GW_160

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1965 (1000 + / 965 −)

genes with fdr < 0.1 = 1565 (769 + / 796 −)

genes with fdr < 0.05 = 1390 (681 + / 709 −)

genes with fdr < 0.01 = 937 (442 + / 495 −)

genes in genesets = 16332

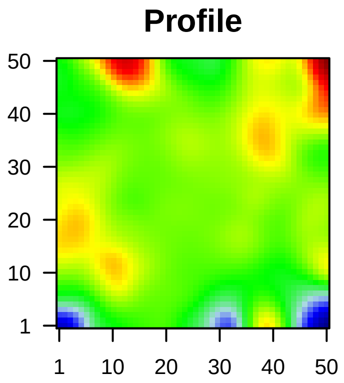
<FC> = 0

<shrinkage−t> = 0

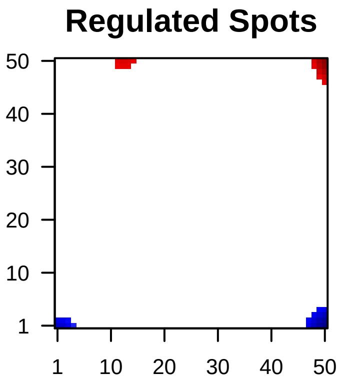
<p−value> = 0.1

<fdr> = 0.85

Profile



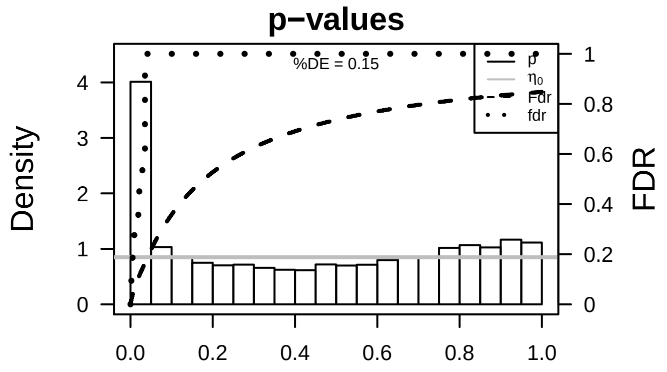
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10551	2.55	2e−16	5e−14	50 x 10	anterior gradient 2 [Source:HGNC Symbol;Acc:328]
2	8644	2.68	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
3	1109	2.62	2e−16	5e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
4	216	1.82	2e−16	5e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
5	218	2.76	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	92747	3.18	2e−16	5e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
7	760	−1.81	2e−16	5e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
8	26256	1.82	2e−16	5e−14	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
9	6347	−1.97	2e−16	5e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
10	414062	−2.13	2e−16	5e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
11	1066	2.34	2e−16	5e−14	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
12	9073	1.89	2e−16	5e−14	8 x 50	claudin 8 [Source:HGNC Symbol;Acc:2050]
13	1308	−2.09	2e−16	5e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
14	1277	−2.29	2e−16	5e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
15	1278	−2.12	2e−16	5e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
16	1281	−1.84	2e−16	5e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
17	1289	−2.04	2e−16	5e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
18	1290	−1.83	2e−16	5e−14	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
19	1293	−1.95	2e−16	5e−14	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
20	49860	−2.38	2e−16	5e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]

p−values



Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	11.72	NULL	743	Chr	Chr 7
2	9.27	NULL	918	Chr	Chr 17
3	8.1	NULL	866	Chr	Chr 12
4	6.86	NULL	16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
5	6.53	NULL	534	Chr	Chr 8
6	6.31	NULL	34	BP	glutathione metabolic process
7	6.26	NULL	25	BP	glutathione derivative biosynthetic process
8	5.45	NULL	19	BP	cellular amino acid biosynthetic process
9	5.41	NULL	119	BP	xenobiotic metabolic process
10	5.39	NULL	1253	BP	small molecule metabolic process
11	5.22	NULL	1318	CC	mitochondrion
12	5.2	NULL	20	MF	glutathione transferase activity
13	5.17	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
14	5.04	NULL	20	TF	MYC_Metabolism UP
15	5.02	NULL	15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
16	5.01	NULL	434	BP	oxidation−reduction process
17	4.85	NULL	16	GSEA C2	KORKOLA_SEMINOMA_UP
18	4.81	NULL	15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
19	4.8	NULL	15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
20	4.76	NULL	12	BP	cellular aldehyde metabolic process

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−21.37	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−18.02	NULL	312	BP	immune response
3	−16.73	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	−16.36	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	−16.36	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	−16.36	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	−16.36	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	−14.57	NULL	572	Disease	GUDJ_psoriasis up
9	−13.71	NULL	417	H.Tiss	WIRTH_Immune system
10	−12.85	NULL	190	CC	extracellular matrix
11	−12.82	NULL	316	Cancer	SPANG_BCL6−index2
12	−12.49	NULL	51	BP	type I interferon signaling pathway
13	−12.32	NULL	1182	CC	extracellular region
14	−12.24	NULL	69	BP	extracellular matrix disassembly
15	−12.15	NULL	60	BP	interferon−gamma−mediated signaling pathway
16	−12.14	NULL	618	Chr	Chr 4
17	−12.04	NULL	683	CC	extracellular space
18	−11.97	NULL	204	BP	cytokine−mediated signaling pathway
19	−11.73	NULL	64	BP	collagen catabolic process
20	−11.52	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE

GW_160

Local Summary

%DE = 0.89

metagenes = 11

genes = 182

genes in genesets = 181

genes with fdr < 0.1 = 137 (134 + / 3 −)

genes with fdr < 0.05 = 121 (120 + / 1 −)

genes with fdr < 0.01 = 104 (103 + / 1 −)

<r> metagenes = 0.98

<r> genes = 0.28

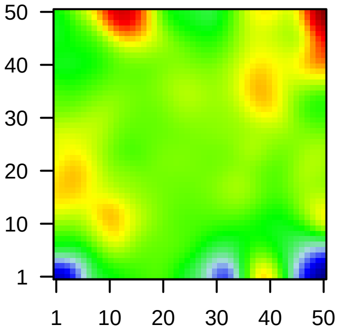
<FC> = 0.78

<shrinkage−t> = 27.19

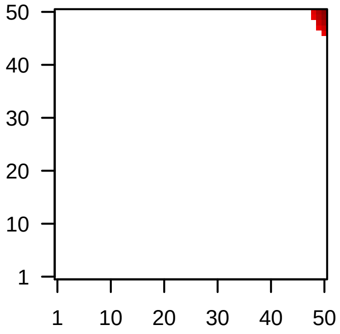
<p−value> = 0

<fdr> = 0.36

Profile



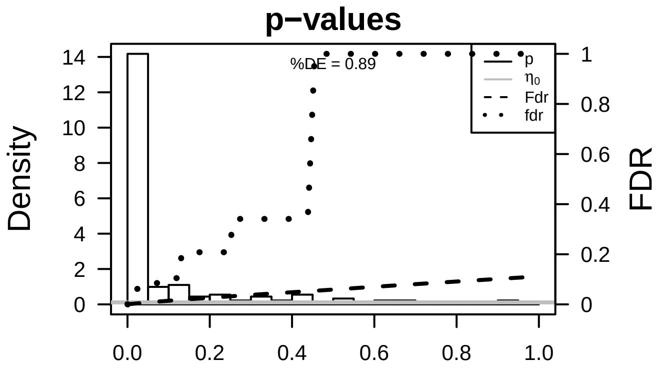
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	1.82	2e−16	6e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	26256	1.82	2e−16	6e−16	50 x 50	calcium binding tyrosine−(Y)−phosphorylation regulated [Sou
3	4072	2.5	2e−16	6e−16	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
4	2719	2.16	2e−16	6e−16	50 x 50	glypican 3 [Source:HGNC Symbol;Acc:4451]
5	2938	1.82	2e−16	6e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
6	3866	1.92	2e−16	6e−16	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
7	7345	2	2e−16	6e−16	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
8	79844	1.86	2e−16	6e−16	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
9	339512	1.74	3e−15	2e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
10	5625	1.74	3e−15	2e−14	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
11	79679	1.74	3e−15	2e−14	50 x 50	V−set domain containing T cell activation inhibitor 1 [Source:
12	2946	1.73	4e−15	3e−14	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
13	3880	1.72	6e−15	3e−14	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
14	214	1.72	6e−15	2e−12	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC S
15	7546	1.64	1e−13	2e−12	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
16	56963	1.62	2e−13	2e−12	50 x 50	repulsive guidance molecule family member a [Source:HGNC
17	10057	1.61	3e−13	2e−12	50 x 50	ATP−binding cassette, sub−family C (CFTR/MRP), member 5
18	400916	1.6	3e−13	4e−12	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [Sou
19	1780	1.59	5e−13	8e−12	50 x 50	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
20	352954	1.57	9e−13	9e−12	50 x 46	

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset
1	16.69	NULL	3 / 8	GSEA C2 LIU_CDX2_TARGETS_DN
2	16.55	NULL	5 / 15	GSEA C2 KEGG_GLUTATHIONE_METABOLISM
3	15.24	NULL	6 / 25	BP glutathione derivative biosynthetic process
4	15.11	NULL	8 / 34	BP glutathione metabolic process
5	13.99	NULL	4 / 15	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_E
6	13.77	NULL	4 / 13	GSEA C2 KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
7	13.37	NULL	3 / 11	GSEA C2 ITO_PTTG1_TARGETS_UP
8	13.21	NULL	5 / 20	MF glutathione transferase activity
9	12.68	NULL	3 / 9	GSEA C2 REACTOME_METABOLISM_OF_AMINO_ACIDS
10	12.63	NULL	1 / 4	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
11	12.44	NULL	3 / 11	MF glutathione binding
12	12.44	NULL	3 / 11	GSEA C2 KEGG_DRUG_METABOLISM_CYTOCHROME_P450
13	11.71	NULL	11 / 119	BP xenobiotic metabolic process
14	11.29	NULL	2 / 7	GSEA C2 FREDERICK_PRKCI_TARGETS
15	10.6	NULL	1 / 2	miRNA target miR−127
16	10.52	NULL	4 / 13	BP regulation of blood vessel size
17	10.21	NULL	2 / 6	GSEA C2 GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
18	9.27	NULL	2 / 11	GSEA C2 SMID_BREAST_CANCER_BASAL_UP
19	9.05	NULL	4 / 15	GSEA C2 REACTOME_GLUTATHIONE_CONJUGATION
20	8.8	NULL	1 / 5	GSEA C2 TURASHVILI_BREAST_CARCINOMA_DUCTAL_VS_LOBULAR_
21	8.78	NULL	3 / 19	BP cellular amino acid biosynthetic process
22	8.7	NULL	3 / 16	GSEA C2 KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
23	8.25	NULL	2 / 12	GSEA C2 KAYO_AGING_MUSCLE_UP
24	8.24	NULL	1 / 6	GSEA C2 KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
25	8.17	NULL	2 / 11	GSEA C2 SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANC
26	7.86	NULL	2 / 13	GSEA C2 BLUM_RESPONSE_TO_SALIRASIB_UP
27	7.81	NULL	2 / 6	GSEA C2 MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7
28	7.66	NULL	2 / 12	GSEA C2 LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN
29	7.64	NULL	3 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
30	7.63	NULL	1 / 8	GSEA C2 MUNSHI_MULTIPLE_MYELOMA_DN
31	7.57	NULL	2 / 14	CC membrane−bounded vesicle
32	7.53	NULL	2 / 9	GSEA C2 REACTOME_GLUCURONIDATION
33	7.48	NULL	3 / 12	GSEA C2 HELLER_SILENCED_BY_METHYLATION_DN
34	7.47	NULL	4 / 32	BP glycosaminoglycan biosynthetic process
35	7.34	NULL	2 / 12	GSEA C2 ONDER_CDH1_TARGETS_1_UP
36	7.29	NULL	3 / 14	GSEA C2 VANTVEER_BREAST_CANCER_METASTASIS_DN
37	7.28	NULL	2 / 16	GSEA C2 VANTVEER_BREAST_CANCER_ESR1_DN
38	7.28	NULL	2 / 16	GSEA C2 SESTO_RESPONSE_TO_UV_C7
39	7.27	NULL	2 / 16	GSEA C2 MAHADEVAN_RESPONSE_TO_MP470_UP
40	7.23	NULL	2 / 12	BP cellular aldehyde metabolic process

GW_160

Local Summary

%DE = 0.72

metagenes = 7

genes = 111

genes in genesets = 110

genes with fdr < 0.1 = 64 (62 + / 2 −)

genes with fdr < 0.05 = 52 (50 + / 2 −)

genes with fdr < 0.01 = 48 (46 + / 2 −)

<r> metagenes = 0.99

<r> genes = 0.28

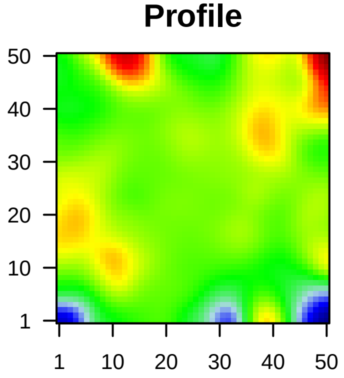
<FC> = 0.64

<shrinkage−t> = 22.45

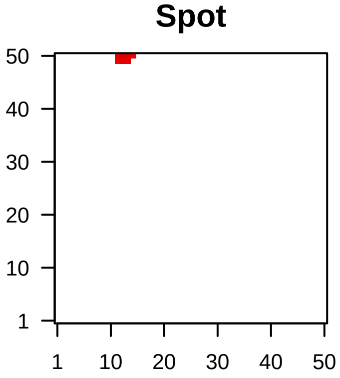
<p−value> = 0

<fdr> = 0.46

Profile



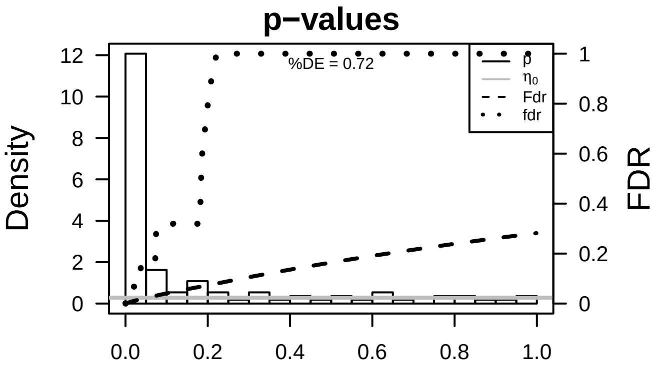
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1109	2.62	2e−16	2e−15	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
2	1066	2.34	2e−16	2e−15	14 x 50	carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
3	57834	1.86	2e−16	2e−15	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
4	10457	1.71	8e−15	1e−12	13 x 50	glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
5	63928	1.67	4e−14	5e−12	13 x 50	calcineurin−like EF−hand protein 2 [Source:HGNC Symbol;A
6	1749	1.61	3e−13	5e−12	13 x 50	distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918]
7	1646	1.6	4e−13	8e−10	13 x 50	aldo−keto reductase family 1, member C2 [Source:HGNC Sy
8	55065	1.45	5e−11	8e−10	14 x 50	solute carrier family 52 (riboflavin transporter), member 1 [So
9	7062	1.45	5e−11	6e−09	13 x 50	trichohyalin [Source:HGNC Symbol;Acc:11791]
10	7296	1.4	2e−10	2e−08	14 x 50	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:12437]
11	140809	1.35	8e−10	2e−07	13 x 50	sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
12	2736	1.24	2e−08	2e−07	14 x 50	GLI family zinc finger 2 [Source:HGNC Symbol;Acc:4318]
13	23108	1.24	2e−08	2e−07	15 x 50	RAP1 GTPase activating protein 2 [Source:HGNC Symbol;Ac
14	2539	1.23	2e−08	7e−07	13 x 50	glucose−6−phosphate dehydrogenase [Source:HGNC Symbo
15	4147	1.19	7e−08	7e−07	15 x 50	matrilin 2 [Source:HGNC Symbol;Acc:6908]
16	1399	1.18	8e−08	7e−07	14 x 50	v−crk avian sarcoma virus CT10 oncogene homolog−like [So
17	51071	1.17	1e−07	7e−07	13 x 50	deoxyribose−phosphate aldolase (putative) [Source:HGNC S
18	7086	1.16	1e−07	7e−07	13 x 50	transketolase [Source:HGNC Symbol;Acc:11834]
19	2690	1.16	2e−07	7e−07	15 x 50	growth hormone receptor [Source:HGNC Symbol;Acc:4263]
20	29948	1.15	2e−07	7e−07	13 x 50	oxidative stress induced growth inhibitor 1 [Source:HGNC Sy

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.51	NULL	1 / 2	miRNA target	miR−124a
2	12.94	NULL	2 / 12	BP	head development
3	12.93	NULL	1 / 2	Cancer	GENTLES_modul8
4	12.59	NULL	3 / 13	GSEA C2	SINGH_NFE2L2_TARGETS
5	12.01	NULL	2 / 10	BP	response to food
6	11.84	NULL	1 / 12	BP	androgen metabolic process
7	11.55	NULL	3 / 19	BP	anatomical structure formation involved in morphogenesis
8	11.53	NULL	1 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
9	10.98	NULL	1 / 6	GSEA C2	ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS
10	10.98	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
11	10.81	NULL	1 / 14	BP	bile acid and bile salt transport
12	10.5	NULL	2 / 15	GSEA C2	KANG_FLUOROURACIL_RESISTANCE_UP
13	9.48	NULL	2 / 15	BP	pentose−phosphate shunt
14	9.37	NULL	3 / 32	MF	NADP binding
15	9.34	NULL	1 / 18	BP	bile acid biosynthetic process
16	9.15	NULL	2 / 44	BP	steroid metabolic process
17	9.14	NULL	3 / 51	BP	osteoblast differentiation
18	9.12	NULL	1 / 9	Glio	Colman_survival_robust
19	8.95	NULL	13 / 434	BP	oxidation−reduction process
20	8.86	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
21	8.64	NULL	2 / 12	BP	nitric oxide biosynthetic process
22	8.56	NULL	1 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
23	8.2	NULL	2 / 22	BP	response to axon injury
24	8.08	NULL	1 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
25	7.95	NULL	2 / 17	MF	proline−rich region binding
26	7.83	NULL	2 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_7
27	7.59	NULL	1 / 11	BP	ear development
28	7.59	NULL	1 / 11	GSEA C2	SU_PLACENTA
29	7.55	NULL	1 / 11	BP	prostaglandin metabolic process
30	7.5	NULL	4 / 63	MF	oxidoreductase activity, acting on paired donors, with incorporation
31	7.45	NULL	2 / 12	BP	positive regulation of protein import into nucleus
32	7.37	NULL	3 / 34	BP	glutathione metabolic process
33	7.31	NULL	1 / 13	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
34	7.02	NULL	1 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
35	6.86	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
36	6.85	NULL	2 / 15	GSEA C2	KEGG_PROPANOATE_METABOLISM
37	6.85	NULL	2 / 35	MF	monooxygenase activity
38	6.84	NULL	3 / 31	BP	positive regulation of actin filament polymerization
39	6.79	NULL	1 / 31	BP	bile acid metabolic process
40	6.73	NULL	2 / 15	BP	leukotriene metabolic process

GW_160

Local Summary

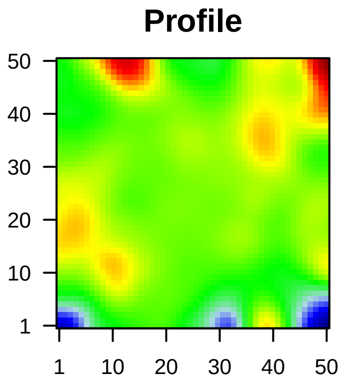
%DE = 0.94
metagenes = 7
genes = 141
genes in genesets = 141

genes with fdr < 0.1 = 131 (6 + / 125 −)
genes with fdr < 0.05 = 131 (6 + / 125 −)
genes with fdr < 0.01 = 124 (6 + / 118 −)

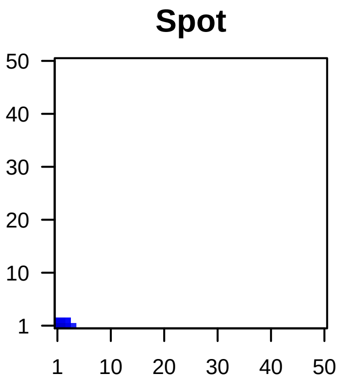
<r> metagenes = 0.99
<r> genes = 0.48

<FC> = −0.98
<shrinkage−t> = −34.41
<p−value> = 0
<fdr> = 0.15

Profile



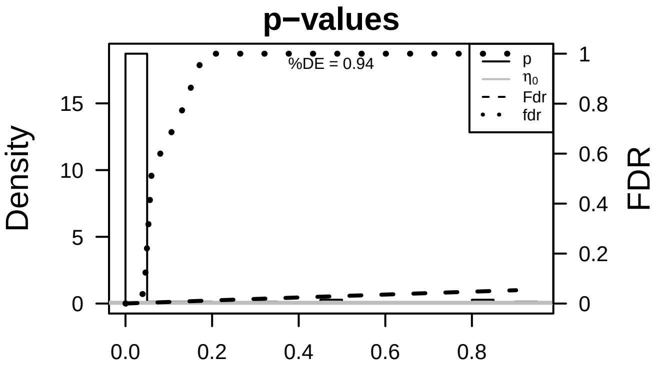
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	414062	−2.13	2e−16	9e−17	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
2	1277	−2.29	2e−16	9e−17	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	−2.12	2e−16	9e−17	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	−1.84	2e−16	9e−17	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1289	−2.04	2e−16	9e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1290	−1.83	2e−16	9e−17	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1293	−1.95	2e−16	9e−17	2 x 1	collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	3491	−1.87	2e−16	9e−17	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
9	3040	−2.05	2e−16	9e−17	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
10	3553	−2.37	2e−16	9e−17	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
11	3576	−2.13	2e−16	9e−17	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
12	3956	−2.02	2e−16	9e−17	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
13	4060	−2.05	2e−16	9e−17	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
14	4312	−2.11	2e−16	9e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
15	4314	−2.84	2e−16	9e−17	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
16	4316	−2.07	2e−16	9e−17	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
17	4318	−1.83	2e−16	9e−17	1 x 1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 9
18	6515	−2.23	2e−16	9e−17	3 x 1	solute carrier family 2 (facilitated glucose transporter), membe
19	7058	−1.91	2e−16	9e−17	2 x 1	thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
20	7431	−1.81	2e−16	9e−17	4 x 1	vimentin [Source:HGNC Symbol;Acc:12692]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−45.6	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
2	−42.26	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
3	−39.93	NULL	28 / 69	BP	extracellular matrix disassembly
4	−39.57	NULL	25 / 64	BP	collagen catabolic process
5	−38.23	NULL	7 / 11	MF	platelet−derived growth factor binding
6	−37.07	NULL	50 / 190	CC	extracellular matrix
7	−33.15	NULL	51 / 250	Lymphoma	LENZ_Stromal signature 1
8	−32.4	NULL	8 / 12	miRNA target	miR−29c
9	−29.79	NULL	49 / 242	BP	extracellular matrix organization
10	−29.04	NULL	10 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
11	−26.49	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
12	−25.91	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
13	−25.75	NULL	13 / 37	BP	collagen fibril organization
14	−24.66	NULL	18 / 57	MF	extracellular matrix structural constituent
15	−24.2	NULL	11 / 19	MF	extracellular matrix binding
16	−23.69	NULL	8 / 40	BP	cellular response to amino acid stimulus
17	−22.46	NULL	5 / 16	GSEA C2	URS_ADIPOCYTE_DIFFERENTIATION_DN
18	−22.06	NULL	4 / 10	BP	protein heterotrimerization
19	−21.69	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
20	−21.34	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
21	−20.54	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
22	−20.28	NULL	6 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
23	−20.18	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
24	−20.18	NULL	5 / 16	GSEA C2	REACTOME_SIGNALING_BY_PDGF
25	−20.15	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
26	−19.97	NULL	5 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
27	−19.88	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
28	−19.88	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
29	−19.51	NULL	4 / 12	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C2
30	−19.42	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
31	−19.24	NULL	20 / 119	Lymphoma	ROSOLOWSKI_green total
32	−18.87	NULL	26 / 183	CC	proteinaceous extracellular matrix
33	−18.76	NULL	5 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
34	−18.72	NULL	69 / 1182	CC	extracellular region
35	−18.21	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
36	−18.17	NULL	51 / 683	CC	extracellular space
37	−18	NULL	46 / 553	Cancer	Lembcke_Colonic Inflammation
38	−17.95	NULL	13 / 68	CC	collagen
39	−17.84	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
40	−17.8	NULL	4 / 12	GSEA C2	LY_AGING_MIDDLE_UP

GW_160

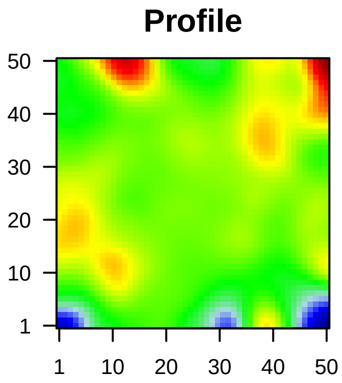
Local Summary

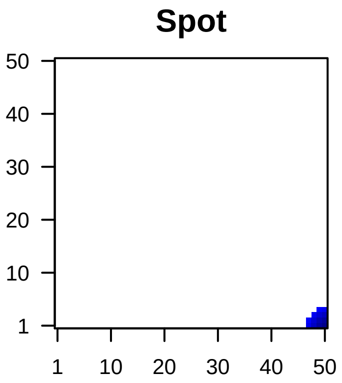
%DE = 0.97
metagenes = 13
genes = 245
genes in genesets = 243

genes with fdr < 0.1 = 224 (4 + / 220 −)
genes with fdr < 0.05 = 224 (4 + / 220 −)
genes with fdr < 0.01 = 210 (4 + / 206 −)

<r> metagenes = 0.99
<r> genes = 0.6

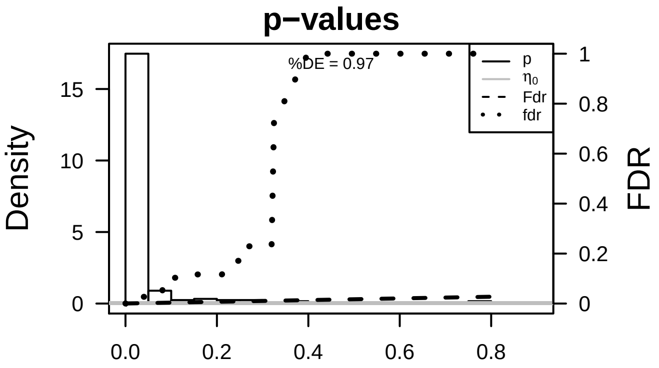
<FC> = −0.82
<shrinkage−t> = −28.76
<p−value> = 0
<fdr> = 0.22


Profile


Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6347	−1.97	2e−16	3e−16	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
2	3113	−1.85	2e−16	3e−16	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
3	3122	−1.98	2e−16	3e−16	50 x 1	major histocompatibility complex, class II, DR alpha [Source:H
4	3936	−2.07	2e−16	3e−16	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Sy
5	5341	−1.88	2e−16	3e−16	50 x 1	pleckstrin [Source:HGNC Symbol;Acc:9070]
6	5552	−1.97	2e−16	3e−16	50 x 1	serglycin [Source:HGNC Symbol;Acc:9361]
7	5880	−1.73	4e−15	6e−14	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small
8	3002	−1.7	1e−14	3e−13	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
9	4283	−1.66	6e−14	3e−13	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
10	5996	−1.64	9e−14	1e−12	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
11	3512	−1.61	2e−13	2e−12	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
12	260436	−1.58	7e−13	2e−12	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
13	23643	−1.58	8e−13	5e−11	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
14	3059	−1.5	1e−11	5e−11	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
15	10537	−1.49	1e−11	9e−11	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
16	23180	−1.47	3e−11	9e−11	50 x 1	raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
17	241	−1.46	4e−11	1e−10	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
18	972	−1.43	8e−11	1e−10	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
19	3689	−1.43	8e−11	1e−10	50 x 1	integrin, beta 2 (complement component 3 receptor 3 and 4 s
20	6352	−1.43	9e−11	1e−10	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−32.4	NULL	12 / 15	CC	MHC class II protein complex
2	−30.27	NULL	86 / 417	H.Tiss	WIRTH_Immune system
3	−23.6	NULL	86 / 553	Cancer	Lembcke_Colonic Inflammation
4	−22.96	NULL	47 / 312	BP	immune response
5	−20.37	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
6	−20.29	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
7	−20.29	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
8	−20.29	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
9	−20.29	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
10	−19.76	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
11	−19.5	NULL	15 / 47	BP	antigen processing and presentation
12	−19.07	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
13	−18.38	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
14	−17.82	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
15	−17.65	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
16	−17.23	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	−16.89	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
18	−16.77	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
19	−16.56	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
20	−16.38	NULL	13 / 60	BP	T cell costimulation
21	−16.38	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
22	−16.05	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
23	−15.92	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
24	−15.24	NULL	17 / 74	BP	regulation of immune response
25	−15.02	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
26	−15.01	NULL	7 / 28	CC	transport vesicle membrane
27	−14.91	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
28	−14.86	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
29	−14.57	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
30	−14.46	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
31	−14.2	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
32	−13.92	NULL	7 / 32	CC	ER to Golgi transport vesicle membrane
33	−13.63	NULL	8 / 35	CC	trans−Golgi network membrane
34	−13.53	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
35	−13.43	NULL	8 / 16	GSEA C2	SU_THYMUS
36	−13.33	NULL	5 / 12	BP	immunoglobulin mediated immune response
37	−13.15	NULL	23 / 162	CC	external side of plasma membrane
38	−12.88	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
39	−12.62	NULL	10 / 60	BP	interferon−gamma−mediated signaling pathway
40	−12.53	NULL	12 / 87	BP	antigen processing and presentation of exogenous peptide antigen