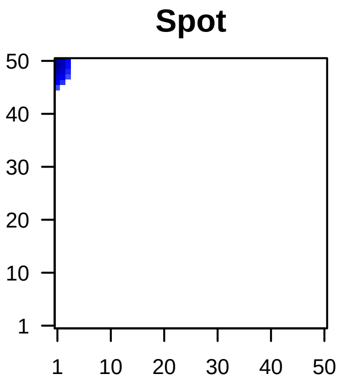
<FC> = −1.43

<shrinkage−t> = −50.53

<p−value> = 0

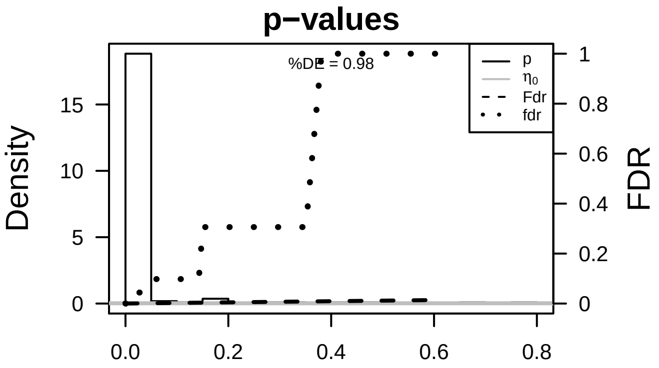
<fdr> = 0.08


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	1.59	2e−16	9e−18	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−2.51	2e−16	9e−18	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−2.56	2e−16	9e−18	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	441282	−2.04	2e−16	9e−18	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	−2.01	2e−16	9e−18	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
6	65124	−1.54	2e−16	9e−18	1 x 45	sosondowah ankyrin repeat domain family member C [Source
7	121551	−1.59	2e−16	9e−18	1 x 47	BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc
8	387695	−2.55	2e−16	9e−18	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
9	64073	−2.45	2e−16	9e−18	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Symb
10	375791	−2.49	2e−16	9e−18	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
11	84290	−1.54	2e−16	9e−18	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
12	1048	−1.81	2e−16	9e−18	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
13	4680	−3.19	2e−16	9e−18	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	9635	−2.93	2e−16	9e−18	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
15	9022	−1.9	2e−16	9e−18	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
16	84518	−2.81	2e−16	9e−18	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	54544	−1.72	2e−16	9e−18	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
18	49860	−2.49	2e−16	9e−18	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
19	1476	−1.43	2e−16	9e−18	1 x 50	cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
20	1672	−2.26	2e−16	9e−18	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−62.21	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
2	−43.54	NULL	18 / 21	CC	cornified envelope
3	−35.82	NULL	24 / 53	BP	keratinocyte differentiation
4	−34.44	NULL	19 / 42	BP	keratinization
5	−31.67	NULL	93 / 572	Disease	GUDJ_psoriasis up
6	−29.92	NULL	23 / 76	BP	epidermis development
7	−26.31	NULL	10 / 19	BP	peptide cross−linking
8	−22.6	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
9	−21.41	NULL	5 / 10	MF	RAGE receptor binding
10	−18.73	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	−18.5	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	−18.13	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	−15.75	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	−14.87	NULL	23 / 186	MF	structural molecule activity
15	−14.64	NULL	6 / 13	BP	negative regulation of peptidase activity
16	−14.63	NULL	10 / 44	CC	keratin filament
17	−14.48	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	−14.01	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
19	−13.8	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
20	−13.68	NULL	16 / 82	CC	intermediate filament
21	−13.53	NULL	12 / 21	CC	desmosome
22	−13.14	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
23	−12.79	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	−12.54	NULL	7 / 38	BP	epithelial cell differentiation
25	−12.41	NULL	10 / 52	BP	negative regulation of endopeptidase activity
26	−12.16	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
27	−11.73	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
28	−11.57	NULL	4 / 25	BP	response to zinc ion
29	−11.56	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
30	−11.31	NULL	3 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
31	−11.3	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
32	−11.05	NULL	7 / 29	BP	regulation of proteolysis
33	−11.01	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
34	−10.56	NULL	55 / 1182	CC	extracellular region
35	−10.37	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
36	−10.2	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
37	−10.19	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
38	−10.04	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
39	−9.96	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
40	−9.79	NULL	4 / 27	BP	response to bacterium