GW_108

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1743 (1029 + / 714 −)

genes with fdr < 0.1 = 1478 (899 + / 579 −)

genes with fdr < 0.05 = 1140 (734 + / 406 −)

genes with fdr < 0.01 = 823 (564 + / 259 −)

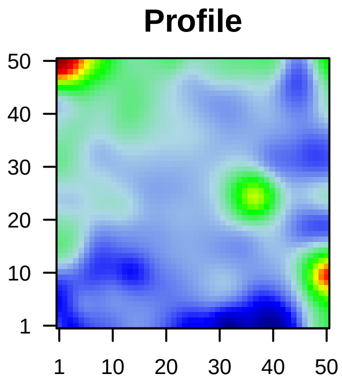
genes in genesets = 16332

<FC> = 0

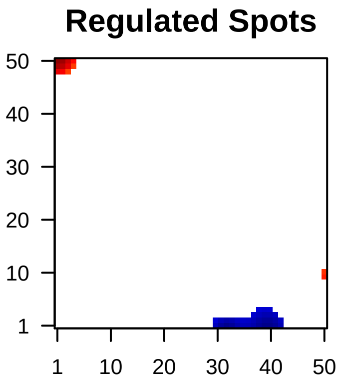
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.86



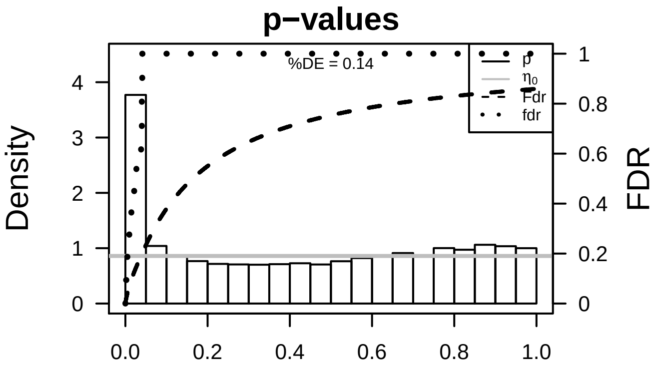
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.4	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	2.18	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	131	1.33	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	10551	2.02	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	216	1.62	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
6	218	1.56	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
7	55107	1.58	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
8	147495	1.55	2e−16	3e−14	2 x 44	adenomatosis polyposis coli down−regulated 1 [Source:HGN
9	347	1.52	2e−16	3e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
10	366	1.85	2e−16	3e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
11	655	1.54	2e−16	3e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
12	684	−2.07	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
13	339512	1.98	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
14	92747	3.6	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
15	29113	1.71	2e−16	3e−14	2 x 47	chromosome 6 open reading frame 15 [Source:HGNC Symbo
16	352999	1.55	2e−16	3e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
17	760	−1.79	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	92291	1.35	2e−16	3e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
19	6347	1.68	2e−16	3e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
20	6364	1.55	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.87	NULL	42	BP	keratinization
2	15.1	NULL	135	H.Tiss	WIRTH_Mucosa
3	13.63	NULL	21	CC	cornified envelope
4	13.57	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
5	10.49	NULL	43	MF	chemokine activity
6	10.41	NULL	76	BP	epidermis development
7	9.86	NULL	53	BP	keratinocyte differentiation
8	9.41	NULL	1182	CC	extracellular region
9	9.26	NULL	9	GSEA C2	GOUYER_TATI_TARGETS_UP
10	9.18	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
11	9.16	NULL	111	BP	chemotaxis
12	8.98	NULL	13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
13	8.91	NULL	10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
14	8.79	NULL	534	Chr	Chr 8
15	8.74	NULL	16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
16	8.68	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
17	8.43	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
18	8.14	NULL	683	CC	extracellular space
19	7.9	NULL	82	CC	intermediate filament
20	7.75	NULL	19	BP	peptide cross−linking
Underexpressed					
1	−10.49	NULL	633	Chr	Chr 9
2	−10.14	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	−9.95	NULL	51	BP	type I interferon signaling pathway
4	−9.92	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	−9.9	NULL	504	Chr	Chr 15
6	−9.24	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
7	−8.97	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	−7.85	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
9	−7.6	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
10	−7.27	NULL	940	MF	nucleic acid binding
11	−7.2	NULL	11	MF	platelet−derived growth factor binding
12	−7	NULL	4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
13	−6.98	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	−6.68	NULL	123	BP	defense response to virus
15	−6.62	NULL	4	MMML CGS	MACIEJ_MMML 47
16	−6.58	NULL	1820	MF	metal ion binding
17	−6.57	NULL	699	Chr	Chr 5
18	−6.46	NULL	127	H.Tiss	WIRTH_Muscle
19	−6.42	NULL	1135	Chr	Chr 19
20	−6.34	NULL	83	CC	basement membrane

GW_108

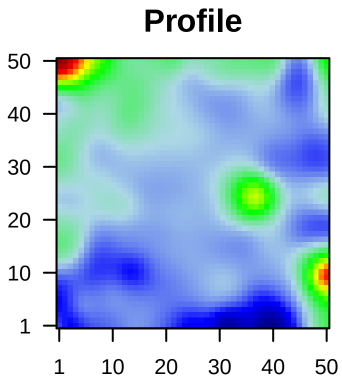
Local Summary

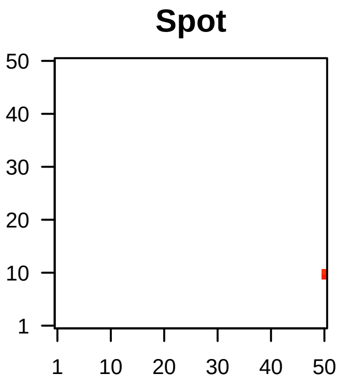
%DE = 0.94
metagenes = 2
genes = 67
genes in genesets = 66

genes with fdr < 0.1 = 54 (53 + / 1 −)
genes with fdr < 0.05 = 51 (51 + / 0 −)
genes with fdr < 0.01 = 45 (45 + / 0 −)

<r> metagenes = 0.99
<r> genes = 0.44

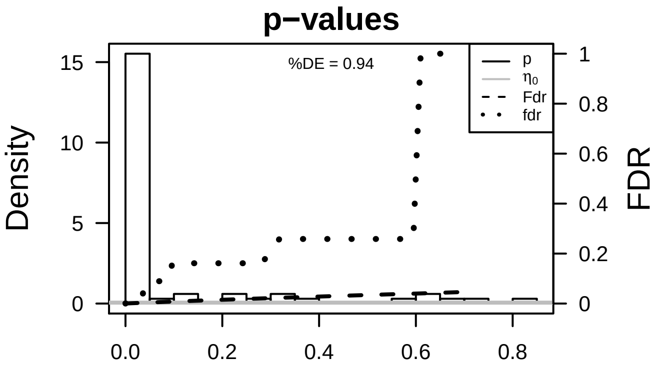
<FC> = 0.98
<shrinkage−t> = 34.46
<p−value> = 0
<fdr> = 0.29


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.4	2e−16	5e−17	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	10551	2.02	2e−16	5e−17	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	92747	3.6	2e−16	5e−17	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
4	352999	1.55	2e−16	5e−17	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
5	92291	1.35	2e−16	5e−17	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
6	57535	1.55	2e−16	5e−17	50 x 10	KIAA1324 [Source:HGNC Symbol;Acc:29618]
7	124220	1.57	2e−16	5e−17	50 x 10	zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
8	10232	2.25	2e−16	5e−17	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
9	4477	2.13	2e−16	5e−17	50 x 11	microseminoprotein, beta− [Source:HGNC Symbol;Acc:7372]
10	94025	1.9	2e−16	5e−17	50 x 11	mucin 16, cell surface associated [Source:HGNC Symbol;Acc
11	5284	2.09	2e−16	5e−17	50 x 10	polymeric immunoglobulin receptor [Source:HGNC Symbol;A
12	5304	1.73	2e−16	5e−17	50 x 10	prolactin−induced protein [Source:HGNC Symbol;Acc:8993]
13	51297	2.83	2e−16	5e−17	50 x 10	BPI fold containing family A, member 1 [Source:HGNC Symb
14	8842	2.28	2e−16	5e−17	50 x 10	prominin 1 [Source:HGNC Symbol;Acc:9454]
15	11272	2.8	2e−16	5e−17	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
16	92304	3.35	2e−16	5e−17	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
17	7018	1.4	2e−16	5e−17	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
18	7033	2.8	2e−16	5e−17	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
19	389816	1.3	7e−16	4e−13	50 x 10	leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
20	4246	1.2	1e−13	5e−12	50 x 10	secretoglobin, family 2A, member 1 [Source:HGNC Symbol;A


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	50.58	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	21.19	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
3	17.88	NULL	2 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
4	16.77	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
5	13.94	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
6	13.43	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
7	13.15	NULL	1 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
8	12.9	NULL	1 / 8	GSEA C2	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_UP
9	12.02	NULL	1 / 15	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN
10	12.02	NULL	1 / 15	GSEA C2	LOPES_METHYLATED_IN_COLON_CANCER_UP
11	11.91	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
12	11.6	NULL	2 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
13	10.97	NULL	1 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
14	10.02	NULL	4 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
15	9.9	NULL	1 / 11	CC	photoreceptor outer segment membrane
16	9.35	NULL	1 / 12	BP	retina layer formation
17	9.16	NULL	2 / 15	GSEA C2	VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
18	8.77	NULL	1 / 4	miRNA target	miR−204
19	8.43	NULL	2 / 21	BP	drug metabolic process
20	8.37	NULL	1 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
21	8.37	NULL	1 / 14	GSEA C2	VALK_AML_WITH_11Q23_REARRANGED
22	8.14	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON
23	8.01	NULL	1 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
24	7.9	NULL	11 / 683	CC	extracellular space
25	7.79	NULL	1 / 16	CC	microvillus membrane
26	7.79	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
27	7.69	NULL	1 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
28	7.69	NULL	1 / 16	GSEA C2	VALK_AML_CLUSTER_9
29	7.42	NULL	2 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
30	7.39	NULL	1 / 5	GSEA C2	LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
31	7.18	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
32	7.16	NULL	1 / 5	GSEA C2	VALK_AML_CLUSTER_7
33	7.13	NULL	1 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
34	7.08	NULL	2 / 12	MF	calcium−dependent cysteine−type endopeptidase activity
35	7.07	NULL	21 / 1182	CC	extracellular region
36	7.07	NULL	2 / 37	BP	digestion
37	6.77	NULL	1 / 20	CC	stereocilium
38	6.63	NULL	1 / 17	Disease	BCHETNIA_EBM up
39	6.62	NULL	3 / 115	MF	lipid binding
40	6.49	NULL	1 / 21	BP	pancreas development

GW_108

Local Summary

%DE = 0.85

metagenes = 11

genes = 168

genes in genesets = 165

genes with fdr < 0.1 = 125 (117 + / 8 −)

genes with fdr < 0.05 = 120 (112 + / 8 −)

genes with fdr < 0.01 = 101 (96 + / 5 −)

<r> metagenes = 0.99

<r> genes = 0.49

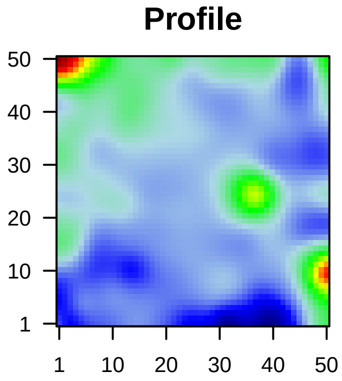
<FC> = 0.7

<shrinkage−t> = 24.71

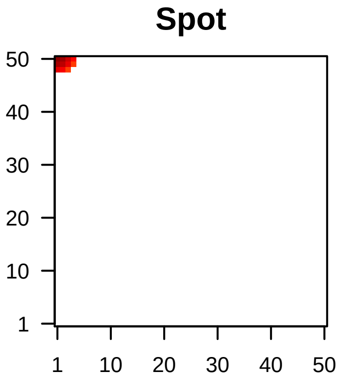
<p−value> = 0

<fdr> = 0.3

Profile

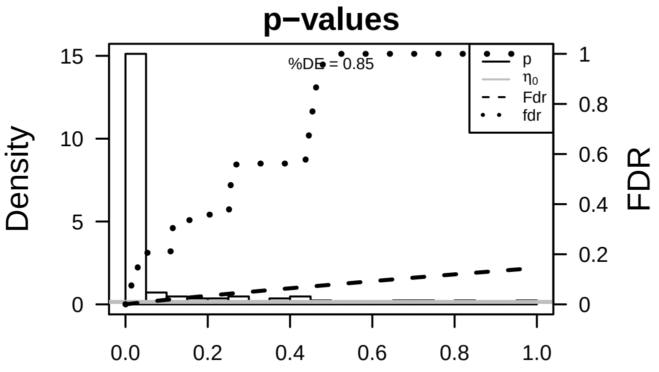


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.33	2e−16	2e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	1.56	2e−16	2e−16	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	1577	1.69	2e−16	2e−16	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
4	92196	2.01	2e−16	2e−16	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
5	1672	1.52	2e−16	2e−16	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
6	3860	1.52	2e−16	2e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
7	192666	1.36	2e−16	2e−16	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
8	3851	2.25	2e−16	2e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
9	388533	1.42	2e−16	2e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
10	84648	1.43	2e−16	2e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
11	3934	1.69	2e−16	2e−16	1 x 50	lipocalin 2 [Source:HGNC Symbol;Acc:6526]
12	4014	2.65	2e−16	2e−16	2 x 48	loricrin [Source:HGNC Symbol;Acc:6663]
13	10874	1.44	2e−16	2e−16	4 x 50	neuromedin U [Source:HGNC Symbol;Acc:7859]
14	6278	1.48	2e−16	2e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
15	338324	1.82	2e−16	2e−16	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
16	6286	1.61	2e−16	2e−16	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
17	374897	1.88	2e−16	2e−16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
18	6337	1.34	2e−16	2e−16	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
19	6590	1.85	2e−16	2e−16	1 x 49	secretory leukocyte peptidase inhibitor [Source:HGNC Symbo
20	6699	1.64	2e−16	2e−16	1 x 50	small proline−rich protein 1B [Source:HGNC Symbol;Acc:112



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	44.12	NULL	71 / 135	H.Tiss	WIRTH_Mucosa
2	43.23	NULL	14 / 21	CC	cornified envelope
3	38.23	NULL	16 / 42	BP	keratinization
4	31.52	NULL	19 / 53	BP	keratinocyte differentiation
5	27.56	NULL	18 / 76	BP	epidermis development
6	24.63	NULL	8 / 19	BP	peptide cross−linking
7	20.88	NULL	72 / 572	Disease	GUDJ_psoriasis up
8	16.86	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
9	15.19	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	15.07	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
11	14.23	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
12	13.28	NULL	5 / 10	MF	RAGE receptor binding
13	13.27	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
14	13.04	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
15	11.86	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	11.85	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	11.78	NULL	13 / 186	MF	structural molecule activity
18	11.46	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
19	11.09	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
20	11.08	NULL	4 / 27	BP	response to bacterium
21	10.78	NULL	3 / 16	GSEA C2	LEE_LIVER_CANCER_ACOX1_UP
22	10.73	NULL	2 / 17	Disease	BCHETNIA_EBM up
23	10.56	NULL	3 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
24	10.42	NULL	2 / 14	GSEA C2	CAIRO_HEPATOBLASTOMA_DN
25	10.32	NULL	3 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
26	10.07	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
27	9.96	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
28	9.92	NULL	3 / 12	BP	cellular aldehyde metabolic process
29	9.75	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
30	9.64	NULL	2 / 16	GSEA C2	ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_
31	9.5	NULL	3 / 13	GSEA C2	HAN_SATB1_TARGETS_DN
32	9.27	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
33	8.7	NULL	2 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
34	8.67	NULL	2 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
35	8.61	NULL	46 / 1182	CC	extracellular region
36	8.49	NULL	2 / 11	GSEA C2	REACTOME_XENOBIOTICS
37	8.47	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
38	8.27	NULL	4 / 44	CC	keratin filament
39	8.22	NULL	2 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
40	8.21	NULL	2 / 12	H.Tiss	WIRTH_Prim. lymphoid organs

GW_108

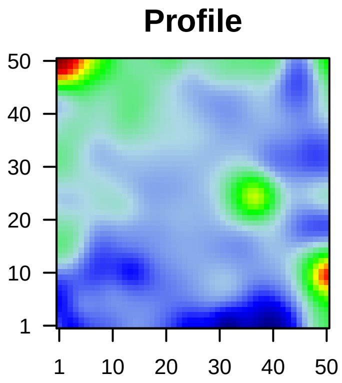
Local Summary

%DE = 0.77
metagenes = 34
genes = 448
genes in genesets = 419

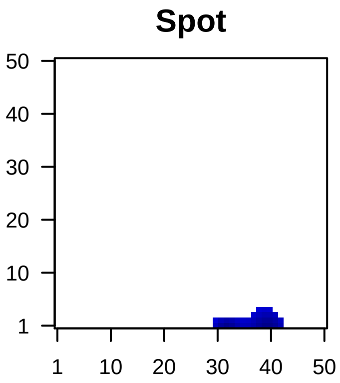
genes with fdr < 0.1 = 264 (13 + / 251 −)
genes with fdr < 0.05 = 206 (11 + / 195 −)
genes with fdr < 0.01 = 134 (6 + / 128 −)

<r> metagenes = 0.77
<r> genes = 0.28

<FC> = −0.34
<shrinkage−t> = −11.97
<p−value> = 0
<fdr> = 0.59



Profile



Spot

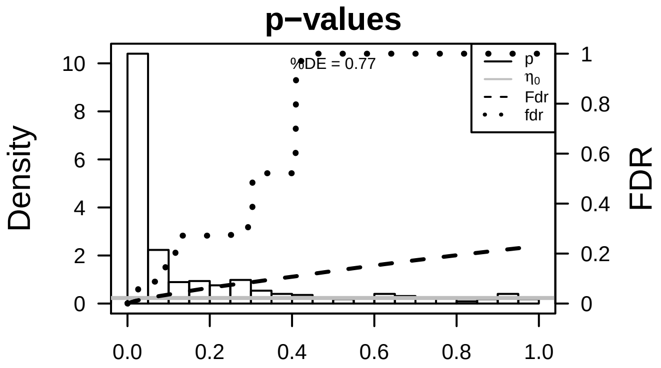
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−2.07	2e−16	3e−15	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	9560	1.79	2e−16	3e−15	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
3	3627	−1.49	2e−16	3e−15	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
4	1591	1.73	2e−16	3e−15	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
5	10561	−1.38	2e−16	3e−15	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
6	10964	−1.68	2e−16	3e−15	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
7	2537	−1.72	2e−16	3e−15	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
8	9636	−2.19	2e−16	3e−15	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
9	94240	−1.31	7e−16	2e−13	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
10	9997	−1.28	3e−15	2e−12	32 x 1	SCO2 cytochrome c oxidase assembly protein [Source:HGNC
11	6772	−1.24	2e−14	7e−12	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
12	51191	−1.21	8e−14	4e−11	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
13	4599	−1.07	5e−13	9e−11	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
14	629	1.15	1e−12	9e−11	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
15	54739	−1.14	2e−12	1e−10	32 x 1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
16	91543	−1.12	4e−12	2e−10	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:I
17	6773	−1.11	6e−12	9e−10	32 x 1	signal transducer and activator of transcription 2, 113kDa [So
18	400818	−1.09	2e−11	9e−10	40 x 1	Neuroblastoma breakpoint family member 1 [Source:UniProt
19	388372	1.08	2e−11	1e−08	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symbo
20	125050	1.04	1e−10	4e−08	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−40.51	NULL	12 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
2	−36.5	NULL	30 / 51	BP	type I interferon signaling pathway
3	−36.3	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	−36.09	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	−32.81	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	−31.58	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
7	−29.43	NULL	14 / 31	BP	negative regulation of viral genome replication
8	−29.24	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	−28.71	NULL	35 / 123	BP	defense response to virus
10	−28.05	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
11	−26.89	NULL	12 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
12	−26.78	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
13	−26.32	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
14	−24.76	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
15	−24.44	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
16	−24.17	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	−24.03	NULL	29 / 109	BP	response to virus
18	−22.87	NULL	7 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
19	−22.19	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
20	−22.02	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
21	−21.5	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
22	−21.11	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
23	−19.73	NULL	35 / 204	BP	cytokine−mediated signaling pathway
24	−18.58	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
25	−18.46	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
26	−18.3	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
27	−18.3	NULL	34 / 274	Lymphoma	SPANG_IL21 DN
28	−18.11	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
29	−18	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
30	−16.8	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
31	−14.95	NULL	6 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
32	−14.92	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
33	−14.86	NULL	4 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	−14.8	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	−14.09	NULL	48 / 572	Disease	GUDJ_psoriasis up
36	−13.71	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
37	−13.63	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
38	−13.51	NULL	3 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
39	−13.47	NULL	3 / 16	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
40	−13.37	NULL	5 / 18	BP	response to interferon−gamma



p−values