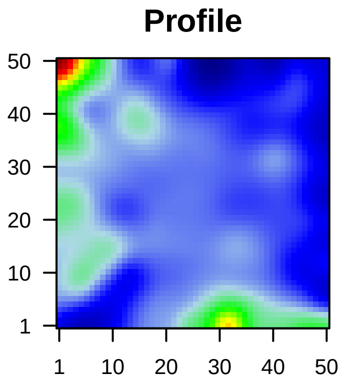
GW_268

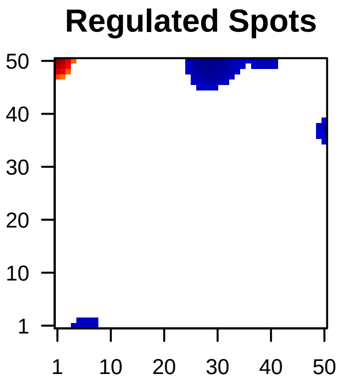
Global Summary

%DE = 0.15
genes with fdr < 0.2 = 1854 (1054 + / 800 −)
genes with fdr < 0.1 = 1489 (888 + / 601 −)
genes with fdr < 0.05 = 1179 (741 + / 438 −)
genes with fdr < 0.01 = 793 (548 + / 245 −)

genes in genesets = 16332

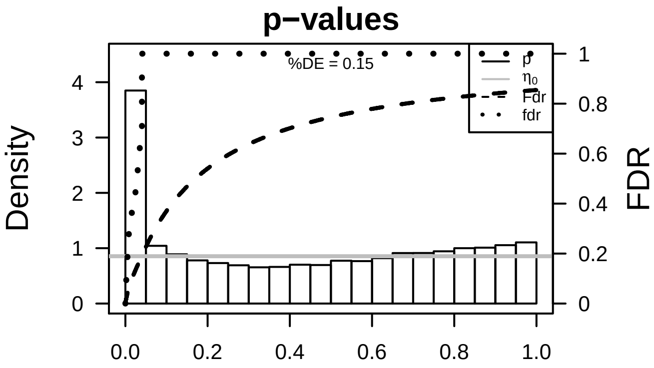
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.11
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.36	2e−16	4e−14	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	58	1.96	2e−16	4e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	1.6	2e−16	4e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	222	1.67	2e−16	4e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
5	242	1.7	2e−16	4e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
6	200315	1.65	2e−16	4e−14	1 x 40	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
7	151516	1.57	2e−16	4e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
8	23120	1.56	2e−16	4e−14	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
9	339512	2.06	2e−16	4e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
10	713	1.51	2e−16	4e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
11	375791	2.45	2e−16	4e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
12	1041	1.43	2e−16	4e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
13	1048	1.69	2e−16	4e−14	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
14	4680	1.49	2e−16	4e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
15	9022	1.84	2e−16	4e−14	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
16	84518	2.01	2e−16	4e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	49860	2.01	2e−16	4e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
18	3627	1.8	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
19	6373	1.6	2e−16	4e−14	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;
20	9547	−1.43	2e−16	4e−14	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	26.83	NULL	572	Disease	GUDJ_psoriasis up
2	26.17	NULL	135	H.Tiss	WIRTH_Mucosa
3	16.93	NULL	633	Chr	Chr 9
4	14.8	NULL	21	CC	cornified envelope
5	13.08	NULL	51	BP	type I interferon signaling pathway
6	13.03	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
7	12.73	NULL	42	BP	keratinization
8	12.62	NULL	53	BP	keratinocyte differentiation
9	12.23	NULL	123	BP	defense response to virus
10	11.8	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
11	11.32	NULL	76	BP	epidermis development
12	10.88	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
13	10.78	NULL	31	BP	negative regulation of viral genome replication
14	10.69	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
15	10.21	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
16	9.74	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
17	9.68	NULL	312	BP	immune response
18	9.58	NULL	15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
19	9.49	NULL	274	Lymphoma	SPANG_IL21 DN
20	9.35	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
Underexpressed					
1	−9.6	NULL	618	Chr	Chr 4
2	−9.38	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
3	−9.05	NULL	914	Chr	Chr 3
4	−8.82	NULL	4	MMML CGS	MACIEJ_MMML 23
5	−8.69	NULL	92	BP	translational elongation
6	−8.23	NULL	81	BP	viral transcription
7	−8.06	NULL	128	BP	translational initiation
8	−8.02	NULL	87	BP	translational termination
9	−8.02	NULL	482	BP	cellular protein metabolic process
10	−7.57	NULL	92	BP	viral life cycle
11	−7.13	NULL	315	miRNA target starBase	hsa−miR−30e
12	−6.98	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
13	−6.83	NULL	253	BP	translation
14	−6.77	NULL	37	CC	cytosolic small ribosomal subunit
15	−6.71	NULL	436	miRNA target starBase	hsa−miR−548n
16	−6.28	NULL	268	miRNA target starBase	hsa−miR−30b
17	−6.26	NULL	534	Chr	Chr 8
18	−6.26	NULL	235	miRNA target starBase	hsa−miR−1252
19	−6.21	NULL	630	Chr	Chr X
20	−6.19	NULL	264	miRNA target starBase	hsa−miR−30a

GW_268

Local Summary

%DE = 0.97

metagenes = 12

genes = 187

genes in genesets = 182

genes with fdr < 0.1 = 170 (163 + / 7 −)

genes with fdr < 0.05 = 170 (163 + / 7 −)

genes with fdr < 0.01 = 152 (148 + / 4 −)

<r> metagenes = 0.98

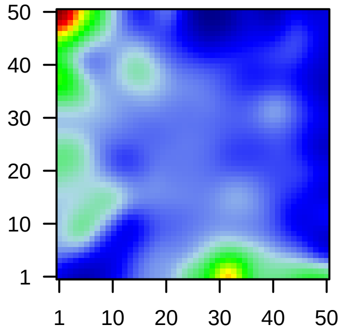
<r> genes = 0.48

<FC> = 0.9

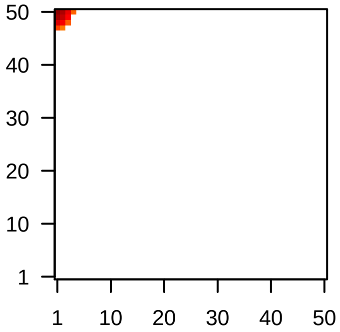
<shrinkage−t> = 31.91

<p−value> = 0

<fdr> = 0.17



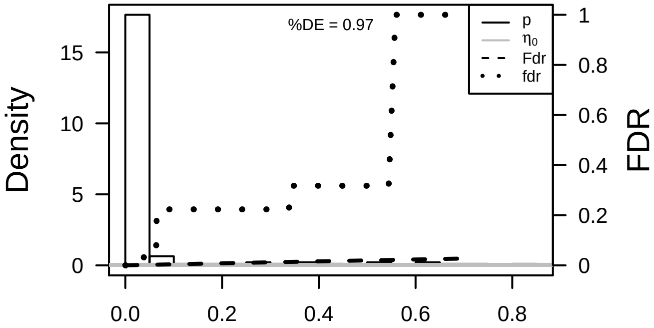
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	79852	1.36	2e−16	3e−17	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	222	1.67	2e−16	3e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGN
3	242	1.7	2e−16	3e−17	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sy
4	23120	1.56	2e−16	3e−17	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
5	375791	2.45	2e−16	3e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
6	1048	1.69	2e−16	3e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [
7	4680	1.49	2e−16	3e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
8	9022	1.84	2e−16	3e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
9	84518	2.01	2e−16	3e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
10	49860	2.01	2e−16	3e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
11	1577	1.55	2e−16	3e−17	4 x 50	cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
12	1673	1.87	2e−16	3e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	1893	1.58	2e−16	3e−17	3 x 50	extracellular matrix protein 1 [Source:HGNC Symbol;Acc:315
14	2312	1.94	2e−16	3e−17	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
15	9245	1.4	2e−16	3e−17	4 x 50	glucosaminyl (N−acetyl) transferase 3, mucin type [Source:H
16	26525	1.36	2e−16	3e−17	1 x 49	interleukin 36 receptor antagonist [Source:HGNC Symbol;Ac
17	56300	1.42	2e−16	3e−17	1 x 47	interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
18	26085	1.36	2e−16	3e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
19	5653	1.45	2e−16	3e−17	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
20	3858	1.45	2e−16	3e−17	1 x 47	keratin 10 [Source:HGNC Symbol;Acc:6413]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	56.48	NULL	74 / 135	H.Tiss	WIRTH_Mucosa
2	37.04	NULL	16 / 21	CC	cornified envelope
3	32.84	NULL	19 / 42	BP	keratinization
4	29.73	NULL	21 / 53	BP	keratinocyte differentiation
5	28.59	NULL	81 / 572	Disease	GUDJ_psoriasis up
6	22.76	NULL	9 / 19	BP	peptide cross−linking
7	22.58	NULL	20 / 76	BP	epidermis development
8	20.3	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	16.8	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
10	15.73	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
11	15.44	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	15.02	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
13	13.88	NULL	5 / 10	MF	RAGE receptor binding
14	13.27	NULL	18 / 186	MF	structural molecule activity
15	13.23	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
16	12.97	NULL	8 / 44	CC	keratin filament
17	12.87	NULL	10 / 82	CC	intermediate filament
18	12.72	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
19	12.61	NULL	4 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
20	12.51	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
21	11.96	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
22	11.39	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
23	11.3	NULL	6 / 13	BP	negative regulation of peptidase activity
24	11.3	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
25	11.26	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
26	11.16	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
27	11.02	NULL	3 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
28	10.92	NULL	3 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
29	10.62	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
30	10.29	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
31	9.69	NULL	7 / 38	BP	epithelial cell differentiation
32	9.59	NULL	8 / 83	CC	anchored to membrane
33	9.34	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
34	9.12	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
35	9.08	NULL	12 / 122	MF	serine−type endopeptidase activity
36	9.04	NULL	49 / 1182	CC	extracellular region
37	8.94	NULL	2 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
38	8.84	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
39	8.6	NULL	3 / 13	GSEA C2	FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
40	8.56	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP

GW_268

Local Summary

%DE = 0.71

metagenes = 9

genes = 184

genes in genesets = 183

genes with fdr < 0.1 = 52 (3 + / 49 −)

genes with fdr < 0.05 = 35 (3 + / 32 −)

genes with fdr < 0.01 = 27 (2 + / 25 −)

<r> metagenes = 0.99

<r> genes = 0.41

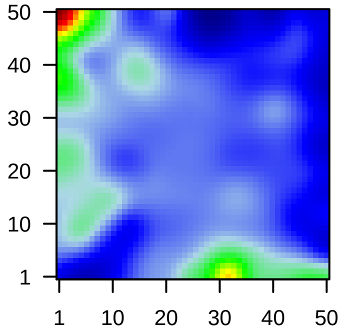
<FC> = −0.27

<shrinkage−t> = −9.3

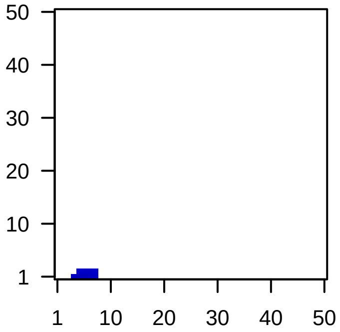
<p−value> = 0.02

<fdr> = 0.76

Profile



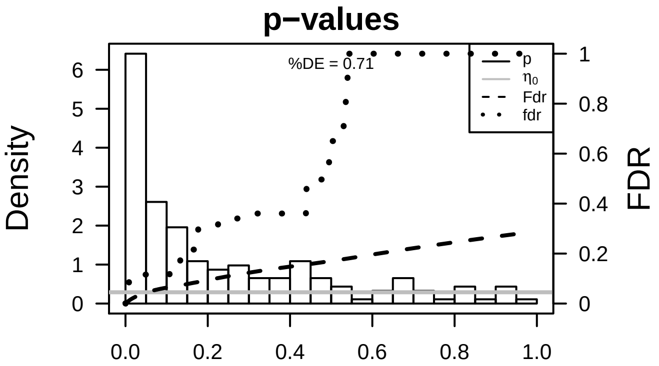
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3039	−1.62	2e−16	4e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
2	3040	−2.54	2e−16	4e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
3	3043	−3.04	2e−16	4e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
4	26064	−1.12	1e−11	1e−07	4 x 1	retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
5	2882	−0.97	4e−09	1e−07	6 x 1	glutathione peroxidase 7 [Source:HGNC Symbol;Acc:4559]
6	2202	−0.97	5e−09	1e−07	5 x 1	EGF containing fibulin−like extracellular matrix protein 1 [Sou
7	5156	−0.96	7e−09	3e−07	5 x 1	platelet−derived growth factor receptor, alpha polypeptide [So
8	8910	−0.93	2e−08	3e−07	6 x 1	sarcoglycan, epsilon [Source:HGNC Symbol;Acc:10808]
9	140606	−0.93	2e−08	3e−05	5 x 1	Selenoprotein M [Source:UniProtKB/Swiss−Prot;Acc:Q8WW
10	7474	−0.82	7e−07	3e−05	6 x 1	wingless−type MMTV integration site family, member 5A [Sou
11	2791	−0.81	1e−06	4e−04	5 x 1	guanine nucleotide binding protein (G protein), gamma 11 [So
12	22920	−0.71	2e−05	4e−04	7 x 1	kinesin−associated protein 3 [Source:HGNC Symbol;Acc:170
13	4692	−0.71	2e−05	3e−03	5 x 1	necdin, melanoma antigen (MAGE) family member [Source:H
14	23531	−0.64	1e−04	3e−03	8 x 1	monocyte to macrophage differentiation−associated [Source:
15	1634	−0.63	1e−04	4e−03	4 x 1	decorin [Source:HGNC Symbol;Acc:2705]
16	9823	−0.61	2e−04	4e−03	7 x 1	armadillo repeat containing, X−linked 2 [Source:HGNC Symb
17	10962	−0.6	3e−04	4e−03	5 x 1	myeloid/lymphoid or mixed−lineage leukemia (trithorax homol
18	130132	−0.59	3e−04	4e−03	8 x 1	raftlin family member 2 [Source:HGNC Symbol;Acc:26402]
19	7076	−0.58	5e−04	4e−03	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc
20	55752	−0.57	5e−04	4e−03	8 x 1	septin 11 [Source:HGNC Symbol;Acc:25589]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−60.21	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
2	−37.32	NULL	3 / 11	MF	oxygen transporter activity
3	−36.39	NULL	2 / 10	CC	hemoglobin complex
4	−34.56	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
5	−30.36	NULL	2 / 14	CC	endocytic vesicle lumen
6	−27.85	NULL	3 / 19	MF	peroxidase activity
7	−27.55	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
8	−25.78	NULL	2 / 19	BP	hydrogen peroxide catabolic process
9	−23.84	NULL	2 / 22	BP	bicarbonate transport
10	−23.56	NULL	3 / 26	MF	oxygen binding
11	−20.57	NULL	2 / 29	BP	positive regulation of cell death
12	−18.64	NULL	1 / 13	BP	regulation of blood vessel size
13	−17.87	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
14	−17.87	NULL	1 / 7	GSEA C2	SCHLESINGER_H3K27ME3_IN_NORMAL_AND_METHYLATED_
15	−16.65	NULL	2 / 43	BP	response to hydrogen peroxide
16	−16.6	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
17	−16.41	NULL	2 / 15	GSEA C2	DELYS_THYROID_CANCER_DN
18	−16.31	NULL	4 / 56	BP	protein heterooligomerization
19	−16.2	NULL	1 / 2	MMML CGS	MACIEJ_MMML 46
20	−14.99	NULL	4 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
21	−13.29	NULL	1 / 12	GSEA C2	SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER
22	−12.96	NULL	2 / 15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
23	−12.8	NULL	1 / 26	BP	positive regulation of nitric oxide biosynthetic process
24	−12.72	NULL	1 / 13	GSEA C2	NIKOLSKY_BREAST_CANCER_16P13_AMPLICON
25	−12.72	NULL	1 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
26	−11.87	NULL	5 / 110	MF	heme binding
27	−11.68	NULL	3 / 13	GSEA C2	REACTOME_CLASS_B2_SECRETIN_FAMILY_RECEPTORS
28	−11.4	NULL	39 / 250	Lymphoma	LENZ_Stromal signature 1
29	−10.52	NULL	4 / 125	MF	iron ion binding
30	−10.48	NULL	3 / 100	Lymphoma	ROSOLOWSKI_blue total
31	−10.32	NULL	3 / 54	BP	regulation of blood pressure
32	−9.83	NULL	1 / 5	Glio	laffaire_hypometh_LGG_vs_control
33	−9.29	NULL	2 / 10	GSEA C2	IIZUKA_RECURRENT_LIVER_CANCER
34	−9.07	NULL	12 / 59	Lymphoma	LENZ_Stromal signature 2
35	−8.84	NULL	26 / 190	CC	extracellular matrix
36	−8.36	NULL	3 / 16	GSEA C2	RUGO_RESPONSE_TO_4NQO
37	−8.36	NULL	3 / 16	GSEA C2	KYNG_DNA_DAMAGE_BY_4NQO
38	−8.19	NULL	1 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
39	−8.12	NULL	3 / 13	GSEA C2	REACTOME_HEMOSTASIS
40	−8.06	NULL	7 / 76	BP	wound healing

GW_268

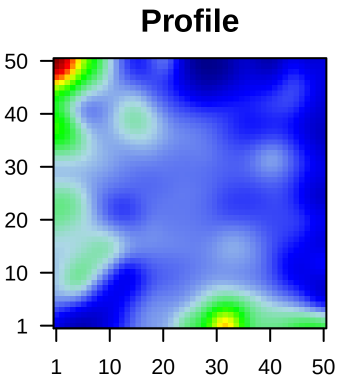
Local Summary

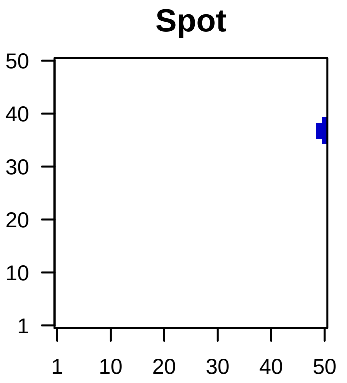
%DE = 0.66
metagenes = 8
genes = 174
genes in genesets = 174

genes with fdr < 0.1 = 49 (1 + / 48 −)
genes with fdr < 0.05 = 37 (1 + / 36 −)
genes with fdr < 0.01 = 18 (1 + / 17 −)

<r> metagenes = 0.98
<r> genes = 0.3

<FC> = −0.24
<shrinkage−t> = −8.32
<p−value> = 0.05
<fdr> = 0.76





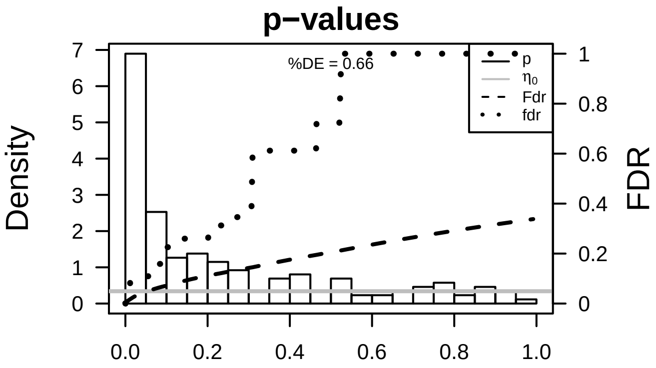
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10314	−0.87	2e−07	2e−05	50 x 35	LanC lantibiotic synthetase component C−like 1 (bacterial) [S
2	4942	−0.83	5e−07	3e−04	50 x 35	ornithine aminotransferase [Source:HGNC Symbol;Acc:8091]
3	29058	−0.7	2e−05	3e−04	50 x 38	transmembrane protein 230 [Source:HGNC Symbol;Acc:1587
4	310	−0.7	2e−05	3e−04	50 x 35	annexin A7 [Source:HGNC Symbol;Acc:545]
5	5431	−0.7	2e−05	3e−04	50 x 37	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [
6	84928	−0.7	3e−05	3e−04	50 x 37	transmembrane protein 209 [Source:HGNC Symbol;Acc:218
7	8723	−0.69	3e−05	3e−03	50 x 36	sorting nexin 4 [Source:HGNC Symbol;Acc:11175]
8	51663	−0.64	1e−04	3e−03	50 x 37	zinc finger RNA binding protein [Source:HGNC Symbol;Acc:1
9	5189	0.63	1e−04	6e−03	50 x 38	peroxisomal biogenesis factor 1 [Source:HGNC Symbol;Acc:
10	10289	−0.6	3e−04	6e−03	50 x 35	eukaryotic translation initiation factor 1B [Source:HGNC Sym
11	1975	−0.59	3e−04	6e−03	50 x 35	eukaryotic translation initiation factor 4B [Source:HGNC Sym
12	51765	−0.58	4e−04	8e−03	50 x 37	Serine/threonine−protein kinase MST4 [Source:UniProtKB/S
13	8443	−0.56	7e−04	8e−03	49 x 38	glyceronephosphate O−acyltransferase [Source:HGNC Symb
14	11212	−0.55	9e−04	8e−03	50 x 39	proline synthetase co−transcribed homolog (bacterial) [Sourc
15	6599	−0.54	1e−03	8e−03	50 x 36	SWI/SNF related, matrix associated, actin dependent regulat
16	9908	−0.54	1e−03	8e−03	50 x 36	GTPase activating protein (SH3 domain) binding protein 2 [S
17	51170	−0.53	1e−03	8e−03	50 x 38	hydroxysteroid (17−beta) dehydrogenase 11 [Source:HGNC
18	4089	−0.53	1e−03	8e−03	50 x 35	SMAD family member 4 [Source:HGNC Symbol;Acc:6770]
19	57092	−0.53	1e−03	1e−02	50 x 35	PEST proteolytic signal containing nuclear protein [Source:H
20	1915	−0.47	2e−03	1e−02	50 x 35	eukaryotic translation elongation factor 1 alpha 1 [Source:HG

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.79	NULL	1 / 2	miRNA target	miR−98
2	−12.37	NULL	1 / 4	miRNA target	let−7c
3	−12.37	NULL	1 / 4	miRNA target	let−7g
4	−9.99	NULL	1 / 6	miRNA target	let−7b
5	−9.99	NULL	1 / 6	miRNA target	let−7d
6	−9.99	NULL	1 / 6	miRNA target	miR−26a
7	−9.81	NULL	2 / 11	GSEA C2	ROZANOV_MMP14_CORRELATED
8	−9.54	NULL	2 / 10	BP	positive regulation of SMAD protein import into nucleus
9	−8.92	NULL	4 / 38	miRNA target starBase	hsa−miR−1277
10	−8.05	NULL	1 / 9	miRNA target	miR−125b
11	−7.97	NULL	8 / 90	miRNA target starBase	hsa−miR−10a
12	−7.91	NULL	2 / 16	GSEA C2	RODWELL_AGING_KIDNEY_NO_BLOOD_DN
13	−7.81	NULL	8 / 93	miRNA target starBase	hsa−miR−10b
14	−7.61	NULL	1 / 10	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_DN
15	−7.54	NULL	1 / 11	MF	glutathione binding
16	−7.23	NULL	1 / 11	miRNA target	let−7a
17	−7.19	NULL	1 / 12	MF	low−density lipoprotein particle receptor binding
18	−7.15	NULL	3 / 11	MF	AU−rich element binding
19	−7.11	NULL	19 / 271	miRNA target starBase	hsa−miR−101
20	−6.89	NULL	1 / 12	GSEA C2	LEE_LIVER_CANCER_E2F1_DN
21	−6.89	NULL	1 / 12	GSEA C2	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERS
22	−6.69	NULL	1 / 5	GSEA C2	KIM_LRRC3B_TARGETS
23	−6.66	NULL	1 / 4	GSEA C2	LUCAS_HNF4A_TARGETS_DN
24	−6.64	NULL	1 / 9	GSEA C2	JAIN_NFKB_SIGNALING
25	−6.6	NULL	1 / 13	GSEA C2	LEE_LIVER_CANCER_CIPROFIBRATE_DN
26	−6.6	NULL	1 / 13	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_DN
27	−6.6	NULL	1 / 13	GSEA C2	LEE_LIVER_CANCER_DENA_DN
28	−6.55	NULL	8 / 95	miRNA 3UTR	GTGGC−365
29	−6.48	NULL	20 / 421	miRNA target starBase	hsa−let−7b
30	−6.38	NULL	4 / 20	BP	protein secretion
31	−6.37	NULL	2 / 21	BP	positive regulation of pathway−restricted SMAD protein phosphoryl
32	−6.34	NULL	1 / 14	GSEA C2	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_UP
33	−6.34	NULL	1 / 14	GSEA C2	KIM_MYCL1_AMPLIFICATION_TARGETS_DN
34	−6.34	NULL	1 / 14	GSEA C2	LEE_LIVER_CANCER_ACOX1_DN
35	−6.31	NULL	8 / 121	miRNA target starBase	hsa−miR−646
36	−6.17	NULL	14 / 313	Glio	willscher_GBM_Verhaak−CL_expression_D_up
37	−6.17	NULL	14 / 313	Glio	willscher_GBM_Verhaak−MES_expression_D_down
38	−6.17	NULL	14 / 313	Glio	willscher_GBM_Verhaak−PNwt_expression_D_up
39	−6.13	NULL	3 / 48	MF	pyridoxal phosphate binding
40	−6.12	NULL	11 / 155	miRNA target starBase	hsa−miR−298



GW_268

Local Summary

%DE = 0.63

metagenes = 62

genes = 893

genes in genesets = 877

genes with fdr < 0.1 = 225 (6 + / 219 −)

genes with fdr < 0.05 = 194 (6 + / 188 −)

genes with fdr < 0.01 = 90 (4 + / 86 −)

<r> metagenes = 0.8

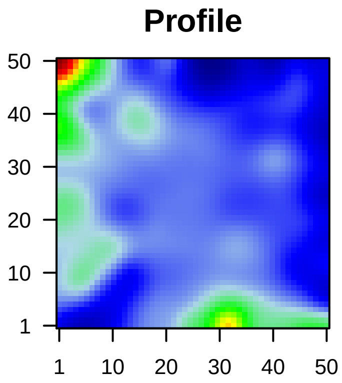
<r> genes = 0.22

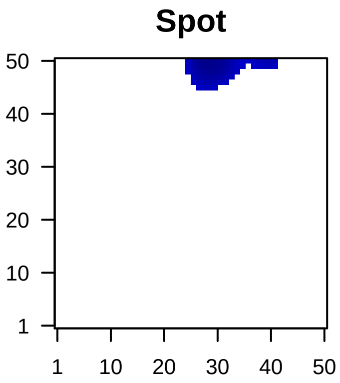
<FC> = −0.25

<shrinkage−t> = −8.78

<p−value> = 0.05

<fdr> = 0.75





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	114908	−1.09	4e−11	1e−07	26 x 50	transmembrane protein 123 [Source:HGNC Symbol;Acc:301
2	100093630	−1.04	4e−10	2e−07	32 x 48	small nucleolar RNA host gene 8 (non−protein coding) [Sourc
3	139886	−1.01	1e−09	1e−06	31 x 50	spindlin family, member 4 [Source:HGNC Symbol;Acc:27040]
4	329	−0.97	5e−09	2e−06	27 x 46	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;A
5	1207	−0.94	1e−08	2e−05	31 x 49	chloride channel, nucleotide−sensitive, 1A [Source:HGNC Sy
6	6156	−0.8	1e−07	2e−05	32 x 48	ribosomal protein L30 [Source:HGNC Symbol;Acc:10333]
7	3945	−0.87	2e−07	5e−05	40 x 50	lactate dehydrogenase B [Source:HGNC Symbol;Acc:6541]
8	10175	−0.83	5e−07	5e−05	28 x 50	cornichon family AMPA receptor auxiliary protein 1 [Source:H
9	1738	−0.83	5e−07	5e−05	28 x 50	dihydrolipoamide dehydrogenase [Source:HGNC Symbol;Acc
10	58505	−0.82	8e−07	5e−05	29 x 50	oligosaccharyltransferase complex subunit (non−catalytic) [S
11	3703	−0.81	8e−07	5e−05	29 x 47	STT3A, subunit of the oligosaccharyltransferase complex (ca
12	51504	−0.81	8e−07	5e−05	38 x 50	tRNA methyltransferase 11−2 homolog (S. cerevisiae) [Sourc
13	64776	−0.81	1e−06	2e−04	32 x 49	chromosome 11 open reading frame 1 [Source:HGNC Symbo
14	60592	−0.79	2e−06	2e−04	28 x 50	short coiled−coil protein [Source:HGNC Symbol;Acc:20335]
15	10413	−0.78	2e−06	2e−04	26 x 50	Yes−associated protein 1 [Source:HGNC Symbol;Acc:16262]
16	38	−0.77	3e−06	2e−04	31 x 48	acetyl−CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:
17	84992	−0.77	3e−06	2e−04	29 x 50	PIGY upstream reading frame [Source:HGNC Symbol;Acc:44
18	583	−0.76	4e−06	2e−04	27 x 46	Bardet−Biedl syndrome 2 [Source:HGNC Symbol;Acc:967]
19	136319	−0.76	4e−06	2e−04	25 x 50	myotrophin [Source:HGNC Symbol;Acc:15667]
20	64216	−0.75	6e−06	2e−04	40 x 50	transcription factor B2, mitochondrial [Source:HGNC Symbol;

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−10.96	NULL	7 / 11	MMML CGS	MACIEJ_MMML 49
2	−10.82	NULL	29 / 109	BP	SRP−dependent cotranslational protein targeting to membrane
3	−10.6	NULL	56 / 253	BP	translation
4	−9.6	NULL	14 / 51	CC	cytosolic large ribosomal subunit
5	−9.34	NULL	66 / 534	Chr	Chr 8
6	−9.15	NULL	21 / 81	BP	viral transcription
7	−9.06	NULL	39 / 153	MF	structural constituent of ribosome
8	−9.05	NULL	6 / 11	BP	ribosomal large subunit biogenesis
9	−8.94	NULL	22 / 92	BP	translational elongation
10	−8.84	NULL	22 / 92	BP	viral life cycle
11	−8.35	NULL	5 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_MS_DN
12	−8.34	NULL	23 / 87	BP	translational termination
13	−8.31	NULL	4 / 13	BP	COPI coating of Golgi vesicle
14	−8.3	NULL	3 / 10	CC	oligosaccharyltransferase complex
15	−8.27	NULL	16 / 62	Glio	Stuehler_Proteins_up_in_STS
16	−8.23	NULL	26 / 128	BP	translational initiation
17	−8.18	NULL	82 / 957	Chr	Chr 11
18	−8.16	NULL	175 / 1318	CC	mitochondrion
19	−8.05	NULL	65 / 482	BP	cellular protein metabolic process
20	−7.91	NULL	91 / 649	BP	gene expression
21	−7.85	NULL	23 / 115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
22	−7.45	NULL	53 / 287	BP	viral process
23	−7.41	NULL	37 / 167	CC	ribosome
24	−7.16	NULL	11 / 36	BP	ribosome biogenesis
25	−7.04	NULL	40 / 242	BP	RNA metabolic process
26	−7.03	NULL	146 / 1233	TF	KIM_MYC targets
27	−6.94	NULL	4 / 15	GSEA C2	HASLINGER_B_CLL_WITH_11Q23_DELETION
28	−6.65	NULL	52 / 618	Chr	Chr 4
29	−6.55	NULL	9 / 61	miRNA target−starBase	hsa−miR−659
30	−6.39	NULL	4 / 5	MMML CGS	MACIEJ_MMML 28
31	−6.34	NULL	53 / 614	CC	endoplasmic reticulum membrane
32	−6.25	NULL	17 / 86	Lymphoma	ROSOLOWSKI_red total
33	−6.25	NULL	3 / 10	GSEA C2	POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN
34	−6.12	NULL	4 / 16	GSEA C2	REACTOME_PYRUVATE_METABOLISM
35	−6.1	NULL	36 / 219	BP	mRNA metabolic process
36	−6.03	NULL	2 / 3	miRNA target	miR−214
37	−5.97	NULL	193 / 2378	CC	cytosol
38	−5.93	NULL	16 / 75	miRNA target−starBase	hsa−miR−592
39	−5.8	NULL	27 / 184	miRNA target−starBase	hsa−miR−586
40	−5.77	NULL	36 / 269	miRNA target−starBase	hsa−miR−1244