GW_088

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2219 (1236 + / 983 −)

genes with fdr < 0.1 = 1863 (1044 + / 819 −)

genes with fdr < 0.05 = 1458 (833 + / 625 −)

genes with fdr < 0.01 = 1053 (606 + / 447 −)

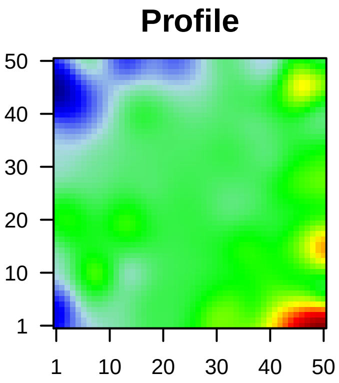
genes in genesets = 16332

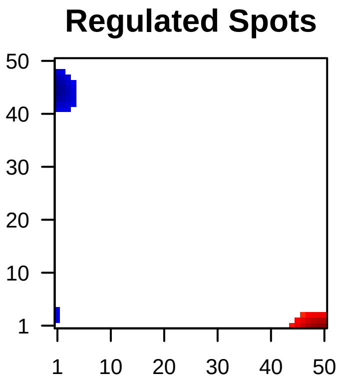
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

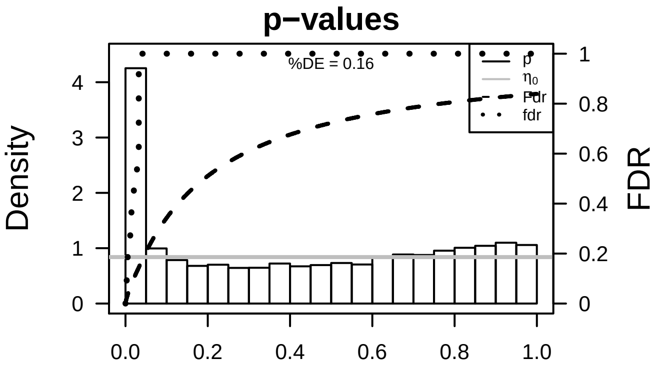
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.47	2e−16	2e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	21	2.11	2e−16	2e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
3	58	1.76	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
4	131	1.87	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	57016	−1.59	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	441282	−1.79	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
7	8644	−2.43	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Syı
8	1109	−2.13	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
9	65124	−1.61	2e−16	2e−14	1 x 45	sosondowah ankyrin repeat domain family member C [Source
10	55107	−1.61	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
11	341	1.62	2e−16	2e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
12	348	1.62	2e−16	2e−14	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
13	445	1.68	2e−16	2e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
14	23120	−1.52	2e−16	2e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
15	10974	1.83	2e−16	2e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:2
16	387695	−1.76	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
17	399948	2.16	2e−16	2e−14	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
18	116028	1.49	2e−16	2e−14	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
19	713	1.7	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
20	343990	1.72	2e−16	2e−14	50 x 12	KIAA1211−like [Source:HGNC Symbol;Acc:33454]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	16.04	NULL	417	H.Tiss	WIRTH_Immune system
2	9.61	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
3	9.51	NULL	12	GSEA C2	BIOCARTA_CTL_PATHWAY
4	9.04	NULL	14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
5	8.83	NULL	1135	Chr	Chr 19
6	8.82	NULL	74	BP	regulation of immune response
7	8.73	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
8	8.01	NULL	312	BP	immune response
9	8	NULL	15	CC	MHC class II protein complex
10	7.81	NULL	7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
11	7.74	NULL	633	Chr	Chr 9
12	7.22	NULL	13	Cancer	GENTLES_modul18
13	7.07	NULL	14	GSEA C2	BIOCARTA_IL12_PATHWAY
14	6.79	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
15	6.79	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
16	6.72	NULL	12	CC	T cell receptor complex
17	6.41	NULL	16	BP	cytolysis
18	6.35	NULL	149	BP	DNA replication
19	6.27	NULL	162	CC	external side of plasma membrane
20	6.11	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
Underexpressed					
1	−12.45	NULL	714	Chr	Chr 6
2	−10.97	NULL	135	H.Tiss	WIRTH_Mucosa
3	−9.52	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−8.75	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
5	−7.92	NULL	76	BP	epidermis development
6	−7.74	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
7	−7.71	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
8	−7.59	NULL	242	BP	extracellular matrix organization
9	−7.55	NULL	190	CC	extracellular matrix
10	−7.23	NULL	16	GSEA C2	ELVIDGE_HYPOXIA_UP
11	−6.94	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
12	−6.93	NULL	572	Disease	GUDJ_psoriasis up
13	−6.86	NULL	59	Lymphoma	LENZ_Stromal signature 2
14	−6.82	NULL	53	BP	keratinocyte differentiation
15	−6.72	NULL	914	Chr	Chr 3
16	−6.67	NULL	83	CC	basement membrane
17	−6.64	NULL	21	CC	desmosome
18	−6.58	NULL	12	BP	hemidesmosome assembly
19	−6.4	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
20	−6.28	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP

GW_088

Local Summary

%DE = 0.93

metagenes = 18

genes = 294

genes in genesets = 291

genes with fdr < 0.1 = 247 (245 + / 2 −)

genes with fdr < 0.05 = 244 (242 + / 2 −)

genes with fdr < 0.01 = 217 (216 + / 1 −)

<r> metagenes = 0.98

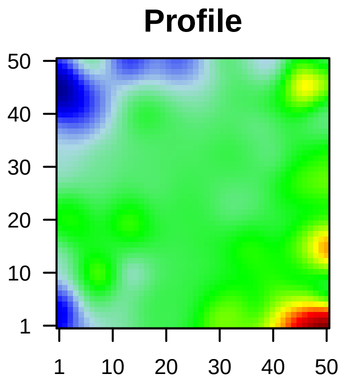
<r> genes = 0.58

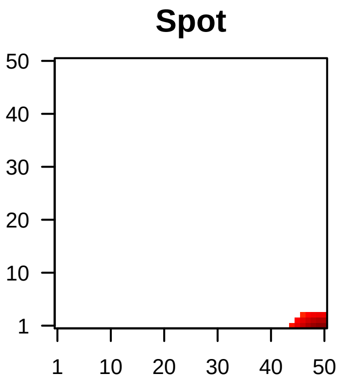
<FC> = 0.83

<shrinkage−t> = 29.23

<p−value> = 0

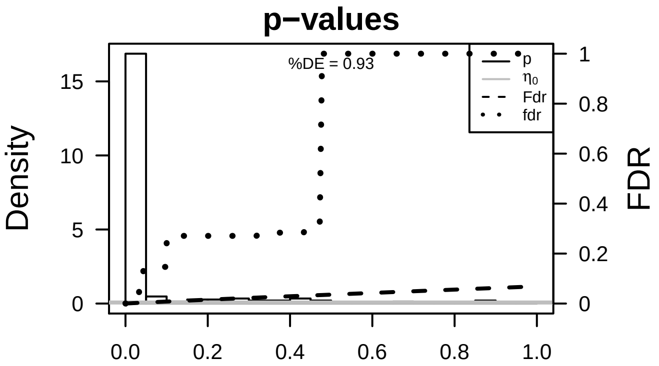
<fdr> = 0.21





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	341	1.62	2e−16	1e−16	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
2	348	1.62	2e−16	1e−16	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	713	1.7	2e−16	1e−16	50 x 1	complement component 1, q subcomponent, B chain [Source
4	260436	3.43	2e−16	1e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
5	914	1.57	2e−16	1e−16	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
6	915	1.88	2e−16	1e−16	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
7	924	1.57	2e−16	1e−16	49 x 1	CD7 molecule [Source:HGNC Symbol;Acc:1695]
8	925	1.5	2e−16	1e−16	48 x 1	CD8a molecule [Source:HGNC Symbol;Acc:1706]
9	169044	1.48	2e−16	1e−16	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
10	6376	1.67	2e−16	1e−16	44 x 1	chemokine (C−X3−C motif) ligand 1 [Source:HGNC Symbol;
11	4283	2.64	2e−16	1e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
12	1593	1.5	2e−16	1e−16	50 x 3	cytochrome P450, family 27, subfamily A, polypeptide 1 [Sou
13	8320	1.67	2e−16	1e−16	48 x 1	eomesodermin [Source:HGNC Symbol;Acc:3372]
14	3001	1.89	2e−16	1e−16	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
15	3002	2.25	2e−16	1e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
16	2999	1.89	2e−16	1e−16	47 x 1	granzyme H (cathepsin G−like 2, protein h−CCPX) [Source:H
17	3003	1.65	2e−16	1e−16	49 x 1	granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol
18	3109	1.49	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
19	3113	1.67	2e−16	1e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
20	3120	1.71	2e−16	1e−16	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.37	NULL	100 / 417	H.Tiss	WIRTH_Immune system
2	24.9	NULL	13 / 15	CC	MHC class II protein complex
3	24.18	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
4	23.83	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
5	21.37	NULL	96 / 553	Cancer	Lembcke_Colonic Inflammation
6	21.17	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
7	20.76	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
8	19.85	NULL	57 / 312	BP	immune response
9	19	NULL	8 / 13	Cancer	GENTLES_modul18
10	18.69	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
11	17.59	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	17.09	NULL	17 / 74	BP	regulation of immune response
13	16.94	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
14	16.67	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
15	16.23	NULL	7 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
16	15.8	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
17	15.27	NULL	15 / 47	BP	antigen processing and presentation
18	14.99	NULL	4 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
19	14.92	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	14.92	NULL	40 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
21	14.92	NULL	40 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
22	14.92	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
23	14.92	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
24	14.56	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
25	14.32	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
26	14.27	NULL	4 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
27	14.01	NULL	5 / 12	CC	T cell receptor complex
28	13.95	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
29	13.32	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
30	13.23	NULL	4 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
31	13.23	NULL	4 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
32	12.83	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
33	12.82	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
34	12.66	NULL	6 / 13	MMML CGS	MACIEJ_MMML 6
35	12.63	NULL	28 / 162	CC	external side of plasma membrane
36	12.51	NULL	26 / 204	BP	cell surface receptor signaling pathway
37	12.4	NULL	4 / 10	GSEA C2	BIOCARTA_LYM_PATHWAY
38	12.35	NULL	18 / 60	BP	T cell costimulation
39	12.23	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
40	12.19	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN

GW_088

Local Summary

%DE = 0.96

metagenes = 3

genes = 66

genes in genesets = 66

genes with fdr < 0.1 = 56 (4 + / 52 −)

genes with fdr < 0.05 = 54 (4 + / 50 −)

genes with fdr < 0.01 = 54 (4 + / 50 −)

<r> metagenes = 0.99

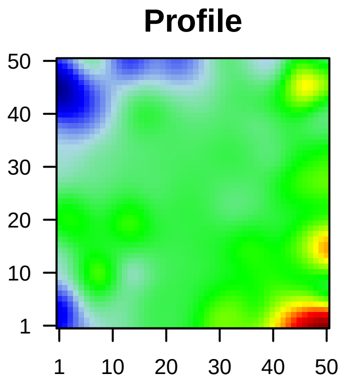
<r> genes = 0.44

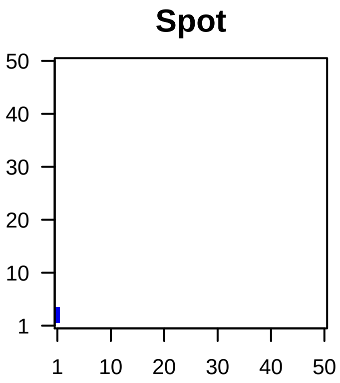
<FC> = −0.61

<shrinkage−t> = −21.33

<p−value> = 0

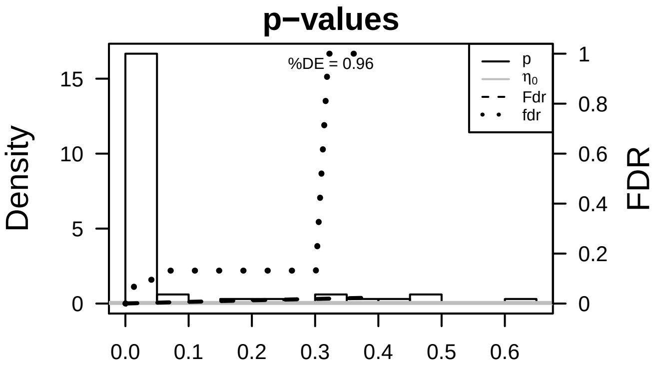
<fdr> = 0.24





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4319	−2.32	2e−16	2e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
2	5054	−1.65	2e−16	2e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
3	3371	−1.78	2e−16	2e−16	1 x 3	tenascin C [Source:HGNC Symbol;Acc:5318]
4	27122	−1.46	4e−16	2e−15	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Sy
5	1687	−1.44	1e−15	4e−15	1 x 4	deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc
6	10512	−1.42	3e−15	2e−11	1 x 4	sema domain, immunoglobulin domain (Ig), short basic doma
7	6591	−1.23	1e−11	2e−11	1 x 4	snail family zinc finger 2 [Source:HGNC Symbol;Acc:11094]
8	4907	−1.21	2e−11	3e−10	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80
9	857	−1.16	1e−10	7e−10	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
10	8870	−1.13	4e−10	2e−09	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:539
11	7045	−1	1e−09	2e−08	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
12	11009	−1.04	8e−09	2e−07	1 x 3	interleukin 24 [Source:HGNC Symbol;Acc:11346]
13	10381	−0.96	1e−07	2e−07	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
14	5328	−0.94	2e−07	2e−07	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
15	56603	−0.93	2e−07	3e−07	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
16	3918	−0.91	4e−07	3e−07	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
17	4322	−0.91	4e−07	1e−06	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
18	259217	−0.89	9e−07	5e−06	1 x 4	heat shock 70kDa protein 12A [Source:HGNC Symbol;Acc:1
19	51050	−0.85	3e−06	6e−05	1 x 2	peptidase inhibitor 15 [Source:HGNC Symbol;Acc:8946]
20	5270	−0.74	4e−05	6e−05	1 x 3	serpin peptidase inhibitor, clade E (nexin, plasminogen activa



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.18	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
2	−22.23	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
3	−21.98	NULL	3 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	−19.58	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
5	−18.93	NULL	2 / 10	BP	regulation of receptor activity
6	−18.93	NULL	2 / 10	GSEA C2	BIOCARTA_FIBRINOLYSIS_PATHWAY
7	−18.92	NULL	1 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
8	−18.91	NULL	2 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
9	−17.85	NULL	2 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
10	−17.57	NULL	2 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
11	−17.46	NULL	2 / 10	BP	negative regulation of blood coagulation
12	−17.33	NULL	3 / 37	Glio	Christensen_hypomethylated_in_ependymoma
13	−17.19	NULL	3 / 15	BP	fibrinolysis
14	−17.04	NULL	2 / 13	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP
15	−16.96	NULL	1 / 10	GSEA C2	LI_CISPLATIN_RESISTANCE_DN
16	−16.91	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C8
17	−16.83	NULL	3 / 15	BP	negative regulation of anoikis
18	−16.69	NULL	1 / 6	GSEA C2	MAINA_HYPOXIA_VHL_TARGETS_UP
19	−16.54	NULL	5 / 35	Glio	Colman_survival_associated
20	−15.66	NULL	1 / 2	miRNA target	miR−101b
21	−15.44	NULL	2 / 16	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_UP
22	−15.15	NULL	1 / 12	GSEA C2	LY_AGING_MIDDLE_UP
23	−15.06	NULL	1 / 7	GSEA C2	GAUTSCHI_SRC_SIGNALING
24	−15.06	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
25	−14.43	NULL	1 / 13	GSEA C2	AUNG_GASTRIC_CANCER
26	−14.36	NULL	2 / 15	GSEA C2	OSADA_ASCL1_TARGETS_DN
27	−13.92	NULL	3 / 16	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_UP
28	−13.81	NULL	1 / 8	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
29	−13.81	NULL	1 / 8	GSEA C2	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
30	−13.8	NULL	1 / 14	GSEA C2	COWLING_MYCN_TARGETS
31	−13.78	NULL	2 / 14	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN
32	−13.71	NULL	1 / 2	TF	MYC_ECM cell adhesion DOWN
33	−13.62	NULL	20 / 683	CC	extracellular space
34	−13.24	NULL	1 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
35	−12.96	NULL	1 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
36	−12.96	NULL	1 / 10	BP	prostate gland epithelium morphogenesis
37	−12.74	NULL	1 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
38	−12.74	NULL	1 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
39	−12.5	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
40	−12.44	NULL	7 / 190	CC	extracellular matrix

GW_088

Local Summary

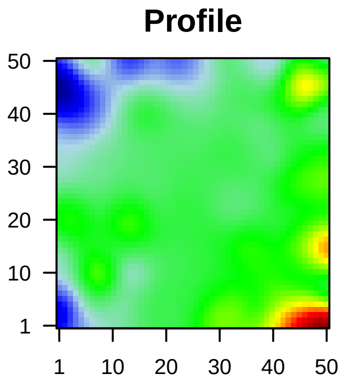
%DE = 0.88
metagenes = 28
genes = 309
genes in genesets = 303

genes with fdr < 0.1 = 254 (14 + / 240 −)
genes with fdr < 0.05 = 241 (14 + / 227 −)
genes with fdr < 0.01 = 201 (12 + / 189 −)

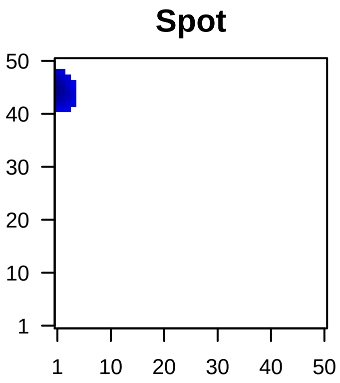
<r> metagenes = 0.92
<r> genes = 0.37

<FC> = −0.65
<shrinkage−t> = −22.96
<p−value> = 0
<fdr> = 0.27

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	65124	−1.61	2e−16	3e−16	1 x 45	sosondowah ankyrin repeat domain family member C [Source
2	771	−1.91	2e−16	3e−16	1 x 44	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
3	9635	−2.23	2e−16	3e−16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
4	51200	−1.48	2e−16	3e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
5	9547	−2.1	2e−16	3e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
6	2150	−1.74	2e−16	3e−16	1 x 44	coagulation factor II (thrombin) receptor−like 1 [Source:HGN
7	2171	−2.31	2e−16	3e−16	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H
8	9982	−1.78	2e−16	3e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
9	2697	−1.76	2e−16	3e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
10	10804	−1.92	2e−16	3e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
11	56169	−1.5	2e−16	3e−16	1 x 46	gasdermin C [Source:HGNC Symbol;Acc:7151]
12	3489	−2.02	2e−16	3e−16	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
13	53833	−1.96	2e−16	3e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
14	3861	−2.62	2e−16	3e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
15	3868	−1.65	2e−16	3e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
16	5744	−2.2	2e−16	3e−16	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
17	5836	−1.82	2e−16	3e−16	1 x 44	phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:9
18	23682	−2.05	2e−16	3e−16	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
19	5947	−1.62	2e−16	3e−16	1 x 43	retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
20	338324	−2.08	2e−16	3e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.63	NULL	40 / 135	H.Tiss	WIRTH_Mucosa
2	−22.4	NULL	8 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	−18.58	NULL	84 / 572	Disease	GUDJ_psoriasis up
4	−17.08	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
5	−16.6	NULL	11 / 21	CC	desmosome
6	−15.19	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
7	−14.68	NULL	2 / 2	miRNA target	miR−199a*
8	−14.49	NULL	19 / 82	CC	intermediate filament
9	−14.28	NULL	17 / 76	BP	epidermis development
10	−13.57	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
11	−13.17	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
12	−12.59	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
13	−12.49	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
14	−11.93	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
15	−11.82	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
16	−11.66	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
17	−11.44	NULL	5 / 21	CC	gap junction
18	−11.33	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
19	−11.15	NULL	4 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
20	−11.08	NULL	3 / 15	CC	connexon complex
21	−10.71	NULL	5 / 12	BP	hemidesmosome assembly
22	−10.68	NULL	9 / 44	CC	keratin filament
23	−9.97	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
24	−9.81	NULL	3 / 10	MF	gap junction channel activity
25	−9.73	NULL	4 / 38	BP	epithelial cell differentiation
26	−9.41	NULL	12 / 82	MF	structural constituent of cytoskeleton
27	−9.22	NULL	3 / 25	BP	response to zinc ion
28	−9.2	NULL	2 / 12	MF	fatty acid binding
29	−9.04	NULL	6 / 21	CC	cornified envelope
30	−8.83	NULL	2 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
31	−8.82	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
32	−8.71	NULL	3 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
33	−8.29	NULL	3 / 10	BP	negative regulation of interleukin−2 production
34	−8.22	NULL	2 / 15	GSEA C2	NGUYEN_NOTCH1_TARGETS_UP
35	−8.2	NULL	2 / 15	GSEA C2	RIGGINS_TAMOXIFEN_RESISTANCE_DN
36	−8.1	NULL	21 / 186	MF	structural molecule activity
37	−8.09	NULL	1 / 5	GSEA C2	BUSA_SAM68_TARGETS_UP
38	−8.05	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
39	−7.89	NULL	2 / 15	GSEA C2	STOSSI_RESPONSE_TO_ESTRADIOL
40	−7.84	NULL	6 / 48	Glio	Noushmehr_Pron_GCIMP_hypermeth_DN

p−values