GW_234

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1712 (920 + / 792 −)

genes with fdr < 0.1 = 1390 (769 + / 621 −)

genes with fdr < 0.05 = 1104 (631 + / 473 −)

genes with fdr < 0.01 = 840 (491 + / 349 −)

genes in genesets = 16332

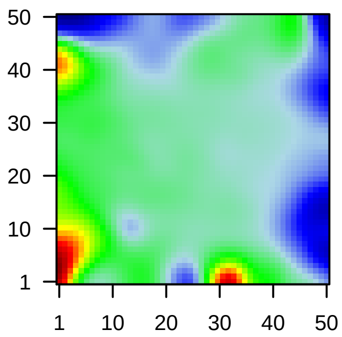
<FC> = 0

<shrinkage−t> = 0

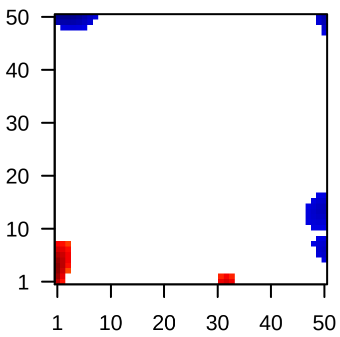
<p−value> = 0.11

<fdr> = 0.87

Profile



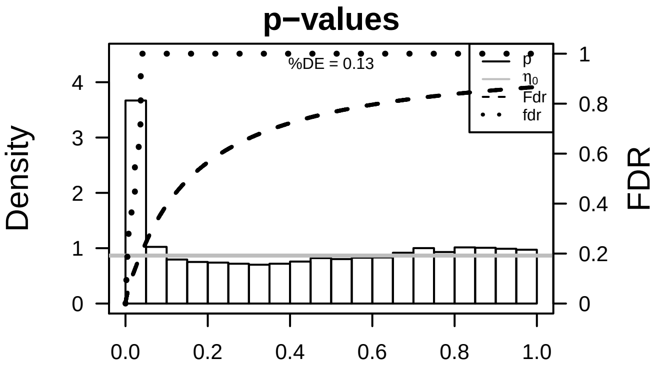
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	−1.44	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	87	1.33	2e−16	3e−14	1 x 3	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
3	131	−2.52	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	216	−1.5	2e−16	3e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	218	−1.64	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	163782	1.4	2e−16	3e−14	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
7	118429	1.3	2e−16	3e−14	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
8	306	1.46	2e−16	3e−14	4 x 42	annexin A3 [Source:HGNC Symbol;Acc:541]
9	23780	1.29	2e−16	3e−14	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
10	684	1.31	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
11	140851	1.38	2e−16	3e−14	1 x 5	
12	834	1.32	2e−16	3e−14	32 x 1	caspase 1, apoptosis−related cysteine peptidase [Source:HG
13	857	1.31	2e−16	3e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
14	629	1.96	2e−16	3e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
15	9076	−1.22	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
16	1258	1.42	2e−16	3e−14	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
17	1308	1.65	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
18	1437	1.31	2e−16	3e−14	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
19	1469	1.89	2e−16	3e−14	9 x 6	cystatin SN [Source:HGNC Symbol;Acc:2473]
20	2919	1.38	2e−16	3e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	14.85	NULL	51	BP	type I interferon signaling pathway
2	14.15	NULL	123	BP	defense response to virus
3	13.65	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	12.67	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
5	11.8	NULL	572	Disease	GUDJ_psoriasis up
6	11.73	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
7	11.4	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
8	11.35	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
9	11.16	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
10	11.14	NULL	31	BP	negative regulation of viral genome replication
11	10.97	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	10.73	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
13	10.12	NULL	109	BP	response to virus
14	9.99	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
15	9.99	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
16	9.86	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
17	9.62	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
18	9.59	NULL	242	BP	extracellular matrix organization
19	9.58	NULL	12	BP	hemidesmosome assembly
20	9.46	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
Underexpressed					
1	−8.13	NULL	135	H.Tiss	WIRTH_Mucosa
2	−7.28	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
3	−6.98	NULL	7	MMML CGS	MACIEJ_MMML 5
4	−6.67	NULL	743	Chr	Chr 7
5	−6.35	NULL	92	BP	translational elongation
6	−6.17	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
7	−6.17	NULL	128	BP	translational initiation
8	−6.12	NULL	127	H.Tiss	WIRTH_Muscle
9	−6.08	NULL	33	BP	cholesterol biosynthetic process
10	−5.91	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
11	−5.83	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−5.78	NULL	87	BP	translational termination
13	−5.76	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
14	−5.74	NULL	81	BP	viral transcription
15	−5.62	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
16	−5.61	NULL	15	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
17	−5.58	NULL	11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
18	−5.37	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
19	−5.27	NULL	92	BP	viral life cycle
20	−5.21	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_

GW_234

Local Summary

%DE = 0.83

metagenes = 22

genes = 332

genes in genesets = 329

genes with fdr < 0.1 = 223 (217 + / 6 −)

genes with fdr < 0.05 = 214 (208 + / 6 −)

genes with fdr < 0.01 = 182 (177 + / 5 −)

<r> metagenes = 0.94

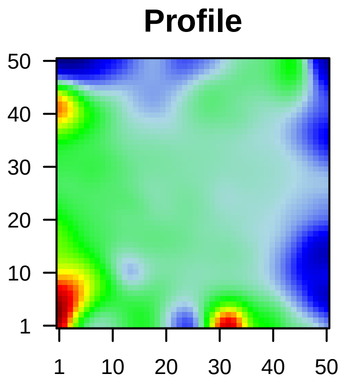
<r> genes = 0.32

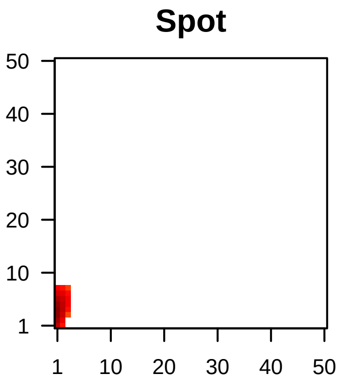
<FC> = 0.55

<shrinkage−t> = 19.22

<p−value> = 0

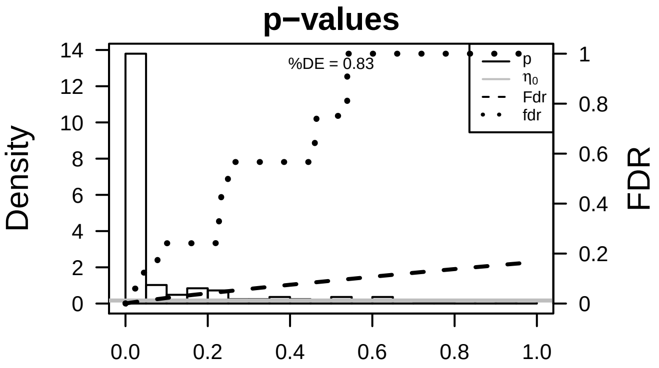
<fdr> = 0.38





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	87	1.33	2e−16	4e−16	1 x 3	actinin, alpha 1 [Source:HGNC Symbol;Acc:163]
2	163782	1.4	2e−16	4e−16	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
3	118429	1.3	2e−16	4e−16	2 x 1	anthrax toxin receptor 2 [Source:HGNC Symbol;Acc:21732]
4	140851	1.38	2e−16	4e−16	1 x 5	
5	857	1.31	2e−16	4e−16	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
6	1258	1.42	2e−16	4e−16	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
7	1437	1.31	2e−16	4e−16	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
8	2919	1.38	2e−16	4e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
9	285761	1.51	2e−16	4e−16	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
10	27122	1.44	2e−16	4e−16	1 x 3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC S
11	2201	1.88	2e−16	4e−16	1 x 5	fibrillin 2 [Source:HGNC Symbol;Acc:3604]
12	3678	1.58	2e−16	4e−16	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
13	3909	1.54	2e−16	4e−16	1 x 5	laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
14	3918	1.29	2e−16	4e−16	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
15	4312	2.68	2e−16	4e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
16	4319	2.02	2e−16	4e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
17	4314	2.66	2e−16	4e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
18	4489	1.32	2e−16	4e−16	1 x 4	metallothionein 1A [Source:HGNC Symbol;Acc:7393]
19	4493	1.35	2e−16	4e−16	1 x 5	metallothionein 1E [Source:HGNC Symbol;Acc:7397]
20	4502	1.8	2e−16	4e−16	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.41	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	22.44	NULL	59 / 242	BP	extracellular matrix organization
3	21.27	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
4	17.9	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
5	16.34	NULL	11 / 35	Glio	Colman_survival_associated
6	16.3	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
7	16.29	NULL	7 / 16	MF	fibronectin binding
8	15.48	NULL	6 / 12	BP	hemidesmosome assembly
9	15.02	NULL	55 / 403	BP	cell adhesion
10	14.79	NULL	21 / 64	BP	collagen catabolic process
11	14.74	NULL	37 / 190	CC	extracellular matrix
12	14.61	NULL	44 / 250	Lymphoma	LENZ_Stromal signature 1
13	14.56	NULL	3 / 10	BP	cellular response to zinc ion
14	14.55	NULL	22 / 69	BP	extracellular matrix disassembly
15	14.17	NULL	100 / 1182	CC	extracellular region
16	14.06	NULL	67 / 683	CC	extracellular space
17	13.93	NULL	5 / 8	GSEA C2	SASAKI_TARGETS_OF_TP73_AND_TP63
18	13.55	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
19	13.32	NULL	26 / 183	CC	proteinaceous extracellular matrix
20	13.27	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP
21	13.05	NULL	17 / 83	CC	basement membrane
22	12.68	NULL	8 / 51	BP	regulation of cell migration
23	12.62	NULL	6 / 19	MF	laminin binding
24	12.51	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
25	12.46	NULL	8 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
26	12.46	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
27	12.3	NULL	3 / 11	GSEA C2	VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
28	12.15	NULL	2 / 7	MMML CGS	MACIEJ_MMML 13
29	12.12	NULL	5 / 13	GSEA C2	BRUECKNER_TARGETS_OF_MIRLET7A3_DN
30	11.88	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
31	11.79	NULL	3 / 15	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
32	11.63	NULL	4 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
33	11.57	NULL	2 / 12	GSEA C2	GEISS_RESPONSE_TO_DSRNA_DN
34	11.56	NULL	3 / 15	BP	negative regulation of growth
35	11.31	NULL	4 / 11	GSEA C2	LIU_SOX4_TARGETS_UP
36	11.12	NULL	14 / 85	MF	integrin binding
37	11.09	NULL	4 / 16	GSEA C2	KEGG_BLADDER_CANCER
38	11.09	NULL	10 / 16	MMML CGS	MACIEJ_MMML 1
39	10.95	NULL	3 / 10	GSEA C2	VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN
40	10.95	NULL	3 / 10	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_DN

GW_234

Local Summary

%DE = 0.95

metagenes = 6

genes = 114

genes in genesets = 112

genes with fdr < 0.1 = 106 (105 + / 1 −)

genes with fdr < 0.05 = 101 (100 + / 1 −)

genes with fdr < 0.01 = 95 (94 + / 1 −)

<r> metagenes = 1

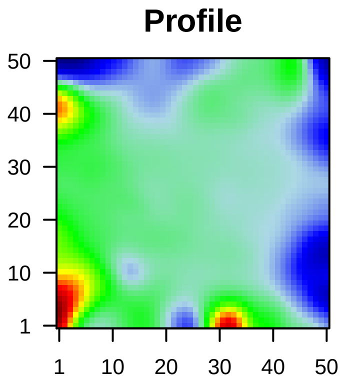
<r> genes = 0.47

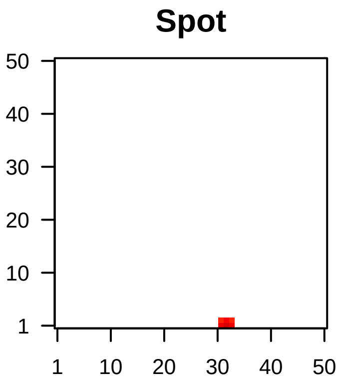
<FC> = 0.79

<shrinkage−t> = 27.92

<p−value> = 0

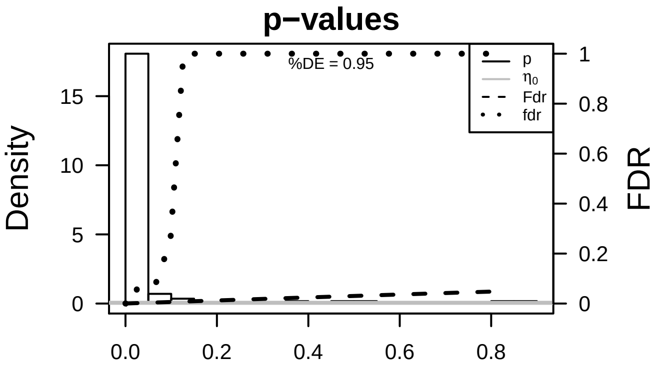
<fdr> = 0.14





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23780	1.29	2e−16	6e−17	32 x 1	apolipoprotein L, 2 [Source:HGNC Symbol;Acc:619]
2	684	1.31	2e−16	6e−17	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
3	834	1.32	2e−16	6e−17	32 x 1	caspase 1, apoptosis−related cysteine peptidase [Source:HG
4	629	1.96	2e−16	6e−17	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
5	3627	2.18	2e−16	6e−17	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
6	94240	1.41	2e−16	6e−17	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
7	2633	1.23	2e−16	6e−17	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN
8	115362	1.44	2e−16	6e−17	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
9	51191	1.33	2e−16	6e−17	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
10	55008	1.3	2e−16	6e−17	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
11	3430	1.38	2e−16	6e−17	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53
12	10561	1.28	2e−16	6e−17	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
13	10964	1.61	2e−16	6e−17	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
14	2537	1.9	2e−16	6e−17	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
15	3433	1.6	2e−16	6e−17	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
16	8519	1.27	2e−16	6e−17	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
17	10581	1.14	2e−16	6e−17	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC
18	10410	1.29	2e−16	6e−17	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
19	9636	2.28	2e−16	6e−17	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
20	4061	1.39	2e−16	6e−17	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	53.65	NULL	29 / 51	BP	type I interferon signaling pathway
2	52.72	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
3	47.69	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
4	46.89	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	42.37	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	41.36	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	41.15	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
8	39.97	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
9	38.55	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
10	37.37	NULL	31 / 123	BP	defense response to virus
11	36.62	NULL	13 / 31	BP	negative regulation of viral genome replication
12	35.83	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
13	34.32	NULL	27 / 109	BP	response to virus
14	31.78	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
15	31.77	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
16	30.71	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
17	30.57	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
18	29.67	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
19	29.25	NULL	34 / 204	BP	cytokine−mediated signaling pathway
20	28.16	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
21	27.51	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	27.44	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
23	26.88	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
24	25.61	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
25	24.73	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
26	23.84	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
27	23.39	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
28	23.17	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
29	22.87	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
30	22.64	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
31	22.1	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
32	22	NULL	46 / 572	Disease	GUDJ_psoriasis up
33	21.63	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
34	21.63	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
35	21.17	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
36	20.92	NULL	7 / 10	CC	MHC class I protein complex
37	20.24	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
38	19.97	NULL	5 / 18	BP	response to interferon−gamma
39	19.69	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
40	19.55	NULL	3 / 5	GSEA C2	BROWNE_INTERFERON_RESPONSIVE_GENES

GW_234

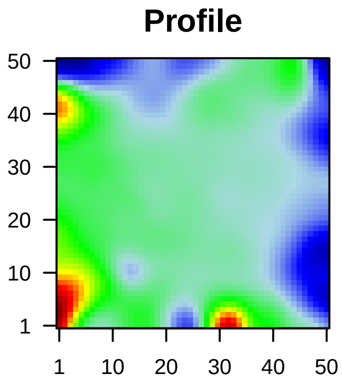
Local Summary

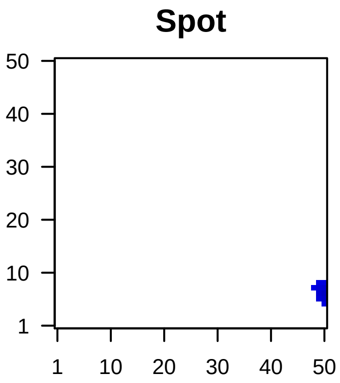
%DE = 0.84
metagenes = 10
genes = 142
genes in genesets = 142

genes with fdr < 0.1 = 91 (4 + / 87 −)
genes with fdr < 0.05 = 85 (4 + / 81 −)
genes with fdr < 0.01 = 49 (4 + / 45 −)

<r> metagenes = 0.95
<r> genes = 0.37

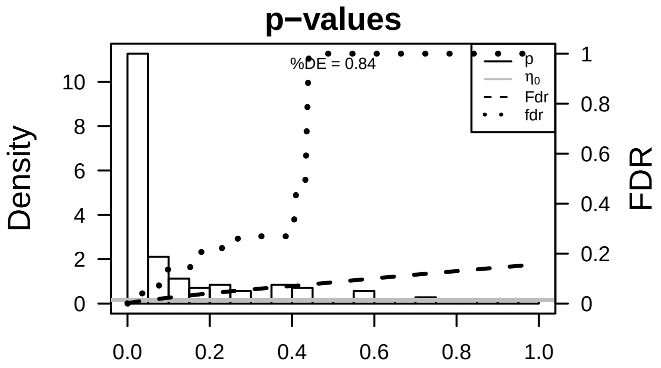
<FC> = −0.33
<shrinkage−t> = −11.6
<p−value> = 0
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3488	−1.38	2e−16	2e−15	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
2	6192	−2.21	2e−16	2e−15	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
3	3426	1.17	6e−15	2e−12	50 x 8	complement factor I [Source:HGNC Symbol;Acc:5394]
4	7832	−1.11	1e−13	2e−12	49 x 6	BTG family, member 2 [Source:HGNC Symbol;Acc:1131]
5	79901	−1.1	2e−13	3e−12	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
6	1363	−1.09	3e−13	3e−09	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
7	347	−0.96	1e−10	4e−09	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	4239	−0.93	5e−10	4e−09	50 x 6	microfibrillar−associated protein 4 [Source:HGNC Symbol;Ac
9	10253	−0.92	7e−10	4e−09	50 x 8	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:1
10	8284	−0.92	7e−10	1e−08	48 x 8	lysine (K)−specific demethylase 5D [Source:HGNC Symbol;A
11	4256	−0.9	2e−09	1e−08	50 x 6	matrix Gla protein [Source:HGNC Symbol;Acc:7060]
12	338773	−0.9	2e−09	1e−07	50 x 5	transmembrane protein 119 [Source:HGNC Symbol;Acc:2788
13	2532	−0.86	8e−09	1e−07	50 x 5	Duffy blood group, atypical chemokine receptor [Source:HGN
14	7049	−0.86	1e−08	1e−07	50 x 9	transforming growth factor, beta receptor III [Source:HGNC S
15	3075	0.85	1e−08	3e−06	50 x 7	complement factor H [Source:HGNC Symbol;Acc:4883]
16	6867	−0.77	3e−07	3e−06	50 x 6	transforming, acidic coiled−coil containing protein 1 [Source:H
17	6358	−0.77	3e−07	2e−05	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
18	1359	−0.73	1e−06	2e−05	50 x 7	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
19	1396	0.71	2e−06	2e−04	50 x 5	cysteine−rich protein 1 (intestinal) [Source:HGNC Symbol;Ac
20	1362	0.66	9e−06	2e−04	50 x 9	carboxypeptidase D [Source:HGNC Symbol;Acc:2301]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.54	NULL	2 / 7	MMML CGS	MACIEJ_MMML 5
2	−26.43	NULL	2 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
3	−22.22	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
4	−20.08	NULL	1 / 7	GSEA C2	LEE_NAIVE_T_LYMPHOCYTE
5	−18.6	NULL	1 / 8	GSEA C2	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
6	−17.38	NULL	1 / 9	GSEA C2	KEGG_RIBOSOME
7	−17.38	NULL	1 / 9	GSEA C2	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
8	−17.38	NULL	1 / 9	GSEA C2	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_
9	−17.38	NULL	1 / 9	GSEA C2	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_
10	−17.38	NULL	1 / 9	GSEA C2	REACTOME_PEPTIDE_CHAIN_ELONGATION
11	−17.38	NULL	1 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
12	−17.38	NULL	1 / 9	GSEA C2	REACTOME_VIRAL_MRNA_TRANSLATION
13	−16.37	NULL	1 / 10	GSEA C2	TAKAO_RESPONSE_TO_UVB_RADIATION_UP
14	−16.37	NULL	1 / 10	GSEA C2	REACTOME_TRANSLATION
15	−15.82	NULL	2 / 20	Lymphoma	ROSOLOWSKI_red UP
16	−15.51	NULL	1 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
17	−14.81	NULL	4 / 13	Cancer	GENTLES_modul17
18	−14.76	NULL	1 / 12	GSEA C2	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND
19	−14.76	NULL	1 / 12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
20	−14.76	NULL	1 / 12	GSEA C2	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATIO
21	−14.32	NULL	3 / 13	H.Tiss	WIRTH_Sec. lymphoid organs
22	−14.11	NULL	1 / 13	GSEA C2	KANG_IMMORTALIZED_BY_TERT_UP
23	−14.11	NULL	1 / 13	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP
24	−13.66	NULL	1 / 6	GSEA C2	TRAYNOR_RETT_SYNDROM_DN
25	−13.08	NULL	4 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
26	−13.02	NULL	1 / 15	GSEA C2	FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_DN
27	−12.55	NULL	1 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
28	−12.55	NULL	1 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
29	−12.17	NULL	1 / 5	GSEA C2	DONATO_CELL_CYCLE_TRETINOIN
30	−12.05	NULL	2 / 11	BP	negative regulation of smooth muscle cell migration
31	−12.01	NULL	2 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
32	−11.78	NULL	2 / 34	Chr	Chr Y
33	−11.61	NULL	2 / 8	GSEA C2	LEE_SP4_THYMOCYTE
34	−11.31	NULL	3 / 15	GSEA C2	NADERI_BREAST_CANCER_PROGNOSIS_DN
35	−11.29	NULL	3 / 27	BP	negative regulation of smooth muscle cell proliferation
36	−11.28	NULL	2 / 12	BP	regulation of glucose metabolic process
37	−11.24	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
38	−10.94	NULL	2 / 15	GSEA C2	ABE_INNER_EAR
39	−10.77	NULL	1 / 21	CC	polysome
40	−10.51	NULL	3 / 10	BP	germ cell migration

GW_234

Local Summary

%DE = 0.72

metagenes = 24

genes = 259

genes in genesets = 256

genes with fdr < 0.1 = 117 (9 + / 108 −)

genes with fdr < 0.05 = 80 (5 + / 75 −)

genes with fdr < 0.01 = 64 (4 + / 60 −)

<r> metagenes = 0.92

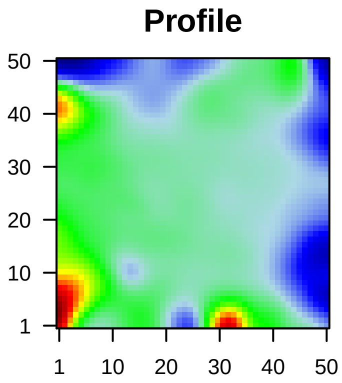
<r> genes = 0.28

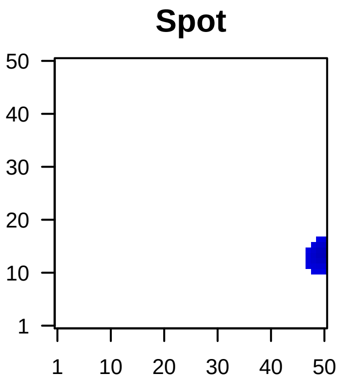
<FC> = −0.27

<shrinkage−t> = −9.35

<p−value> = 0.01

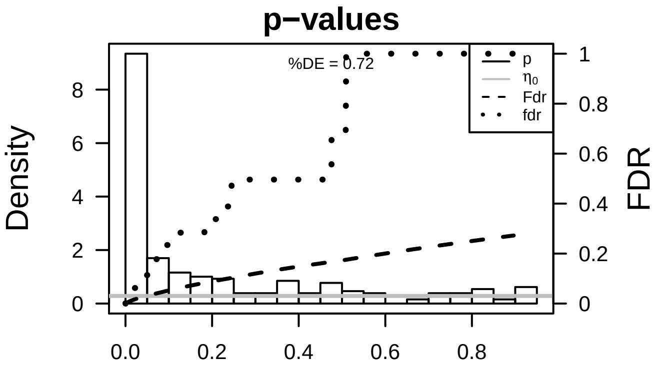
<fdr> = 0.65


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79085	−1.1	2e−13	3e−10	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr
2	10439	−1.03	5e−12	9e−10	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
3	94025	1.01	2e−11	2e−08	50 x 11	mucin 16, cell surface associated [Source:HGNC Symbol;Acc
4	909	−0.94	3e−10	5e−08	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
5	8857	0.9	2e−09	5e−08	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
6	10232	−0.9	2e−09	2e−07	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
7	23521	−0.88	4e−09	4e−07	47 x 12	ribosomal protein L13a [Source:HGNC Symbol;Acc:10304]
8	23171	−0.86	1e−08	4e−07	50 x 12	glycerol−3−phosphate dehydrogenase 1−like [Source:HGNC
9	6542	−0.85	1e−08	3e−06	50 x 16	solute carrier family 7 (cationic amino acid transporter, y+ sys
10	79161	−0.81	6e−08	3e−06	49 x 16	transmembrane protein 243, mitochondrial [Source:HGNC Sy
11	3248	−0.8	1e−07	3e−06	50 x 13	hydroxyprostaglandin dehydrogenase 15−(NAD) [Source:HGI
12	3670	0.78	2e−07	3e−06	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
13	2205	−0.78	2e−07	3e−06	50 x 13	Fc fragment of IgE, high affinity I, receptor for; alpha polypept
14	6414	−0.78	2e−07	3e−05	48 x 11	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:10751
15	260293	−0.75	6e−07	3e−05	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
16	83699	−0.73	1e−06	3e−05	50 x 11	SH3 domain binding glutamic acid−rich protein like 2 [Source
17	2568	−0.71	2e−06	3e−05	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
18	23401	−0.7	2e−06	3e−05	50 x 14	frequently rearranged in advanced T−cell lymphomas 2 [Sour
19	4602	−0.7	3e−06	3e−05	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
20	114915	−0.7	3e−06	3e−05	47 x 14	EPB41L4A antisense RNA 1 [Source:HGNC Symbol;Acc:307


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.06	NULL	5 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	−10.9	NULL	1 / 3	miRNA 3UTR	ACCGC−210
3	−10.72	NULL	2 / 9	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_DN
4	−10.49	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
5	−9.28	NULL	3 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
6	−9.13	NULL	2 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
7	−9	NULL	1 / 2	TF	MYC_Cell cycle DOWN
8	−8.66	NULL	4 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
9	−8.11	NULL	3 / 15	GSEA C2	NAKAJIMA_MAST_CELL
10	−7.55	NULL	2 / 12	BP	nitric oxide biosynthetic process
11	−7.21	NULL	4 / 21	BP	drug metabolic process
12	−7.2	NULL	2 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN
13	−6.7	NULL	1 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
14	−6.69	NULL	1 / 10	GSEA C2	BROWNE_HCMV_INFECTION_12HR_UP
15	−6.69	NULL	1 / 10	GSEA C2	XU_GH1_AUTOCRINE_TARGETS_DN
16	−6.66	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
17	−6.51	NULL	4 / 39	MF	NAD binding
18	−6.3	NULL	2 / 14	GSEA C2	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_DN
19	−6.17	NULL	2 / 16	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
20	−6.11	NULL	1 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
21	−6.04	NULL	2 / 16	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_UP
22	−6.03	NULL	1 / 12	GSEA C2	CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_4
23	−6.03	NULL	1 / 12	GSEA C2	RIZKI_TUMOR_INVASIVENESS_3D_DN
24	−6.03	NULL	1 / 12	GSEA C2	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
25	−5.9	NULL	2 / 12	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
26	−5.78	NULL	2 / 12	MF	NAD+ binding
27	−5.76	NULL	1 / 13	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_UP
28	−5.76	NULL	1 / 13	GSEA C2	STEIN_ESR1_TARGETS
29	−5.74	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
30	−5.74	NULL	3 / 11	BP	DNA integration
31	−5.71	NULL	2 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
32	−5.65	NULL	1 / 10	CC	large ribosomal subunit
33	−5.64	NULL	1 / 15	GSEA C2	CORRE_MULTIPLE_MYELOMA_UP
34	−5.64	NULL	1 / 5	GSEA C2	ZIRN_TRETINOIN_RESPONSE_WT1_DN
35	−5.58	NULL	7 / 92	BP	viral life cycle
36	−5.52	NULL	1 / 14	GSEA C2	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASS
37	−5.52	NULL	1 / 14	GSEA C2	POMEROY_MEDULLOBLASTOMA_DESMOPLASIC_VS_CLASS
38	−5.52	NULL	1 / 14	GSEA C2	MASSARWEH_TAMOXIFEN_RESISTANCE_DN
39	−5.52	NULL	1 / 14	GSEA C2	STEIN_ESTROGEN_RESPONSE_NOT_VIA_ESRRA
40	−5.52	NULL	1 / 14	GSEA C2	BROWNE_HCMV_INFECTION_16HR_UP

GW_234

Local Summary

%DE = 0.81

metagenes = 6

genes = 133

genes in genesets = 132

genes with fdr < 0.1 = 92 (7 + / 85 −)

genes with fdr < 0.05 = 79 (6 + / 73 −)

genes with fdr < 0.01 = 66 (6 + / 60 −)

<r> metagenes = 0.99

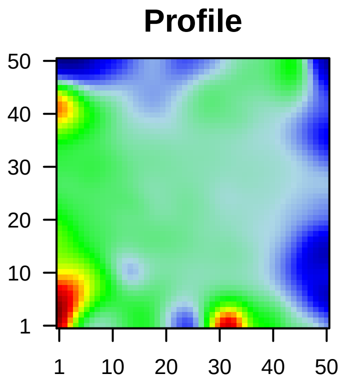
<r> genes = 0.3

<FC> = −0.38

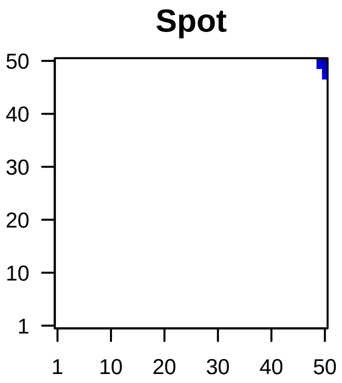
<shrinkage−t> = −13.33

<p−value> = 0

<fdr> = 0.43



Profile



Spot

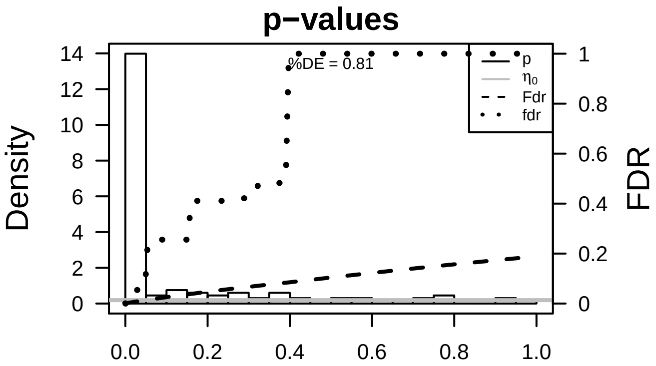
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.5	2e−16	8e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN(
2	9076	−1.22	2e−16	8e−16	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
3	3880	−1.63	2e−16	8e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
4	3856	1.31	2e−16	8e−16	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
5	4922	−1.26	2e−16	8e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
6	29968	−1.27	2e−16	8e−16	49 x 50	phosphoserine aminotransferase 1 [Source:HGNC Symbol;A
7	11166	−1.28	2e−16	8e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Symb
8	6657	−1.14	3e−14	5e−12	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symbo
9	4780	−1.1	2e−13	7e−12	50 x 50	nuclear factor, erythroid 2−like 2 [Source:HGNC Symbol;Acc:
10	154664	−1.08	5e−13	5e−10	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
11	256764	−1	2e−11	1e−09	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
12	655	0.98	7e−11	6e−09	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
13	2222	−0.94	3e−10	2e−08	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
14	10966	−0.91	1e−09	3e−07	50 x 50	RAB40B, member RAS oncogene family [Source:HGNC Sym
15	84707	−0.85	1e−08	6e−07	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
16	56922	−0.82	4e−08	7e−07	50 x 50	methylcrotonoyl−CoA carboxylase 1 (alpha) [Source:HGNC S
17	339512	−0.81	7e−08	7e−07	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
18	4915	−0.79	1e−07	7e−07	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
19	604	−0.79	1e−07	2e−06	50 x 50	B−cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:1001]
20	2947	−0.77	2e−07	2e−06	50 x 50	glutathione S−transferase mu 3 (brain) [Source:HGNC Symbo

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−27.15	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−20.1	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	−14.76	NULL	1 / 2	miRNA target	miR−127
4	−13.7	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
5	−13.7	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
6	−12.78	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
7	−12.48	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
8	−12.31	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
9	−12.27	NULL	2 / 10	GSEA C2	CONRAD_STEM_CELL
10	−11.07	NULL	3 / 11	MF	glutathione binding
11	−11.07	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
12	−11.03	NULL	8 / 34	BP	glutathione metabolic process
13	−10.86	NULL	3 / 13	BP	regulation of blood vessel size
14	−10.75	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
15	−10.75	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
16	−10.72	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
17	−10.42	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
18	−10.37	NULL	6 / 25	BP	glutathione derivative biosynthetic process
19	−10.33	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
20	−10.21	NULL	2 / 23	BP	stem cell differentiation
21	−10.11	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
22	−10.11	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
23	−9.59	NULL	2 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
24	−9.45	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
25	−9.44	NULL	1 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
26	−9.44	NULL	1 / 7	miRNA target	miR−145
27	−9.31	NULL	5 / 20	MF	glutathione transferase activity
28	−9.06	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
29	−8.99	NULL	2 / 12	BP	cellular aldehyde metabolic process
30	−8.87	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
31	−8.71	NULL	1 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
32	−8.71	NULL	1 / 8	miRNA 3UTR	CTGCA−450
33	−8.7	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
34	−8.7	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
35	−8.39	NULL	1 / 8	MMML CGS	MACIEJ_MMML 50
36	−8.38	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
37	−8.38	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
38	−8.3	NULL	1 / 14	MF	Ras GTPase activator activity
39	−8.3	NULL	1 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
40	−8.3	NULL	1 / 14	GSEA C2	MAHADEVAN_IMATINIB_RESISTANCE_UP



p−values

GW_234

Local Summary

%DE = 0.73

metagenes = 20

genes = 314

genes in genesets = 309

genes with fdr < 0.1 = 170 (19 + / 151 −)

genes with fdr < 0.05 = 152 (18 + / 134 −)

genes with fdr < 0.01 = 128 (16 + / 112 −)

<r> metagenes = 0.97

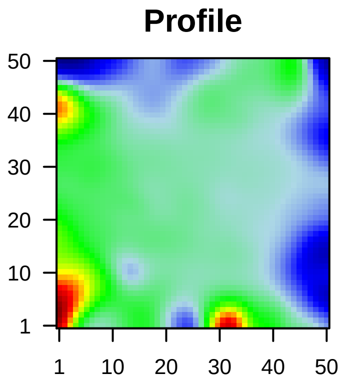
<r> genes = 0.41

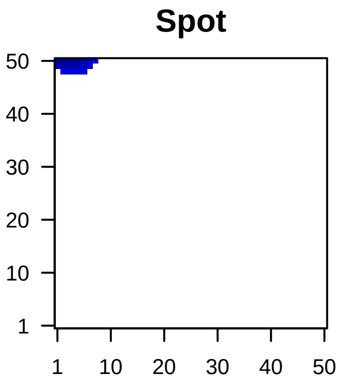
<FC> = −0.33

<shrinkage−t> = −11.62

<p−value> = 0

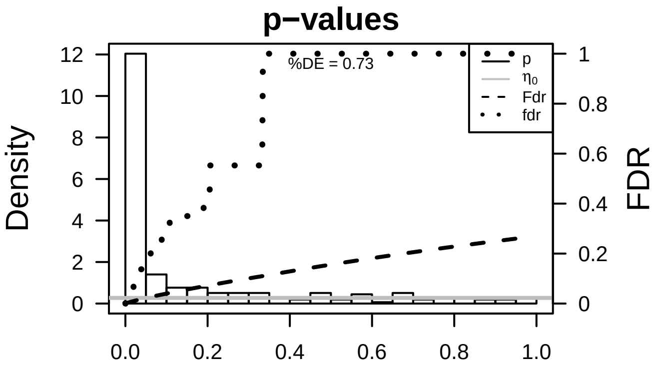
<fdr> = 0.49





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.52	2e−16	2e−15	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	−1.64	2e−16	2e−15	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	1577	−1.38	2e−16	2e−15	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
4	92196	−1.71	2e−16	2e−15	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
5	51228	−1.12	2e−16	2e−15	2 x 50	glycolipid transfer protein [Source:HGNC Symbol;Acc:24867]
6	2877	−2.5	2e−16	2e−15	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
7	3851	−1.95	2e−16	2e−15	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
8	51195	−1.39	2e−16	2e−15	5 x 50	Rap guanine nucleotide exchange factor (GEF)−like 1 [Sourc
9	6947	1.79	2e−16	2e−15	2 x 50	transcobalamin I (vitamin B12 binding protein, R binder family
10	1050	−1.21	9e−16	3e−14	6 x 50	CCAAT/enhancer binding protein (C/EBP), alpha [Source:HG
11	6337	−1.19	2e−15	3e−14	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
12	100134938	−1.19	2e−15	3e−14	6 x 50	polymerase (RNA) II (DNA directed) polypeptide J3 [Source:
13	6701	−1.19	2e−15	8e−14	1 x 49	small proline−rich protein 2B [Source:HGNC Symbol;Acc:112
14	84290	−1.18	3e−15	1e−12	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
15	1475	−1.15	2e−14	1e−12	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
16	1999	−1.14	3e−14	2e−11	5 x 50	E74−like factor 3 (ets domain transcription factor, epithelial−s
17	3157	−1.09	3e−13	2e−10	7 x 50	3−hydroxy−3−methylglutaryl−CoA synthase 1 (soluble) [Sour
18	1622	−1.05	3e−12	2e−10	6 x 50	diazepam binding inhibitor (GABA receptor modulator, acyl−C
19	6286	−1.03	5e−12	7e−10	1 x 50	S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
20	114569	−1.01	1e−11	7e−10	4 x 50	mal, T−cell differentiation protein 2 (gene/pseudogene) [Sour



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−30.97	NULL	74 / 135	H.Tiss	WIRTH_Mucosa
2	−17.37	NULL	5 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
3	−14.24	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
4	−13.21	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
5	−12.6	NULL	5 / 15	MF	retinol dehydrogenase activity
6	−12.33	NULL	7 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
7	−12.22	NULL	3 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
8	−12.04	NULL	3 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
9	−11.67	NULL	1 / 2	Cancer	GENTLES_modul8
10	−11.61	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
11	−11.32	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
12	−11.18	NULL	3 / 12	BP	cellular aldehyde metabolic process
13	−10.73	NULL	3 / 11	GSEA C2	REACTOME_XENOBIOTICS
14	−10.69	NULL	2 / 14	MF	glutathione peroxidase activity
15	−10.4	NULL	2 / 9	GSEA C2	REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRA
16	−10.4	NULL	2 / 9	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUNE
17	−10.03	NULL	2 / 13	BP	retinoic acid metabolic process
18	−9.73	NULL	8 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
19	−9.63	NULL	1 / 12	MF	retinol binding
20	−9.28	NULL	2 / 11	GSEA C2	REACTOME_BIOLOGICAL_OXIDATIONS
21	−9.12	NULL	1 / 13	BP	temperature homeostasis
22	−9.05	NULL	14 / 21	CC	cornified envelope
23	−8.91	NULL	19 / 53	BP	keratinocyte differentiation
24	−8.71	NULL	76 / 572	Disease	GUDJ_psoriasis up
25	−8.52	NULL	4 / 18	BP	retinol metabolic process
26	−8.29	NULL	8 / 38	BP	epithelial cell differentiation
27	−8.09	NULL	2 / 10	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
28	−8.06	NULL	5 / 39	BP	retinoid metabolic process
29	−7.94	NULL	3 / 16	miRNA target starBase	hsa−miR−1298
30	−7.79	NULL	2 / 7	GSEA C2	KEGG_STEROID_HORMONE_BIOSYNTHESIS
31	−7.64	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
32	−7.62	NULL	4 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
33	−7.44	NULL	10 / 119	BP	xenobiotic metabolic process
34	−7.41	NULL	3 / 16	GSEA C2	FRASOR_TAMOXIFEN_RESPONSE_UP
35	−7.32	NULL	17 / 76	BP	epidermis development
36	−7.29	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
37	−7.27	NULL	20 / 434	BP	oxidation−reduction process
38	−7.25	NULL	4 / 35	MF	monooxygenase activity
39	−7.15	NULL	3 / 16	CC	microvillus membrane
40	−7.15	NULL	6 / 44	BP	steroid metabolic process