GW_148

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1616 (978 + / 638 −)

genes with fdr < 0.1 = 1376 (855 + / 521 −)

genes with fdr < 0.05 = 1043 (663 + / 380 −)

genes with fdr < 0.01 = 805 (540 + / 265 −)

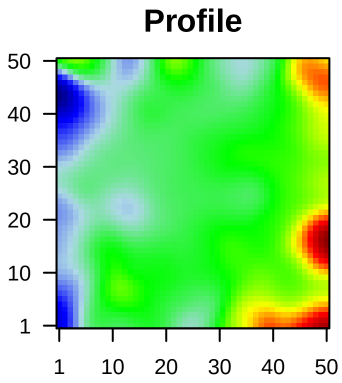
genes in genesets = 16332

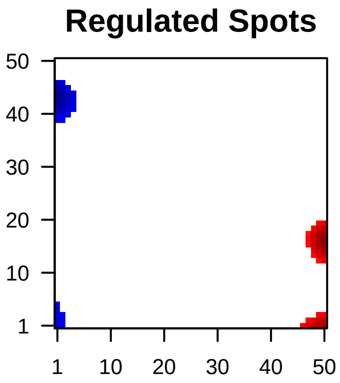
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

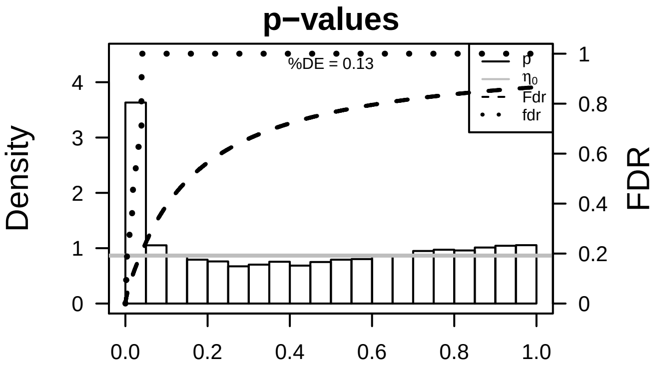
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.85	2e−16	4e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	348	1.37	2e−16	4e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	330	1.32	2e−16	4e−14	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
4	84830	1.42	2e−16	4e−14	15 x 1	androgen−dependent TFPI−regulating protein [Source:HGNC
5	771	−1.35	2e−16	4e−14	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
6	760	−1.38	2e−16	4e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
7	793	1.83	2e−16	4e−14	39 x 50	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
8	51806	1.47	2e−16	4e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
9	909	1.36	2e−16	4e−14	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
10	972	1.55	2e−16	4e−14	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
11	1048	1.37	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
12	1056	1.66	2e−16	4e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
13	22802	1.97	2e−16	4e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
14	9076	1.64	2e−16	4e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
15	9071	1.65	2e−16	4e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
16	1365	1.54	2e−16	4e−14	50 x 15	claudin 3 [Source:HGNC Symbol;Acc:2045]
17	54102	1.32	2e−16	4e−14	50 x 10	chloride intracellular channel 6 [Source:HGNC Symbol;Acc:2
18	169044	2.4	2e−16	4e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
19	49860	2.67	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
20	10563	1.41	2e−16	4e−14	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.44	NULL	15	CC	MHC class II protein complex
2	10.3	NULL	47	BP	antigen processing and presentation
3	8.86	NULL	534	Chr	Chr 8
4	8.42	NULL	24	TF Tissue	VAQUERIZAS_Trachea
5	8.19	NULL	57	Glio	developing astrocytes
6	8.18	NULL	52	Chr	Chr HSCHR6_MHC_QBL
7	8.11	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
8	7.9	NULL	823	MF	sequence−specific DNA binding transcription factor activity
9	7.75	NULL	1749	MF	DNA binding
10	7.73	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
11	7.55	NULL	417	H.Tiss	WIRTH_Immune system
12	7.55	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
13	7.4	NULL	187	Chr	Chr 21
14	7.28	NULL	714	Chr	Chr 6
15	7.26	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
16	7.23	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
17	7.19	NULL	4640	CC	nucleus
18	7.11	NULL	280	Chr	Chr 13
19	6.84	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
20	6.84	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
Underexpressed					
1	−10.36	NULL	957	Chr	Chr 11
2	−7.78	NULL	1720	Chr	Chr 1
3	−6.86	NULL	519	Chr	Chr 14
4	−6.56	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	−6.39	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
6	−6.14	NULL	10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
7	−5.78	NULL	10	BP	cellular response to zinc ion
8	−5.57	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
9	−5.5	NULL	10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
10	−5.38	NULL	618	Chr	Chr 4
11	−5.29	NULL	7	MMML CGS	MACIEJ_MMML 13
12	−5.22	NULL	1182	CC	extracellular region
13	−5.22	NULL	1318	CC	mitochondrion
14	−5.1	NULL	15	MF	interleukin−1 receptor binding
15	−5.01	NULL	15	BP	negative regulation of growth
16	−4.99	NULL	717	Chr	Chr 16
17	−4.76	NULL	183	CC	proteinaceous extracellular matrix
18	−4.73	NULL	190	CC	extracellular matrix
19	−4.69	NULL	1253	BP	small molecule metabolic process
20	−4.66	NULL	572	Disease	GUDJ_psoriasis up

GW_148

Local Summary

%DE = 0.64

metagenes = 11

genes = 232

genes in genesets = 230

genes with fdr < 0.1 = 89 (86 + / 3 −)

genes with fdr < 0.05 = 84 (82 + / 2 −)

genes with fdr < 0.01 = 64 (63 + / 1 −)

<r> metagenes = 0.99

<r> genes = 0.62

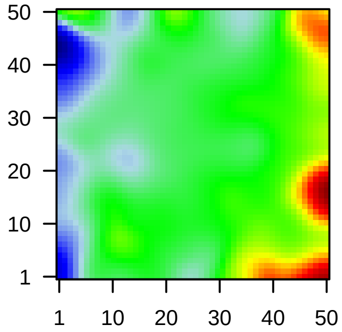
<FC> = 0.43

<shrinkage−t> = 14.94

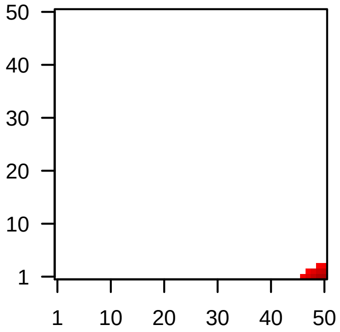
<p−value> = 0

<fdr> = 0.59

Profile



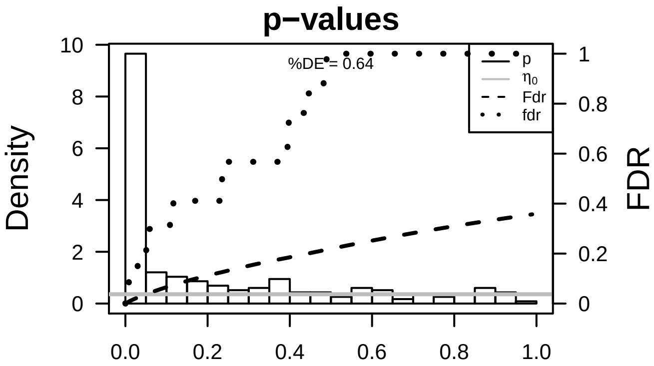
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	1.37	2e−16	1e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	330	1.32	2e−16	1e−15	47 x 1	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
3	972	1.55	2e−16	1e−15	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
4	10563	1.41	2e−16	1e−15	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
5	3113	1.67	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
6	3122	1.25	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
7	3126	1.55	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
8	3128	1.85	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
9	3512	1.47	2e−16	1e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
10	25849	2.13	2e−16	1e−15	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
11	5996	1.43	2e−16	1e−15	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
12	57484	1.89	2e−16	1e−15	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
13	9806	1.91	2e−16	1e−15	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
14	10537	2.68	2e−16	1e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
15	6352	1.29	2e−15	4e−13	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
16	3543	1.16	6e−15	4e−13	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
17	115701	1.25	1e−14	1e−12	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
18	4050	1.23	2e−14	1e−11	50 x 1	lymphotoxin beta (TNF superfamily, member 3) [Source:HGN
19	5168	1.19	2e−13	2e−11	50 x 2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
20	4283	1.17	4e−13	2e−11	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	49.09	NULL	12 / 15	CC	MHC class II protein complex
2	28.66	NULL	14 / 47	BP	antigen processing and presentation
3	26.49	NULL	49 / 312	BP	immune response
4	25.84	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
5	24.58	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
6	23.36	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
7	22.08	NULL	7 / 28	CC	transport vesicle membrane
8	20.55	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
9	20.53	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
10	20.27	NULL	14 / 60	BP	T cell costimulation
11	20.24	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
12	19.79	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
13	19.74	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
14	19.55	NULL	7 / 35	CC	trans−Golgi network membrane
15	19.27	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
16	18.35	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
17	17.44	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
18	17.1	NULL	8 / 52	Chr	Chr HSCHR6_MHC_QBL
19	17.04	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
20	16.82	NULL	7 / 46	CC	endocytic vesicle membrane
21	16.66	NULL	85 / 417	H.Tiss	WIRTH_Immune system
22	15.74	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
23	15.18	NULL	4 / 13	BP	lymph node development
24	14.72	NULL	4 / 12	BP	dendritic cell chemotaxis
25	14.47	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
26	14.43	NULL	12 / 84	BP	T cell receptor signaling pathway
27	14.29	NULL	11 / 60	BP	interferon−gamma−mediated signaling pathway
28	14.17	NULL	7 / 43	MF	chemokine activity
29	13.88	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
30	13.71	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
31	13.66	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
32	13.46	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
33	13.39	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
34	13.34	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
35	13.13	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
36	12.86	NULL	82 / 553	Cancer	Lembcke_Colonic Inflammation
37	12.13	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
38	11.95	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
39	11.8	NULL	3 / 10	BP	negative thymic T cell selection
40	11.58	NULL	24 / 162	CC	external side of plasma membrane

GW_148

Local Summary

%DE = 0.72

metagenes = 25

genes = 282

genes in genesets = 280

genes with fdr < 0.1 = 142 (138 + / 4 −)

genes with fdr < 0.05 = 134 (131 + / 3 −)

genes with fdr < 0.01 = 96 (95 + / 1 −)

<r> metagenes = 0.94

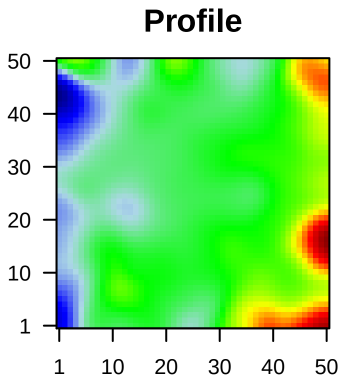
<r> genes = 0.3

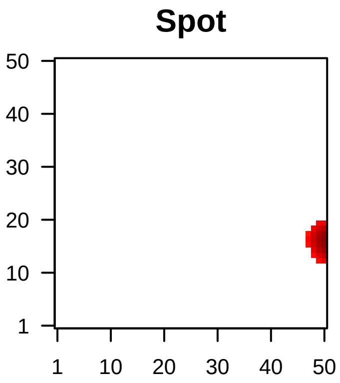
<FC> = 0.46

<shrinkage−t> = 16.28

<p−value> = 0

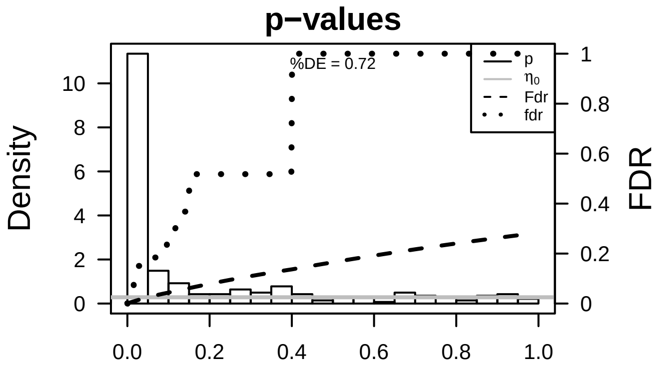
<fdr> = 0.51





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.85	2e−16	1e−15	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	909	1.36	2e−16	1e−15	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
3	1365	1.54	2e−16	1e−15	50 x 15	claudin 3 [Source:HGNC Symbol;Acc:2045]
4	221061	1.33	2e−16	1e−15	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
5	8857	2.08	2e−16	1e−15	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
6	2568	2.58	2e−16	1e−15	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
7	728715	2.02	2e−16	1e−15	50 x 18	
8	26002	1.43	2e−16	1e−15	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
9	7994	1.5	2e−16	1e−15	50 x 16	K(lysine) acetyltransferase 6A [Source:HGNC Symbol;Acc:13
10	9603	1.38	2e−16	1e−15	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
11	4948	1.71	2e−16	1e−15	50 x 17	oculocutaneous albinism II [Source:HGNC Symbol;Acc:8101]
12	51316	1.41	2e−16	1e−15	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
13	162494	1.34	2e−16	1e−15	50 x 17	rhomboid, veinlet−like 3 (Drosophila) [Source:HGNC Symbol;
14	494470	1.82	2e−16	1e−15	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
15	6263	2.18	2e−16	1e−15	50 x 18	ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
16	57556	1.61	2e−16	1e−15	50 x 17	sema domain, transmembrane domain (TM), and cytoplasmic
17	9189	1.4	2e−16	1e−15	50 x 18	zinc finger, BED−type containing 1 [Source:HGNC Symbol;Ac
18	391267	1.31	7e−16	7e−14	50 x 13	ankyrin repeat domain 20 family, member A11, pseudogene [
19	399948	1.28	2e−15	7e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
20	4602	1.27	3e−15	7e−14	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.29	NULL	6 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	15.11	NULL	2 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	14.67	NULL	1 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
4	14.13	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
5	12.45	NULL	2 / 6	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_UP
6	11.18	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
7	10.95	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
8	9.83	NULL	1 / 10	MF	GABA−A receptor activity
9	9.77	NULL	2 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
10	9.77	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
11	9.34	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
12	9.3	NULL	1 / 11	GSEA C2	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
13	9.27	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
14	8.3	NULL	2 / 13	BP	developmental pigmentation
15	8.28	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
16	8.25	NULL	1 / 10	GSEA C2	KEGG_ALZHEIMERS_DISEASE
17	8.12	NULL	1 / 2	miRNA target	miR−153
18	8.09	NULL	1 / 14	GSEA C2	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
19	8.09	NULL	1 / 14	GSEA C2	RIZKI_TUMOR_INVASIVENESS_2D_DN
20	7.9	NULL	2 / 12	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
21	7.85	NULL	1 / 3	miRNA target	miR−148a
22	7.8	NULL	1 / 11	GSEA C2	HUTTMANN_B_CLL_POOR_SURVIVAL_UP
23	7.8	NULL	1 / 11	GSEA C2	KEGG_CALCIUM_SIGNALING_PATHWAY
24	7.77	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
25	7.77	NULL	1 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
26	7.54	NULL	2 / 15	BP	embryonic digestive tract development
27	7.49	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
28	7.43	NULL	6 / 69	miRNA 3UTR	AGGCT−28
29	7.2	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
30	7.09	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
31	6.78	NULL	1 / 14	GSEA C2	ROSS_AML_OF_FAB_M7_TYPE
32	6.75	NULL	1 / 13	GSEA C2	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP
33	6.73	NULL	1 / 5	GSEA C2	VALK_AML_WITH_T_8_21_TRANSLOCATION
34	6.66	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
35	6.5	NULL	1 / 15	BP	striated muscle contraction
36	6.46	NULL	1 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
37	6.41	NULL	3 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
38	6.39	NULL	1 / 10	BP	melanin biosynthetic process
39	6.28	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
40	6.21	NULL	1 / 15	GSEA C2	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN

GW_148

Local Summary

%DE = 0.84

metagenes = 8

genes = 164

genes in genesets = 162

genes with fdr < 0.1 = 117 (15 + / 102 −)

genes with fdr < 0.05 = 98 (14 + / 84 −)

genes with fdr < 0.01 = 80 (11 + / 69 −)

<r> metagenes = 0.97

<r> genes = 0.38

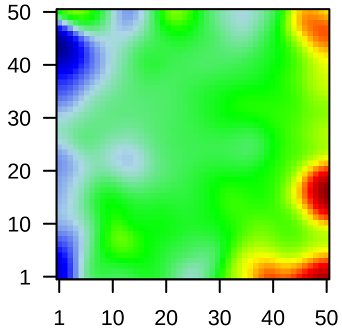
<FC> = −0.37

<shrinkage−t> = −12.88

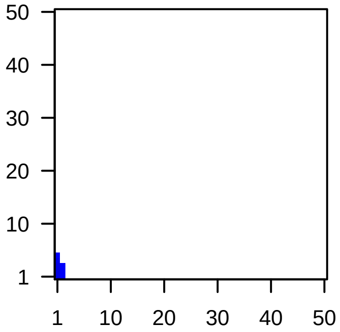
<p−value> = 0

<fdr> = 0.41

Profile



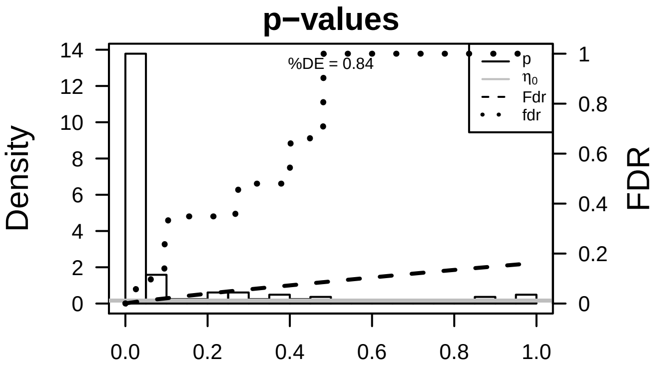
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3576	−1.77	2e−16	6e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
2	4312	−1.28	3e−15	4e−14	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
3	55714	1.28	3e−15	2e−11	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
4	5328	−1.16	7e−13	9e−11	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
5	55107	−1.11	6e−12	9e−11	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
6	4502	−1.11	7e−12	1e−10	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
7	4316	1.1	1e−11	2e−10	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
8	4489	−1	2e−11	2e−09	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
9	644314	−1.05	8e−11	4e−09	1 x 5	
10	10381	−1.01	4e−10	4e−09	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
11	10409	−1	6e−10	4e−09	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
12	4314	−1	6e−10	4e−09	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
13	25907	−1	6e−10	9e−09	1 x 1	transmembrane protein 158 (gene/pseudogene) [Source:HG
14	10631	−0.98	1e−09	9e−09	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;A
15	51330	−0.97	2e−09	9e−09	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
16	79783	−0.97	2e−09	9e−09	1 x 5	succinylCoA:glutarate−CoA transferase [Source:HGNC Symb
17	1290	−0.97	2e−09	9e−09	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
18	10468	−0.97	2e−09	1e−08	1 x 5	follistatin [Source:HGNC Symbol;Acc:3971]
19	1464	0.96	3e−09	1e−08	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
20	401138	−0.96	3e−09	2e−08	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.17	NULL	7 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
2	−21.41	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
3	−20.6	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
4	−19.72	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
5	−19.15	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP
6	−16.18	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
7	−16.05	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
8	−15.42	NULL	35 / 250	Lymphoma	LENZ_Stromal signature 1
9	−15.28	NULL	52 / 683	CC	extracellular space
10	−15.21	NULL	3 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
11	−15.03	NULL	1 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOC
12	−14.58	NULL	45 / 242	BP	extracellular matrix organization
13	−14.55	NULL	3 / 10	BP	cellular response to zinc ion
14	−14.49	NULL	10 / 37	BP	collagen fibril organization
15	−14.32	NULL	3 / 10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
16	−14.23	NULL	9 / 35	Glio	Colman_survival_associated
17	−14.12	NULL	33 / 190	CC	extracellular matrix
18	−13.48	NULL	1 / 6	GSEA C2	MIZUKAMI_HYPOXIA_DN
19	−13.48	NULL	1 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
20	−13.07	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
21	−13.05	NULL	2 / 13	Glio	Christensen_hypomethylated_in_grade2_oligodendroglioma
22	−12.51	NULL	2 / 12	GSEA C2	GEISS_RESPONSE_TO_DSRNA_DN
23	−12.31	NULL	1 / 7	GSEA C2	BIOCARTA_FREE_PATHWAY
24	−12.28	NULL	20 / 183	CC	proteinaceous extracellular matrix
25	−12.24	NULL	29 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
26	−12.24	NULL	29 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
27	−12.24	NULL	29 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
28	−12.24	NULL	29 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
29	−12.1	NULL	2 / 13	BP	induction of positive chemotaxis
30	−12.07	NULL	2 / 6	Glio	Martinez_Glio_hypometh
31	−11.89	NULL	3 / 10	BP	negative regulation of cell−substrate adhesion
32	−11.84	NULL	70 / 1182	CC	extracellular region
33	−11.73	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
34	−11.67	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
35	−11.55	NULL	3 / 15	BP	negative regulation of growth
36	−11.55	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
37	−11.38	NULL	2 / 10	GSEA C2	CHEN_HOXA5_TARGETS_6HR_UP
38	−11.31	NULL	10 / 40	BP	cellular response to amino acid stimulus
39	−11.23	NULL	2 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
40	−10.83	NULL	2 / 12	GSEA C2	SHI_SPARC_TARGETS_UP

GW_148

Local Summary

%DE = 0.74

metagenes = 26

genes = 299

genes in genesets = 294

genes with fdr < 0.1 = 158 (7 + / 151 −)

genes with fdr < 0.05 = 158 (7 + / 151 −)

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

<r> metagenes = 0.95

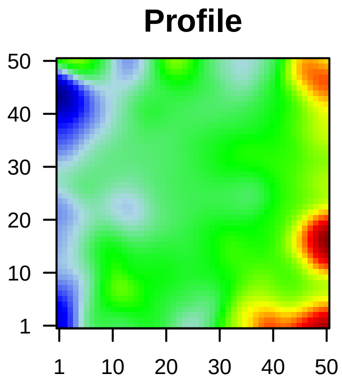
<r> genes = 0.34

<FC> = −0.4

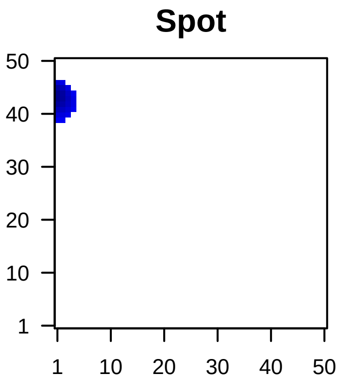
<shrinkage−t> = −13.93

<p−value> = 0

<fdr> = 0.49



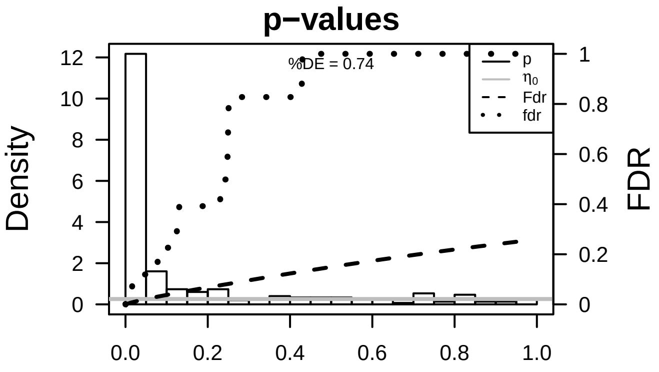
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	771	−1.35	2e−16	3e−15	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
2	760	−1.38	2e−16	3e−15	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	2167	−1.57	2e−16	3e−15	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
4	3489	−1.69	2e−16	3e−15	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
5	3861	−1.49	2e−16	3e−15	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
6	5744	−1.74	2e−16	3e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
7	8942	−1.28	2e−15	1e−13	1 x 40	kynureninase [Source:HGNC Symbol;Acc:6469]
8	780851	−1.27	4e−15	5e−13	2 x 39	small nucleolar RNA, C/D box 3A [Source:HGNC Symbol;Acc
9	7277	−1.25	1e−14	1e−11	1 x 45	tubulin, alpha 4a [Source:HGNC Symbol;Acc:12407]
10	6513	−1.19	2e−13	2e−10	1 x 43	solute carrier family 2 (facilitated glucose transporter), membe
11	6665	−1.11	5e−12	2e−10	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Symb
12	8111	−1.11	7e−12	2e−10	1 x 42	G protein−coupled receptor 68 [Source:HGNC Symbol;Acc:4
13	90102	−1.11	7e−12	3e−10	1 x 42	pleckstrin homology−like domain, family B, member 2 [Source
14	1001	−1.09	1e−11	3e−10	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
15	3552	−1.09	1e−11	3e−09	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
16	146802	−1.06	5e−11	3e−09	1 x 45	solute carrier family 47 (multidrug and toxin extrusion), memb
17	4015	−1.04	1e−10	3e−09	1 x 41	lysyl oxidase [Source:HGNC Symbol;Acc:6664]
18	135398	1.04	1e−10	2e−08	1 x 40	chromosome 6 open reading frame 141 [Source:HGNC Symb
19	9547	−1.02	3e−10	2e−08	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
20	83882	−1	7e−10	2e−08	1 x 43	tetraspanin 10 [Source:HGNC Symbol;Acc:29942]



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−12.59	NULL	62 / 572	Disease	GUDJ_psoriasis up
2	−12.27	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	−11.02	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
4	−10.42	NULL	14 / 76	BP	epidermis development
5	−9.94	NULL	3 / 25	BP	response to zinc ion
6	−9.76	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
7	−9.61	NULL	2 / 12	MF	fatty acid binding
8	−9.37	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
9	−9.31	NULL	2 / 16	Glio	VERHAAK_MES subtype
10	−9.02	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
11	−8.93	NULL	5 / 12	BP	hemidesmosome assembly
12	−8.87	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
13	−8.81	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
14	−8.6	NULL	3 / 38	BP	epithelial cell differentiation
15	−8.42	NULL	2 / 9	GSEA C2	KORKOLA_CORRELATED_WITH_POU5F1
16	−8.23	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
17	−8.04	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
18	−7.95	NULL	3 / 15	Pathw Ac	GUSTAFSON_PI3K_DN
19	−7.88	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
20	−7.76	NULL	2 / 22	BP	bicarbonate transport
21	−7.73	NULL	3 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
22	−7.7	NULL	1 / 5	GSEA C2	RODRIGUES_DCC_TARGETS_UP
23	−7.67	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
24	−7.63	NULL	1 / 10	BP	surfactant homeostasis
25	−7.57	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
26	−7.55	NULL	2 / 15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
27	−7.49	NULL	1 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
28	−7.44	NULL	3 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
29	−7.39	NULL	3 / 15	GSEA C2	NAKAMURA_METASTASIS_MODEL_DN
30	−7.27	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
31	−7.2	NULL	2 / 25	BP	one−carbon metabolic process
32	−7.13	NULL	2 / 10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
33	−7.07	NULL	2 / 16	GSEA C2	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP
34	−7	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
35	−6.85	NULL	1 / 10	BP	white fat cell differentiation
36	−6.84	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
37	−6.72	NULL	1 / 5	GSEA C2	ELVIDGE_HIF2A_TARGETS_UP
38	−6.64	NULL	1 / 12	GSEA C2	SANCHEZ_MDM2_TARGETS
39	−6.54	NULL	1 / 13	H.Tiss	WIRTH_Thalamus
40	−6.49	NULL	2 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN