GW_261

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1620 (980 + / 640 −)

genes with fdr < 0.1 = 1290 (804 + / 486 −)

genes with fdr < 0.05 = 1135 (711 + / 424 −)

genes with fdr < 0.01 = 791 (513 + / 278 −)

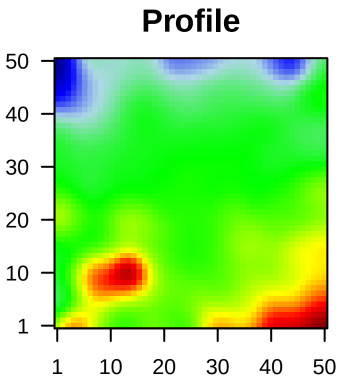
genes in genesets = 16332

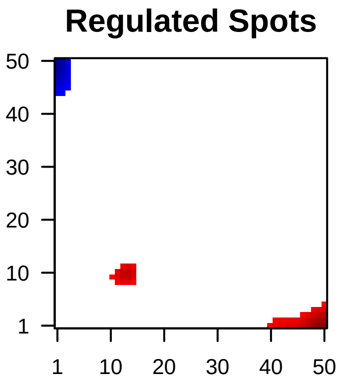
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.11

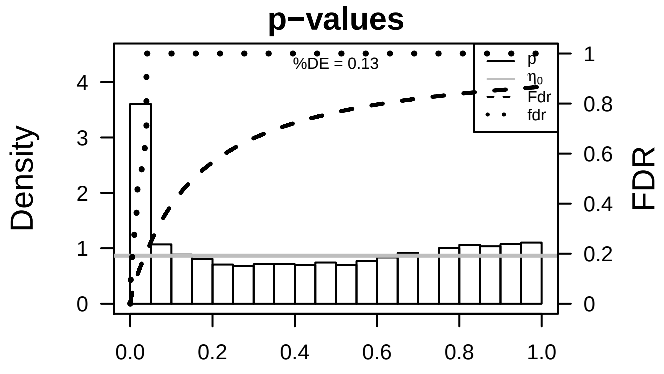
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.42	2e−16	4e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.47	2e−16	4e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.92	2e−16	4e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	347	2.68	2e−16	4e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
5	684	1.71	2e−16	4e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
6	57172	2.02	2e−16	4e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
7	6363	2.21	2e−16	4e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
8	1056	2.58	2e−16	4e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
9	169044	2.78	2e−16	4e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
10	51755	1.75	2e−16	4e−14	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
11	49860	−1.87	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
12	1475	−1.77	2e−16	4e−14	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
13	441520	2.76	2e−16	4e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
14	414325	−2.15	2e−16	4e−14	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	1673	−1.94	2e−16	4e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
16	1830	−1.95	2e−16	4e−14	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
17	1843	−1.87	2e−16	4e−14	22 x 50	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30
18	1917	2.15	2e−16	4e−14	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
19	8320	1.69	2e−16	4e−14	48 x 1	eomesodermin [Source:HGNC Symbol;Acc:3372]
20	2064	1.84	2e−16	4e−14	6 x 50	v−erb−b2 avian erythroblastic leukemia viral oncogene homol


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	9.91	NULL	1135	Chr	Chr 19
2	9.59	NULL	417	H.Tiss	WIRTH_Immune system
3	9.17	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	8.94	NULL	190	CC	extracellular matrix
5	8.46	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
6	8.39	NULL	250	Lymphoma	LENZ_Stromal signature 1
7	8.12	NULL	6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
8	7.69	NULL	51	BP	type I interferon signaling pathway
9	7.4	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
10	7.35	NULL	74	BP	regulation of immune response
11	7.32	NULL	717	Chr	Chr 16
12	6.89	NULL	183	CC	proteinaceous extracellular matrix
13	6.48	NULL	15	CC	MHC class II protein complex
14	6.4	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
15	6.4	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
16	6.4	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
17	6.4	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
18	6.37	NULL	15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
19	6.24	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
20	6.21	NULL	52	Chr	Chr HSCHR6_MHC_QBL
Underexpressed					
1	−22.57	NULL	572	Disease	GUDJ_psoriasis up
2	−20.45	NULL	135	H.Tiss	WIRTH_Mucosa
3	−15.48	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
4	−15.48	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
5	−15.43	NULL	21	CC	cornified envelope
6	−14.04	NULL	53	BP	keratinocyte differentiation
7	−13.89	NULL	42	BP	keratinization
8	−11.42	NULL	76	BP	epidermis development
9	−10.27	NULL	370	BP	mitotic cell cycle
10	−9.99	NULL	530	Cancer	Lembcke_Normal vs Adenoma
11	−9.65	NULL	19	BP	peptide cross−linking
12	−8.03	NULL	15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
13	−7.67	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
14	−7.36	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
15	−7.28	NULL	15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
16	−7.15	NULL	232	BP	mitosis
17	−6.87	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
18	−6.8	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
19	−6.77	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
20	−6.75	NULL	421	miRNA target−starBase	hsa−let−7b

GW_261

Local Summary

%DE = 0.89

metagenes = 30

genes = 472

genes in genesets = 461

genes with fdr < 0.1 = 384 (378 + / 6 −)

genes with fdr < 0.05 = 339 (333 + / 6 −)

genes with fdr < 0.01 = 285 (283 + / 2 −)

<r> metagenes = 0.89

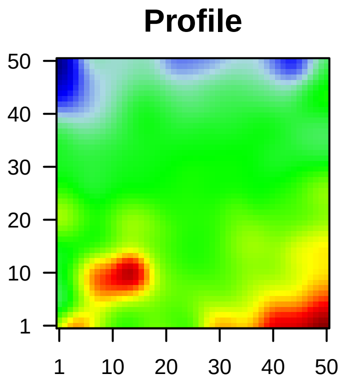
<r> genes = 0.44

<FC> = 0.69

<shrinkage−t> = 24.26

<p−value> = 0

<fdr> = 0.34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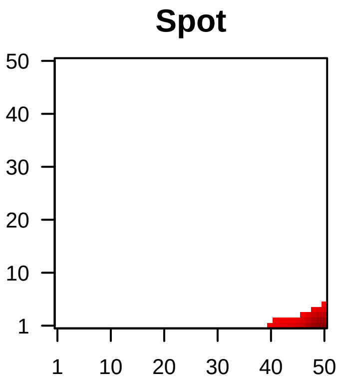
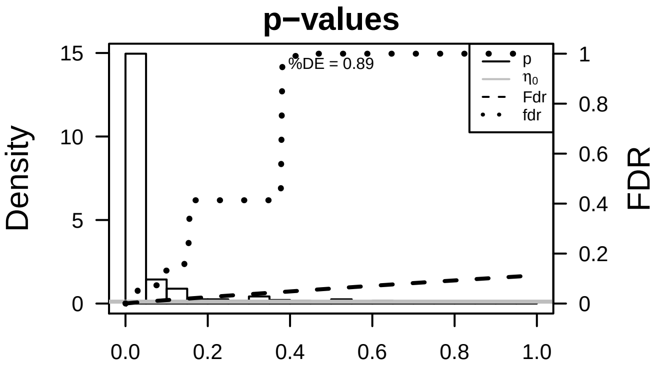

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	2.02	2e−16	1e−15	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	6363	2.21	2e−16	1e−15	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	169044	2.78	2e−16	1e−15	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:229
4	51755	1.75	2e−16	1e−15	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
5	8320	1.69	2e−16	1e−15	48 x 1	eomesodermin [Source:HGNC Symbol;Acc:3372]
6	54855	1.73	2e−16	1e−15	49 x 1	family with sequence similarity 46, member C [Source:HGNC
7	3128	1.73	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
8	5920	1.76	2e−16	1e−15	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
9	10537	1.76	2e−16	1e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
10	930	1.67	4e−16	4e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
11	125050	1.65	1e−15	5e−14	40 x 1	RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
12	3543	1.5	2e−15	2e−13	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
13	3512	1.61	7e−15	2e−13	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
14	939	1.6	8e−15	4e−13	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
15	84446	1.58	2e−14	1e−12	43 x 1	BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:18
16	401261	1.56	4e−14	3e−12	41 x 1	
17	3109	1.54	9e−14	3e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
18	126306	1.52	1e−13	3e−12	49 x 1	junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
19	692084	1.52	2e−13	6e−12	48 x 4	small nucleolar RNA, C/D box 13 [Source:HGNC Symbol;Acc
20	84824	1.5	4e−13	6e−12	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	23.2	NULL	107 / 417	H.Tiss	WIRTH_Immune system
2	17.67	NULL	14 / 15	CC	MHC class II protein complex
3	16.72	NULL	107 / 553	Cancer	Lembcke_Colonic Inflammation
4	16.14	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	15.53	NULL	65 / 312	BP	immune response
6	14.86	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
7	14.03	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
8	13.96	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
9	13.52	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
10	13.32	NULL	6 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
11	13.06	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
12	13.02	NULL	19 / 74	BP	regulation of immune response
13	12.38	NULL	22 / 60	BP	T cell costimulation
14	12.08	NULL	17 / 47	BP	antigen processing and presentation
15	11.91	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	11.66	NULL	8 / 13	Cancer	GENTLES_modul18
17	11.41	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
18	11.22	NULL	5 / 12	BP	dendritic cell chemotaxis
19	11.2	NULL	7 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
20	11.03	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
21	10.72	NULL	5 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
22	10.66	NULL	48 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
23	10.66	NULL	48 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
24	10.66	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
25	10.66	NULL	48 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
26	10.54	NULL	5 / 12	BP	immunoglobulin mediated immune response
27	10.11	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
28	9.91	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
29	9.82	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
30	9.7	NULL	5 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
31	9.62	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
32	9.59	NULL	4 / 13	BP	positive regulation of endocytosis
33	9.49	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
34	9.4	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
35	9.31	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
36	9.22	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE
37	9.19	NULL	5 / 11	BP	positive regulation of B cell differentiation
38	9.16	NULL	30 / 204	BP	cell surface receptor signaling pathway
39	9.05	NULL	4 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
40	8.97	NULL	5 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB

GW_261

Local Summary

%DE = 0.76

metagenes = 16

genes = 80

genes in genesets = 63

genes with fdr < 0.1 = 56 (56 + / 0 −)

genes with fdr < 0.05 = 54 (54 + / 0 −)

genes with fdr < 0.01 = 49 (49 + / 0 −)

<r> metagenes = 0.96

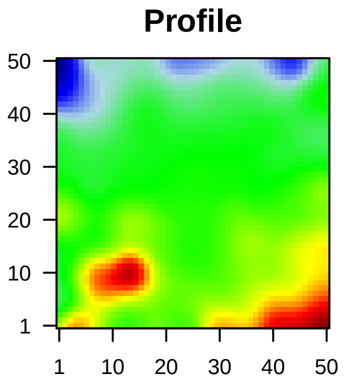
<r> genes = 0.31

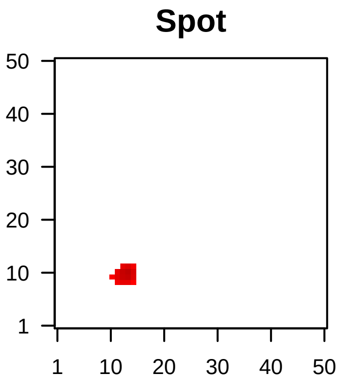
<FC> = 1.21

<shrinkage−t> = 42.48

<p−value> = 0

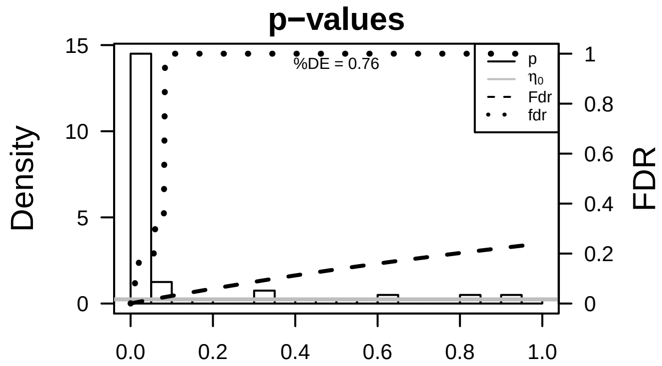
<fdr> = 0.32





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	441520	2.76	2e−16	2e−16	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
2	729428	3.3	2e−16	2e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
3	729422	3.8	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	3.18	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	2.86	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.52	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	3.44	2e−16	2e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729447	2.49	2e−16	2e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
9	645037	3.66	2e−16	2e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
10	26749	2.46	2e−16	2e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
11	2576	3.01	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
12	2577	3.32	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2578	1.9	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2579	3.06	2e−16	2e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
15	100101629	1.69	2e−16	2e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
16	121355	1.91	2e−16	2e−16	14 x 11	gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
17	4100	1.75	2e−16	2e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
18	4109	3.25	2e−16	2e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
19	55655	1.78	2e−16	2e−16	15 x 11	NLR family, pyrin domain containing 2 [Source:HGNC Symbo
20	402381	1.69	2e−16	2e−16	13 x 11	spermatogenesis and oogenesis specific basic helix−loop−he



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	17.47	NULL	26 / 630	Chr	Chr X
2	15.46	NULL	1 / 11	GSEA C2	SU_PLACENTA
3	14.61	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
4	13.27	NULL	1 / 14	GSEA C2	NIELSEN_GIST
5	12.81	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
6	12.71	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
7	10.9	NULL	1 / 2	miRNA target	miR−107
8	10.42	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
9	9.37	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
10	9.31	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
11	8.33	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
12	6.33	NULL	1 / 17	BP	positive regulation of interleukin−1 beta secretion
13	6.32	NULL	7 / 120	H.Tiss	WIRTH_Testis
14	6.24	NULL	1 / 11	Glio	willscher_GBM_Verhaak−CL_expression_M_down
15	6.24	NULL	1 / 11	Glio	willscher_GBM_Verhaak−MES_expression_M_down
16	6.24	NULL	1 / 11	Glio	willscher_GBM_Verhaak−PNmut_expression_M_up
17	6.02	NULL	1 / 10	GSEA C2	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
18	5.65	NULL	1 / 11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
19	5.59	NULL	1 / 19	BP	oogenesis
20	5.56	NULL	1 / 10	GSEA C2	XU_RESPONSE_TO_TRETINOIN_DN
21	5.48	NULL	1 / 13	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_DN
22	5.48	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
23	5.45	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
24	5.33	NULL	1 / 12	GSEA C2	HSIAO_LIVER_SPECIFIC_GENES
25	5.22	NULL	1 / 14	BP	negative regulation of retinoic acid receptor signaling pathway
26	5.22	NULL	1 / 14	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN
27	5.17	NULL	1 / 13	CC	mitochondrial respiratory chain
28	5.06	NULL	1 / 13	GSEA C2	HOSHIDA_LIVER_CANCER_SURVIVAL_DN
29	5.03	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
30	5	NULL	1 / 15	GSEA C2	LI_WILMS_TUMOR
31	4.79	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
32	4.77	NULL	1 / 10	BP	leukocyte tethering or rolling
33	4.61	NULL	1 / 15	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
34	4.61	NULL	1 / 15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
35	4.61	NULL	1 / 15	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4
36	4.61	NULL	1 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
37	4.6	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_UP
38	4.42	NULL	7 / 419	CC	cellular_component
39	4.42	NULL	1 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
40	4.42	NULL	1 / 16	GSEA C2	JI_METASTASIS_REPRESSED_BY_STK11

GW_261

Local Summary

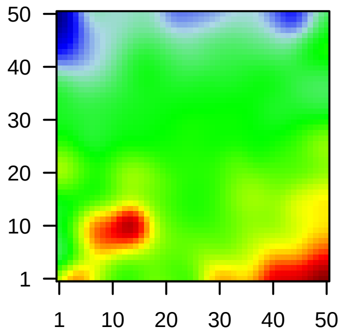
%DE = 0.87
metagenes = 20
genes = 271
genes in genesets = 264

genes with fdr < 0.1 = 202 (6 + / 196 −)
genes with fdr < 0.05 = 202 (6 + / 196 −)
genes with fdr < 0.01 = 175 (3 + / 172 −)

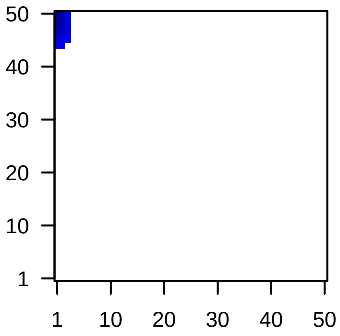
<r> metagenes = 0.92
<r> genes = 0.41

<FC> = −0.8
<shrinkage−t> = −28.24
<p−value> = 0
<fdr> = 0.31

Profile



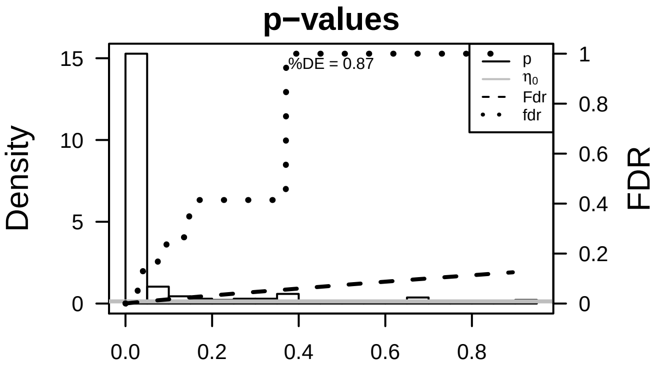
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.42	2e−16	3e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	−2.47	2e−16	3e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.92	2e−16	3e−16	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC S
4	49860	−1.87	2e−16	3e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
5	1475	−1.77	2e−16	3e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
6	414325	−2.15	2e−16	3e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
7	1673	−1.94	2e−16	3e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
8	1830	−1.95	2e−16	3e−16	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
9	9982	−2.58	2e−16	3e−16	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
10	163351	−1.77	2e−16	3e−16	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
11	10804	−2.43	2e−16	3e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
12	56300	−1.88	2e−16	3e−16	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
13	53833	−1.86	2e−16	3e−16	1 x 46	interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
14	3861	−1.92	2e−16	3e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
15	286887	−3.23	2e−16	3e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
16	388533	−2.69	2e−16	3e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGN
17	84648	−1.86	2e−16	3e−16	1 x 48	late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
18	6283	−1.79	2e−16	3e−16	1 x 49	S100 calcium binding protein A12 [Source:HGNC Symbol;Ac
19	6273	−1.76	2e−16	3e−16	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
20	374897	−2.16	2e−16	3e−16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−48.62	NULL	87 / 135	H.Tiss	WIRTH_Mucosa
2	−42.77	NULL	18 / 21	CC	cornified envelope
3	−36.17	NULL	19 / 42	BP	keratinization
4	−34.28	NULL	24 / 53	BP	keratinocyte differentiation
5	−30.33	NULL	104 / 572	Disease	GUDJ_psoriasis up
6	−27.03	NULL	10 / 19	BP	peptide cross−linking
7	−26.2	NULL	24 / 76	BP	epidermis development
8	−19.04	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
9	−18.36	NULL	12 / 21	CC	desmosome
10	−16.56	NULL	27 / 186	MF	structural molecule activity
11	−15.52	NULL	19 / 82	CC	intermediate filament
12	−14.74	NULL	12 / 44	CC	keratin filament
13	−13.27	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
14	−13.11	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
15	−12.92	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
16	−12.37	NULL	9 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	−12.34	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
18	−12.07	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
19	−11.78	NULL	5 / 10	MF	RAGE receptor binding
20	−10.9	NULL	3 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
21	−10.87	NULL	6 / 13	BP	negative regulation of peptidase activity
22	−10.86	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
23	−10.51	NULL	2 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
24	−10.47	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
25	−10.36	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
26	−9.76	NULL	3 / 12	BP	cellular aldehyde metabolic process
27	−9.74	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
28	−9.58	NULL	3 / 15	CC	connexon complex
29	−9.3	NULL	5 / 25	BP	response to zinc ion
30	−9.24	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
31	−9.13	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
32	−8.88	NULL	4 / 21	CC	gap junction
33	−8.71	NULL	7 / 51	MF	protein binding, bridging
34	−8.66	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
35	−8.53	NULL	4 / 15	MF	retinol dehydrogenase activity
36	−8.43	NULL	62 / 1182	CC	extracellular region
37	−8.12	NULL	7 / 38	BP	epithelial cell differentiation
38	−7.98	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
39	−7.93	NULL	2 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
40	−7.86	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U