GW_140

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2018 (1120 + / 898 −)

genes with fdr < 0.1 = 1643 (918 + / 725 −)

genes with fdr < 0.05 = 1412 (806 + / 606 −)

genes with fdr < 0.01 = 989 (567 + / 422 −)

genes in genesets = 16332

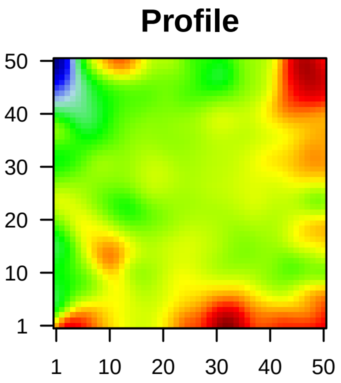
<FC> = 0

<shrinkage−t> = 0

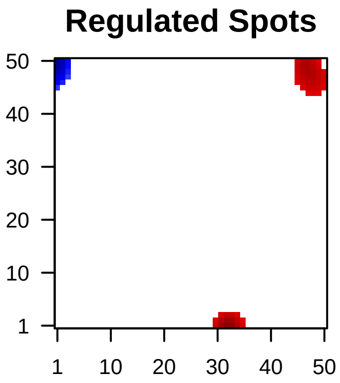
<p−value> = 0.08

<fdr> = 0.85

Profile



Regulated Spots



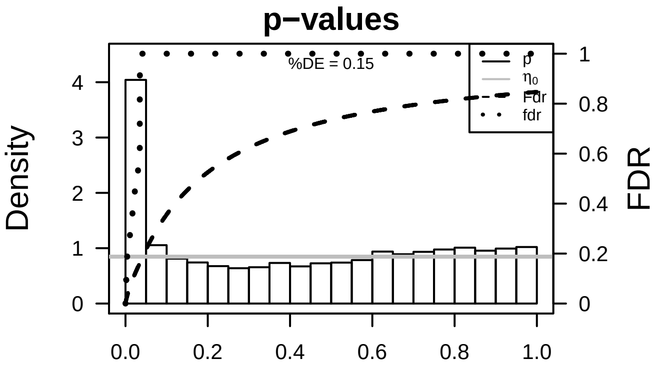
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.48	2e−16	3e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	70	1.29	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	−2.03	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	113146	−1.33	2e−16	3e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
5	57016	1.37	2e−16	3e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
6	441282	1.3	2e−16	3e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
7	216	−1.35	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
8	10840	1.19	2e−16	3e−14	50 x 12	aldehyde dehydrogenase 1 family, member L1 [Source:HGNC
9	8120	1.29	2e−16	3e−14	11 x 14	adaptor−related protein complex 3, beta 2 subunit [Source:HC
10	341	1.23	2e−16	3e−14	50 x 1	apolipoprotein C−I [Source:HGNC Symbol;Acc:607]
11	64207	−1.42	2e−16	3e−14	50 x 40	interferon regulatory factor 2 binding protein−like [Source:HG
12	440712	1.49	2e−16	3e−14	1 x 39	chromosome 1 open reading frame 186 [Source:HGNC Symb
13	149563	1.24	2e−16	3e−14	34 x 23	chromosome 1 open reading frame 64 [Source:HGNC Symbo
14	713	1.25	2e−16	3e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
15	56892	1.25	2e−16	3e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
16	375791	−1.41	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
17	51806	1.43	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
18	857	−1.22	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
19	595	−1.27	2e−16	3e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
20	1056	1.95	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	15.32	NULL	504	Chr	Chr 15
2	14.55	NULL	1720	Chr	Chr 1
3	8.65	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	7.02	NULL	9	GSEA C2	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
5	6.87	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
6	6.61	NULL	13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
7	6.53	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
8	6.38	NULL	250	Lymphoma	LENZ_Stromal signature 1
9	6.36	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	6.33	NULL	14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
11	6.26	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
12	6.09	NULL	47	BP	embryonic skeletal system morphogenesis
13	6.08	NULL	15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
14	6.08	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
15	5.77	NULL	7	MMML CGS	MACIEJ_MMML 9
16	5.76	NULL	119	Lymphoma	ROSOLOWSKI_green total
17	5.69	NULL	14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
18	5.63	NULL	123	BP	defense response to virus
19	5.63	NULL	699	Chr	Chr 5
20	5.57	NULL	15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
Underexpressed					
1	−14.24	NULL	519	Chr	Chr 14
2	−10.31	NULL	135	H.Tiss	WIRTH_Mucosa
3	−10.03	NULL	957	Chr	Chr 11
4	−8.93	NULL	12	BP	hemidesmosome assembly
5	−8.68	NULL	717	Chr	Chr 16
6	−8.25	NULL	4	MMML CGS	MACIEJ_MMML 23
7	−7.95	NULL	42	BP	keratinization
8	−6.2	NULL	1146	TF	HEBENSTREIT_low expression TF
9	−6.06	NULL	21	CC	cornified envelope
10	−5.67	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
11	−5.64	NULL	232	Chr	Chr 18
12	−5.57	NULL	10	CC	hemoglobin complex
13	−5.24	NULL	618	Chr	Chr 4
14	−5.1	NULL	128	BP	translational initiation
15	−5.1	NULL	21	CC	desmosome
16	−5.07	NULL	11	MF	oxygen transporter activity
17	−5.06	NULL	534	Chr	Chr 8
18	−5.04	NULL	92	BP	translational elongation
19	−5.03	NULL	13	BP	intermediate filament cytoskeleton organization
20	−4.98	NULL	5	GSEA C2	BUSA_SAM68_TARGETS_UP

p−values



GW_140

Local Summary

%DE = 0.73

metagenes = 16

genes = 163

genes in genesets = 160

genes with fdr < 0.1 = 87 (75 + / 12 −)

genes with fdr < 0.05 = 84 (73 + / 11 −)

genes with fdr < 0.01 = 65 (59 + / 6 −)

<r> metagenes = 0.96

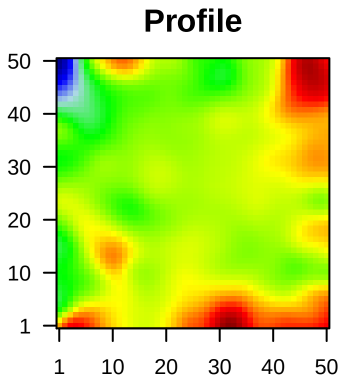
<r> genes = 0.38

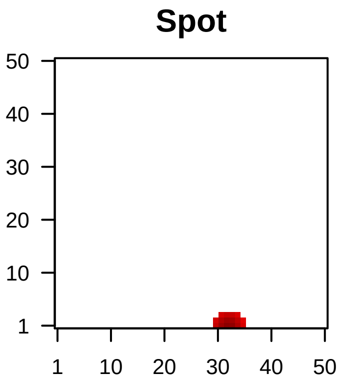
<FC> = 0.28

<shrinkage−t> = 9.98

<p−value> = 0

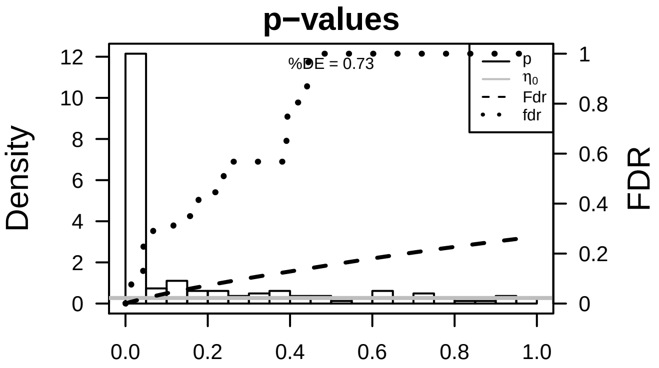
<fdr> = 0.48


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4321	−1.28	2e−16	1e−14	32 x 1	matrix metallopeptidase 12 (macrophage elastase) [Source:H
2	91543	1.11	3e−14	8e−12	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:I
3	10561	1.07	2e−13	1e−11	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
4	27074	1.06	4e−13	6e−11	32 x 1	lysosomal−associated membrane protein 3 [Source:HGNC Sy
5	2633	1.02	2e−12	6e−11	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN
6	100	1.02	3e−12	1e−10	30 x 1	adenosine deaminase [Source:HGNC Symbol;Acc:186]
7	64135	1	6e−12	1e−10	32 x 1	interferon induced with helicase C domain 1 [Source:HGNC S
8	629	1	8e−12	1e−10	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
9	23780	0.99	1e−11	1e−10	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
10	6890	0.98	1e−11	5e−10	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
11	83666	0.97	3e−11	5e−10	32 x 1	poly (ADP−ribose) polymerase family, member 9 [Source:HG
12	219285	0.96	4e−11	2e−09	32 x 1	sterile alpha motif domain containing 9−like [Source:HGNC S
13	3628	0.94	1e−10	2e−09	33 x 1	inositol polyphosphate−1−phosphatase [Source:HGNC Symb
14	3627	0.94	1e−10	4e−09	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
15	55092	0.91	4e−10	4e−09	33 x 2	transmembrane protein 51 [Source:HGNC Symbol;Acc:2548
16	103	0.91	4e−10	4e−09	33 x 1	adenosine deaminase, RNA−specific [Source:HGNC Symbol
17	6772	0.91	5e−10	5e−09	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
18	4940	0.9	6e−10	8e−09	32 x 1	2'−5'−oligoadenylate synthetase 3, 100kDa [Source:HGNC S
19	64167	0.9	8e−10	2e−08	35 x 2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Sym
20	684	0.89	1e−09	5e−08	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	45.91	NULL	13 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	36.9	NULL	12 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	35.1	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
4	28.74	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
5	28.45	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
6	27.21	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
7	27.16	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
8	24.67	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
9	24.67	NULL	33 / 123	BP	defense response to virus
10	24.63	NULL	29 / 51	BP	type I interferon signaling pathway
11	23.06	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
12	22.72	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
13	21.48	NULL	15 / 31	BP	negative regulation of viral genome replication
14	20.78	NULL	5 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
15	20.17	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
16	19.99	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
17	19.99	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
18	19.98	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
19	19.38	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
20	19.08	NULL	3 / 5	GSEA C2	BROWNE_INTERFERON_RESPONSIVE_GENES
21	19.01	NULL	7 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
22	18.76	NULL	4 / 15	GSEA C2	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
23	18.76	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
24	18.65	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
25	18.1	NULL	4 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
26	17.94	NULL	27 / 109	BP	response to virus
27	17.42	NULL	4 / 16	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
28	17.06	NULL	33 / 274	Lymphoma	SPANG_IL21 DN
29	16.93	NULL	4 / 16	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP
30	16.73	NULL	3 / 8	GSEA C2	KEGG_PRIMARY_IMMUNODEFICIENCY
31	16.66	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
32	15.77	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
33	15.55	NULL	34 / 204	BP	cytokine−mediated signaling pathway
34	15.25	NULL	49 / 572	Disease	GUDJ_psoriasis up
35	14.77	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
36	14.64	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
37	14.07	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
38	13.81	NULL	5 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_LB_DN
39	13.62	NULL	11 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
40	13.5	NULL	3 / 15	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP

GW_140

Local Summary

%DE = 0.63

metagenes = 36

genes = 348

genes in genesets = 345

genes with fdr < 0.1 = 119 (105 + / 14 −)

genes with fdr < 0.05 = 109 (96 + / 13 −)

genes with fdr < 0.01 = 76 (71 + / 5 −)

<r> metagenes = 0.91

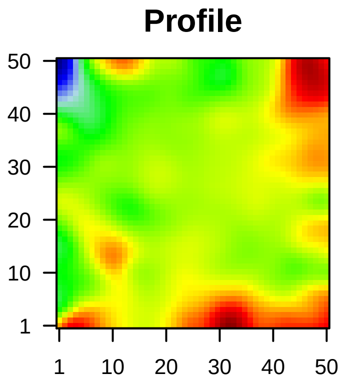
<r> genes = 0.28

<FC> = 0.23

<shrinkage−t> = 7.96

<p−value> = 0.01

<fdr> = 0.64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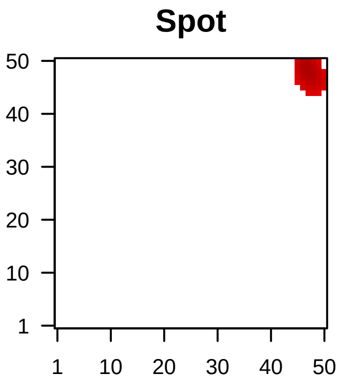
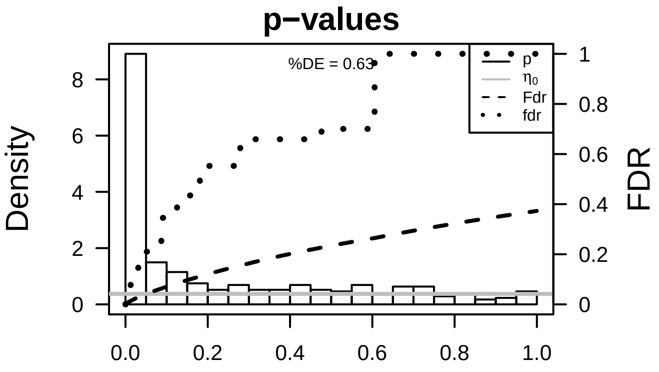

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3992	1.26	2e−16	6e−15	45 x 50	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
2	3202	1.79	2e−16	6e−15	49 x 47	homeobox A5 [Source:HGNC Symbol;Acc:5106]
3	3205	1.97	2e−16	6e−15	49 x 45	homeobox A9 [Source:HGNC Symbol;Acc:5109]
4	139728	1.45	2e−16	6e−15	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
5	59342	1.33	2e−16	6e−15	50 x 47	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:29507
6	55897	1.16	1e−15	4e−13	50 x 45	mesoderm posterior 1 homolog (mouse) [Source:HGNC Sym
7	9055	1.14	4e−15	3e−12	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
8	387103	1.11	3e−14	5e−12	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
9	8884	1.09	7e−14	2e−11	48 x 44	solute carrier family 5 (sodium/multivitamin and iodide cotrans
10	7345	1.07	2e−13	2e−11	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
11	7037	0.97	3e−13	1e−09	47 x 50	transferrin receptor [Source:HGNC Symbol;Acc:11763]
12	54913	1	9e−12	2e−09	48 x 47	ribonuclease P/MRP 25kDa subunit [Source:HGNC Symbol;
13	7546	0.97	2e−11	3e−08	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
14	113802	0.92	3e−10	3e−08	46 x 46	HEN1 methyltransferase homolog 1 (Arabidopsis) [Source:H
15	51133	0.91	4e−10	3e−08	49 x 50	potassium channel tetramerization domain containing 3 [Sour
16	116832	0.9	6e−10	3e−08	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
17	55086	0.9	8e−10	9e−08	48 x 50	chromosome X open reading frame 57 [Source:HGNC Symb
18	23580	0.88	2e−09	4e−07	47 x 45	CDC42 effector protein (Rho GTPase binding) 4 [Source:HG
19	109	0.85	5e−09	4e−07	48 x 46	adenylate cyclase 3 [Source:HGNC Symbol;Acc:234]
20	168002	−0.84	7e−09	1e−06	50 x 46	dishevelled−binding antagonist of beta−catenin 2 [Source:HG


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.73	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_7P15_AMPLICON
2	15.71	NULL	37 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	15.71	NULL	37 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	14.83	NULL	1 / 5	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29
5	14.83	NULL	1 / 5	miRNA target	miR−126
6	13.49	NULL	3 / 21	Glio	Martinez_Glio_hypermeth
7	13.34	NULL	5 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
8	12.62	NULL	4 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
9	12.24	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
10	10.93	NULL	2 / 12	TF Tissue	VAQUERIZAS_Kidney
11	10.78	NULL	2 / 13	GSEA C2	LEE_INTRATHYMIC_T_PROGENITOR
12	10.63	NULL	3 / 13	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
13	10.61	NULL	5 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
14	10.58	NULL	3 / 37	BP	embryonic skeletal system development
15	10.52	NULL	5 / 16	GSEA C2	MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
16	9.52	NULL	5 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
17	9.06	NULL	4 / 9	GSEA C2	SEMBA_FHIT_TARGETS_DN
18	8.91	NULL	7 / 26	BP	cellular response to ionizing radiation
19	8.89	NULL	2 / 15	TF Tissue	VAQUERIZAS_Adrenal gland
20	8.78	NULL	1 / 13	TF Tissue	VAQUERIZAS_Skin
21	8.73	NULL	2 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
22	8.7	NULL	4 / 53	Glio	Christensen_hypermethylated_in_primary_glioblastoma
23	8.62	NULL	5 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
24	8.42	NULL	1 / 14	GSEA C2	GOLUB_ALL_VS_AML_DN
25	8.32	NULL	5 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
26	8.15	NULL	10 / 163	miRNA target	hsa−miR−1297
27	8.1	NULL	1 / 15	BP	definitive hemopoiesis
28	7.94	NULL	1 / 13	BP	epithelial tube branching involved in lung morphogenesis
29	7.94	NULL	1 / 13	BP	mammary gland alveolus development
30	7.9	NULL	1 / 5	miRNA target	miR−320
31	7.85	NULL	30 / 149	BP	DNA replication
32	7.83	NULL	5 / 26	BP	chromosome organization
33	7.83	NULL	13 / 57	Glio	developing astrocytes
34	7.82	NULL	1 / 16	TF Tissue	VAQUERIZAS_Pancreas
35	7.77	NULL	4 / 16	GSEA C2	BENPORATH_PROLIFERATION
36	7.73	NULL	65 / 914	Chr	Chr 3
37	7.57	NULL	4 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
38	7.49	NULL	4 / 15	GSEA C2	CHANG_CYCLING_GENES
39	7.45	NULL	4 / 92	BP	anterior/posterior pattern specification
40	7.44	NULL	2 / 13	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_C

GW_140

Local Summary

%DE = 0.93

metagenes = 15

genes = 222

genes in genesets = 216

genes with fdr < 0.1 = 191 (48 + / 143 −)

genes with fdr < 0.05 = 180 (45 + / 135 −)

genes with fdr < 0.01 = 159 (37 + / 122 −)

<r> metagenes = 0.95

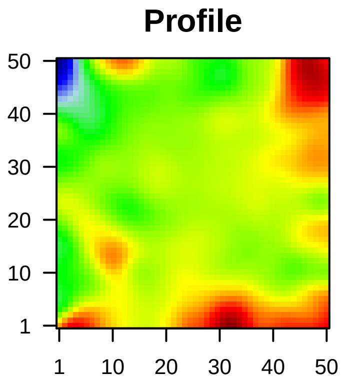
<r> genes = 0.45

<FC> = −0.42

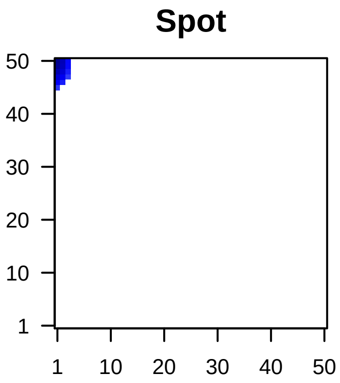
<shrinkage−t> = −14.69

<p−value> = 0

<fdr> = 0.25



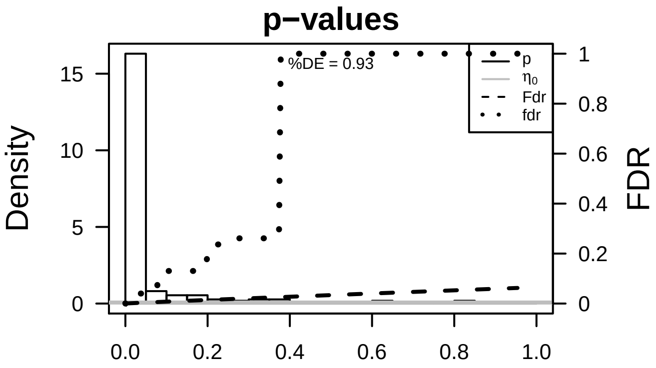
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.03	2e−16	9e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.37	2e−16	9e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	1.3	2e−16	9e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	375791	−1.41	2e−16	9e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
5	84518	−1.5	2e−16	9e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
6	1382	1.69	2e−16	9e−17	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
7	54544	−1.47	2e−16	9e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
8	49860	−1.96	2e−16	9e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	9547	−1.55	2e−16	9e−17	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
10	1672	−1.41	2e−16	9e−17	1 x 50	defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
11	414325	−1.65	2e−16	9e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	1673	−1.46	2e−16	9e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1828	−1.39	2e−16	9e−17	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
14	26525	−1.31	2e−16	9e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
15	5653	−1.29	2e−16	9e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
16	3848	−1.37	2e−16	9e−17	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
17	3861	−3.12	2e−16	9e−17	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
18	192666	−1.28	2e−16	9e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
19	3851	−1.73	2e−16	9e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
20	388533	−2.55	2e−16	9e−17	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.39	NULL	82 / 135	H.Tiss	WIRTH_Mucosa
2	−19.26	NULL	19 / 42	BP	keratinization
3	−18.06	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
4	−17	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
5	−16.33	NULL	18 / 21	CC	cornified envelope
6	−14.44	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
7	−14.27	NULL	10 / 19	BP	peptide cross−linking
8	−14.14	NULL	12 / 21	CC	desmosome
9	−13.52	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
10	−12.24	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
11	−11.98	NULL	7 / 38	BP	epithelial cell differentiation
12	−11.45	NULL	2 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
13	−11.45	NULL	16 / 82	CC	intermediate filament
14	−10.86	NULL	24 / 53	BP	keratinocyte differentiation
15	−10.8	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
16	−10.49	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−10.47	NULL	10 / 44	CC	keratin filament
18	−10.29	NULL	2 / 15	BP	fibrinolysis
19	−10.29	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
20	−9.8	NULL	1 / 12	BP	hemidesmosome assembly
21	−9.15	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
22	−9.14	NULL	93 / 572	Disease	GUDJ_psoriasis up
23	−8.67	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
24	−8.59	NULL	3 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
25	−8.52	NULL	1 / 10	GSEA C2	BIOCARTA_FIBRINOLYSIS_PATHWAY
26	−8.5	NULL	23 / 186	MF	structural molecule activity
27	−8.39	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
28	−8.04	NULL	3 / 18	BP	retinol metabolic process
29	−8.04	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
30	−7.82	NULL	8 / 82	MF	structural constituent of cytoskeleton
31	−7.58	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
32	−7.39	NULL	4 / 27	BP	response to bacterium
33	−7.1	NULL	1 / 12	GSEA C2	ODONNELL_METASTASIS_DN
34	−7.1	NULL	1 / 12	GSEA C2	SYED_ESTRADIOL_RESPONSE
35	−7.01	NULL	5 / 23	MF	peptidase inhibitor activity
36	−6.82	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
37	−6.72	NULL	4 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
38	−6.62	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_24HR
39	−6.56	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
40	−6.52	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY