GW_135

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1747 (1032 + / 715 −)

genes with fdr < 0.1 = 1338 (818 + / 520 −)

genes with fdr < 0.05 = 1118 (694 + / 424 −)

genes with fdr < 0.01 = 747 (496 + / 251 −)

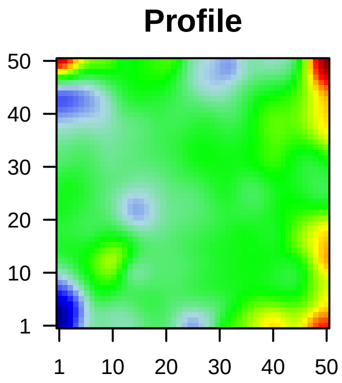
genes in genesets = 16332

<FC> = 0

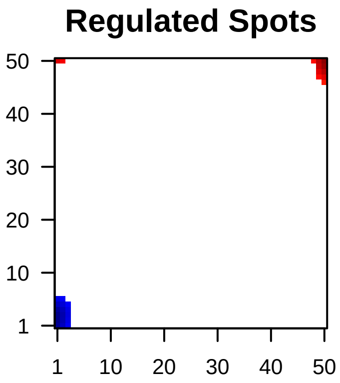
<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.86



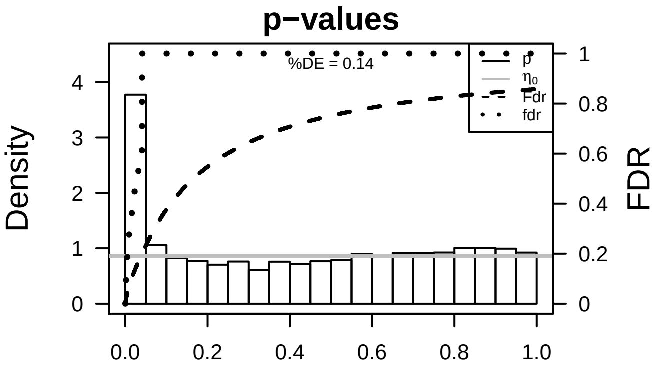
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.87	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	2.6	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	131	1.6	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	200810	1.25	2e−16	3e−14	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransferas
5	55107	1.51	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
6	440	1.2	2e−16	3e−14	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HGN
7	151516	1.51	2e−16	3e−14	1 x 46	aspartic peptidase, retroviral−like 1 [Source:HGNC Symbol;A
8	445	1.13	2e−16	3e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:758
9	339512	2.1	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
10	768	−1.2	2e−16	3e−14	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
11	57172	1.39	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
12	84290	1.14	2e−16	3e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
13	868	1.17	2e−16	3e−14	8 x 5	Cbl proto−oncogene B, E3 ubiquitin protein ligase [Source:HC
14	1056	2.31	2e−16	3e−14	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
15	1152	1.52	2e−16	3e−14	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
16	9076	1.32	2e−16	3e−14	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
17	1288	1.5	2e−16	3e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
18	49860	1.66	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
19	1515	−1.34	2e−16	3e−14	1 x 44	cathepsin V [Source:HGNC Symbol;Acc:2538]
20	57007	−1.22	2e−16	3e−14	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.82	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
2	10.66	NULL	7	MMML CGS	MACIEJ_MMML 5
3	10.27	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
4	9.63	NULL	15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
5	9.14	NULL	135	H.Tiss	WIRTH_Mucosa
6	8.52	NULL	34	Chr	Chr Y
7	7.36	NULL	21	CC	cornified envelope
8	7.35	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
9	7.3	NULL	24	TF Tissue	VAQUERIZAS_Trachea
10	7.21	NULL	53	BP	keratinocyte differentiation
11	6.98	NULL	1749	MF	DNA binding
12	6.96	NULL	13	BP	regulation of blood vessel size
13	6.84	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
14	6.83	NULL	918	Chr	Chr 17
15	6.64	NULL	7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
16	6.63	NULL	99	MF	double−stranded DNA binding
17	6.31	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	6.15	NULL	7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
19	6.08	NULL	20	Lymphoma	ROSOLOWSKI_red UP
20	6.06	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
Underexpressed					
1	−13.73	NULL	633	Chr	Chr 9
2	−11.18	NULL	699	Chr	Chr 5
3	−7.73	NULL	534	Chr	Chr 8
4	−7.52	NULL	16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
5	−6.98	NULL	16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
6	−6.93	NULL	280	Chr	Chr 13
7	−5.75	NULL	35	Glio	Colman_survival_associated
8	−5.35	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
9	−5.01	NULL	36	BP	muscle filament sliding
10	−4.85	NULL	15	GSEA C2	KARAKAS_TGFB1_SIGNALING
11	−4.84	NULL	250	Lymphoma	LENZ_Stromal signature 1
12	−4.77	NULL	11	MMML CGS	MACIEJ_MMML 31
13	−4.52	NULL	33	BP	cholesterol biosynthetic process
14	−4.5	NULL	42	BP	positive regulation of cell division
15	−4.46	NULL	242	BP	extracellular matrix organization
16	−4.43	NULL	39	BP	glycolysis
17	−4.42	NULL	15	GSEA C2	SEMENZA_HIF1_TARGETS
18	−4.38	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_240_MCF10A
19	−4.34	NULL	9	GSEA C2	KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
20	−4.26	NULL	127	H.Tiss	WIRTH_Muscle

GW_135

Local Summary

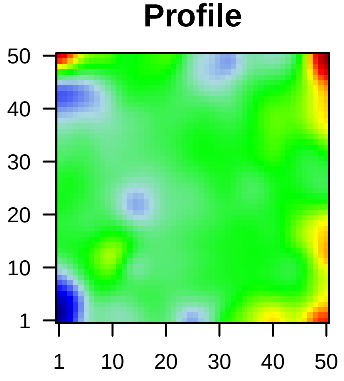
%DE = 0.7
metagenes = 10
genes = 178
genes in genesets = 177

genes with fdr < 0.1 = 90 (73 + / 17 −)
genes with fdr < 0.05 = 89 (72 + / 17 −)
genes with fdr < 0.01 = 66 (61 + / 5 −)

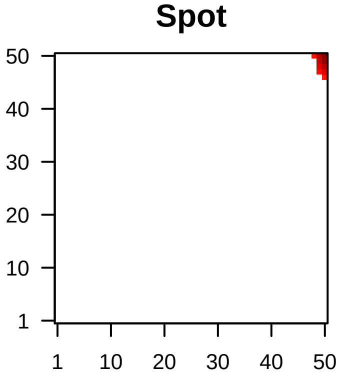
<r> metagenes = 0.98
<r> genes = 0.28

<FC> = 0.33
<shrinkage−t> = 11.73
<p−value> = 0
<fdr> = 0.5

Profile



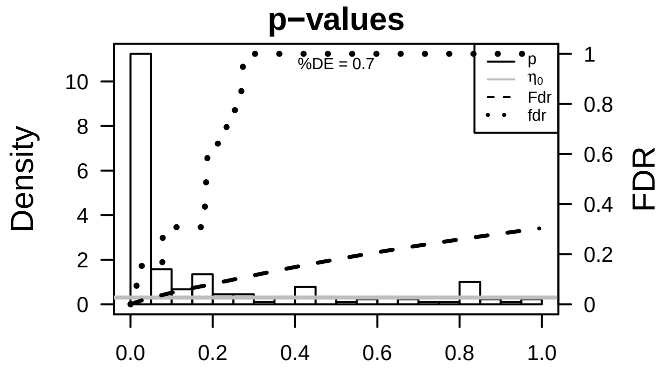
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	200810	1.25	2e−16	7e−16	49 x 50	ALG1, chitobiosyldiphosphodolichol beta−mannosyltransfera
2	440	1.2	2e−16	7e−16	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HG
3	445	1.13	2e−16	7e−16	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
4	339512	2.1	2e−16	7e−16	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
5	1056	2.31	2e−16	7e−16	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
6	9076	1.32	2e−16	7e−16	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
7	25975	1.22	2e−16	7e−16	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
8	2938	2.24	2e−16	7e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
9	3304	1.07	2e−16	7e−16	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
10	57291	1.11	2e−16	7e−16	50 x 50	differentiation antagonizing non−protein coding RNA [Source:
11	3880	1.23	2e−16	7e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
12	4922	3.76	2e−16	7e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
13	5013	1.2	2e−16	7e−16	50 x 50	orthodenticle homeobox 1 [Source:HGNC Symbol;Acc:8521]
14	26227	1.12	2e−16	7e−16	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
15	6446	1.28	2e−16	7e−16	50 x 50	serum/glucocorticoid regulated kinase 1 [Source:HGNC Sym
16	256764	1.9	2e−16	7e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
17	79844	1.91	2e−16	7e−16	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
18	9182	1.09	7e−16	6e−14	50 x 50	Ras association (RalGDS/AF−6) domain family (N−terminal)
19	875	1.08	2e−15	2e−13	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
20	26047	−1.05	8e−15	2e−13	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;A

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	23.21	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	20.36	NULL	4 / 13	BP	regulation of blood vessel size
3	19.51	NULL	1 / 2	GSEA C2	KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
4	18.48	NULL	2 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
5	17.39	NULL	1 / 11	Glio	neurons_glio
6	16.51	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
7	15.09	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
8	14.59	NULL	1 / 15	MF	neuropeptide hormone activity
9	13.03	NULL	3 / 12	GSEA C2	BROCKE_APOPTOSIS_REVERSED_BY_IL6
10	12.8	NULL	1 / 8	GSEA C2	KEGG_GLYCEROLIPID_METABOLISM
11	12.66	NULL	2 / 10	GSEA C2	MOHANKUMAR_TLX1_TARGETS_DN
12	12.6	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	12.4	NULL	2 / 9	GSEA C2	BROWNE_HCMV_INFECTION_8HR_UP
14	10.7	NULL	1 / 5	GSEA C2	DASU_IL6_SIGNALING_UP
15	10.63	NULL	1 / 11	GSEA C2	BROWNE_HCMV_INFECTION_10HR_UP
16	10.48	NULL	5 / 20	MF	glutathione transferase activity
17	9.97	NULL	2 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
18	9.66	NULL	1 / 13	MF	triglyceride lipase activity
19	9.58	NULL	1 / 6	GSEA C2	SESTO_RESPONSE_TO_UV_C0
20	9.58	NULL	1 / 6	GSEA C2	BIOCARTA_TID_PATHWAY
21	9.52	NULL	2 / 13	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
22	9.26	NULL	1 / 14	GSEA C2	WATANABE_COLON_CANCER_MSI_VS_MSS_DN
23	9.02	NULL	3 / 19	BP	cellular amino acid biosynthetic process
24	8.84	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
25	8.78	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
26	8.77	NULL	2 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
27	8.77	NULL	2 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
28	8.73	NULL	1 / 7	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_UP
29	8.61	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
30	8.61	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
31	8.59	NULL	2 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
32	8.45	NULL	2 / 16	GSEA C2	IGARASHI_ATF4_TARGETS_DN
33	8.45	NULL	2 / 16	GSEA C2	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
34	8.4	NULL	2 / 11	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
35	8.29	NULL	1 / 41	CC	transport vesicle
36	8.22	NULL	1 / 5	GSEA C2	NIELSEN_SCHWANNOMA_DN
37	8.19	NULL	2 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN
38	8.14	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
39	8.06	NULL	1 / 8	GSEA C2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
40	8.06	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN

GW_135

Local Summary

%DE = 0.77

metagenes = 2

genes = 71

genes in genesets = 70

genes with fdr < 0.1 = 46 (42 + / 4 −)

genes with fdr < 0.05 = 41 (39 + / 2 −)

genes with fdr < 0.01 = 36 (35 + / 1 −)

<r> metagenes = 1

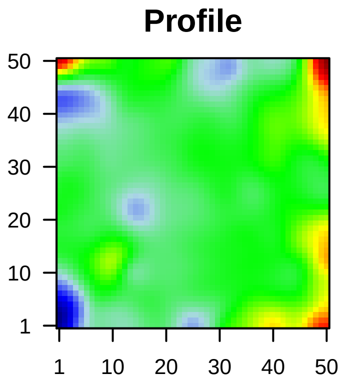
<r> genes = 0.58

<FC> = 0.53

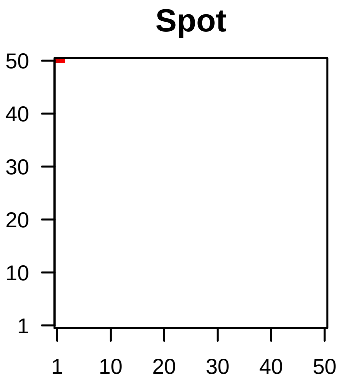
<shrinkage−t> = 18.74

<p−value> = 0

<fdr> = 0.38



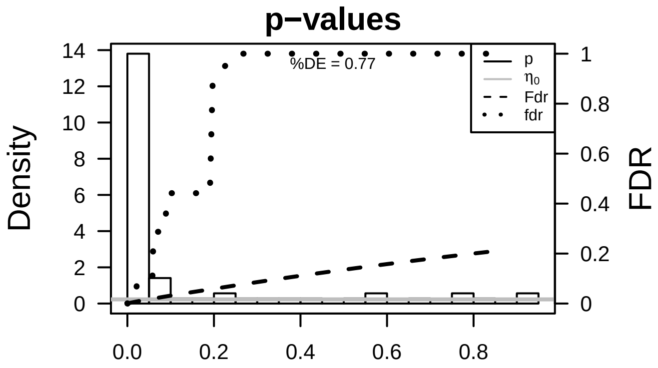
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.6	2e−16	3e−16	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	84290	1.14	2e−16	3e−16	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
3	49860	1.66	2e−16	3e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
4	2877	1.61	2e−16	3e−16	1 x 50	glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy
5	3860	1.29	2e−16	3e−16	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
6	3851	1.23	2e−16	3e−16	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
7	6700	1.44	2e−16	3e−16	1 x 50	small proline−rich protein 2A [Source:HGNC Symbol;Acc:112
8	6702	1.97	2e−16	3e−16	1 x 50	
9	6704	1.69	2e−16	3e−16	1 x 50	small proline−rich protein 2E [Source:HGNC Symbol;Acc:112
10	6705	1.37	2e−16	3e−16	1 x 50	small proline−rich protein 2F [Source:HGNC Symbol;Acc:112
11	6707	1.38	2e−16	3e−16	1 x 50	small proline−rich protein 3 [Source:HGNC Symbol;Acc:1126
12	339967	1.28	2e−16	3e−16	2 x 50	transmembrane protease, serine 11A [Source:HGNC Symbol
13	5653	1.09	9e−16	7e−15	1 x 50	kallikrein−related peptidase 6 [Source:HGNC Symbol;Acc:63
14	7053	1.09	1e−15	3e−14	1 x 50	transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
15	26085	1.07	3e−15	6e−14	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
16	6698	0.97	7e−15	6e−14	1 x 50	small proline−rich protein 1A [Source:HGNC Symbol;Acc:112
17	4680	1.04	1e−14	6e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
18	218	1.04	1e−14	5e−13	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
19	23120	1.02	4e−14	2e−10	1 x 50	ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543
20	6699	0.92	1e−11	2e−10	1 x 50	small proline−rich protein 1B [Source:HGNC Symbol;Acc:112



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	39.72	NULL	10 / 21	CC	cornified envelope
2	36.67	NULL	39 / 135	H.Tiss	WIRTH_Mucosa
3	35.78	NULL	11 / 42	BP	keratinization
4	30.59	NULL	12 / 53	BP	keratinocyte differentiation
5	27.98	NULL	7 / 19	BP	peptide cross−linking
6	20.64	NULL	9 / 76	BP	epidermis development
7	19.32	NULL	4 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	18.72	NULL	4 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
9	17.08	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
10	16.4	NULL	3 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	16.31	NULL	2 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
12	14.97	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
13	13.23	NULL	1 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
14	13.01	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
15	12.93	NULL	10 / 186	MF	structural molecule activity
16	12.42	NULL	29 / 572	Disease	GUDJ_psoriasis up
17	12.4	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER
18	12.4	NULL	1 / 5	GSEA C2	NAKAMURA_LUNG_CANCER_MARKERS
19	11.27	NULL	2 / 15	MF	retinol dehydrogenase activity
20	11.21	NULL	2 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
21	11.07	NULL	9 / 122	MF	serine−type endopeptidase activity
22	10.83	NULL	1 / 12	MF	retinol binding
23	10.64	NULL	1 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
24	10.37	NULL	1 / 13	BP	temperature homeostasis
25	10.3	NULL	1 / 13	BP	retinoic acid metabolic process
26	10.01	NULL	1 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
27	9.91	NULL	1 / 14	MF	glutathione peroxidase activity
28	9.74	NULL	2 / 12	BP	cellular aldehyde metabolic process
29	9.43	NULL	2 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
30	9.43	NULL	2 / 16	GSEA C2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_
31	8.76	NULL	1 / 15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
32	8.64	NULL	1 / 10	GSEA C2	BIOCARTA_P35ALZHEIMERS_PATHWAY
33	8.43	NULL	1 / 18	BP	retinol metabolic process
34	8.42	NULL	1 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
35	8.09	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
36	7.75	NULL	3 / 39	BP	retinoid metabolic process
37	7.72	NULL	3 / 44	CC	keratin filament
38	7.71	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
39	7.41	NULL	2 / 13	GSEA C2	LUI_THYROID_CANCER_PAX8_PPARG_UP
40	7.31	NULL	1 / 13	GSEA C2	BIOCARTA_MEF2D_PATHWAY

GW_135

Local Summary

%DE = 0.72

metagenes = 17

genes = 259

genes in genesets = 257

genes with fdr < 0.1 = 161 (20 + / 141 −)

genes with fdr < 0.05 = 129 (18 + / 111 −)

genes with fdr < 0.01 = 110 (14 + / 96 −)

<r> metagenes = 0.96

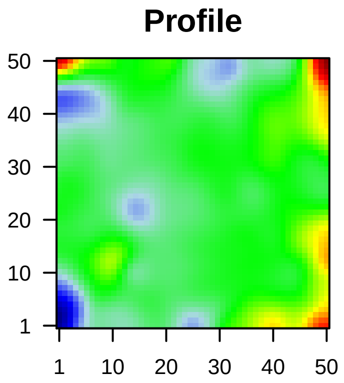
<r> genes = 0.36

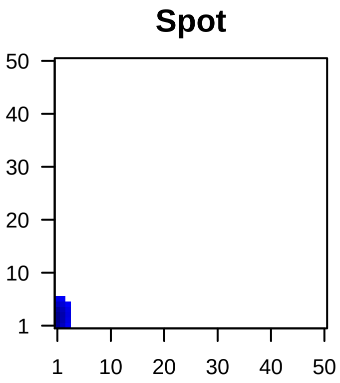
<FC> = −0.28

<shrinkage−t> = −9.74

<p−value> = 0

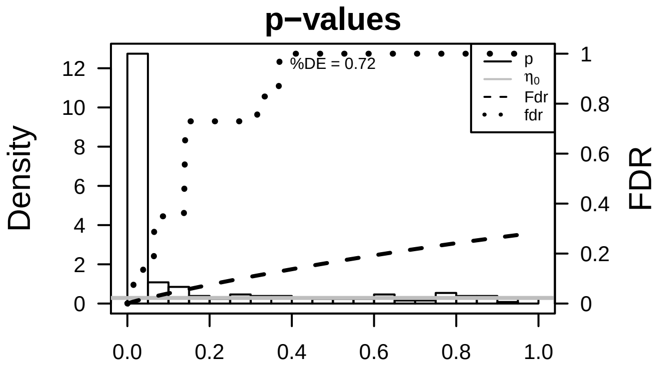
<fdr> = 0.45





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	1.51	2e−16	2e−15	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	768	−1.2	2e−16	2e−15	1 x 6	carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
3	3486	−1.36	2e−16	2e−15	1 x 6	insulin−like growth factor binding protein 3 [Source:HGNC Sy
4	3678	−1.12	2e−16	2e−15	1 x 1	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Sou
5	3918	−1.17	2e−16	2e−15	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
6	3956	−1.21	2e−16	2e−15	1 x 1	lectin, galactoside−binding, soluble, 1 [Source:HGNC Symbol
7	4060	1.89	2e−16	2e−15	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
8	4314	−1.15	2e−16	2e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
9	5328	−1.14	2e−16	2e−15	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
10	5743	1.46	2e−16	2e−15	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
11	55714	−1.09	9e−16	1e−13	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
12	6662	−1.09	9e−16	1e−13	2 x 5	SRY (sex determining region Y)−box 9 [Source:HGNC Symbo
13	4628	−1.06	4e−15	1e−13	1 x 5	myosin, heavy chain 10, non−muscle [Source:HGNC Symbol;
14	2274	−1.06	4e−15	1e−12	1 x 4	four and a half LIM domains 2 [Source:HGNC Symbol;Acc:37
15	10381	1.04	2e−14	4e−12	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
16	8988	−1.01	9e−14	4e−12	1 x 4	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248
17	4502	−1	1e−13	4e−12	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
18	4312	−1	2e−13	1e−09	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
19	3553	−0.9	3e−11	1e−09	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
20	1948	−0.89	4e−11	1e−09	1 x 5	ephrin−B2 [Source:HGNC Symbol;Acc:3227]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−17.65	NULL	12 / 35	Glio	Colman_survival_associated
2	−17.38	NULL	57 / 242	BP	extracellular matrix organization
3	−15.35	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
4	−14.83	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
5	−13.66	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
6	−13.2	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
7	−12.81	NULL	38 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
8	−12.81	NULL	38 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
9	−12.81	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
10	−12.81	NULL	38 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
11	−12.63	NULL	58 / 250	Lymphoma	LENZ_Stromal signature 1
12	−12.48	NULL	5 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
13	−12.44	NULL	4 / 13	GSEA C2	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FAC
14	−12.06	NULL	68 / 683	CC	extracellular space
15	−12.05	NULL	25 / 69	BP	extracellular matrix disassembly
16	−11.94	NULL	32 / 183	CC	proteinaceous extracellular matrix
17	−11.77	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
18	−11.66	NULL	4 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
19	−11.52	NULL	6 / 19	MF	L−ascorbic acid binding
20	−11.46	NULL	24 / 64	BP	collagen catabolic process
21	−11.4	NULL	8 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
22	−11.33	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
23	−11.24	NULL	51 / 403	BP	cell adhesion
24	−10.98	NULL	4 / 9	GSEA C2	WEINMANN_ADAPTATION_TO_HYPOXIA_DN
25	−10.78	NULL	4 / 16	GSEA C2	HENDRICKS_SMARCA4_TARGETS_UP
26	−10.63	NULL	46 / 190	CC	extracellular matrix
27	−10.63	NULL	3 / 10	BP	cellular response to zinc ion
28	−10.48	NULL	17 / 117	Glio	GIEZELT_GBM_WT_up_VS_mut
29	−10.37	NULL	3 / 10	BP	negative regulation of cell−substrate adhesion
30	−10.19	NULL	4 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
31	−10.14	NULL	4 / 17	BP	negative regulation of signal transduction
32	−10.11	NULL	5 / 11	MMML CGS	MACIEJ_MMML 31
33	−10.04	NULL	2 / 12	GSEA C2	GEISS_RESPONSE_TO_DSRNA_DN
34	−10.03	NULL	2 / 11	BP	negative regulation of smooth muscle cell migration
35	−9.83	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
36	−9.71	NULL	5 / 16	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C1
37	−9.62	NULL	3 / 9	GSEA C2	REACTOME_SIGNALING_BY_VEGF
38	−9.53	NULL	3 / 10	GSEA C2	NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP
39	−9.49	NULL	4 / 15	BP	negative regulation of anoikis
40	−9.48	NULL	2 / 12	GSEA C2	LI_LUNG_CANCER