GW_076

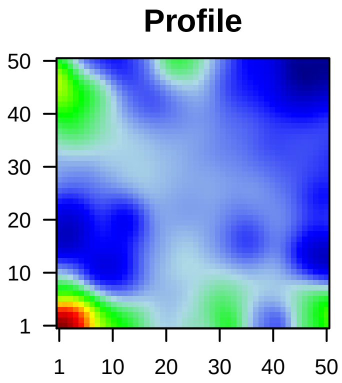
Global Summary

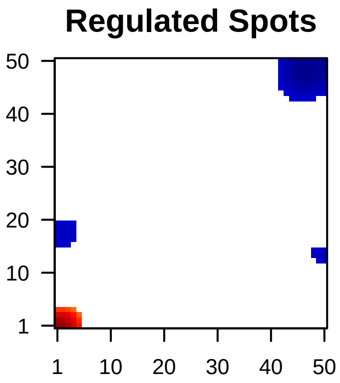
%DE = 0.16

genes with fdr < 0.2 = 1785 (1140 + / 645 −)
genes with fdr < 0.1 = 1564 (1035 + / 529 −)
genes with fdr < 0.05 = 1276 (885 + / 391 −)
genes with fdr < 0.01 = 888 (678 + / 210 −)

genes in genesets = 16332

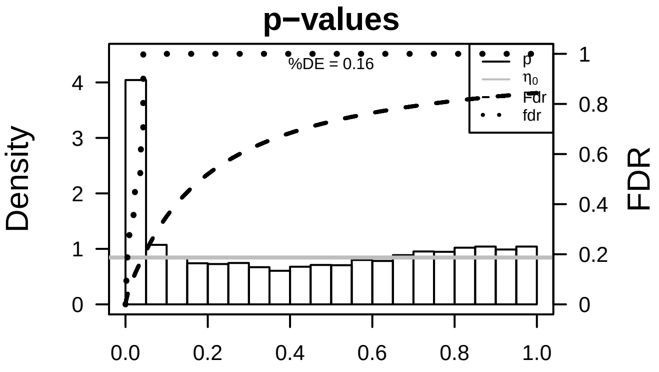
<FC> = 0
<shrinkage−t> = 0
<p−value> = 0.09
<fdr> = 0.84





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	218	−3.07	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
2	23452	1.84	2e−16	3e−14	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
3	164284	1.83	2e−16	3e−14	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:
4	366	2.29	2e−16	3e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
5	650	1.71	2e−16	3e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1
6	260436	2.15	2e−16	3e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
7	29923	2.11	2e−16	3e−14	4 x 44	hypoxia inducible lipid droplet−associated [Source:HGNC Sy
8	6347	1.98	2e−16	3e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
9	6364	3.07	2e−16	3e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
10	6348	2.29	2e−16	3e−14	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
11	6349	1.91	2e−16	3e−14	5 x 5	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
12	414062	3.13	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
13	9560	2.62	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
14	388372	2.05	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
15	6355	2.02	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
16	1041	1.97	2e−16	3e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
17	4680	1.92	2e−16	3e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
18	1116	2.21	2e−16	3e−14	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
19	1306	1.77	2e−16	3e−14	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
20	169044	2.26	2e−16	3e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	25.54	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	22.02	NULL	1182	CC	extracellular region
3	20.73	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	20.45	NULL	683	CC	extracellular space
5	19.22	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	19.22	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	19.22	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	19.22	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	17.85	NULL	190	CC	extracellular matrix
10	17.2	NULL	242	BP	extracellular matrix organization
11	17.2	NULL	312	BP	immune response
12	16.26	NULL	572	Disease	GUDJ_psoriasis up
13	15.54	NULL	269	BP	inflammatory response
14	13.99	NULL	69	BP	extracellular matrix disassembly
15	13.85	NULL	64	BP	collagen catabolic process
16	13.14	NULL	274	Lymphoma	SPANG_IL21 DN
17	12.76	NULL	43	MF	chemokine activity
18	12.68	NULL	16	MMML CGS	MACIEJ_MMML 1
19	12.29	NULL	2659	CC	plasma membrane
20	12.1	NULL	111	BP	chemotaxis
Underexpressed					
1	−13.88	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−13.88	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−11.72	NULL	370	BP	mitotic cell cycle
4	−10.9	NULL	1318	CC	mitochondrion
5	−10.3	NULL	649	BP	gene expression
6	−10.21	NULL	940	MF	nucleic acid binding
7	−9.79	NULL	4640	CC	nucleus
8	−9.3	NULL	949	CC	nucleoplasm
9	−9.3	NULL	595	MF	RNA binding
10	−9.14	NULL	149	BP	DNA replication
11	−9.05	NULL	298	BP	DNA repair
12	−8.89	NULL	253	BP	translation
13	−8.74	NULL	232	BP	mitosis
14	−8.57	NULL	1233	TF	KIM_MYC targets
15	−8.39	NULL	153	MF	structural constituent of ribosome
16	−8.37	NULL	242	BP	RNA metabolic process
17	−8.33	NULL	167	CC	ribosome
18	−8.07	NULL	579	CC	nucleolus
19	−7.93	NULL	220	CC	mitochondrial matrix
20	−7.52	NULL	304	CC	mitochondrial inner membrane

GW_076

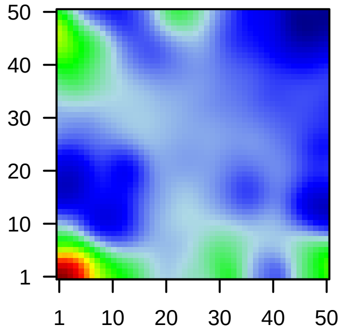
Local Summary

%DE = 0.93
metagenes = 19
genes = 275
genes in genesets = 274

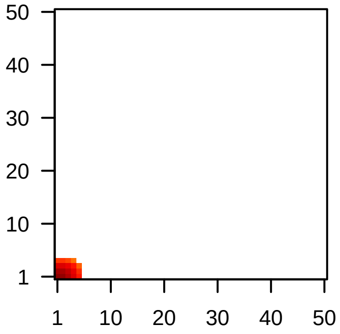
genes with fdr < 0.1 = 245 (245 + / 0 −)
genes with fdr < 0.05 = 245 (245 + / 0 −)
genes with fdr < 0.01 = 224 (224 + / 0 −)

<r> metagenes = 0.96
<r> genes = 0.39

<FC> = 1.08
<shrinkage−t> = 37.85
<p−value> = 0
<fdr> = 0.14



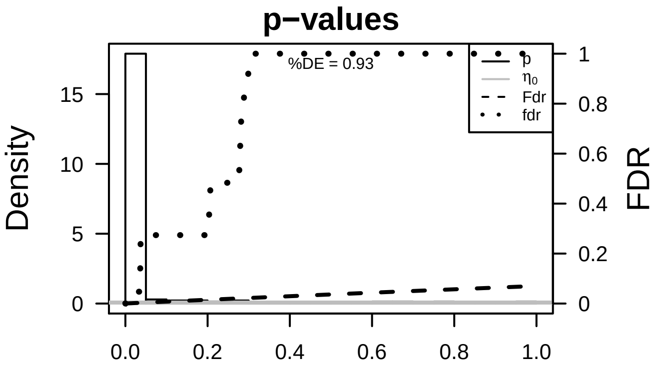
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	23452	1.84	2e−16	1e−16	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
2	164284	1.83	2e−16	1e−16	1 x 3	adenomatosis polyposis coli down−regulated 1−like [Source:H
3	366	2.29	2e−16	1e−16	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
4	650	1.71	2e−16	1e−16	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:10
5	6348	2.29	2e−16	1e−16	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:
6	414062	3.13	2e−16	1e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
7	1306	1.77	2e−16	1e−16	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
8	1281	1.91	2e−16	1e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
9	1290	1.72	2e−16	1e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
10	1291	1.79	2e−16	1e−16	2 x 1	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
11	1293	1.81	2e−16	1e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	1437	2.34	2e−16	1e−16	1 x 4	colony stimulating factor 2 (granulocyte−macrophage) [Sourc
13	2919	1.73	2e−16	1e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
14	2920	2.13	2e−16	1e−16	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
15	6374	2.45	2e−16	1e−16	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
16	6372	2.38	2e−16	1e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
17	84624	1.74	2e−16	1e−16	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
18	2619	1.87	2e−16	1e−16	2 x 1	growth arrest−specific 1 [Source:HGNC Symbol;Acc:4165]
19	8870	2.03	2e−16	1e−16	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:5392
20	3553	2.45	2e−16	1e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	35.05	NULL	63 / 190	CC	extracellular matrix
2	34.15	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
3	32.52	NULL	32 / 69	BP	extracellular matrix disassembly
4	31.84	NULL	67 / 242	BP	extracellular matrix organization
5	30.61	NULL	28 / 64	BP	collagen catabolic process
6	29.23	NULL	73 / 250	Lymphoma	LENZ_Stromal signature 1
7	27.54	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
8	26.35	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
9	25.95	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
10	25.61	NULL	8 / 11	MF	platelet−derived growth factor binding
11	24.1	NULL	82 / 683	CC	extracellular space
12	22.45	NULL	108 / 1182	CC	extracellular region
13	22.37	NULL	8 / 12	miRNA target	miR−29c
14	22.35	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
15	21.19	NULL	65 / 553	Cancer	Lembcke_Colonic Inflammation
16	20.75	NULL	38 / 183	CC	proteinaceous extracellular matrix
17	19.77	NULL	20 / 57	MF	extracellular matrix structural constituent
18	19.72	NULL	11 / 19	MF	extracellular matrix binding
19	19.45	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
20	19.09	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
21	18.91	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
22	18.83	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
23	18.83	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
24	18.83	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
25	18.83	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
26	18.76	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
27	18.52	NULL	15 / 37	BP	collagen fibril organization
28	18.46	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
29	18.21	NULL	3 / 6	Glio	Martinez_Glio_hypometh
30	18.02	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
31	17.92	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
32	16.8	NULL	12 / 40	BP	cellular response to amino acid stimulus
33	16.53	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
34	16.51	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
35	16.41	NULL	4 / 12	GSEA C2	BIOCARTA_ERYTH_PATHWAY
36	16.35	NULL	22 / 83	CC	basement membrane
37	16.27	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
38	16.27	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
39	16.23	NULL	5 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
40	16	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP

GW_076

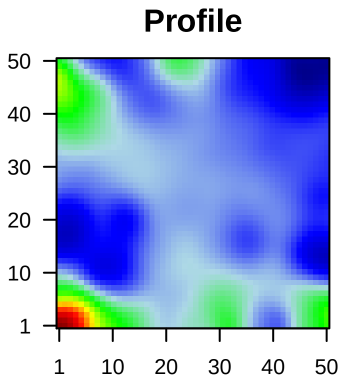
Local Summary

%DE = 0.94
metagenes = 8
genes = 79
genes in genesets = 79

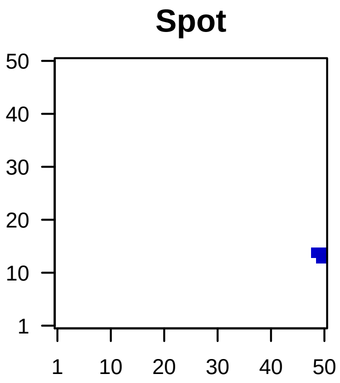
genes with fdr < 0.1 = 66 (4 + / 62 −)
genes with fdr < 0.05 = 58 (1 + / 57 −)
genes with fdr < 0.01 = 46 (1 + / 45 −)

<r> metagenes = 0.98
<r> genes = 0.34

<FC> = −0.51
<shrinkage−t> = −17.89
<p−value> = 0
<fdr> = 0.46



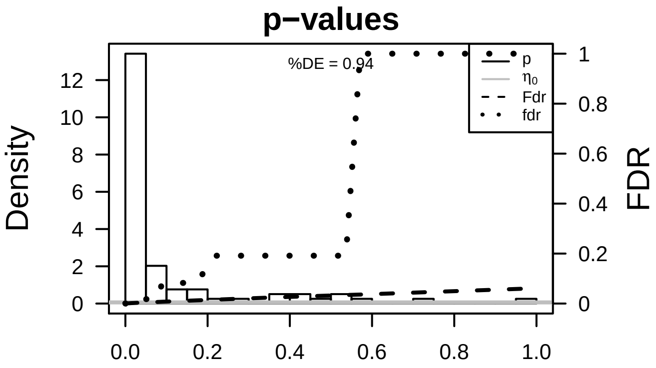
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8857	−1.8	2e−16	1e−15	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
2	55268	−1.4	2e−11	4e−09	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy
3	6920	−1.28	8e−10	2e−06	50 x 13	transcription elongation factor A (SII), 3 [Source:HGNC Symb
4	28958	−1.04	7e−07	2e−06	49 x 13	cytochrome c oxidase assembly factor 3 [Source:HGNC Sym
5	2568	−1.02	9e−07	2e−06	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
6	260293	−1.01	1e−06	2e−06	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
7	6228	−1	2e−06	2e−06	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
8	2139	−0.99	2e−06	8e−06	50 x 13	eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;
9	293	−0.97	4e−06	8e−06	50 x 15	solute carrier family 25 (mitochondrial carrier; adenine nucleo
10	2053	−0.95	5e−06	1e−05	50 x 14	epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc
11	4255	−0.94	7e−06	1e−05	48 x 15	O−6−methylguanine−DNA methyltransferase [Source:HGNC
12	79762	−0.93	9e−06	3e−05	50 x 15	chromosome 1 open reading frame 115 [Source:HGNC Symb
13	79085	−0.9	2e−05	1e−04	50 x 13	solute carrier family 25 (mitochondrial carrier; phosphate carr
14	498	−0.79	4e−05	2e−04	48 x 15	ATP synthase, H+ transporting, mitochondrial F1 complex, al
15	3033	−0.82	8e−05	2e−04	50 x 14	hydroxyacyl−CoA dehydrogenase [Source:HGNC Symbol;Ac
16	55930	−0.81	1e−04	1e−03	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
17	2205	−0.74	4e−04	1e−03	50 x 13	Fc fragment of IgE, high affinity I, receptor for; alpha polypept
18	66002	−0.71	6e−04	1e−03	50 x 13	cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
19	84064	−0.7	8e−04	1e−03	48 x 14	haloacid dehalogenase−like hydrolase domain containing 2 [
20	9249	−0.69	1e−03	1e−03	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.33	NULL	1 / 4	GSEA C2	NICK_RESPONSE_TO_PROC_TREATMENT_UP
2	−17.93	NULL	2 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−17.35	NULL	3 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
4	−15.83	NULL	2 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
5	−14.66	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_DN
6	−13.69	NULL	2 / 11	GSEA C2	BIOCARTA_ETC_PATHWAY
7	−13.16	NULL	2 / 10	BP	epoxygenase P450 pathway
8	−12.22	NULL	1 / 13	GSEA C2	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP
9	−12.22	NULL	1 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
10	−11.71	NULL	1 / 14	GSEA C2	WANG_BARRETTS_ESOPHAGUS_UP
11	−11.44	NULL	2 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
12	−11.44	NULL	2 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
13	−11.25	NULL	1 / 15	GSEA C2	FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN
14	−11.08	NULL	1 / 10	GSEA C2	YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
15	−10.85	NULL	1 / 16	GSEA C2	WATTEL_AUTONOMOUS_THYROID_ADENOMA_UP
16	−10.48	NULL	1 / 11	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_DN
17	−10.13	NULL	1 / 3	miRNA target	miR−223
18	−9.68	NULL	2 / 18	MF	aromatase activity
19	−9.17	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
20	−9.1	NULL	1 / 14	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN
21	−9.1	NULL	2 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
22	−9.1	NULL	2 / 10	GSEA C2	KEGG_LIMONENE_AND_PINENE_DEGRADATION
23	−9.05	NULL	1 / 12	BP	regulation of DNA−dependent transcription, elongation
24	−8.85	NULL	3 / 15	GSEA C2	KEGG_PROPANOATE_METABOLISM
25	−8.75	NULL	1 / 15	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP
26	−8.75	NULL	1 / 15	GSEA C2	VALK_AML_CLUSTER_15
27	−8.75	NULL	1 / 15	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN
28	−8.6	NULL	2 / 11	BP	neurotransmitter biosynthetic process
29	−8.57	NULL	2 / 21	BP	drug metabolic process
30	−8.46	NULL	2 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
31	−8.42	NULL	1 / 16	GSEA C2	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_DN
32	−8.42	NULL	1 / 16	GSEA C2	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_DN
33	−8.42	NULL	1 / 16	GSEA C2	ALCALAY_AML_BY_NPM1_LOCALIZATION_UP
34	−8.36	NULL	1 / 8	GSEA C2	SCHLESINGER_METHYLATED_IN_COLON_CANCER
35	−8.32	NULL	2 / 15	GSEA C2	MARTINEZ_RESPONSE_TO_TRABECTEDIN
36	−8.12	NULL	1 / 10	CC	integral to mitochondrial inner membrane
37	−8.03	NULL	1 / 10	MF	GABA−A receptor activity
38	−7.82	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
39	−7.81	NULL	2 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
40	−7.76	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_

GW_076

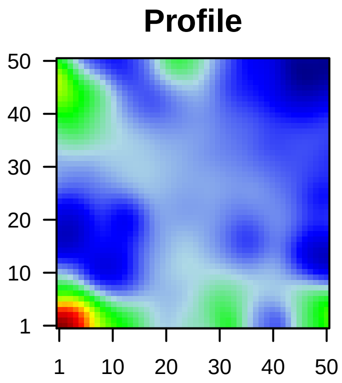
Local Summary

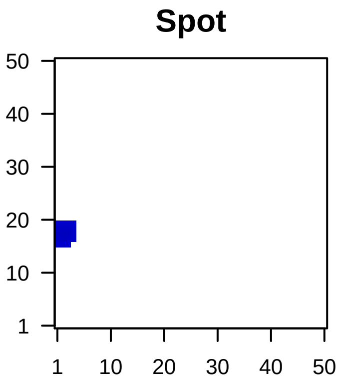
%DE = 0.7
metagenes = 19
genes = 212
genes in genesets = 211

genes with fdr < 0.1 = 93 (3 + / 90 −)
genes with fdr < 0.05 = 69 (1 + / 68 −)
genes with fdr < 0.01 = 32 (0 + / 32 −)

<r> metagenes = 0.97
<r> genes = 0.32

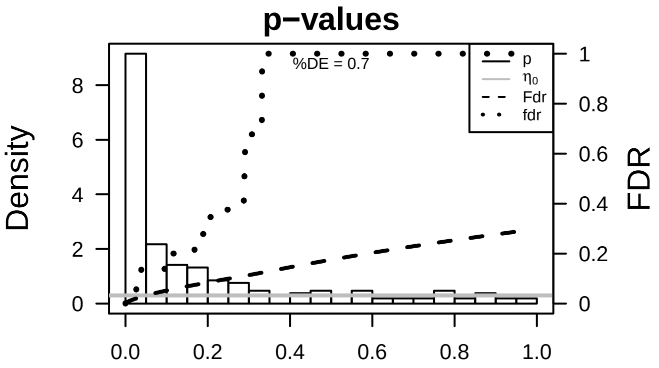
<FC> = −0.37
<shrinkage−t> = −12.97
<p−value> = 0.03
<fdr> = 0.65





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2194	−1.31	4e−10	2e−05	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
2	51373	−1.06	4e−07	2e−05	1 x 16	28S ribosomal protein S17, mitochondrial; HCG1984214, isof
3	3237	−1.03	7e−07	8e−05	1 x 16	homeobox D11 [Source:HGNC Symbol;Acc:5134]
4	991	−0.97	3e−06	8e−05	1 x 16	cell division cycle 20 [Source:HGNC Symbol;Acc:1723]
5	389541	−0.97	3e−06	2e−03	3 x 19	late endosomal/lysosomal adaptor, MAPK and MTOR activato
6	57418	−0.84	6e−05	2e−03	2 x 19	WD repeat domain 18 [Source:HGNC Symbol;Acc:17956]
7	27339	−0.84	6e−05	2e−03	3 x 18	pre−mRNA processing factor 19 [Source:HGNC Symbol;Acc:
8	10162	−0.8	1e−04	2e−03	3 x 20	lysophosphatidylcholine acyltransferase 3 [Source:HGNC Syr
9	11331	−0.78	2e−04	2e−03	4 x 18	prohibitin 2 [Source:HGNC Symbol;Acc:30306]
10	201254	−0.78	2e−04	2e−03	4 x 20	stimulated by retinoic acid 13 [Source:HGNC Symbol;Acc:114
11	4704	−0.77	2e−04	2e−03	3 x 19	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 3
12	2288	−0.77	2e−04	2e−03	1 x 19	FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:3
13	113655	−0.77	2e−04	2e−03	1 x 18	major facilitator superfamily domain containing 3 [Source:HGI
14	57109	−0.77	2e−04	2e−03	1 x 20	REX4, RNA exonuclease 4 homolog (S. cerevisiae) [Source:H
15	11004	−0.76	3e−04	2e−03	2 x 16	kinesin family member 2C [Source:HGNC Symbol;Acc:6393]
16	430	−0.76	3e−04	3e−03	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
17	55226	−0.75	3e−04	3e−03	2 x 17	N−acetyltransferase 10 (GCN5−related) [Source:HGNC Symb
18	284085	−0.74	4e−04	3e−03	3 x 18	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
19	7205	−0.72	6e−04	3e−03	2 x 16	thyroid hormone receptor interactor 6 [Source:HGNC Symbol
20	30833	−0.72	6e−04	3e−03	3 x 19	5', 3'−nucleotidase, cytosolic [Source:HGNC Symbol;Acc:171



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.21	NULL	3 / 9	GSEA C2	MOREIRA_RESPONSE_TO_TSA_UP
2	−11.47	NULL	6 / 19	CC	mitochondrial small ribosomal subunit
3	−11.22	NULL	2 / 4	TF	MYC_Cell growth and proliferation UP
4	−11.07	NULL	2 / 9	GSEA C2	KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
5	−10.18	NULL	2 / 6	GSEA C2	KORKOLA_CHORIOCARCINOMA_UP
6	−10.16	NULL	63 / 1318	CC	mitochondrion
7	−10.14	NULL	3 / 15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
8	−9.73	NULL	20 / 153	MF	structural constituent of ribosome
9	−9.68	NULL	3 / 16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
10	−9.44	NULL	18 / 167	CC	ribosome
11	−9.22	NULL	3 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
12	−8.64	NULL	2 / 15	GSEA C2	JI_RESPONSE_TO_FSH_UP
13	−8.47	NULL	2 / 7	GSEA C2	PARK_HSC_MARKERS
14	−8.42	NULL	2 / 15	GSEA C2	DIRMEIER_LMP1_RESPONSE_LATE_UP
15	−8.37	NULL	2 / 15	GSEA C2	LY_AGING_MIDDLE_DN
16	−8.14	NULL	11 / 96	BP	rRNA processing
17	−8.02	NULL	2 / 16	GSEA C2	WALLACE_PROSTATE_CANCER_UP
18	−7.81	NULL	1 / 10	MF	NADPH binding
19	−7.81	NULL	1 / 10	BP	pantothenate metabolic process
20	−7.81	NULL	1 / 10	BP	positive regulation of cellular metabolic process
21	−7.81	NULL	1 / 10	GSEA C2	REACTOME_TRIACYLGLYCERIDE_BIOSYNTHESIS
22	−7.81	NULL	1 / 10	GSEA C2	REACTOME_VITAMIN_B5_(PANTOTHENATE)_METABOLISM
23	−7.62	NULL	1 / 6	GSEA C2	WAESCH_ANAPHASE_PROMOTING_COMPLEX
24	−7.56	NULL	18 / 304	CC	mitochondrial inner membrane
25	−7.41	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_UP
26	−7.22	NULL	2 / 10	MF	NADH dehydrogenase activity
27	−7.22	NULL	1 / 3	TF	MYC_Tumor supressor genes UP
28	−7.16	NULL	3 / 16	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
29	−7.06	NULL	1 / 12	Glio	willscher_GBM_Verhaak−PNwt_expression_I_up
30	−7.06	NULL	1 / 12	Glio	willscher_GBM_Verhaak−PNmut_expression_I_up
31	−7.05	NULL	21 / 253	BP	translation
32	−6.98	NULL	3 / 16	GSEA C2	SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN
33	−6.91	NULL	1 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
34	−6.88	NULL	4 / 34	MF	NADH dehydrogenase (ubiquinone) activity
35	−6.76	NULL	4 / 35	BP	mitochondrial electron transport, NADH to ubiquinone
36	−6.71	NULL	24 / 579	CC	nucleolus
37	−6.65	NULL	4 / 36	CC	mitochondrial respiratory chain complex I
38	−6.64	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POC
39	−6.64	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_MODERATELY_VS_POC
40	−6.62	NULL	1 / 5	GSEA C2	NIELSEN_LIPOSARCOMA_DN

GW_076

Local Summary

%DE = 0.77

metagenes = 67

genes = 738

genes in genesets = 732

genes with fdr < 0.1 = 401 (11 + / 390 −)

genes with fdr < 0.05 = 274 (5 + / 269 −)

genes with fdr < 0.01 = 138 (2 + / 136 −)

<r> metagenes = 0.86

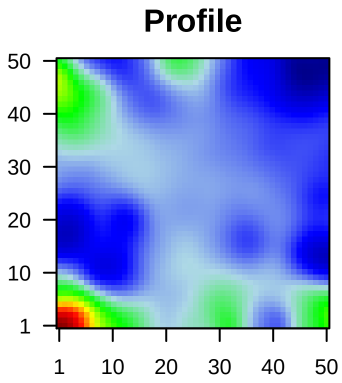
<r> genes = 0.24

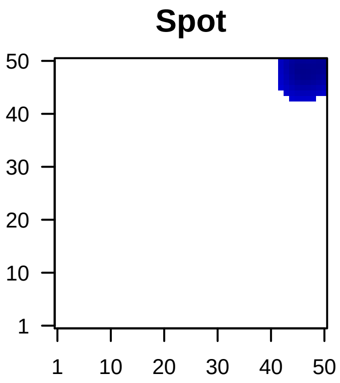
<FC> = −0.4

<shrinkage−t> = −14.1

<p−value> = 0.02

<fdr> = 0.63





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	256764	−2.85	2e−16	4e−14	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
2	4922	−1.6	1e−14	3e−10	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
3	200634	−1.46	2e−12	3e−10	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
4	25975	1.45	3e−12	4e−09	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
5	3880	−1.38	3e−11	4e−09	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
6	115749	−1.37	4e−11	4e−08	50 x 50	chromosome 12 open reading frame 56 [Source:HGNC Sym
7	4072	−1.32	3e−10	9e−08	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
8	339512	−1.28	8e−10	3e−07	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
9	7153	−1.24	2e−09	3e−07	45 x 49	topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symb
10	9133	−1.23	4e−09	3e−07	45 x 49	cyclin B2 [Source:HGNC Symbol;Acc:1580]
11	8364	−1.11	6e−09	3e−07	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
12	56256	−1.21	7e−09	1e−06	50 x 50	SERTA domain containing 4 [Source:HGNC Symbol;Acc:252
13	9918	−1.18	2e−08	1e−06	45 x 49	non−SMC condensin I complex, subunit D2 [Source:HGNC S
14	9055	−1.17	2e−08	3e−06	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:
15	1870	−1.13	5e−08	3e−06	46 x 45	E2F transcription factor 2 [Source:HGNC Symbol;Acc:3114]
16	26227	−1.13	6e−08	3e−06	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
17	113130	−1.12	7e−08	3e−06	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
18	139728	−1.12	8e−08	5e−06	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
19	899	−1.1	1e−07	5e−06	45 x 46	cyclin F [Source:HGNC Symbol;Acc:1591]
20	116832	−1.1	1e−07	5e−06	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−42.84	NULL	100 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−42.84	NULL	100 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−24.77	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
4	−24.52	NULL	118 / 370	BP	mitotic cell cycle
5	−21.78	NULL	26 / 57	Glio	developing astrocytes
6	−21.11	NULL	55 / 149	BP	DNA replication
7	−20.67	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
8	−20.14	NULL	121 / 530	Cancer	Lembcke_Normal vs Adenoma
9	−20.01	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
10	−19.64	NULL	21 / 30	BP	DNA strand elongation involved in DNA replication
11	−18.96	NULL	68 / 232	BP	mitosis
12	−18.72	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	−17.94	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
14	−17.86	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
15	−17.48	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
16	−17.06	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
17	−16.82	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
18	−16.12	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
19	−15.97	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
20	−15.88	NULL	12 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
21	−15.82	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
22	−15.66	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
23	−15.65	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
24	−15.5	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
25	−15.36	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
26	−15.25	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
27	−14.99	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
28	−14.95	NULL	10 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
29	−14.75	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
30	−14.43	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
31	−14.38	NULL	10 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
32	−14.27	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
33	−14.23	NULL	11 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
34	−14.18	NULL	15 / 21	BP	telomere maintenance via semi−conservative replication
35	−14.07	NULL	26 / 56	CC	chromosome, centromeric region
36	−13.94	NULL	9 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
37	−13.89	NULL	14 / 22	BP	DNA replication initiation
38	−13.89	NULL	16 / 24	BP	telomere maintenance via recombination
39	−13.69	NULL	59 / 298	BP	DNA repair
40	−13.64	NULL	8 / 16	GSEA C2	LY_AGING_PREMATURE_DN