GW_300

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1919 (1163 + / 756 −)

genes with fdr < 0.1 = 1531 (957 + / 574 −)

genes with fdr < 0.05 = 1308 (824 + / 484 −)

genes with fdr < 0.01 = 881 (571 + / 310 −)

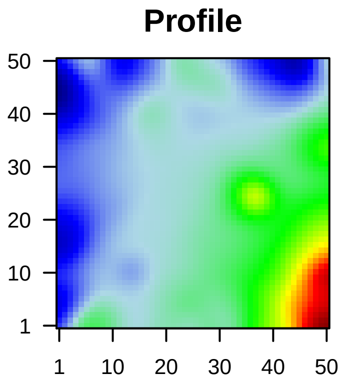
genes in genesets = 16332

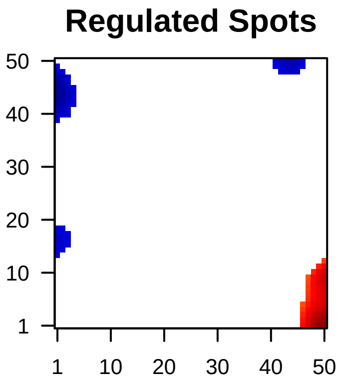
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

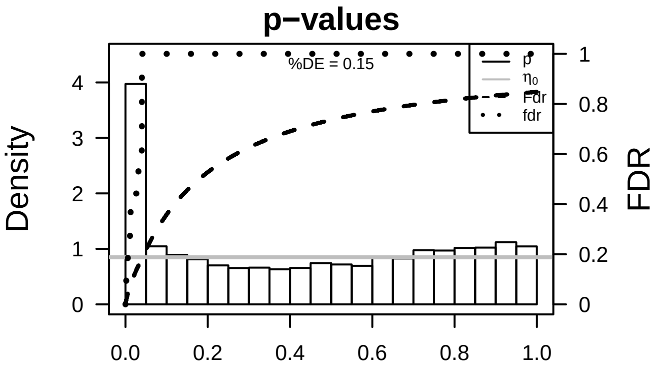
<fdr> = 0.85


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	2.14	2e−16	4e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	25890	2.25	2e−16	4e−14	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
3	124	2.77	2e−16	4e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
4	126	1.94	2e−16	4e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
5	10551	1.92	2e−16	4e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
6	216	2.32	2e−16	4e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
7	347	2.53	2e−16	4e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	92747	4.66	2e−16	4e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
9	730	1.95	2e−16	4e−14	49 x 7	complement component 7 [Source:HGNC Symbol;Acc:1346]
10	6358	1.83	2e−16	4e−14	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
11	6363	3.38	2e−16	4e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
12	6366	2.79	2e−16	4e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
13	1236	2.15	2e−16	4e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
14	930	2.74	2e−16	4e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
15	919	1.79	2e−16	4e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
16	939	1.83	2e−16	4e−14	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
17	962	2.37	2e−16	4e−14	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
18	1043	2.03	2e−16	4e−14	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
19	1545	2.01	2e−16	4e−14	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
20	2532	1.99	2e−16	4e−14	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN


p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	20.64	NULL	417	H.Tiss	WIRTH_Immune system
2	17.22	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
3	14.33	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	10.02	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
5	9.85	NULL	51	Glio	willscher_GBM_Verhaak−PNmut_expression_G_down
6	9.46	NULL	312	BP	immune response
7	9.14	NULL	162	CC	external side of plasma membrane
8	8.95	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
9	8.29	NULL	28	BP	B cell receptor signaling pathway
10	8.16	NULL	74	BP	regulation of immune response
11	7.85	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
12	7.84	NULL	15	CC	MHC class II protein complex
13	7.8	NULL	60	BP	T cell costimulation
14	7.68	NULL	12	BP	dendritic cell chemotaxis
15	7.6	NULL	375	Disease	GUDJ_psoriasis down
16	7.44	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
17	7.42	NULL	10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
18	7.37	NULL	16	GSEA C2	SU_THYMUS
19	7.26	NULL	13	Cancer	GENTLES_modul18
20	7.02	NULL	84	BP	T cell receptor signaling pathway
Underexpressed					
1	−18.97	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−18.97	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−18.21	NULL	572	Disease	GUDJ_psoriasis up
4	−15.01	NULL	530	Cancer	Lembcke_Normal vs Adenoma
5	−12.45	NULL	135	H.Tiss	WIRTH_Mucosa
6	−11.87	NULL	370	BP	mitotic cell cycle
7	−10.25	NULL	76	BP	epidermis development
8	−9.13	NULL	1233	TF	KIM_MYC targets
9	−9.05	NULL	1318	CC	mitochondrion
10	−8.83	NULL	15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
11	−8.3	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
12	−7.84	NULL	21	CC	cornified envelope
13	−7.82	NULL	232	BP	mitosis
14	−7.8	NULL	53	BP	keratinocyte differentiation
15	−7.74	NULL	949	CC	nucleoplasm
16	−7.58	NULL	148	BP	G1/S transition of mitotic cell cycle
17	−7.45	NULL	12	BP	hemidesmosome assembly
18	−7.34	NULL	1253	BP	small molecule metabolic process
19	−7.3	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
20	−7.24	NULL	10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP

GW_300

Local Summary

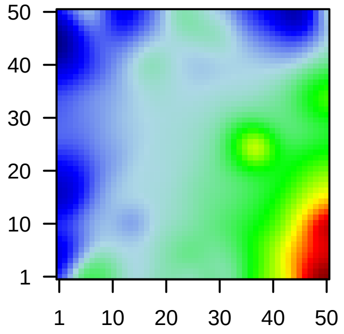
%DE = 0.92
metagenes = 51
genes = 663
genes in genesets = 660

genes with fdr < 0.1 = 581 (580 + / 1 −)
genes with fdr < 0.05 = 561 (561 + / 0 −)
genes with fdr < 0.01 = 497 (497 + / 0 −)

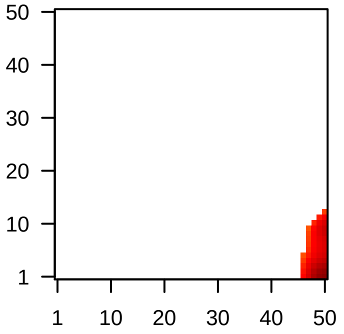
<r> metagenes = 0.82
<r> genes = 0.33

<FC> = 0.98
<shrinkage−t> = 34.41
<p−value> = 0
<fdr> = 0.22

Profile

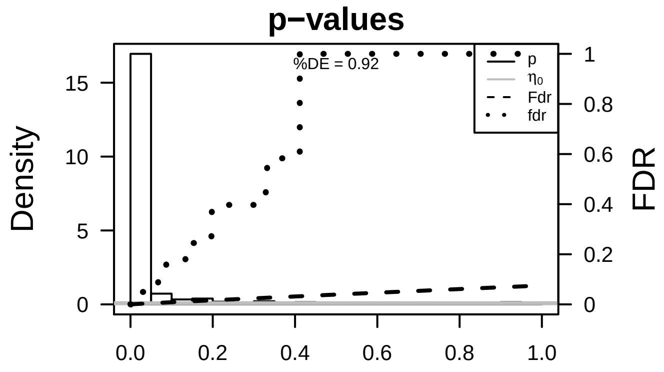


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	25890	2.25	2e−16	2e−16	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
2	124	2.77	2e−16	2e−16	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
3	126	1.94	2e−16	2e−16	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
4	10551	1.92	2e−16	2e−16	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	347	2.53	2e−16	2e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
6	92747	4.66	2e−16	2e−16	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
7	730	1.95	2e−16	2e−16	49 x 7	complement component 7 [Source:HGNC Symbol;Acc:1346]
8	6358	1.83	2e−16	2e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
9	6363	3.38	2e−16	2e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
10	6366	2.79	2e−16	2e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
11	1236	2.15	2e−16	2e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
12	930	2.74	2e−16	2e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
13	919	1.79	2e−16	2e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
14	939	1.83	2e−16	2e−16	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
15	962	2.37	2e−16	2e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
16	1043	2.03	2e−16	2e−16	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
17	1545	2.01	2e−16	2e−16	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
18	2532	1.99	2e−16	2e−16	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
19	1805	1.89	2e−16	2e−16	50 x 5	dermatopontin [Source:HGNC Symbol;Acc:3011]
20	9214	2.23	2e−16	2e−16	49 x 1	Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.97	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	24.66	NULL	111 / 417	H.Tiss	WIRTH_Immune system
3	23.75	NULL	142 / 553	Cancer	Lembcke_Colonic Inflammation
4	15.6	NULL	12 / 15	CC	MHC class II protein complex
5	15.57	NULL	72 / 312	BP	immune response
6	14.97	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
7	13.84	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
8	13.09	NULL	5 / 12	BP	dendritic cell chemotaxis
9	12.92	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
10	12.83	NULL	39 / 162	CC	external side of plasma membrane
11	12.56	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
12	12.54	NULL	4 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
13	12.25	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
14	12.15	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
15	12.12	NULL	13 / 28	BP	B cell receptor signaling pathway
16	11.91	NULL	79 / 683	CC	extracellular space
17	11.85	NULL	68 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
18	11.85	NULL	68 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
19	11.85	NULL	68 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
20	11.85	NULL	68 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
21	11.74	NULL	5 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
22	11.68	NULL	19 / 60	BP	T cell costimulation
23	10.96	NULL	8 / 13	Cancer	GENTLES_modul18
24	10.83	NULL	4 / 7	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
25	10.78	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
26	10.69	NULL	18 / 47	BP	antigen processing and presentation
27	10.65	NULL	20 / 74	BP	regulation of immune response
28	10.58	NULL	8 / 16	GSEA C2	SU_THYMUS
29	10.09	NULL	6 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
30	9.83	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
31	9.81	NULL	12 / 43	MF	chemokine activity
32	9.78	NULL	48 / 327	Lymphoma	SPANG_CD40 6hrs UP
33	9.66	NULL	6 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
34	9.55	NULL	114 / 1182	CC	extracellular region
35	9.53	NULL	7 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
36	9.52	NULL	7 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
37	9.51	NULL	7 / 14	GSEA C2	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
38	9.2	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
39	9.18	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
40	9.11	NULL	7 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA

GW_300

Local Summary

%DE = 0.97

metagenes = 14

genes = 192

genes in genesets = 191

genes with fdr < 0.1 = 179 (1 + / 178 −)

genes with fdr < 0.05 = 174 (0 + / 174 −)

genes with fdr < 0.01 = 128 (0 + / 128 −)

<r> metagenes = 0.97

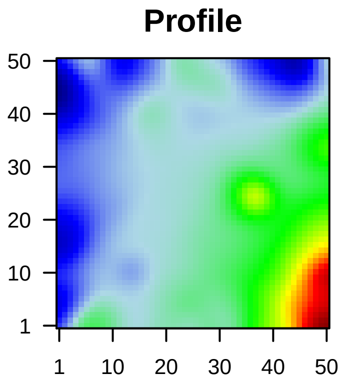
<r> genes = 0.31

<FC> = −0.54

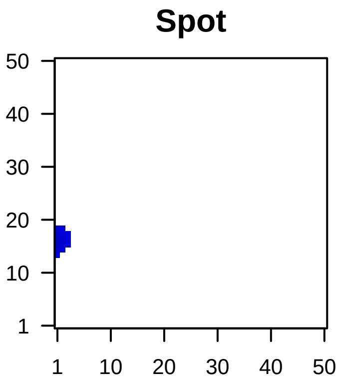
<shrinkage−t> = −18.96

<p−value> = 0.01

<fdr> = 0.48



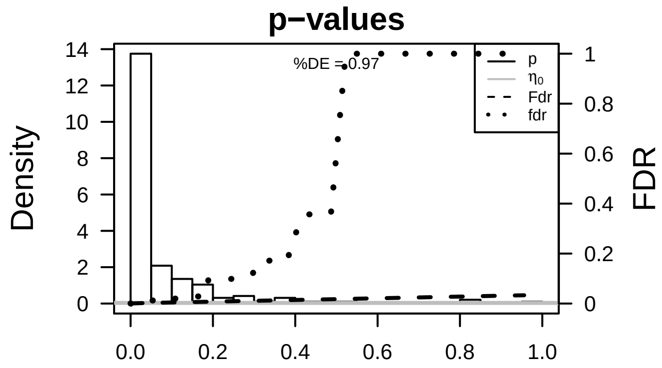
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	991	−1.42	8e−11	2e−06	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
2	51373	−1.11	4e−07	2e−06	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
3	3237	−1.09	6e−07	2e−06	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
4	2288	−1.07	1e−06	2e−06	1 x 19	FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:
5	4495	−1.07	1e−06	2e−06	1 x 16	metallothionein 1G [Source:HGNC Symbol;Acc:7399]
6	2597	−0.96	2e−06	2e−06	2 x 17	glyceraldehyde−3−phosphate dehydrogenase [Source:HGNC
7	2194	−1.05	2e−06	2e−06	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
8	8772	−1.05	2e−06	2e−05	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
9	286016	−0.98	8e−06	2e−05	1 x 19	
10	64979	−0.98	8e−06	3e−05	1 x 16	mitochondrial ribosomal protein L36 [Source:HGNC Symbol;
11	705	−0.94	2e−05	3e−05	1 x 16	bystin−like [Source:HGNC Symbol;Acc:1157]
12	23246	−0.94	2e−05	3e−05	1 x 16	block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
13	2023	−0.86	2e−05	4e−05	1 x 14	enolase 1, (alpha) [Source:HGNC Symbol;Acc:3350]
14	8079	−0.92	3e−05	4e−05	3 x 18	myeloid leukemia factor 2 [Source:HGNC Symbol;Acc:7126]
15	26873	−0.91	3e−05	4e−05	1 x 17	5−oxoprolinase (ATP−hydrolysing) [Source:HGNC Symbol;Ac
16	3217	−0.89	5e−05	4e−05	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
17	4715	−0.88	5e−05	4e−05	1 x 17	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
18	219927	−0.88	6e−05	4e−05	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
19	5690	−0.88	6e−05	7e−05	1 x 15	proteasome (prosome, macropain) subunit, beta type, 2 [Sou
20	84300	−0.87	7e−05	7e−05	2 x 18	ubiquinol−cytochrome c reductase complex assembly factor



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−14.29	NULL	3 / 9	GSEA C2 BIOCARTA_GLYCOLYSIS_PATHWAY
2	−12.13	NULL	2 / 9	GSEA C2 KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
3	−11.64	NULL	3 / 13	GSEA C2 REACTOME_GLYCOLYSIS
4	−11.25	NULL	8 / 66	BP positive regulation of ubiquitin−protein ligase activity involved in mit
5	−11.11	NULL	16 / 153	MF structural constituent of ribosome
6	−10.87	NULL	8 / 70	BP regulation of ubiquitin−protein ligase activity involved in mitotic cell
7	−10.85	NULL	3 / 15	GSEA C2 LY_AGING_MIDDLE_DN
8	−10.83	NULL	7 / 62	BP negative regulation of ubiquitin−protein ligase activity involved in m
9	−10.74	NULL	3 / 15	GSEA C2 REACTOME_GLUCONEOGENESIS
10	−10.63	NULL	3 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
11	−10.52	NULL	8 / 74	BP anaphase−promoting complex−dependent proteasomal ubiquitin−
12	−9.99	NULL	15 / 167	CC ribosome
13	−9.79	NULL	2 / 8	GSEA C2 NIKOLSKY_BREAST_CANCER_5P15_AMPLICON
14	−9.75	NULL	7 / 55	CC proteasome complex
15	−9.7	NULL	2 / 9	GSEA C2 MOREIRA_RESPONSE_TO_TSA_UP
16	−9.63	NULL	1 / 6	GSEA C2 WAESCH_ANAPHASE_PROMOTING_COMPLEX
17	−9.45	NULL	19 / 253	BP translation
18	−9.22	NULL	6 / 48	BP regulation of cellular amino acid metabolic process
19	−9.08	NULL	2 / 7	GSEA C2 REACTOME_SIGNALING_BY_WNT
20	−9.08	NULL	4 / 19	CC mitochondrial small ribosomal subunit
21	−8.93	NULL	1 / 4	GSEA C2 DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
22	−8.76	NULL	11 / 96	BP rRNA processing
23	−8.44	NULL	3 / 17	CC proteasome accessory complex
24	−8.44	NULL	2 / 13	GSEA C2 NADERI_BREAST_CANCER_PROGNOSIS_UP
25	−8.35	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
26	−8.11	NULL	3 / 15	CC mitochondrial large ribosomal subunit
27	−7.83	NULL	6 / 63	BP DNA damage response, signal transduction by p53 class mediator
28	−7.81	NULL	3 / 14	GSEA C2 NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
29	−7.69	NULL	3 / 17	CC proteasome core complex
30	−7.67	NULL	3 / 13	BP ribosomal small subunit biogenesis
31	−7.63	NULL	3 / 16	GSEA C2 GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
32	−7.62	NULL	2 / 7	GSEA C2 PARK_HSC_MARKERS
33	−7.58	NULL	6 / 63	TF MYC_Targets UP
34	−7.44	NULL	3 / 18	MF threonine−type endopeptidase activity
35	−7.41	NULL	4 / 39	BP gluconeogenesis
36	−7.41	NULL	4 / 39	BP glycolysis
37	−7.34	NULL	6 / 70	BP antigen processing and presentation of exogenous peptide antigen
38	−7.31	NULL	3 / 14	GSEA C2 KEGG_COLORECTAL_CANCER
39	−7.25	NULL	2 / 15	GSEA C2 DIRMEIER_LMP1_RESPONSE_LATE_UP
40	−7.19	NULL	1 / 10	BP regulation of dendrite development

GW_300

Local Summary

%DE = 0.89

metagenes = 32

genes = 376

genes in genesets = 368

genes with fdr < 0.1 = 301 (6 + / 295 −)

genes with fdr < 0.05 = 269 (5 + / 264 −)

genes with fdr < 0.01 = 200 (4 + / 196 −)

<r> metagenes = 0.9

<r> genes = 0.35

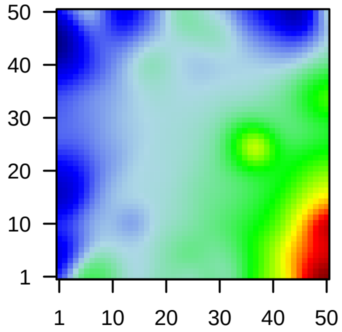
<FC> = −0.67

<shrinkage−t> = −23.69

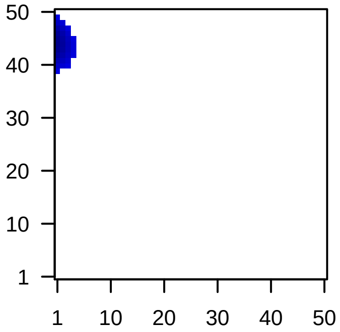
<p−value> = 0

<fdr> = 0.4

Profile

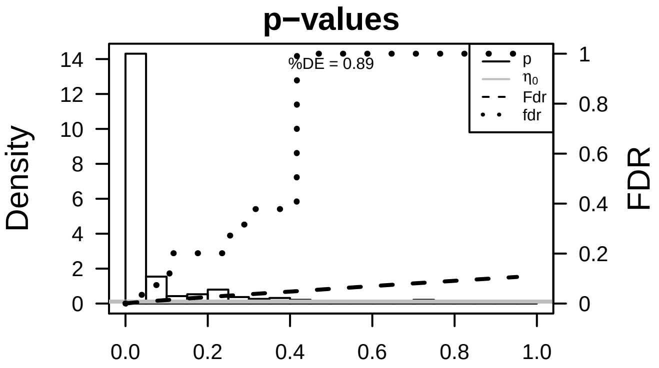


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1673	−1.95	2e−16	8e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
2	10804	−2.02	2e−16	8e−16	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
3	3552	−1.95	2e−16	8e−16	1 x 43	interleukin 1, alpha [Source:HGNC Symbol;Acc:5991]
4	3868	−2.02	2e−16	8e−16	1 x 46	keratin 16 [Source:HGNC Symbol;Acc:6423]
5	3852	−1.78	2e−16	8e−16	1 x 44	keratin 5 [Source:HGNC Symbol;Acc:6442]
6	286887	−2.69	2e−16	8e−16	1 x 47	keratin 6C [Source:HGNC Symbol;Acc:20406]
7	388533	−2.47	2e−16	8e−16	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
8	3963	−1.84	2e−16	8e−16	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
9	6278	−2.08	2e−16	8e−16	1 x 49	S100 calcium binding protein A7 [Source:HGNC Symbol;Acc:
10	374897	−2	2e−16	8e−16	1 x 49	suprabasin [Source:HGNC Symbol;Acc:24950]
11	8140	−1.97	2e−16	8e−16	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
12	6706	−1.91	2e−16	8e−16	1 x 48	small proline−rich protein 2G [Source:HGNC Symbol;Acc:112
13	338324	−1.78	4e−16	3e−13	1 x 48	S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
14	653499	−1.7	7e−15	3e−13	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
15	56300	−1.69	1e−14	3e−13	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
16	1515	−1.67	3e−14	3e−13	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
17	2706	−1.53	3e−14	5e−13	1 x 47	gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
18	5317	−1.65	4e−14	5e−13	1 x 46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
19	414325	−1.65	5e−14	3e−11	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
20	5650	−1.55	2e−12	3e−11	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.37	NULL	47 / 135	H.Tiss	WIRTH_Mucosa
2	−26.26	NULL	104 / 572	Disease	GUDJ_psoriasis up
3	−22.69	NULL	22 / 76	BP	epidermis development
4	−19.95	NULL	11 / 21	CC	desmosome
5	−18.53	NULL	21 / 82	CC	intermediate filament
6	−15.63	NULL	10 / 44	CC	keratin filament
7	−15.3	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
8	−14.77	NULL	5 / 12	BP	hemidesmosome assembly
9	−14.2	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
10	−13.66	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
11	−13.51	NULL	5 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
12	−13.48	NULL	15 / 53	BP	keratinocyte differentiation
13	−13.43	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	−12.78	NULL	7 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
15	−12.27	NULL	4 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
16	−11.91	NULL	5 / 15	CC	connexon complex
17	−11.54	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
18	−10.94	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
19	−10.56	NULL	6 / 21	CC	gap junction
20	−9.83	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
21	−9.81	NULL	3 / 10	MF	RAGE receptor binding
22	−9.76	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
23	−9.71	NULL	23 / 186	MF	structural molecule activity
24	−9.64	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
25	−9.6	NULL	3 / 15	MF	interleukin−1 receptor binding
26	−9.54	NULL	6 / 32	CC	cell−cell adherens junction
27	−9.44	NULL	8 / 21	CC	cornified envelope
28	−9.3	NULL	3 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
29	−9.15	NULL	4 / 10	MF	gap junction channel activity
30	−8.93	NULL	12 / 82	MF	structural constituent of cytoskeleton
31	−8.74	NULL	4 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
32	−8.7	NULL	2 / 2	miRNA target	miR−199a*
33	−8.46	NULL	5 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
34	−8.39	NULL	2 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
35	−8.36	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
36	−8.28	NULL	2 / 5	miRNA target	miR−196a
37	−8.21	NULL	3 / 16	GSEA C2	LANDEMAINE_LUNG_METASTASIS
38	−8.14	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
39	−8.12	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
40	−8.11	NULL	4 / 25	BP	response to zinc ion

GW_300

Local Summary

%DE = 0.92

metagenes = 16

genes = 226

genes in genesets = 224

genes with fdr < 0.1 = 190 (0 + / 190 −)

genes with fdr < 0.05 = 171 (0 + / 171 −)

genes with fdr < 0.01 = 130 (0 + / 130 −)

<r> metagenes = 0.96

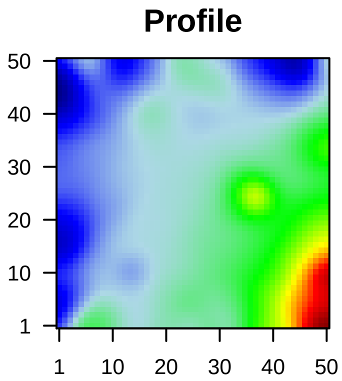
<r> genes = 0.42

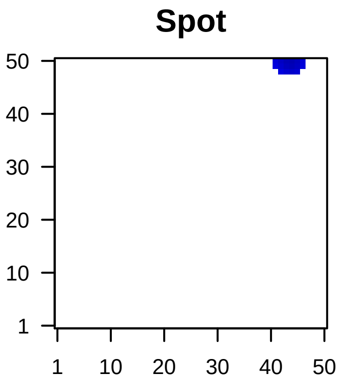
<FC> = −0.62

<shrinkage−t> = −21.88

<p−value> = 0

<fdr> = 0.42





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55165	−1.41	1e−10	2e−09	44 x 50	centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161
2	113130	−1.39	2e−10	4e−09	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
3	8318	−1.37	4e−10	4e−09	45 x 49	cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
4	9055	−1.35	6e−10	5e−09	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
5	387103	−1.34	9e−10	7e−09	45 x 49	centromere protein W [Source:HGNC Symbol;Acc:21488]
6	7153	−1.32	1e−09	7e−09	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbo
7	259266	−1.31	2e−09	7e−09	45 x 49	asp (abnormal spindle) homolog, microcephaly associated (D
8	26255	−1.31	2e−09	9e−09	44 x 48	pituitary tumor−transforming 3, pseudogene [Source:HGNC
9	54443	−1.3	3e−09	2e−08	43 x 50	anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
10	1163	−1.28	6e−09	2e−08	44 x 50	CDC28 protein kinase regulatory subunit 1B [Source:HGNC
11	7083	−1.27	6e−09	2e−08	45 x 49	thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
12	51203	−1.27	6e−09	7e−08	45 x 48	nucleolar and spindle associated protein 1 [Source:HGNC Sy
13	1894	−1.25	1e−08	3e−07	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
14	9212	−1.2	4e−08	3e−07	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
15	890	−1.18	7e−08	3e−07	44 x 50	cyclin A2 [Source:HGNC Symbol;Acc:1578]
16	9232	−1.17	8e−08	3e−07	44 x 48	pituitary tumor−transforming 1 [Source:HGNC Symbol;Acc:96
17	22974	−1.17	9e−08	3e−07	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
18	29899	−1.17	1e−07	3e−07	41 x 50	G−protein signaling modulator 2 [Source:HGNC Symbol;Acc:
19	9133	−1.16	1e−07	1e−06	45 x 49	cyclin B2 [Source:HGNC Symbol;Acc:1580]
20	81831	−1.14	2e−07	1e−06	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−64.22	NULL	72 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−64.22	NULL	72 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−38.41	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
4	−34.49	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
5	−34.13	NULL	13 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
6	−32.33	NULL	12 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
7	−32.08	NULL	20 / 57	Glio	developing astrocytes
8	−31.45	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
9	−30.98	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	−30.92	NULL	11 / 14	MMML CGS	MACIEJ_MMML 4
11	−29.33	NULL	10 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
12	−28.84	NULL	10 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
13	−25.86	NULL	62 / 370	BP	mitotic cell cycle
14	−25.63	NULL	66 / 530	Cancer	Lembcke_Normal vs Adenoma
15	−25.32	NULL	8 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
16	−25	NULL	59 / 572	Disease	GUDJ_psoriasis up
17	−24.93	NULL	11 / 18	BP	spindle organization
18	−23.29	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
19	−22.88	NULL	9 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
20	−22.38	NULL	7 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
21	−22.06	NULL	37 / 232	BP	mitosis
22	−21.95	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
23	−21.83	NULL	7 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
24	−21.62	NULL	9 / 15	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
25	−21.32	NULL	9 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
26	−20.91	NULL	8 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
27	−19.72	NULL	7 / 15	GSEA C2	LY_AGING_MIDDLE_DN
28	−19.72	NULL	6 / 12	BP	mitotic chromosome condensation
29	−19.69	NULL	6 / 13	GSEA C2	REN_BOUND_BY_E2F
30	−19.44	NULL	6 / 15	GSEA C2	TANG_SENESCENCE_TP53_TARGETS_DN
31	−19.24	NULL	10 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
32	−19.15	NULL	6 / 16	Cancer	RHODES_UNDIFFERENTIATED_CANCER
33	−18.99	NULL	6 / 15	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
34	−18.86	NULL	16 / 56	CC	chromosome, centromeric region
35	−18.17	NULL	4 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
36	−18.11	NULL	6 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
37	−18	NULL	6 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
38	−17.92	NULL	7 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
39	−17.85	NULL	6 / 15	GSEA C2	CHANG_CYCLING_GENES
40	−17.34	NULL	5 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS