GW_236

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1671 (930 + / 741 −)

genes with fdr < 0.1 = 1435 (823 + / 612 −)

genes with fdr < 0.05 = 1136 (685 + / 451 −)

genes with fdr < 0.01 = 818 (541 + / 277 −)

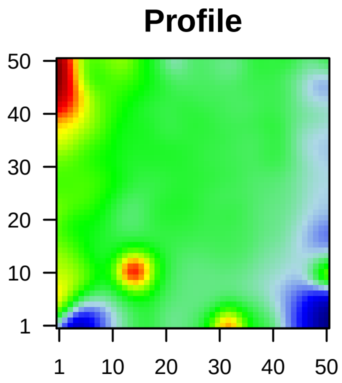
genes in genesets = 16332

<FC> = 0

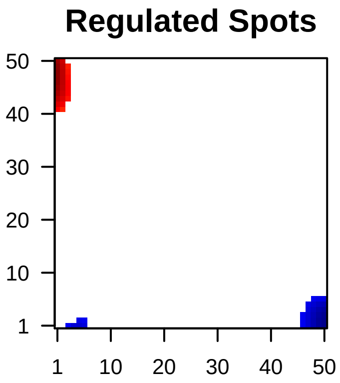
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.87



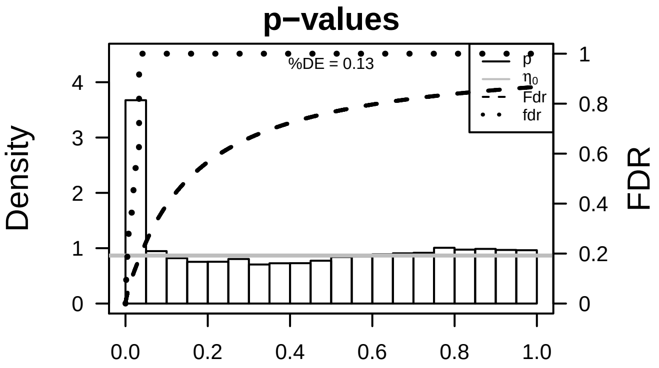
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	1.35	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	57016	1.39	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	1109	1.52	2e−16	3e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	222	1.75	2e−16	3e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
5	147495	1.54	2e−16	3e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
6	348	−1.34	2e−16	3e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	80341	1.47	2e−16	3e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
8	684	1.23	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
9	339512	1.23	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
10	92747	3.75	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
11	140683	1.33	2e−16	3e−14	18 x 37	BPI fold containing family A, member 2 [Source:HGNC Symb
12	260436	1.56	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
13	57172	−1.5	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
14	857	1.37	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
15	1041	2.17	2e−16	3e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
16	629	1.28	2e−16	3e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
17	1308	1.98	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	170712	1.35	2e−16	3e−14	15 x 11	cytochrome c oxidase subunit VIIb2 [Source:HGNC Symbol;A
19	51200	2.05	2e−16	3e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
20	49860	1.76	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	17.2	NULL	572	Disease	GUDJ_psoriasis up
2	17.13	NULL	135	H.Tiss	WIRTH_Mucosa
3	12.29	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	12.29	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
5	12.25	NULL	957	Chr	Chr 11
6	12.2	NULL	76	BP	epidermis development
7	11.32	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
8	10.73	NULL	51	BP	type I interferon signaling pathway
9	10.5	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
10	9.96	NULL	21	CC	cornified envelope
11	9.51	NULL	12	BP	hemidesmosome assembly
12	9.16	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
13	9	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
14	8.8	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
15	8.79	NULL	31	BP	negative regulation of viral genome replication
16	8.7	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
17	8.61	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
18	8.6	NULL	123	BP	defense response to virus
19	8.3	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
20	8.25	NULL	82	CC	intermediate filament
Underexpressed					
1	−11.19	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
2	−10.23	NULL	504	Chr	Chr 15
3	−9.99	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
4	−8.6	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
5	−8.39	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
6	−8.35	NULL	250	Lymphoma	LENZ_Stromal signature 1
7	−8.07	NULL	553	Cancer	Lembcke_Colonic Inflammation
8	−7.82	NULL	417	H.Tiss	WIRTH_Immune system
9	−7.52	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
10	−7.18	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_40_MCF10A
11	−7.04	NULL	699	Chr	Chr 5
12	−6.89	NULL	190	CC	extracellular matrix
13	−6.87	NULL	16	GSEA C2	BROWNE_HCMV_INFECTION_2HR_UP
14	−6.61	NULL	16	GSEA C2	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP
15	−6.51	NULL	81	BP	viral transcription
16	−6.47	NULL	87	BP	translational termination
17	−6.45	NULL	92	BP	translational elongation
18	−6.41	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
19	−6.33	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
20	−6.24	NULL	16	MMML CGS	MACIEJ_MMML 1

GW_236

Local Summary

%DE = 0.78

metagenes = 27

genes = 357

genes in genesets = 350

genes with fdr < 0.1 = 207 (198 + / 9 −)

genes with fdr < 0.05 = 197 (188 + / 9 −)

genes with fdr < 0.01 = 184 (176 + / 8 −)

<r> metagenes = 0.87

<r> genes = 0.35

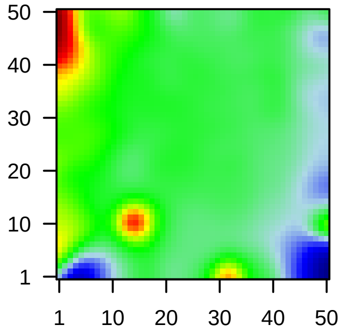
<FC> = 0.51

<shrinkage−t> = 18.1

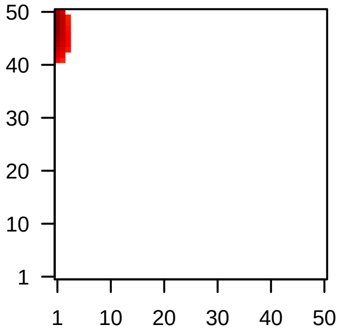
<p−value> = 0

<fdr> = 0.42

Profile



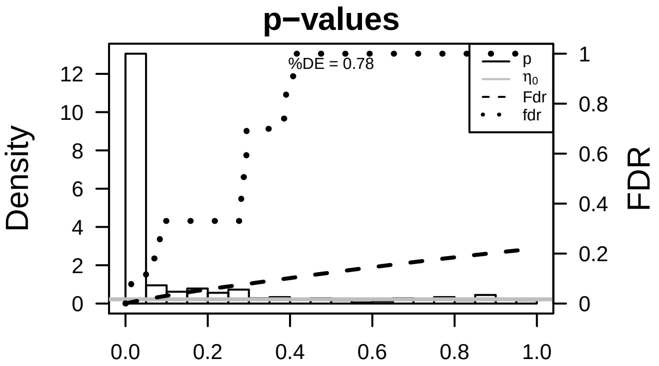
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.39	2e−16	4e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	222	1.75	2e−16	4e−16	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	147495	1.54	2e−16	4e−16	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
4	1041	2.17	2e−16	4e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
5	1308	1.98	2e−16	4e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
6	51200	2.05	2e−16	4e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
7	49860	1.76	2e−16	4e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
8	9547	1.51	2e−16	4e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
9	55894	1.54	2e−16	4e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	414325	2.02	2e−16	4e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1673	1.23	2e−16	4e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	1828	1.37	2e−16	4e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	9982	1.32	2e−16	4e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
14	2352	1.89	2e−16	4e−16	1 x 42	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
15	2877	1.53	2e−16	4e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
16	3429	1.47	2e−16	4e−16	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
17	374918	1.58	2e−16	4e−16	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093
18	53833	1.46	2e−16	4e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
19	3613	1.33	2e−16	4e−16	1 x 46	inositol(myo)−1(or 4)−monophosphatase 2 [Source:HGNC Sy
20	5653	1.72	2e−16	4e−16	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	33.99	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
2	25.25	NULL	18 / 21	CC	cornified envelope
3	25.13	NULL	27 / 76	BP	epidermis development
4	23.73	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
5	23.61	NULL	122 / 572	Disease	GUDJ_psoriasis up
6	20.96	NULL	25 / 53	BP	keratinocyte differentiation
7	19.96	NULL	20 / 42	BP	keratinization
8	19.15	NULL	22 / 82	CC	intermediate filament
9	18.4	NULL	13 / 44	CC	keratin filament
10	15.69	NULL	12 / 21	CC	desmosome
11	15.68	NULL	4 / 12	BP	hemidesmosome assembly
12	14.98	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	14.63	NULL	30 / 186	MF	structural molecule activity
14	13.94	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	13.89	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	13.17	NULL	5 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
17	11.8	NULL	3 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
18	11.78	NULL	4 / 12	H.Tiss	WIRTH_Prim. lymphoid organs
19	11.66	NULL	10 / 19	BP	peptide cross−linking
20	11.65	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
21	11.43	NULL	2 / 15	BP	fibrinolysis
22	11.39	NULL	4 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
23	10.85	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
24	10.79	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
25	10.62	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
26	10.36	NULL	3 / 12	BP	cellular aldehyde metabolic process
27	10.24	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
28	10.19	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
29	10.03	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
30	9.82	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
31	9.65	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
32	9.59	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
33	9.58	NULL	4 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
34	9.48	NULL	3 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
35	9.36	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
36	8.72	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
37	8.64	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
38	8.63	NULL	2 / 2	miRNA target	miR−199a*
39	8.61	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
40	8.47	NULL	5 / 10	MF	RAGE receptor binding

GW_236

Local Summary

%DE = 0.84

metagenes = 6

genes = 144

genes in genesets = 143

genes with fdr < 0.1 = 100 (3 + / 97 −)

genes with fdr < 0.05 = 100 (3 + / 97 −)

genes with fdr < 0.01 = 82 (2 + / 80 −)

<r> metagenes = 0.99

<r> genes = 0.48

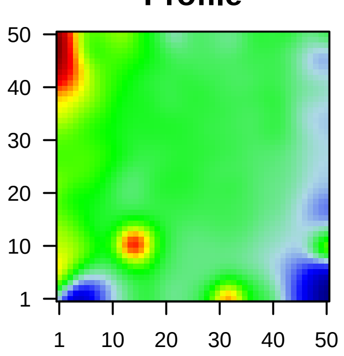
<FC> = −0.49

<shrinkage−t> = −17.16

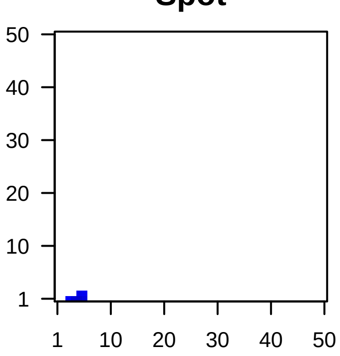
<p−value> = 0

<fdr> = 0.36

Profile



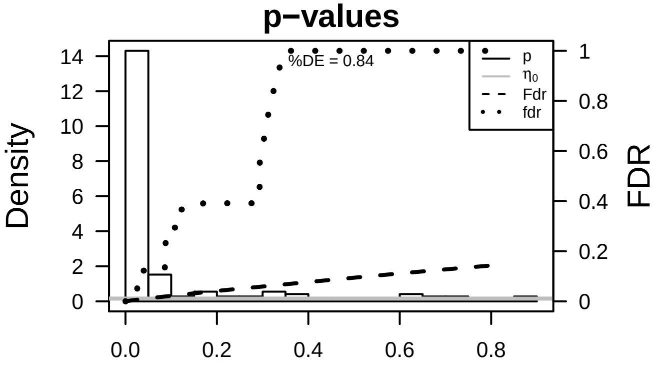
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	115908	−1.29	2e−16	8e−16	3 x 1	collagen triple helix repeat containing 1 [Source:HGNC Symb
2	1809	−1.4	2e−16	8e−16	6 x 1	dihydropyrimidinase−like 3 [Source:HGNC Symbol;Acc:3015]
3	3043	−1.38	2e−16	8e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
4	4320	−1.31	2e−16	8e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
5	50861	−1.46	2e−16	8e−16	6 x 2	
6	7431	−1.33	2e−16	8e−16	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]
7	3040	−1.19	1e−15	9e−13	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	8076	1.12	4e−14	2e−12	4 x 1	microfibrillar associated protein 5 [Source:HGNC Symbol;Acc
9	1009	−1.1	2e−13	2e−12	3 x 1	cadherin 11, type 2, OB−cadherin (osteoblast) [Source:HGNC
10	5997	−1.09	3e−13	2e−12	5 x 1	regulator of G−protein signaling 2, 24kDa [Source:HGNC Syn
11	2199	−1.08	3e−13	1e−11	4 x 1	fibulin 2 [Source:HGNC Symbol;Acc:3601]
12	6515	−1.06	9e−13	1e−11	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
13	6423	−1.05	2e−12	2e−11	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
14	165	−1.04	3e−12	2e−11	3 x 1	AE binding protein 1 [Source:HGNC Symbol;Acc:303]
15	5919	−1.04	3e−12	9e−10	5 x 1	retinoic acid receptor responder (tazarotene induced) 2 [Sour
16	387914	−0.98	4e−11	1e−09	6 x 1	shisa family member 2 [Source:HGNC Symbol;Acc:20366]
17	1490	−0.96	1e−10	1e−09	3 x 1	connective tissue growth factor [Source:HGNC Symbol;Acc:2
18	7291	−0.95	2e−10	1e−09	3 x 1	twist family bHLH transcription factor 1 [Source:HGNC Symbo
19	3671	−0.95	2e−10	2e−08	4 x 1	immunoglobulin superfamily containing leucine−rich repeat [S
20	6876	−0.91	1e−09	2e−08	3 x 1	transgelin [Source:HGNC Symbol;Acc:11553]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.17	NULL	45 / 250	Lymphoma	LENZ_Stromal signature 1
2	−25.31	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
3	−21.97	NULL	33 / 190	CC	extracellular matrix
4	−21.21	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
5	−18.97	NULL	7 / 19	MF	extracellular matrix binding
6	−18.45	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
7	−18.27	NULL	4 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
8	−16.93	NULL	5 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
9	−16.77	NULL	3 / 11	MF	oxygen transporter activity
10	−16.74	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
11	−16.54	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
12	−15.96	NULL	3 / 14	CC	endocytic vesicle lumen
13	−15.92	NULL	1 / 2	miRNA target	miR−18
14	−15.85	NULL	4 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
15	−14.59	NULL	2 / 10	CC	hemoglobin complex
16	−14.48	NULL	4 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
17	−14.39	NULL	3 / 11	BP	dermatan sulfate biosynthetic process
18	−14.21	NULL	3 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
19	−14.08	NULL	2 / 8	GSEA C2	ZHAN_MULTIPLE_MYELOMA_SPIKED
20	−13.8	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
21	−13.74	NULL	4 / 11	MMML CGS	MACIEJ_MMML 31
22	−13.69	NULL	5 / 25	BP	chondroitin sulfate biosynthetic process
23	−13.61	NULL	25 / 242	BP	extracellular matrix organization
24	−13.43	NULL	4 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH
25	−12.8	NULL	2 / 10	GSEA C2	IIZUKA_RECURRENT_LIVER_CANCER
26	−12.51	NULL	3 / 14	BP	chondroitin sulfate catabolic process
27	−12.49	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
28	−12.41	NULL	2 / 5	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C6
29	−12.34	NULL	17 / 183	CC	proteinaceous extracellular matrix
30	−12.26	NULL	3 / 19	MF	peroxidase activity
31	−12.16	NULL	2 / 10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP
32	−12.14	NULL	4 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
33	−12.09	NULL	1 / 5	GSEA C2	CALVET_IRINOTECAN_SENSITIVE_VS_REVERTED_UP
34	−11.98	NULL	11 / 69	BP	extracellular matrix disassembly
35	−11.17	NULL	3 / 29	BP	positive regulation of cell death
36	−11.08	NULL	47 / 1182	CC	extracellular region
37	−11	NULL	3 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
38	−10.8	NULL	3 / 15	Cancer	LIU_PROSTATE_CANCER_DN
39	−10.77	NULL	33 / 683	CC	extracellular space
40	−10.53	NULL	4 / 16	GSEA C2	NEWMAN_ERCC6_TARGETS_DN

GW_236

Local Summary

%DE = 0.88

metagenes = 26

genes = 371

genes in genesets = 369

genes with fdr < 0.1 = 270 (15 + / 255 −)

genes with fdr < 0.05 = 233 (12 + / 221 −)

genes with fdr < 0.01 = 162 (8 + / 154 −)

<r> metagenes = 0.97

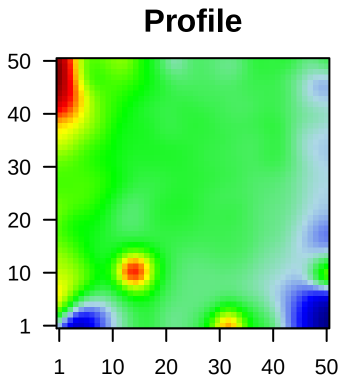
<r> genes = 0.52

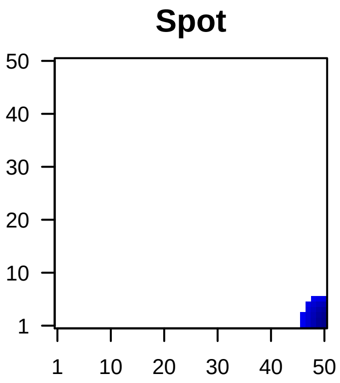
<FC> = −0.36

<shrinkage−t> = −12.63

<p−value> = 0

<fdr> = 0.46





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	348	−1.34	2e−16	3e−15	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
2	260436	1.56	2e−16	3e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
3	57172	−1.5	2e−16	3e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
4	3543	−1.45	2e−16	3e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
5	6363	−1.17	3e−15	5e−13	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
6	10365	−1.15	1e−14	1e−12	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
7	930	−1.12	4e−14	2e−11	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
8	4283	1.07	7e−13	2e−11	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
9	1396	−1.07	8e−13	3e−11	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
10	51755	−1.05	1e−12	3e−11	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	5730	−1.05	2e−12	6e−11	50 x 1	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Syn
12	10563	−1.04	3e−12	1e−10	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
13	5996	−1.02	6e−12	1e−10	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
14	126306	−1.02	9e−12	1e−10	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
15	23231	−1.01	1e−11	2e−10	48 x 2	sel−1 suppressor of lin−12−like 3 (C. elegans) [Source:HGN
16	5552	−1	2e−11	8e−09	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
17	969	−0.95	2e−10	1e−08	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
18	338773	−0.93	5e−10	4e−08	50 x 5	transmembrane protein 119 [Source:HGNC Symbol;Acc:278
19	5734	−0.9	1e−09	4e−08	50 x 3	prostaglandin E receptor 4 (subtype EP4) [Source:HGNC Sy
20	54855	−0.87	4e−09	4e−08	49 x 1	family with sequence similarity 46, member C [Source:HGNC

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−22.15	NULL	102 / 417	H.Tiss	WIRTH_Immune system
2	−21.78	NULL	119 / 553	Cancer	Lembcke_Colonic Inflammation
3	−19.53	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
4	−16.22	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
5	−14.85	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	−14.48	NULL	55 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−14.48	NULL	55 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−14.48	NULL	55 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−14.48	NULL	55 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−13.61	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
11	−12.86	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
12	−12.6	NULL	12 / 28	BP	B cell receptor signaling pathway
13	−12.55	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
14	−12.27	NULL	61 / 312	BP	immune response
15	−11.31	NULL	5 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
16	−11.01	NULL	3 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
17	−10.92	NULL	5 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
18	−10.52	NULL	5 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
19	−10.36	NULL	20 / 74	BP	regulation of immune response
20	−10.23	NULL	4 / 13	BP	positive regulation of endocytosis
21	−10.21	NULL	12 / 15	CC	MHC class II protein complex
22	−9.92	NULL	5 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
23	−9.89	NULL	4 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
24	−9.73	NULL	4 / 13	Lymphoma	BENTINK_mBL DOWN
25	−9.55	NULL	8 / 16	Lymphoma	WRIGHT_ABC UP
26	−9.52	NULL	3 / 12	BP	negative regulation of cytokine secretion
27	−9.44	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
28	−9.34	NULL	34 / 327	Lymphoma	SPANG_CD40 6hrs UP
29	−9.31	NULL	5 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
30	−9.31	NULL	2 / 7	Cancer	ZHANG_MGUS up
31	−9.15	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
32	−9.14	NULL	6 / 14	GSEA C2	FINETTI_BREAST_CANCER_KINOME_GREEN
33	−9.14	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow
34	−9.14	NULL	2 / 11	BP	high−density lipoprotein particle remodeling
35	−9.05	NULL	31 / 162	CC	external side of plasma membrane
36	−8.97	NULL	4 / 15	GSEA C2	HUMMEL_BURKITTS_LYMPHOMA_DN
37	−8.67	NULL	8 / 16	GSEA C2	SU_THYMUS
38	−8.67	NULL	3 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
39	−8.58	NULL	4 / 10	GSEA C2	BIOCARTA_MONOCYTE_PATHWAY
40	−8.55	NULL	4 / 16	GSEA C2	CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP