GW_079

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1532 (1066 + / 466 −)

genes with fdr < 0.1 = 1170 (883 + / 287 −)

genes with fdr < 0.05 = 1034 (810 + / 224 −)

genes with fdr < 0.01 = 796 (672 + / 124 −)

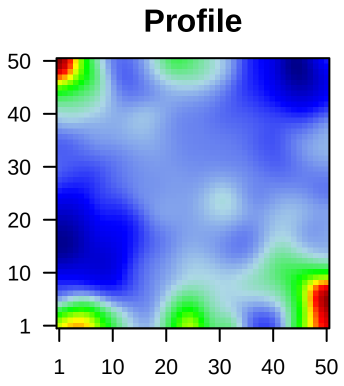
genes in genesets = 16332

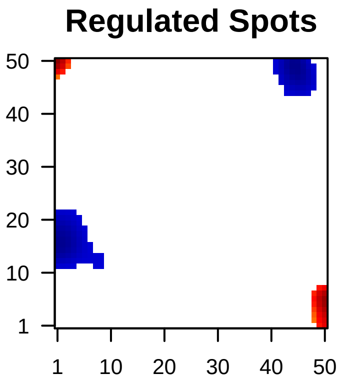
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

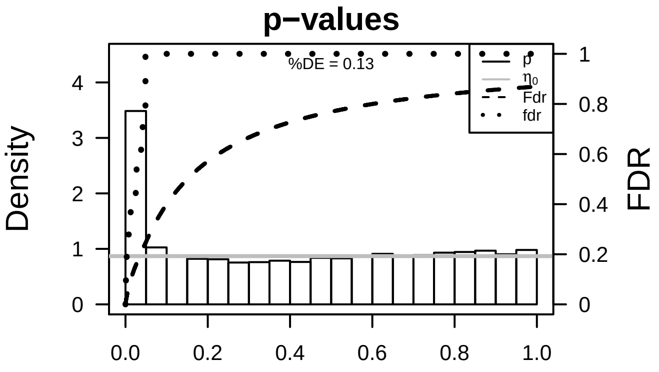
<fdr> = 0.87


Profile


Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2	1.34	2e−16	2e−14	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
2	25890	1.33	2e−16	2e−14	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
3	58	2.41	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
4	9510	1.18	2e−16	2e−14	6 x 1	ADAM metallopeptidase with thrombospondin type 1 motif, 1
5	196883	1.18	2e−16	2e−14	50 x 7	adenylate cyclase 4 [Source:HGNC Symbol;Acc:235]
6	131	1.82	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
7	218	1.34	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	347	2.15	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
9	81575	1.44	2e−16	2e−14	7 x 1	apolipoprotein L domain containing 1 [Source:HGNC Symbol;
10	10974	1.2	2e−16	2e−14	5 x 50	adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24
11	56892	2.02	2e−16	2e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
12	375791	1.5	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
13	57172	2.07	2e−16	2e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
14	6358	1.99	2e−16	2e−14	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
15	6347	1.4	2e−16	2e−14	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
16	6366	1.34	2e−16	2e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
17	6355	1.29	2e−16	2e−14	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:
18	22918	1.4	2e−16	2e−14	4 x 1	CD93 molecule [Source:HGNC Symbol;Acc:15855]
19	1675	2.28	2e−16	2e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
20	3075	1.24	2e−16	2e−14	50 x 7	complement factor H [Source:HGNC Symbol;Acc:4883]


p−values

Global Geneset Analysis

Overexpressed

Rank	GSZ	p−value	#all	Geneset	
1	20.96	NULL	135	H.Tiss	WIRTH_Mucosa
2	19.74	NULL	553	Cancer	Lembcke_Colonic Inflammation
3	17.83	NULL	683	CC	extracellular space
4	17.8	NULL	1182	CC	extracellular region
5	14.4	NULL	312	BP	immune response
6	13.12	NULL	190	CC	extracellular matrix
7	12.99	NULL	572	Disease	GUDJ_psoriasis up
8	12.87	NULL	53	BP	keratinocyte differentiation
9	12.58	NULL	21	CC	cornified envelope
10	12.25	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
11	12.2	NULL	250	Lymphoma	LENZ_Stromal signature 1
12	12.2	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	12.2	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	12.2	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	12.2	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	11.52	NULL	127	H.Tiss	WIRTH_Muscle
17	11.48	NULL	59	Lymphoma	LENZ_Stromal signature 2
18	11.31	NULL	19	BP	peptide cross−linking
19	11.27	NULL	16	H.Tiss	WIRTH_Hippocampus
20	10.9	NULL	129	BP	response to lipopolysaccharide

Underexpressed

Rank	GSZ	p−value	#all	Geneset	
1	−14.03	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−14.03	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−11.73	NULL	370	BP	mitotic cell cycle
4	−10.36	NULL	949	CC	nucleoplasm
5	−8.46	NULL	530	Cancer	Lembcke_Normal vs Adenoma
6	−7.98	NULL	4640	CC	nucleus
7	−7.96	NULL	298	BP	DNA repair
8	−7.86	NULL	1233	TF	KIM_MYC targets
9	−7.83	NULL	232	BP	mitosis
10	−7.32	NULL	649	BP	gene expression
11	−7.13	NULL	149	BP	DNA replication
12	−6.39	NULL	30	BP	DNA strand elongation involved in DNA replication
13	−6.37	NULL	1318	CC	mitochondrion
14	−6.16	NULL	940	MF	nucleic acid binding
15	−6.09	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
16	−5.96	NULL	56	CC	chromosome, centromeric region
17	−5.92	NULL	163	BP	mRNA splicing, via spliceosome
18	−5.92	NULL	1749	MF	DNA binding
19	−5.86	NULL	16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
20	−5.71	NULL	717	Chr	Chr 16

GW_079

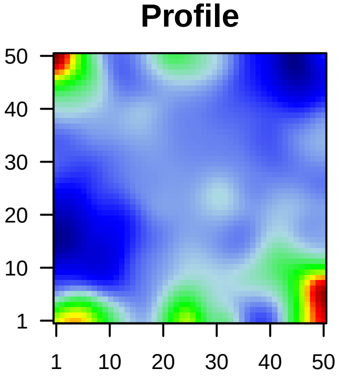
Local Summary

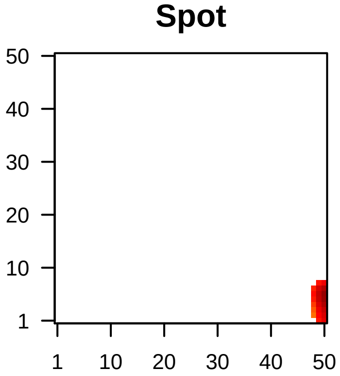
%DE = 0.87
metagenes = 22
genes = 347
genes in genesets = 346

genes with fdr < 0.1 = 288 (284 + / 4 −)
genes with fdr < 0.05 = 258 (255 + / 3 −)
genes with fdr < 0.01 = 232 (230 + / 2 −)

<r> metagenes = 0.92
<r> genes = 0.44

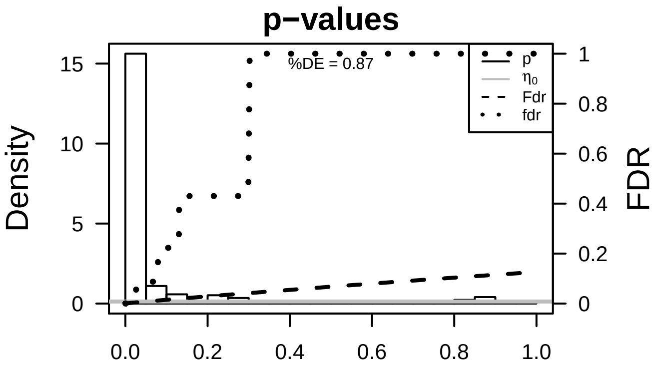
<FC> = 0.62
<shrinkage−t> = 21.6
<p−value> = 0
<fdr> = 0.28





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2	1.34	2e−16	2e−16	50 x 5	alpha−2−macroglobulin [Source:HGNC Symbol;Acc:7]
2	25890	1.33	2e−16	2e−16	50 x 4	ABI family, member 3 (NESH) binding protein [Source:HGNC
3	196883	1.18	2e−16	2e−16	50 x 7	adenylate cyclase 4 [Source:HGNC Symbol;Acc:235]
4	347	2.15	2e−16	2e−16	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
5	56892	2.02	2e−16	2e−16	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
6	57172	2.07	2e−16	2e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
7	6358	1.99	2e−16	2e−16	50 x 7	chemokine (C−C motif) ligand 14 [Source:HGNC Symbol;Acc
8	6347	1.4	2e−16	2e−16	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
9	6366	1.34	2e−16	2e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
10	3075	1.24	2e−16	2e−16	50 x 7	complement factor H [Source:HGNC Symbol;Acc:4883]
11	5010	1.29	2e−16	2e−16	50 x 7	claudin 11 [Source:HGNC Symbol;Acc:8514]
12	7122	1.39	2e−16	2e−16	50 x 6	claudin 5 [Source:HGNC Symbol;Acc:2047]
13	7123	1.14	2e−16	2e−16	50 x 7	C−type lectin domain family 3, member B [Source:HGNC Sy
14	1359	1.24	2e−16	2e−16	50 x 7	carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
15	1363	1.5	2e−16	2e−16	50 x 7	carboxypeptidase E [Source:HGNC Symbol;Acc:2303]
16	51755	1.73	2e−16	2e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
17	1511	1.49	2e−16	2e−16	50 x 7	cathepsin G [Source:HGNC Symbol;Acc:2532]
18	6387	1.35	2e−16	2e−16	50 x 6	chemokine (C−X−C motif) ligand 12 [Source:HGNC Symbol;
19	79901	1.31	2e−16	2e−16	50 x 7	cytochrome b reductase 1 [Source:HGNC Symbol;Acc:20797
20	1545	1.6	2e−16	2e−16	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	20.54	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
2	17.37	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
3	16.37	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
4	15.84	NULL	7 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
5	14.83	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
6	14.54	NULL	45 / 312	BP	immune response
7	14.1	NULL	88 / 553	Cancer	Lembcke_Colonic Inflammation
8	13.33	NULL	4 / 15	GSEA C2	NAKAJIMA_MAST_CELL
9	12.87	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
10	12.85	NULL	6 / 15	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULO
11	12.63	NULL	4 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
12	12.36	NULL	10 / 43	MF	chemokine activity
13	12.28	NULL	50 / 683	CC	extracellular space
14	12.2	NULL	3 / 11	GSEA C2	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
15	11.94	NULL	10 / 15	CC	MHC class II protein complex
16	11.82	NULL	69 / 1182	CC	extracellular region
17	11.41	NULL	4 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
18	10.58	NULL	4 / 10	GSEA C2	LU_TUMOR_VASCULATURE_DN
19	10.56	NULL	3 / 14	MF	lipid transporter activity
20	10.47	NULL	4 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP
21	10.39	NULL	3 / 14	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
22	10.28	NULL	42 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
23	10.28	NULL	42 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
24	10.28	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
25	10.28	NULL	42 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
26	10.06	NULL	6 / 59	Lymphoma	LENZ_Stromal signature 2
27	9.96	NULL	6 / 15	Cancer	GENTLES_modul13
28	9.93	NULL	3 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
29	9.77	NULL	4 / 10	BP	germ cell migration
30	9.62	NULL	16 / 112	MF	heparin binding
31	9.51	NULL	66 / 417	H.Tiss	WIRTH_Immune system
32	9.51	NULL	4 / 10	GSEA C2	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
33	9.49	NULL	3 / 7	GSEA C2	WALLACE_PROSTATE_CANCER_RACE_UP
34	9.29	NULL	3 / 21	BP	chemokine−mediated signaling pathway
35	9.16	NULL	5 / 14	BP	ruffle organization
36	9.15	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
37	9.14	NULL	6 / 16	GSEA C2	BOQUEST_STEM_CELL_CULTURED_VS_FRESH_DN
38	9.09	NULL	4 / 27	BP	negative regulation of smooth muscle cell proliferation
39	9.01	NULL	7 / 20	BP	complement activation
40	9.01	NULL	8 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1

GW_079

Local Summary

%DE = 0.93

metagenes = 9

genes = 158

genes in genesets = 153

genes with fdr < 0.1 = 144 (141 + / 3 −)

genes with fdr < 0.05 = 125 (124 + / 1 −)

genes with fdr < 0.01 = 122 (121 + / 1 −)

<r> metagenes = 0.98

<r> genes = 0.5

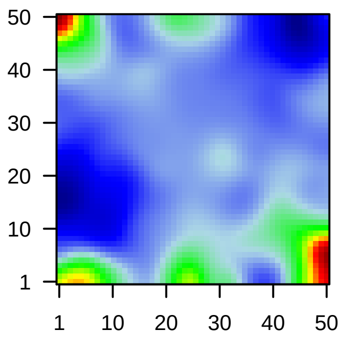
<FC> = 0.81

<shrinkage−t> = 28.75

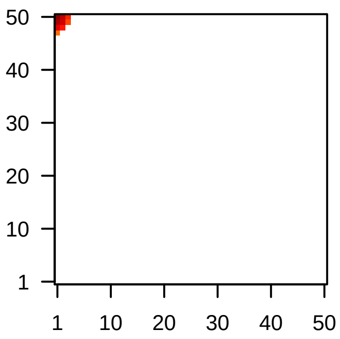
<p−value> = 0

<fdr> = 0.21

Profile



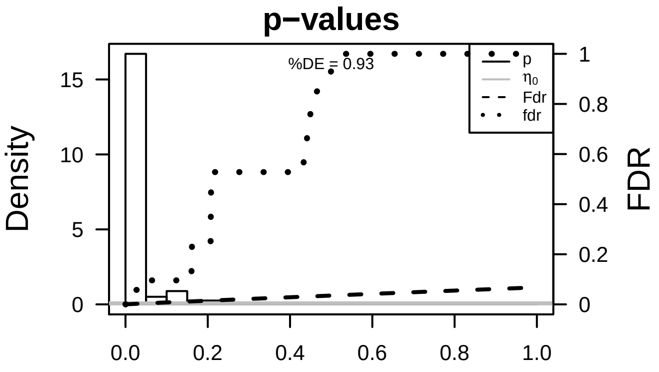
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	1.82	2e−16	6e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	1.34	2e−16	6e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	375791	1.5	2e−16	6e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symb
4	22802	2.13	2e−16	6e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
5	9022	1.32	2e−16	6e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
6	84518	1.49	2e−16	6e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	54544	1.55	2e−16	6e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
8	49860	3.18	2e−16	6e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
9	414325	1.29	2e−16	6e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	2312	2.08	2e−16	6e−17	1 x 49	filaggrin [Source:HGNC Symbol;Acc:3748]
11	163351	1.42	2e−16	6e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S
12	26085	1.2	2e−16	6e−17	1 x 50	kallikrein−related peptidase 13 [Source:HGNC Symbol;Acc:6
13	5650	1.55	2e−16	6e−17	1 x 49	kallikrein−related peptidase 7 [Source:HGNC Symbol;Acc:63
14	3848	1.6	2e−16	6e−17	1 x 47	keratin 1 [Source:HGNC Symbol;Acc:6412]
15	3860	1.4	2e−16	6e−17	1 x 50	keratin 13 [Source:HGNC Symbol;Acc:6415]
16	192666	−1.37	2e−16	6e−17	1 x 50	keratin 24 [Source:HGNC Symbol;Acc:18527]
17	3851	2.25	2e−16	6e−17	1 x 50	keratin 4 [Source:HGNC Symbol;Acc:6441]
18	196374	1.64	2e−16	6e−17	1 x 50	keratin 78 [Source:HGNC Symbol;Acc:28926]
19	388533	1.8	2e−16	6e−17	1 x 49	keratinocyte differentiation−associated protein [Source:HGNC
20	3963	1.24	2e−16	6e−17	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	56.17	NULL	67 / 135	H.Tiss	WIRTH_Mucosa
2	35.19	NULL	15 / 21	CC	cornified envelope
3	31.15	NULL	18 / 42	BP	keratinization
4	30.56	NULL	20 / 53	BP	keratinocyte differentiation
5	24.99	NULL	8 / 19	BP	peptide cross−linking
6	22.18	NULL	18 / 76	BP	epidermis development
7	22.03	NULL	73 / 572	Disease	GUDJ_psoriasis up
8	19.8	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
9	18.27	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	16.09	NULL	5 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
11	15.3	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
12	14.85	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
13	14.28	NULL	6 / 13	BP	negative regulation of peptidase activity
14	13.93	NULL	8 / 44	CC	keratin filament
15	12.12	NULL	17 / 186	MF	structural molecule activity
16	12.11	NULL	4 / 10	MF	RAGE receptor binding
17	11.69	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
18	11.66	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
19	11.28	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
20	10.9	NULL	2 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
21	10.65	NULL	3 / 16	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G24
22	10.54	NULL	10 / 82	CC	intermediate filament
23	9.81	NULL	11 / 122	MF	serine−type endopeptidase activity
24	9.51	NULL	10 / 79	MF	serine−type endopeptidase inhibitor activity
25	9.42	NULL	44 / 1182	CC	extracellular region
26	9.23	NULL	1 / 11	Glio	VERHAAK_Brain
27	9.2	NULL	5 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
28	8.81	NULL	1 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
29	8.75	NULL	1 / 12	MF	channel activity
30	8.42	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
31	8.41	NULL	5 / 38	BP	epithelial cell differentiation
32	8.34	NULL	1 / 13	GSEA C2	HASLINGER_B_CLL_WITH_MUTATED_VH_GENES
33	8.25	NULL	4 / 16	GSEA C2	LEE_LIVER_CANCER_MYC_TGFA_UP
34	8.22	NULL	3 / 16	GSEA C2	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN
35	8.13	NULL	4 / 15	MF	retinol dehydrogenase activity
36	8	NULL	3 / 13	H.Tiss	WIRTH_Tonsil
37	7.92	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
38	7.86	NULL	2 / 12	MF	retinol binding
39	7.79	NULL	2 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
40	7.75	NULL	4 / 23	MF	peptidase inhibitor activity

GW_079

Local Summary

%DE = 0.73

metagenes = 70

genes = 583

genes in genesets = 579

genes with fdr < 0.1 = 242 (3 + / 239 −)

genes with fdr < 0.05 = 171 (0 + / 171 −)

genes with fdr < 0.01 = 40 (0 + / 40 −)

<r> metagenes = 0.87

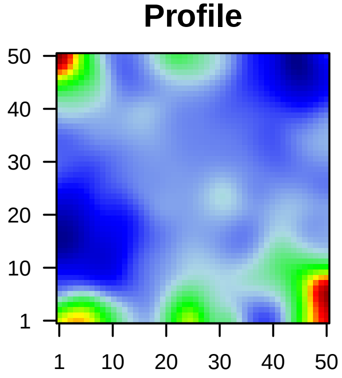
<r> genes = 0.24

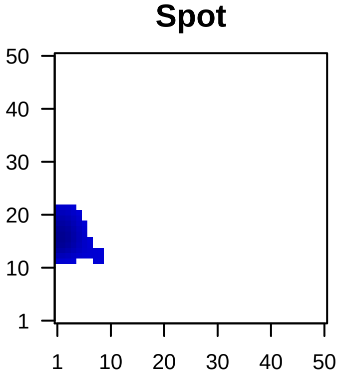
<FC> = −0.23

<shrinkage−t> = −8.12

<p−value> = 0.05

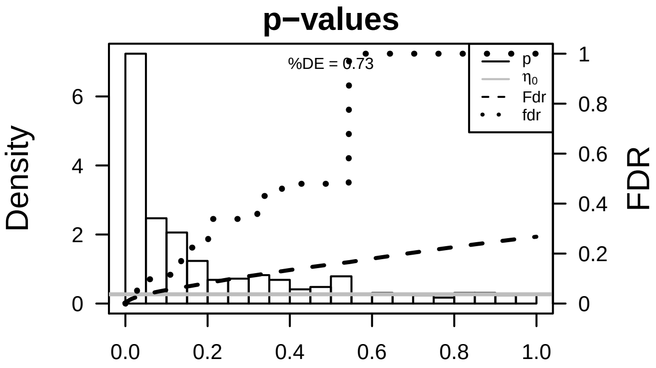
<fdr> = 0.75





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	284085	−1.2	2e−16	3e−14	3 x 18	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
2	10428	−1.11	1e−15	6e−07	1 x 15	craniofacial development protein 1 [Source:HGNC Symbol;Ac
3	3217	−0.82	4e−09	6e−06	1 x 15	homeobox B7 [Source:HGNC Symbol;Acc:5118]
4	1152	−0.75	7e−08	6e−06	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
5	27237	−0.75	8e−08	1e−04	2 x 20	Rho guanine nucleotide exchange factor (GEF) 16 [Source:H
6	51367	−0.68	1e−06	1e−04	1 x 17	processing of precursor 5, ribonuclease P/MRP subunit (S. ce
7	3326	−0.65	2e−06	1e−04	1 x 14	heat shock protein 90kDa alpha (cytosolic), class B member
8	5214	−0.66	2e−06	3e−04	1 x 13	phosphofructokinase, platelet [Source:HGNC Symbol;Acc:88
9	51069	−0.63	5e−06	3e−04	2 x 18	mitochondrial ribosomal protein L2 [Source:HGNC Symbol;Ac
10	6389	−0.62	9e−06	3e−04	1 x 12	succinate dehydrogenase complex, subunit A, flavoprotein (F
11	5693	−0.61	1e−05	3e−04	1 x 16	proteasome (prosome, macropain) subunit, beta type, 5 [Sou
12	8570	−0.61	1e−05	3e−04	2 x 19	KH−type splicing regulatory protein [Source:HGNC Symbol;A
13	220064	−0.61	1e−05	3e−04	1 x 14	oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
14	29763	−0.61	1e−05	3e−04	1 x 20	protein kinase C and casein kinase substrate in neurons 3 [S
15	10963	−0.6	2e−05	3e−04	1 x 16	stress−induced−phosphoprotein 1 [Source:HGNC Symbol;Ac
16	8772	−0.6	2e−05	3e−04	1 x 14	Fas (TNFRSF6)−associated via death domain [Source:HGNC
17	89780	−0.59	2e−05	3e−04	4 x 15	wingless−type MMTV integration site family, member 3A [Sou
18	5702	−0.59	2e−05	3e−04	1 x 19	proteasome (prosome, macropain) 26S subunit, ATPase, 3 [S
19	430	−0.59	2e−05	3e−04	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
20	219927	−0.59	3e−05	2e−03	1 x 15	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;A



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−9.36	NULL	4 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
2	−9.31	NULL	5 / 13	GSEA C2	REACTOME_GLYCOLYSIS
3	−8.77	NULL	10 / 37	CC	mitochondrial nucleoid
4	−8.51	NULL	14 / 66	BP	positive regulation of ubiquitin−protein ligase activity involved in mit
5	−8.4	NULL	12 / 48	BP	regulation of cellular amino acid metabolic process
6	−8.31	NULL	118 / 1318	CC	mitochondrion
7	−8.19	NULL	14 / 70	BP	regulation of ubiquitin−protein ligase activity involved in mitotic cell
8	−8.14	NULL	12 / 55	CC	proteasome complex
9	−8.1	NULL	5 / 16	GSEA C2	BIOCARTA_PTDINS_PATHWAY
10	−7.9	NULL	14 / 74	BP	anaphase−promoting complex−dependent proteasomal ubiquitin−c
11	−7.89	NULL	13 / 62	BP	negative regulation of ubiquitin−protein ligase activity involved in m
12	−7.87	NULL	6 / 15	GSEA C2	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
13	−7.82	NULL	6 / 17	CC	proteasome accessory complex
14	−7.71	NULL	1 / 2	miRNA target	miR−16−1
15	−7.54	NULL	4 / 11	MMML CGS	MACIEJ_MMML 15
16	−7.29	NULL	4 / 9	GSEA C2	BIOCARTA_GLYCOLYSIS_PATHWAY
17	−7.25	NULL	26 / 153	MF	structural constituent of ribosome
18	−7.07	NULL	4 / 9	GSEA C2	CAFFAREL_RESPONSE_TO_THC_8HR_3_DN
19	−6.95	NULL	54 / 530	Cancer	Lembcke_Normal vs Adenoma
20	−6.94	NULL	26 / 242	BP	RNA metabolic process
21	−6.74	NULL	6 / 14	GSEA C2	LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
22	−6.71	NULL	32 / 253	BP	translation
23	−6.7	NULL	11 / 63	BP	DNA damage response, signal transduction by p53 class mediator
24	−6.61	NULL	5 / 16	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP
25	−6.34	NULL	56 / 649	BP	gene expression
26	−6.32	NULL	2 / 10	BP	creatine metabolic process
27	−6.31	NULL	3 / 11	GSEA C2	BIOCARTA_ETC_PATHWAY
28	−6.25	NULL	20 / 96	BP	rRNA processing
29	−6.23	NULL	11 / 70	BP	antigen processing and presentation of exogenous peptide antigen
30	−6.17	NULL	5 / 17	CC	proteasome core complex
31	−6.15	NULL	18 / 167	BP	cellular nitrogen compound metabolic process
32	−6.1	NULL	69 / 949	CC	nucleoplasm
33	−6.06	NULL	22 / 167	CC	ribosome
34	−6.05	NULL	6 / 25	BP	proteolysis involved in cellular protein catabolic process
35	−6.04	NULL	3 / 10	GSEA C2	HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
36	−6.01	NULL	5 / 27	MF	four−way junction helicase activity
37	−5.99	NULL	11 / 74	BP	antigen processing and presentation of exogenous peptide antigen
38	−5.97	NULL	15 / 96	BP	DNA recombination
39	−5.97	NULL	3 / 8	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_25
40	−5.96	NULL	5 / 10	GSEA C2	REACTOME_HIV_LIFE_CYCLE

GW_079

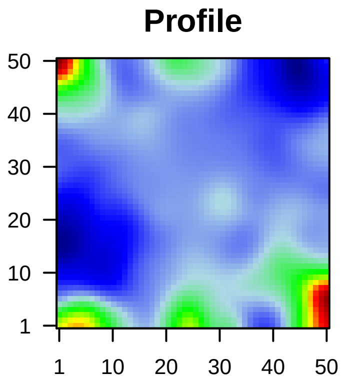
Local Summary

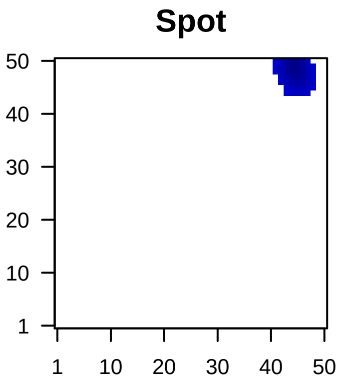
%DE = 0.68
metagenes = 48
genes = 520
genes in genesets = 517

genes with fdr < 0.1 = 220 (4 + / 216 −)
genes with fdr < 0.05 = 171 (1 + / 170 −)
genes with fdr < 0.01 = 101 (0 + / 101 −)

<r> metagenes = 0.89
<r> genes = 0.32

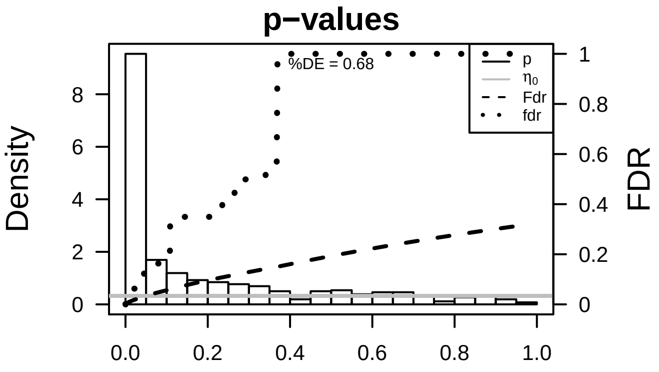
<FC> = −0.26
<shrinkage−t> = −9.01
<p−value> = 0.02
<fdr> = 0.64





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	51659	−1.12	7e−16	1e−12	44 x 50	GINS complex subunit 2 (Psf2 homolog) [Source:HGNC Sym
2	4171	−1.08	8e−15	8e−08	46 x 48	minichromosome maintenance complex component 2 [Source
3	79682	−0.86	5e−10	2e−07	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
4	9319	−0.82	3e−09	2e−07	43 x 50	thyroid hormone receptor interactor 13 [Source:HGNC Symbo
5	9212	−0.82	4e−09	2e−07	45 x 48	aurora kinase B [Source:HGNC Symbol;Acc:11390]
6	113130	−0.81	5e−09	2e−07	44 x 49	cell division cycle associated 5 [Source:HGNC Symbol;Acc:1
7	55872	−0.81	6e−09	4e−06	45 x 49	PDZ binding kinase [Source:HGNC Symbol;Acc:18282]
8	91057	−0.75	7e−08	4e−06	46 x 47	coiled−coil domain containing 34 [Source:HGNC Symbol;Acc
9	899	−0.74	9e−08	4e−06	45 x 46	cyclin F [Source:HGNC Symbol;Acc:1591]
10	9055	−0.74	9e−08	4e−06	45 x 49	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc
11	89891	−0.74	1e−07	3e−05	46 x 45	WD repeat domain 34 [Source:HGNC Symbol;Acc:28296]
12	55355	−0.7	4e−07	3e−05	44 x 49	Holliday junction recognition protein [Source:HGNC Symbol;
13	8364	−0.64	5e−07	4e−05	47 x 46	histone cluster 2, H4a [Source:HGNC Symbol;Acc:4794]
14	84823	−0.69	8e−07	4e−05	44 x 49	lamin B2 [Source:HGNC Symbol;Acc:6638]
15	124222	−0.68	1e−06	5e−05	45 x 46	progestin and adipoQ receptor family member IV [Source:HG
16	10721	−0.67	1e−06	5e−05	46 x 48	polymerase (DNA directed), theta [Source:HGNC Symbol;Ac
17	22974	−0.67	2e−06	7e−05	44 x 50	TPX2, microtubule−associated [Source:HGNC Symbol;Acc:1
18	5050	−0.65	3e−06	7e−05	47 x 45	platelet−activating factor acetylhydrolase 1b, catalytic subunit
19	3978	−0.65	3e−06	7e−05	46 x 45	ligase I, DNA, ATP−dependent [Source:HGNC Symbol;Acc:6
20	55723	−0.65	3e−06	7e−05	46 x 47	anti−silencing function 1B histone chaperone [Source:HGNC



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−57.34	NULL	98 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	−57.34	NULL	98 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	−32.86	NULL	122 / 370	BP	mitotic cell cycle
4	−28.88	NULL	26 / 57	Glio	developing astrocytes
5	−28.42	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
6	−28.4	NULL	117 / 530	Cancer	Lembcke_Normal vs Adenoma
7	−27.26	NULL	55 / 149	BP	DNA replication
8	−26.42	NULL	21 / 30	BP	DNA strand elongation involved in DNA replication
9	−24.97	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
10	−24.83	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
11	−24.83	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
12	−23.21	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
13	−22.9	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
14	−22.88	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
15	−22.06	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
16	−21.76	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
17	−21.63	NULL	61 / 232	BP	mitosis
18	−21.06	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	−20.71	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
20	−20.45	NULL	12 / 15	GSEA C2	CHANG_CYCLING_GENES
21	−20.37	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
22	−19.99	NULL	12 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
23	−19.51	NULL	25 / 56	CC	chromosome, centromeric region
24	−19.3	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
25	−18.9	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
26	−18.84	NULL	14 / 22	BP	DNA replication initiation
27	−18.81	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
28	−18.62	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
29	−18.57	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
30	−18.44	NULL	12 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
31	−18.44	NULL	15 / 21	BP	telomere maintenance via semi−conservative replication
32	−18.33	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
33	−18.28	NULL	9 / 15	GSEA C2	KEGG_DNA_REPLICATION
34	−18.18	NULL	11 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
35	−18.17	NULL	136 / 949	CC	nucleoplasm
36	−18.07	NULL	16 / 24	BP	telomere maintenance via recombination
37	−18	NULL	11 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
38	−18	NULL	11 / 16	GSEA C2	REACTOME_G2_M_CHECKPOINTS
39	−17.93	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
40	−17.84	NULL	13 / 18	BP	spindle organization