GW_051

Global Summary

%DE = 0.13

\# genes with fdr < 0.2 = 1531 (1009 + / 522 −)

\# genes with fdr < 0.1 = 1243 (863 + / 380 −)

\# genes with fdr < 0.05 = 934 (698 + / 236 −)

\# genes with fdr < 0.01 = 605 (507 + / 98 −)

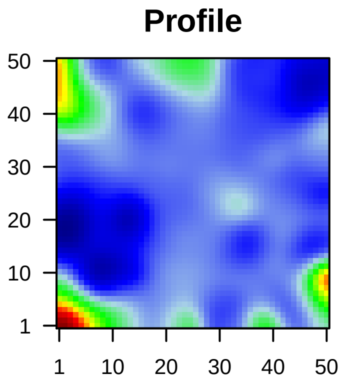
\# genes in genesets = 16332

<FC> = 0

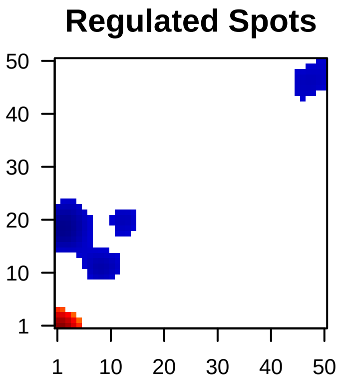
<shrinkage−t> = 0

<p−value> = 0.12

<fdr> = 0.87



Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	1.96	2e−16	3e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	1.42	2e−16	3e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	10551	1.9	2e−16	3e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
4	242	1.36	2e−16	3e−14	1 x 48	arachidonate 12−lipoxygenase, 12R type [Source:HGNC Sym
5	401138	2.62	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
6	25805	1.54	2e−16	3e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC S
7	590	1.51	2e−16	3e−14	16 x 50	butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
8	80341	1.4	2e−16	3e−14	50 x 10	BPI fold containing family B, member 2 [Source:HGNC Symb
9	79949	1.29	2e−16	3e−14	50 x 10	pleckstrin homology domain containing, family S member 1 [S
10	92747	3.79	2e−16	3e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
11	352999	2.01	2e−16	3e−14	50 x 10	chromosome 6 open reading frame 58 [Source:HGNC Symbo
12	760	1.57	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	51806	−1.27	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
14	92291	1.52	2e−16	3e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
15	84290	1.38	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	29775	1.19	2e−16	3e−14	1 x 42	caspase recruitment domain family, member 10 [Source:HGN
17	131076	1.23	2e−16	3e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
18	6352	1.46	2e−16	3e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:1
19	1041	1.31	2e−16	3e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
20	1114	1.53	2e−16	3e−14	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc

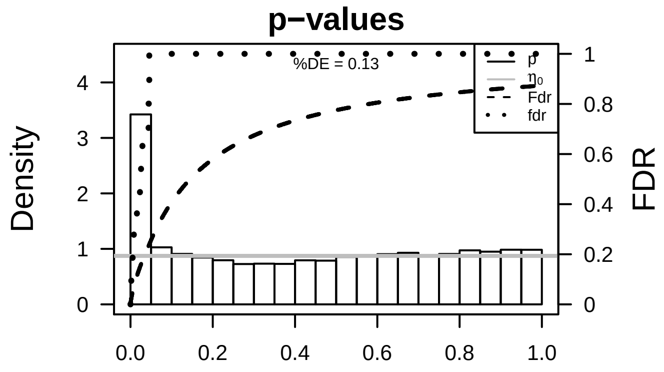
Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	21.26	NULL	1182	CC	extracellular region
2	20.4	NULL	250	Lymphoma	LENZ_Stromal signature 1
3	19.54	NULL	190	CC	extracellular matrix
4	18.44	NULL	242	BP	extracellular matrix organization
5	17.9	NULL	683	CC	extracellular space
6	17.01	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
7	16.93	NULL	69	BP	extracellular matrix disassembly
8	16.07	NULL	64	BP	collagen catabolic process
9	14.32	NULL	183	CC	proteinaceous extracellular matrix
10	13.11	NULL	553	Cancer	Lembcke_Colonic Inflammation
11	12.93	NULL	16	MMML CGS	MACIEJ_MMML 1
12	12.41	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
13	12.27	NULL	57	MF	extracellular matrix structural constituent
14	12.18	NULL	403	BP	cell adhesion
15	11.62	NULL	83	CC	basement membrane
16	11.36	NULL	42	BP	keratinization
17	10.9	NULL	21	CC	cornified envelope
18	10.76	NULL	76	BP	epidermis development
19	10.66	NULL	1146	TF	HEBENSTREIT_low expression TF
20	10.5	NULL	572	Disease	GUDJ_psoriasis up

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−9.77	NULL	1135	Chr	Chr 19
2	−9.35	NULL	4640	CC	nucleus
3	−7.79	NULL	649	BP	gene expression
4	−7.64	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
5	−7.54	NULL	1574	BP	transcription, DNA−templated
6	−7.47	NULL	253	BP	translation
7	−7.33	NULL	949	CC	nucleoplasm
8	−7.06	NULL	153	MF	structural constituent of ribosome
9	−7.06	NULL	1318	CC	mitochondrion
10	−7.05	NULL	242	BP	RNA metabolic process
11	−7.05	NULL	92	BP	translational elongation
12	−7.02	NULL	81	BP	viral transcription
13	−7.01	NULL	128	BP	translational initiation
14	−6.96	NULL	595	MF	RNA binding
15	−6.86	NULL	219	BP	mRNA metabolic process
16	−6.85	NULL	87	BP	translational termination
17	−6.67	NULL	92	BP	viral life cycle
18	−6.49	NULL	167	CC	ribosome
19	−6.48	NULL	1749	MF	DNA binding
20	−6.47	NULL	940	MF	nucleic acid binding



p−values

GW_051

Local Summary

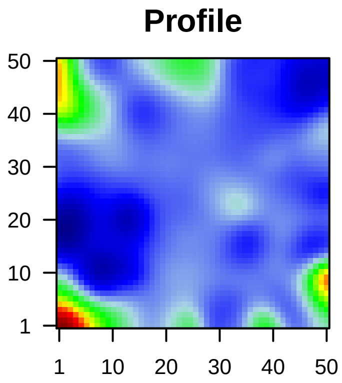
%DE = 0.92
metagenes = 16
genes = 258
genes in genesets = 257

genes with fdr < 0.1 = 221 (212 + / 9 −)
genes with fdr < 0.05 = 203 (197 + / 6 −)
genes with fdr < 0.01 = 187 (182 + / 5 −)

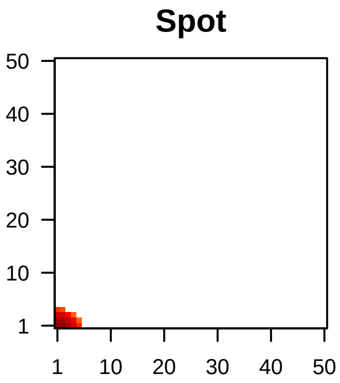
<r> metagenes = 0.96
<r> genes = 0.4

<FC> = 0.61
<shrinkage−t> = 21.3
<p−value> = 0
<fdr> = 0.25

Profile



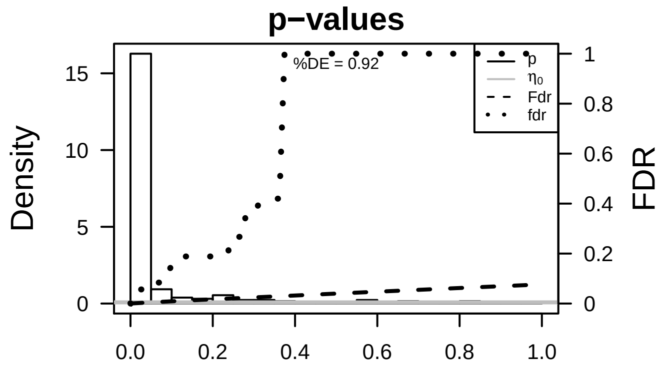
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1306	1.24	2e−16	2e−16	4 x 1	collagen, type XV, alpha 1 [Source:HGNC Symbol;Acc:2192]
2	1277	1.5	2e−16	2e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	1.45	2e−16	2e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	1.49	2e−16	2e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1289	1.51	2e−16	2e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1290	1.39	2e−16	2e−16	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1293	1.35	2e−16	2e−16	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	1464	1.37	2e−16	2e−16	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
9	84624	1.41	2e−16	2e−16	3 x 1	fibronectin type III domain containing 1 [Source:HGNC Symb
10	4060	1.53	2e−16	2e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
11	55384	1.2	2e−16	2e−16	4 x 1	maternally expressed 3 (non−protein coding) [Source:HGNC
12	4312	2.23	2e−16	2e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
13	4319	1.75	2e−16	2e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
14	4322	1.83	2e−16	2e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
15	4314	1.37	2e−16	2e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
16	4316	1.63	2e−16	2e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
17	55714	1.27	2e−16	2e−16	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
18	10631	1.48	2e−16	2e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
19	112464	1.26	2e−16	2e−16	1 x 1	protein kinase C, delta binding protein [Source:HGNC Symbo
20	12	2.36	2e−16	2e−16	1 x 1	

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	41.83	NULL	62 / 190	CC	extracellular matrix
2	38.26	NULL	30 / 69	BP	extracellular matrix disassembly
3	37.89	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
4	37.14	NULL	27 / 64	BP	collagen catabolic process
5	34.82	NULL	71 / 250	Lymphoma	LENZ_Stromal signature 1
6	34.74	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	34.41	NULL	65 / 242	BP	extracellular matrix organization
8	31.98	NULL	8 / 11	MF	platelet−derived growth factor binding
9	27.9	NULL	8 / 12	miRNA target	miR−29c
10	24.72	NULL	19 / 57	MF	extracellular matrix structural constituent
11	24.41	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
12	24.34	NULL	14 / 37	BP	collagen fibril organization
13	24.15	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	23.86	NULL	35 / 183	CC	proteinaceous extracellular matrix
15	21.05	NULL	76 / 683	CC	extracellular space
16	20.12	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
17	20.07	NULL	12 / 40	BP	cellular response to amino acid stimulus
18	19.98	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
19	19.68	NULL	102 / 1182	CC	extracellular region
20	19.63	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
21	19.6	NULL	11 / 19	MF	extracellular matrix binding
22	19.52	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
23	18.77	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
24	18.31	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
25	18.31	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
26	17.74	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
27	17.56	NULL	17 / 68	CC	collagen
28	17.22	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
29	16.88	NULL	61 / 553	Cancer	Lembcke_Colonic Inflammation
30	16.87	NULL	21 / 83	CC	basement membrane
31	16.48	NULL	5 / 11	BP	dermatan sulfate biosynthetic process
32	16.4	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
33	16.21	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
34	16.04	NULL	4 / 10	BP	protein heterotrimerization
35	15.95	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
36	15.95	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
37	15.95	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
38	15.95	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
39	15.87	NULL	17 / 85	MF	integrin binding
40	15.68	NULL	4 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP

GW_051

Local Summary

%DE = 0.63

metagenes = 99

genes = 827

genes in genesets = 816

genes with fdr < 0.1 = 247 (8 + / 239 −)

genes with fdr < 0.05 = 155 (8 + / 147 −)

genes with fdr < 0.01 = 63 (2 + / 61 −)

<r> metagenes = 0.81

<r> genes = 0.22

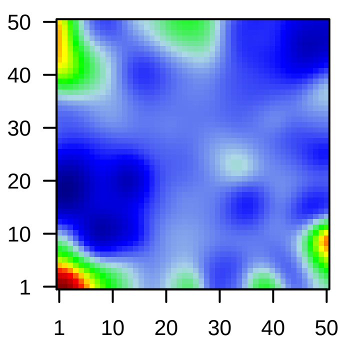
<FC> = −0.21

<shrinkage−t> = −7.41

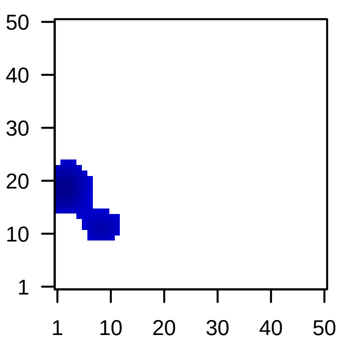
<p−value> = 0.05

<fdr> = 0.75

Profile



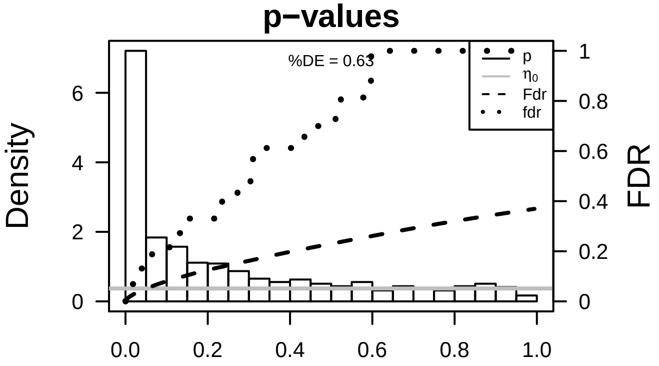
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131076	1.23	2e−16	3e−14	1 x 16	coiled−coil domain containing 58 [Source:HGNC Symbol;Acc
2	2026	−1.22	2e−16	3e−14	10 x 10	enolase 2 (gamma, neuronal) [Source:HGNC Symbol;Acc:33
3	389541	−1.06	2e−13	8e−11	3 x 19	late endosomal/lysosomal adaptor, MAPK and MTOR activat
4	2288	−1.05	5e−13	5e−07	1 x 19	FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:
5	55653	−0.87	2e−09	5e−06	9 x 10	breast carcinoma amplified sequence 4 [Source:HGNC Symb
6	219927	−0.82	2e−08	1e−05	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;
7	2597	−0.72	7e−08	1e−05	2 x 17	glyceraldehyde−3−phosphate dehydrogenase [Source:HGNC
8	25894	−0.77	1e−07	4e−05	12 x 11	pleckstrin homology domain containing, family G (with RhoGe
9	30968	−0.75	2e−07	4e−04	2 x 20	stomatin (EPB72)−like 2 [Source:HGNC Symbol;Acc:14559]
10	57176	−0.7	2e−06	7e−04	9 x 11	Valine−−tRNA ligase, mitochondrial [Source:UniProtKB/TrEM
11	23338	−0.67	4e−06	7e−04	10 x 12	jade family PHD finger 2 [Source:HGNC Symbol;Acc:22984]
12	2194	−0.65	7e−06	7e−04	1 x 17	fatty acid synthase [Source:HGNC Symbol;Acc:3594]
13	10428	−0.64	1e−05	7e−04	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
14	8570	−0.63	1e−05	7e−04	2 x 19	KH−type splicing regulatory protein [Source:HGNC Symbol;A
15	51367	−0.63	1e−05	2e−03	1 x 17	processing of precursor 5, ribonuclease P/MRP subunit (S. ce
16	6499	−0.61	2e−05	2e−03	7 x 11	superkiller viralicidic activity 2−like (S. cerevisiae) [Source:HG
17	112724	−0.6	3e−05	2e−03	1 x 23	retinol dehydrogenase 13 (all−trans/9−cis) [Source:HGNC Sy
18	83715	−0.59	4e−05	2e−03	2 x 22	espin [Source:HGNC Symbol;Acc:13281]
19	51181	−0.59	4e−05	2e−03	2 x 21	dicarbonyl/L−xylulose reductase [Source:HGNC Symbol;Acc:
20	79081	−0.59	5e−05	2e−03	2 x 19	chromosome 11 open reading frame 48 [Source:HGNC Symb

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−11.48	NULL	4 / 13	GSEA C2	REACTOME_GLYCOLYSIS
2	−11.2	NULL	6 / 16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
3	−9.6	NULL	5 / 10	MF	NADH dehydrogenase activity
4	−9.51	NULL	3 / 15	GSEA C2	REACTOME_GLUCONEOGENESIS
5	−9.01	NULL	5 / 9	GSEA C2	MOREIRA_RESPONSE_TO_TSA_UP
6	−7.82	NULL	3 / 14	GSEA C2	TOMIDA_METASTASIS_DN
7	−7.73	NULL	3 / 9	GSEA C2	BIOCARTA_GLYCOLYSIS_PATHWAY
8	−7.32	NULL	130 / 1318	CC	mitochondrion
9	−7.18	NULL	38 / 253	BP	translation
10	−7.09	NULL	5 / 16	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP
11	−7.08	NULL	2 / 5	GSEA C2	REACTOME_ELECTRON_TRANSPORT_CHAIN
12	−7.08	NULL	5 / 39	BP	glycolysis
13	−6.97	NULL	15 / 83	BP	respiratory electron transport chain
14	−6.9	NULL	89 / 717	Chr	Chr 16
15	−6.89	NULL	28 / 153	MF	structural constituent of ribosome
16	−6.74	NULL	28 / 167	CC	ribosome
17	−6.73	NULL	112 / 1135	Chr	Chr 19
18	−6.7	NULL	4 / 10	MF	oxidoreductase activity, acting on NAD(P)H
19	−6.6	NULL	4 / 13	GSEA C2	MOOTHA_VOXPHOS
20	−6.58	NULL	6 / 15	GSEA C2	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
21	−6.48	NULL	3 / 13	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
22	−6.46	NULL	13 / 64	BP	tRNA processing
23	−6.45	NULL	39 / 304	CC	mitochondrial inner membrane
24	−6.4	NULL	4 / 39	BP	gluconeogenesis
25	−6.4	NULL	2 / 6	GSEA C2	KORKOLA_CHORIOCARCINOMA_UP
26	−6.4	NULL	2 / 15	GSEA C2	MOOTHA_GLYCOLYSIS
27	−6.24	NULL	13 / 93	miRNA target	hsa−miR−125a−5p
28	−6.22	NULL	2 / 5	GSEA C2	GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
29	−6.15	NULL	2 / 16	GSEA C2	MOOTHA_GLUCONEOGENESIS
30	−6.11	NULL	4 / 16	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
31	−6.01	NULL	11 / 37	CC	mitochondrial nucleoid
32	−5.95	NULL	8 / 34	MF	NADH dehydrogenase (ubiquinone) activity
33	−5.95	NULL	6 / 14	GSEA C2	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
34	−5.95	NULL	3 / 14	BP	mitochondrial ATP synthesis coupled proton transport
35	−5.85	NULL	20 / 96	BP	rRNA processing
36	−5.84	NULL	5 / 12	GSEA C2	CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
37	−5.78	NULL	20 / 152	BP	cellular metabolic process
38	−5.78	NULL	7 / 23	Chr	Chr HSCHR6_MHC_DBB
39	−5.73	NULL	8 / 36	CC	mitochondrial respiratory chain complex I
40	−5.73	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D

GW_051

Local Summary

%DE = 0.66

metagenes = 21

genes = 229

genes in genesets = 223

genes with fdr < 0.1 = 69 (1 + / 68 −)

genes with fdr < 0.05 = 48 (1 + / 47 −)

genes with fdr < 0.01 = 17 (0 + / 17 −)

<r> metagenes = 0.94

<r> genes = 0.23

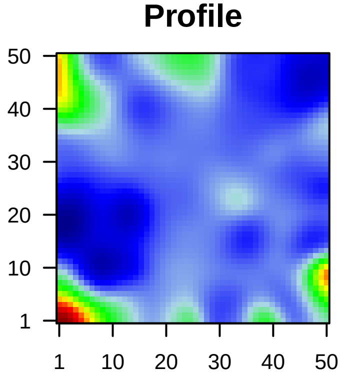
<FC> = −0.23

<shrinkage−t> = −8.03

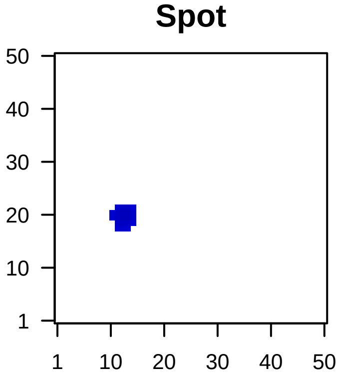
<p−value> = 0.05

<fdr> = 0.74

Profile



Spot



Local Genelist

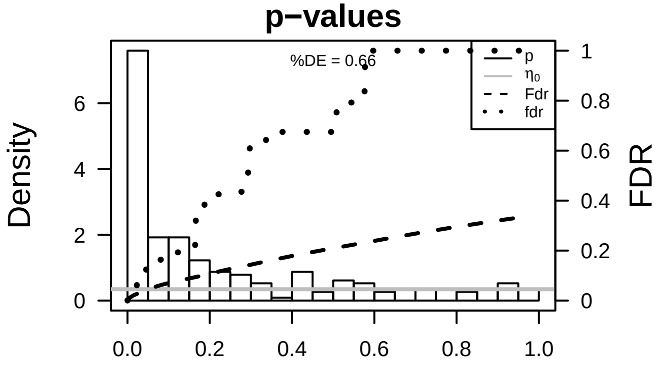
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10591	−0.92	2e−10	5e−05	13 x 20	2'−deoxynucleoside 5'−phosphate N−hydrolase 1 [Source:HG
2	644928	−0.72	6e−07	2e−04	14 x 21	
3	51647	−0.67	4e−06	2e−04	14 x 22	family with sequence similarity 96, member B [Source:HGNC
4	400156	−0.66	5e−06	1e−03	14 x 21	
5	10217	−0.62	2e−05	2e−03	15 x 21	CTD (carboxy−terminal domain, RNA polymerase II, polypept
6	8673	−0.58	6e−05	2e−03	14 x 21	vesicle−associated membrane protein 8 [Source:HGNC Syml
7	10007	−0.56	1e−04	2e−03	13 x 19	glucosamine−6−phosphate deaminase 1 [Source:HGNC Sym
8	54949	−0.56	1e−04	2e−03	14 x 21	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F5
9	286101	−0.56	1e−04	5e−03	13 x 19	zinc finger protein 252, pseudogene [Source:HGNC Symbol;
10	3615	−0.53	3e−04	5e−03	14 x 22	IMP (inosine 5'−monophosphate) dehydrogenase 2 [Source:
11	738	−0.52	3e−04	5e−03	14 x 20	vacuolar protein sorting 51 homolog (S. cerevisiae) [Source:
12	51255	−0.52	3e−04	5e−03	14 x 21	ring finger protein 181 [Source:HGNC Symbol;Acc:28037]
13	27335	−0.51	4e−04	5e−03	13 x 20	eukaryotic translation initiation factor 3, subunit K [Source:HG
14	9296	−0.51	5e−04	5e−03	14 x 21	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F [So
15	60386	−0.5	5e−04	5e−03	13 x 20	solute carrier family 25 (mitochondrial thiamine pyrophosphat
16	285367	−0.5	6e−04	1e−02	14 x 22	RNA pseudouridylate synthase domain containing 3 [Source:
17	51307	−0.49	7e−04	1e−02	15 x 19	family with sequence similarity 53, member C [Source:HGNC
18	5438	−0.49	8e−04	1e−02	13 x 20	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa [
19	7311	−0.48	1e−03	1e−02	13 x 19	ubiquitin A−52 residue ribosomal protein fusion product 1 [So
20	54930	−0.47	1e−03	1e−02	13 x 20	HAUS augmin−like complex, subunit 4 [Source:HGNC Symbo

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.78	NULL	1 / 4	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G5_UP
2	−10.58	NULL	4 / 13	GSEA C2	CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
3	−10.15	NULL	3 / 15	GSEA C2	REACTOME_MRNA_SPLICING_MINOR_PATHWAY
4	−9.6	NULL	3 / 9	GSEA C2	KEGG_RNA_POLYMERASE
5	−9.19	NULL	3 / 12	GSEA C2	REACTOME_NUCLEOTIDE_EXCISION_REPAIR
6	−9.08	NULL	2 / 9	GSEA C2	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_CO
7	−9.08	NULL	2 / 9	GSEA C2	REACTOME_HIV1_TRANSCRIPTION_ELONGATION
8	−8.58	NULL	2 / 10	GSEA C2	REACTOME_DUAL_INCISION_REACTION_IN_TC_NER
9	−8.58	NULL	2 / 10	GSEA C2	REACTOME_HIV1_TRANSCRIPTION_INITIATION
10	−8.58	NULL	2 / 10	GSEA C2	REACTOME_MRNA_PROCESSING
11	−8.58	NULL	2 / 10	GSEA C2	REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_IN
12	−8.15	NULL	2 / 11	GSEA C2	REACTOME_TRANSCRIPTION_COUPLED_NER
13	−7.77	NULL	2 / 12	GSEA C2	KEGG_PYRIMIDINE_METABOLISM
14	−7.77	NULL	2 / 12	GSEA C2	REACTOME_ABORTIVE_ELONGATION_OF_HIV1_TRANSCRIP
15	−7.69	NULL	1 / 12	BP	nucleotide metabolic process
16	−7.44	NULL	2 / 13	GSEA C2	REACTOME_TAT_MEDIATED_HIV1_ELONGATION_ARREST_AN
17	−7.38	NULL	46 / 1233	TF	KIM_MYC targets
18	−7.27	NULL	55 / 1318	CC	mitochondrion
19	−7.22	NULL	2 / 13	CC	eukaryotic 48S preinitiation complex
20	−7.21	NULL	2 / 12	GSEA C2	REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED_
21	−7.14	NULL	2 / 14	GSEA C2	REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS
22	−7.1	NULL	5 / 38	MF	DNA−directed RNA polymerase activity
23	−6.93	NULL	2 / 14	CC	eukaryotic 43S preinitiation complex
24	−6.93	NULL	2 / 14	BP	formation of translation preinitiation complex
25	−6.9	NULL	2 / 13	GSEA C2	REACTOME_FORMATION_AND_MATURATION_OF_MRNA_TRA
26	−6.87	NULL	2 / 15	CC	DNA−directed RNA polymerase II, core complex
27	−6.7	NULL	40 / 1135	Chr	Chr 19
28	−6.67	NULL	2 / 15	CC	eukaryotic translation initiation factor 3 complex
29	−6.63	NULL	2 / 16	GSEA C2	REACTOME_MICRORNA_BIOGENESIS
30	−6.62	NULL	8 / 128	BP	translational initiation
31	−6.62	NULL	2 / 14	GSEA C2	REACTOME_MRNA_SPLICING
32	−6.62	NULL	2 / 14	GSEA C2	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAININ
33	−6.56	NULL	1 / 16	BP	nucleoside metabolic process
34	−6.52	NULL	3 / 10	MF	NADH dehydrogenase activity
35	−6.52	NULL	3 / 25	MF	hydrogen ion transmembrane transporter activity
36	−6.47	NULL	2 / 12	BP	viral protein processing
37	−6.21	NULL	3 / 16	GSEA C2	GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN
38	−6.19	NULL	2 / 13	BP	virion assembly
39	−6.16	NULL	2 / 12	GSEA C2	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AN
40	−6.16	NULL	2 / 12	GSEA C2	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATI

p−values



GW_051

Local Summary

%DE = 0.68

metagenes = 35

genes = 380

genes in genesets = 378

genes with fdr < 0.1 = 118 (12 + / 106 −)

genes with fdr < 0.05 = 106 (11 + / 95 −)

genes with fdr < 0.01 = 37 (6 + / 31 −)

<r> metagenes = 0.91

<r> genes = 0.23

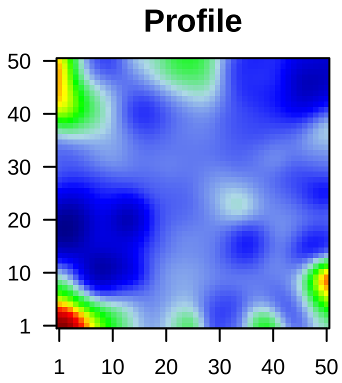
<FC> = −0.19

<shrinkage−t> = −6.71

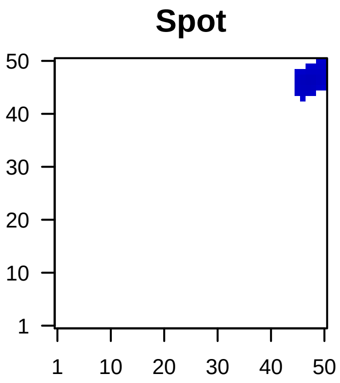
<p−value> = 0.04

<fdr> = 0.73

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2944	−1.34	2e−16	3e−14	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
2	139728	−1.1	3e−14	4e−11	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:I
3	256764	1.05	4e−13	5e−10	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
4	1056	−1	4e−12	2e−08	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
5	339512	−0.91	3e−10	2e−08	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
6	2946	−0.91	3e−10	3e−07	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
7	8492	0.86	3e−09	2e−06	50 x 47	protease, serine, 12 (neurotrypsin, motopsin) [Source:HGNC
8	5050	−0.82	2e−08	4e−06	47 x 45	platelet−activating factor acetylhydrolase 1b, catalytic subunit
9	445	0.79	5e−08	1e−05	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
10	4922	−0.76	1e−07	8e−05	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
11	26227	−0.71	8e−07	8e−05	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
12	116028	−0.7	1e−06	1e−04	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
13	3880	−0.68	3e−06	1e−04	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
14	253782	−0.67	3e−06	7e−04	50 x 47	ceramide synthase 6 [Source:HGNC Symbol;Acc:23826]
15	25804	−0.64	9e−06	1e−03	47 x 47	LSM4 homolog, U6 small nuclear RNA associated (S. cerevis
16	5625	−0.61	2e−05	1e−03	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
17	54578	−0.6	3e−05	1e−03	50 x 50	UDP glucuronosyltransferase 1 family, polypeptide A6 [Sourc
18	7345	−0.59	5e−05	1e−03	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
19	8364	−0.54	5e−05	1e−03	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
20	8317	−0.58	7e−05	1e−03	45 x 47	cell division cycle 7 [Source:HGNC Symbol;Acc:1745]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−13.84	NULL	3 / 11	MF	glutathione binding
2	−13.84	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
3	−13.7	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
4	−12.82	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
5	−12.5	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
6	−12.28	NULL	29 / 149	BP	DNA replication
7	−11.81	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
8	−11.5	NULL	8 / 15	GSEA C2	KEGG_DNA_REPLICATION
9	−11.26	NULL	6 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
10	−11.12	NULL	11 / 30	BP	DNA strand elongation involved in DNA replication
11	−10.9	NULL	5 / 20	MF	glutathione transferase activity
12	−10.76	NULL	6 / 11	GSEA C2	KALMA_E2F1_TARGETS
13	−10.68	NULL	4 / 7	GSEA C2	REACTOME_G1_S_TRANSITION
14	−10.51	NULL	6 / 25	BP	glutathione derivative biosynthetic process
15	−9.79	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
16	−9.74	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
17	−9.38	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
18	−9.32	NULL	5 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
19	−9.2	NULL	6 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
20	−9.13	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
21	−8.93	NULL	8 / 34	BP	glutathione metabolic process
22	−8.93	NULL	7 / 16	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_UP
23	−8.93	NULL	6 / 16	GSEA C2	BIOCARTA_MCM_PATHWAY
24	−8.81	NULL	4 / 13	BP	regulation of blood vessel size
25	−8.61	NULL	7 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
26	−8.48	NULL	6 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
27	−8.46	NULL	4 / 9	miRNA target	miR−24
28	−8.35	NULL	2 / 14	MF	calmodulin−dependent protein kinase activity
29	−8.18	NULL	6 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
30	−8.16	NULL	2 / 11	GSEA C2	BROWNE_HCMV_INFECTION_10HR_UP
31	−8.02	NULL	3 / 15	GSEA C2	REACTOME_PHASE_II_CONJUGATION
32	−7.98	NULL	8 / 24	BP	telomere maintenance via recombination
33	−7.97	NULL	4 / 12	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
34	−7.96	NULL	5 / 16	GSEA C2	KEGG_BASE_EXCISION_REPAIR
35	−7.95	NULL	2 / 16	GSEA C2	GRADE_METASTASIS_DN
36	−7.95	NULL	2 / 16	GSEA C2	ZHANG_PROLIFERATING_VS_QUIESCENT
37	−7.92	NULL	39 / 370	BP	mitotic cell cycle
38	−7.85	NULL	7 / 21	BP	telomere maintenance via semi−conservative replication
39	−7.53	NULL	7 / 22	BP	DNA replication initiation
40	−7.34	NULL	7 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN

p−values