GW_306

Global Summary

%DE = 0.16

genes with fdr < 0.2 = 2281 (1266 + / 1015 −)

genes with fdr < 0.1 = 1739 (981 + / 758 −)

genes with fdr < 0.05 = 1432 (816 + / 616 −)

genes with fdr < 0.01 = 952 (528 + / 424 −)

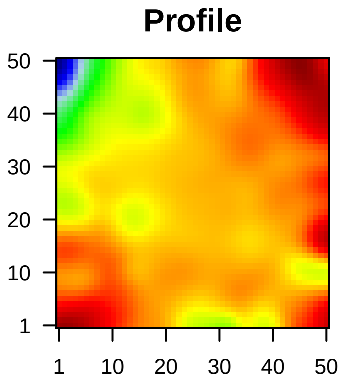
genes in genesets = 16332

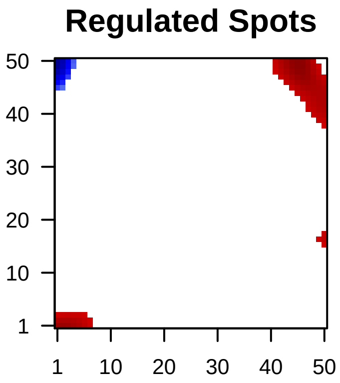
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

<fdr> = 0.84



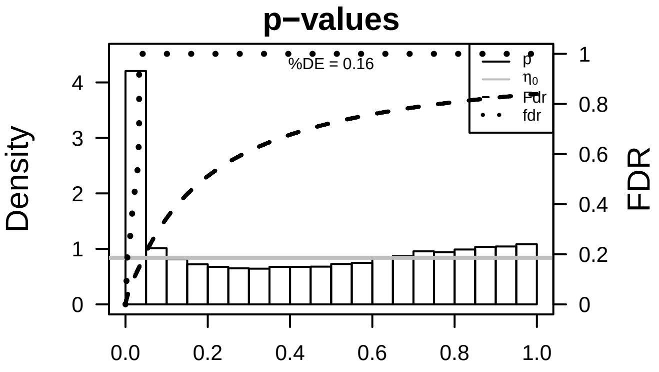


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	113146	−1.64	2e−16	2e−14	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
2	57016	−1.95	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	441282	−1.51	2e−16	2e−14	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
4	8644	−1.55	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
5	1109	−1.83	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
6	218	−2.92	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
7	55107	2.15	2e−16	2e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
8	244	−1.81	2e−16	2e−14	1 x 43	annexin A8−like 2 [Source:HGNC Symbol;Acc:23335]
9	387695	−1.61	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
10	64073	−1.71	2e−16	2e−14	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
11	260436	3.37	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
12	375791	−1.74	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
13	23705	1.58	2e−16	2e−14	50 x 7	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
14	810	−1.36	2e−16	2e−14	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
15	84290	−1.7	2e−16	2e−14	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
16	414062	1.63	2e−16	2e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
17	9560	1.48	2e−16	2e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
18	909	1.6	2e−16	2e−14	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
19	928	2.05	2e−16	2e−14	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
20	1675	−1.61	2e−16	2e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.69	NULL	618	Chr	Chr 4
2	9.59	NULL	4	MMML CGS	MACIEJ_MMML 23
3	9.53	NULL	743	Chr	Chr 7
4	9.4	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
5	9.4	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
6	8.47	NULL	8023	MF	protein binding
7	8.42	NULL	43	MF	chemokine activity
8	8.3	NULL	370	BP	mitotic cell cycle
9	7.6	NULL	426	Lymphoma	SPANG_CD40 6hrs DN
10	7.43	NULL	866	Chr	Chr 12
11	7.42	NULL	949	CC	nucleoplasm
12	7.35	NULL	149	BP	DNA replication
13	7.24	NULL	16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
14	6.95	NULL	57	Glio	developing astrocytes
15	6.92	NULL	4640	CC	nucleus
16	6.85	NULL	10	CC	hemoglobin complex
17	6.72	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
18	6.71	NULL	246	miRNA target starBase	hsa−miR−524−5p
19	6.68	NULL	11	MF	oxygen transporter activity
20	6.65	NULL	436	miRNA target starBase	hsa−miR−548n
Underexpressed					
1	−32.33	NULL	135	H.Tiss	WIRTH_Mucosa
2	−16.69	NULL	572	Disease	GUDJ_psoriasis up
3	−12.96	NULL	1135	Chr	Chr 19
4	−12.72	NULL	76	BP	epidermis development
5	−12.68	NULL	21	CC	cornified envelope
6	−11.79	NULL	42	BP	keratinization
7	−10.34	NULL	53	BP	keratinocyte differentiation
8	−9.5	NULL	82	CC	intermediate filament
9	−9.26	NULL	44	CC	keratin filament
10	−9.09	NULL	19	BP	peptide cross−linking
11	−8.53	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
12	−8.46	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
13	−8.36	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	−8.21	NULL	918	Chr	Chr 17
15	−8.2	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
16	−8.08	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
17	−8.04	NULL	186	MF	structural molecule activity
18	−7.81	NULL	13	H.Tiss	WIRTH_Tonsil
19	−7.77	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
20	−7.66	NULL	16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN



GW_306

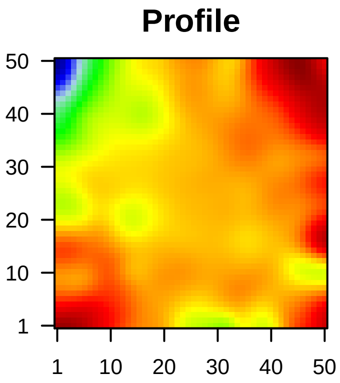
Local Summary

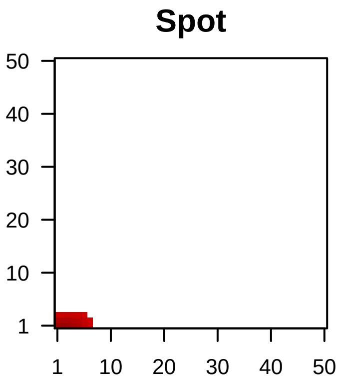
%DE = 0.62
metagenes = 20
genes = 312
genes in genesets = 311

genes with fdr < 0.1 = 136 (118 + / 18 −)
genes with fdr < 0.05 = 125 (111 + / 14 −)
genes with fdr < 0.01 = 118 (104 + / 14 −)

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

<FC> = 0.36
<shrinkage−t> = 12.42
<p−value> = 0
<fdr> = 0.54





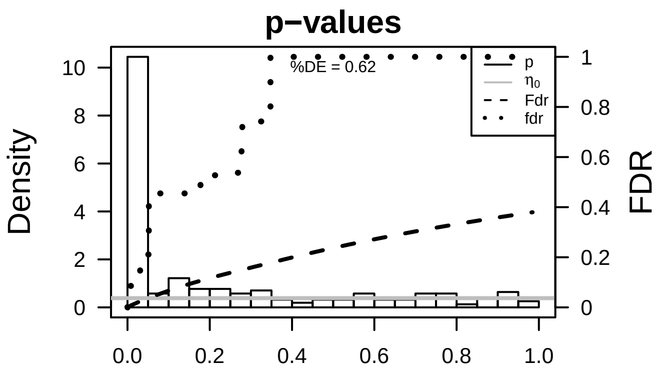
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	414062	1.63	2e−16	2e−15	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
2	1282	1.61	2e−16	2e−15	2 x 1	collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
3	1284	1.52	2e−16	2e−15	2 x 1	collagen, type IV, alpha 2 [Source:HGNC Symbol;Acc:2203]
4	2920	2.26	2e−16	2e−15	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
5	6374	2.44	2e−16	2e−15	1 x 1	chemokine (C−X−C motif) ligand 5 [Source:HGNC Symbol;Ac
6	6372	1.45	2e−16	2e−15	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
7	3491	1.6	2e−16	2e−15	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
8	3039	2.59	2e−16	2e−15	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	3040	2.71	2e−16	2e−15	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
10	3043	2.17	2e−16	2e−15	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
11	4319	−2.13	2e−16	2e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
12	4314	1.88	2e−16	2e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
13	4885	1.52	2e−16	2e−15	5 x 1	neuronal pentraxin II [Source:HGNC Symbol;Acc:7953]
14	26064	1.48	2e−16	2e−15	4 x 1	retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873]
15	387914	3.01	2e−16	2e−15	6 x 1	shisa family member 2 [Source:HGNC Symbol;Acc:20366]
16	7070	1.55	2e−16	2e−15	4 x 1	Thy−1 cell surface antigen [Source:HGNC Symbol;Acc:11801
17	3569	1.4	2e−15	1e−13	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
18	114757	1.4	2e−15	1e−13	5 x 1	cytoglobin [Source:HGNC Symbol;Acc:16505]
19	3576	1.4	3e−15	5e−13	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
20	2919	1.38	7e−15	5e−12	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	27.95	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
2	23.99	NULL	8 / 12	miRNA target	miR−29c
3	22.79	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
4	20.68	NULL	11 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
5	20.58	NULL	3 / 11	MF	oxygen transporter activity
6	18.08	NULL	8 / 11	MF	platelet−derived growth factor binding
7	17.26	NULL	83 / 250	Lymphoma	LENZ_Stromal signature 1
8	16.97	NULL	7 / 43	MF	chemokine activity
9	16.74	NULL	2 / 10	CC	hemoglobin complex
10	16.57	NULL	5 / 19	MF	peroxidase activity
11	15.88	NULL	2 / 11	GSEA C2	BIOCARTA_AHSP_PATHWAY
12	15.46	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
13	15.44	NULL	3 / 14	CC	endocytic vesicle lumen
14	15.22	NULL	21 / 57	MF	extracellular matrix structural constituent
15	14.99	NULL	65 / 242	BP	extracellular matrix organization
16	14.61	NULL	69 / 190	CC	extracellular matrix
17	14.53	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN
18	14.44	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
19	14.34	NULL	2 / 8	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_UP
20	13.99	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
21	13.83	NULL	8 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
22	13.56	NULL	31 / 69	BP	extracellular matrix disassembly
23	13.42	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
24	13.23	NULL	2 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
25	13.21	NULL	114 / 1182	CC	extracellular region
26	13.07	NULL	4 / 26	MF	oxygen binding
27	12.96	NULL	16 / 68	CC	collagen
28	12.85	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
29	12.84	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
30	12.69	NULL	5 / 10	GSEA C2	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
31	12.56	NULL	6 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
32	12.36	NULL	27 / 64	BP	collagen catabolic process
33	12.34	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
34	12.14	NULL	73 / 553	Cancer	Lembcke_Colonic Inflammation
35	12.08	NULL	3 / 19	BP	hydrogen peroxide catabolic process
36	12.02	NULL	10 / 40	BP	cellular response to amino acid stimulus
37	12	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
38	11.85	NULL	4 / 13	GSEA C2	SATO_SILENCED_BY_DEACETYLATION_IN_PANCREATIC_CAN
39	11.84	NULL	3 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
40	11.78	NULL	3 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY



GW_306

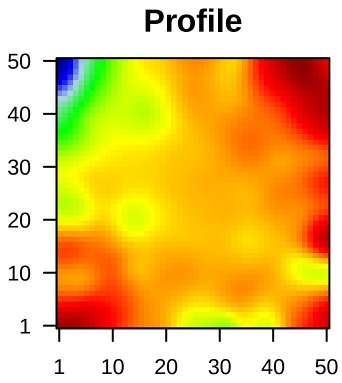
Local Summary

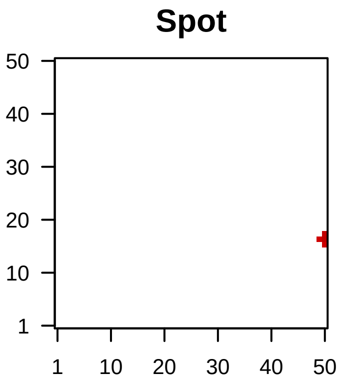
%DE = 0.78
metagenes = 4
genes = 101
genes in genesets = 101

genes with fdr < 0.1 = 60 (57 + / 3 −)
genes with fdr < 0.05 = 60 (57 + / 3 −)
genes with fdr < 0.01 = 53 (53 + / 0 −)

<r> metagenes = 0.99
<r> genes = 0.38

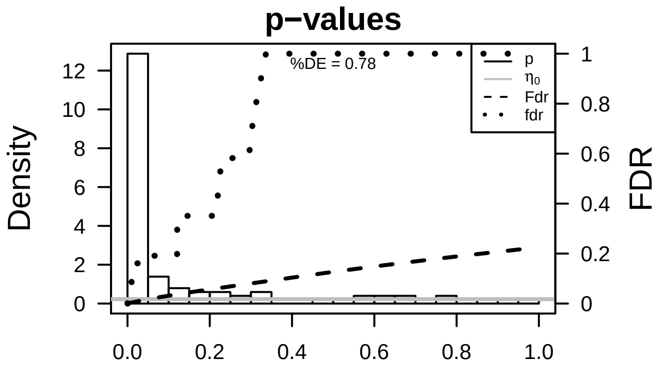
<FC> = 0.59
<shrinkage−t> = 20.75
<p−value> = 0
<fdr> = 0.41





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	909	1.6	2e−16	6e−16	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
2	221061	1.75	2e−16	6e−16	50 x 16	family with sequence similarity 171, member A1 [Source:HGN
3	26002	1.71	2e−16	6e−16	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
4	4602	2.67	2e−16	6e−16	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
5	83988	2.43	2e−16	6e−16	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
6	9603	1.9	2e−16	6e−16	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
7	4948	1.65	2e−16	6e−16	50 x 17	oculocutaneous albinism II [Source:HGNC Symbol;Acc:8101]
8	54959	2.51	2e−16	6e−16	50 x 17	odontogenic, ameloblast asssociated [Source:HGNC Symbol
9	4613	1.44	4e−16	8e−13	50 x 17	v−myc avian myelocytomatosis viral oncogene neuroblastom
10	79805	1.34	4e−14	3e−11	50 x 18	vasohibin 2 [Source:HGNC Symbol;Acc:25723]
11	63917	1.26	1e−12	7e−11	50 x 16	UDP−N−acetyl−alpha−D−galactosamine:polypeptide N−acet
12	1875	1.23	5e−12	3e−09	50 x 17	E2F transcription factor 5, p130−binding [Source:HGNC Sym
13	91461	1.14	1e−10	2e−08	50 x 17	protein kinase domain containing, cytoplasmic [Source:HGNC
14	51768	1.07	2e−09	2e−08	50 x 16	transmembrane 7 superfamily member 3 [Source:HGNC Sym
15	60436	1.06	2e−09	2e−08	50 x 18	TGFB−induced factor homeobox 2 [Source:HGNC Symbol;A
16	55691	1.06	2e−09	3e−08	50 x 18	FERM domain containing 4A [Source:HGNC Symbol;Acc:254
17	494470	1.05	4e−09	3e−08	50 x 17	ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
18	133121	1.04	5e−09	9e−08	50 x 18	ectonucleotide pyrophosphatase/phosphodiesterase 6 [Sourc
19	1298	1.02	9e−09	1e−07	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
20	55846	1	1e−08	3e−07	50 x 18	integrin alpha FG−GAP repeat containing 2 [Source:HGNC S



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	22.22	NULL	4 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	18.41	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
3	17.93	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
4	16.62	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
5	16.38	NULL	2 / 15	BP	embryonic digestive tract development
6	16.07	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
7	15.47	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
8	15.47	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
9	15.12	NULL	1 / 8	GSEA C2	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
10	14.87	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
11	14.53	NULL	2 / 16	GSEA C2	WU_HBX_TARGETS_3_UP
12	14.19	NULL	3 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
13	13.71	NULL	1 / 11	BP	homeostasis of number of cells
14	13.71	NULL	1 / 11	Pathw Act	BENTINK_e2f3.2
15	13.71	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
16	13.71	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
17	13.02	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
18	13	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
19	12.51	NULL	1 / 3	miRNA target	miR−148a
20	12.41	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
21	12.41	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
22	12.41	NULL	1 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
23	11.96	NULL	1 / 5	TF	MYC_TFs
24	11.96	NULL	1 / 5	miRNA target	miR−101
25	11.88	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
26	11.88	NULL	1 / 14	GSEA C2	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
27	11.88	NULL	1 / 14	GSEA C2	TENEDINI_MEGAKARYOCYTE_MARKERS
28	11.88	NULL	1 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
29	11.88	NULL	1 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
30	11.8	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
31	11.76	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
32	11.74	NULL	1 / 2	TF	MYC_Cell cycle DOWN
33	11.69	NULL	1 / 13	GSEA C2	FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN
34	11.49	NULL	2 / 12	GSEA C2	KIM_WT1_TARGETS_12HR_UP
35	11.41	NULL	1 / 15	GSEA C2	LINDGREN_BLADDER_CANCER_CLUSTER_3_DN
36	11.41	NULL	1 / 15	GSEA C2	RUGO_RESPONSE_TO_GAMMA_RADIATION
37	11.41	NULL	1 / 15	GSEA C2	WEI_MIR34A_TARGETS
38	11.41	NULL	1 / 15	GSEA C2	DORSAM_HOXA9_TARGETS_UP
39	11.41	NULL	1 / 15	GSEA C2	KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION
40	11.41	NULL	1 / 15	GSEA C2	KYNG_DNA_DAMAGE_DN

GW_306

Local Summary

%DE = 0.6

metagenes = 75

genes = 824

genes in genesets = 817

genes with fdr < 0.1 = 361 (345 + / 16 −)

genes with fdr < 0.05 = 323 (311 + / 12 −)

genes with fdr < 0.01 = 210 (205 + / 5 −)

<r> metagenes = 0.81

<r> genes = 0.22

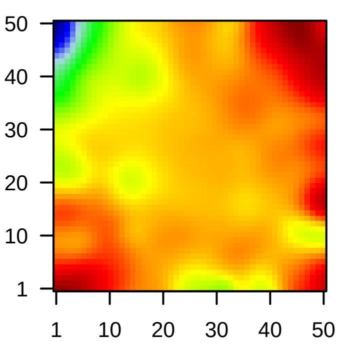
<FC> = 0.34

<shrinkage−t> = 11.94

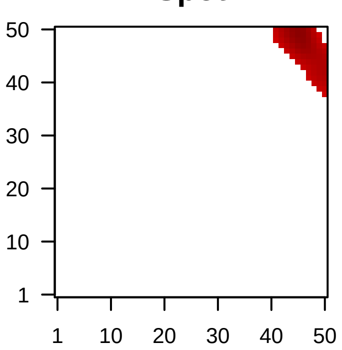
<p−value> = 0.01

<fdr> = 0.59

Profile



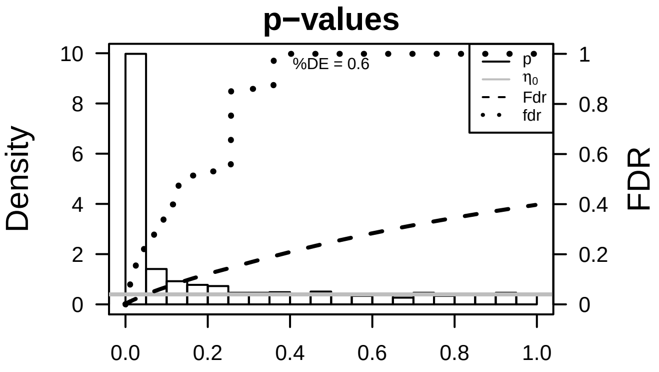
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9965	1.83	2e−16	8e−15	50 x 42	fibroblast growth factor 19 [Source:HGNC Symbol;Acc:3675]
2	57549	1.58	2e−16	8e−15	49 x 47	immunoglobulin superfamily, member 9 [Source:HGNC Symb
3	79682	1.5	2e−16	8e−15	46 x 47	centromere protein U [Source:HGNC Symbol;Acc:21348]
4	4897	1.45	2e−16	8e−15	50 x 45	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:
5	10635	1.63	2e−16	8e−15	45 x 50	RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169
6	157869	1.68	2e−16	8e−15	50 x 42	somatomedin B and thrombospondin, type 1 domain containi
7	6659	1.53	2e−16	8e−15	50 x 45	SRY (sex determining region Y)−box 4 [Source:HGNC Symb
8	7345	2.86	2e−16	8e−15	50 x 46	ubiquitin carboxyl−terminal esterase L1 (ubiquitin thiolesteras
9	7546	1.71	2e−16	8e−15	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
10	64207	1.41	2e−15	5e−13	50 x 40	interferon regulatory factor 2 binding protein−like [Source:HG
11	2119	1.39	4e−15	5e−13	50 x 43	ets variant 5 [Source:HGNC Symbol;Acc:3494]
12	84223	1.38	6e−15	5e−13	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
13	388228	1.38	6e−15	6e−12	50 x 45	SH3 domain binding kinase 1 [Source:HGNC Symbol;Acc:17
14	3148	1.35	2e−14	1e−11	46 x 46	high mobility group box 2 [Source:HGNC Symbol;Acc:5000]
15	55200	1.33	6e−14	2e−11	50 x 46	pleckstrin homology domain containing, family G (with RhoGe
16	3304	−1.21	1e−13	7e−11	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
17	4171	1.29	3e−13	9e−09	46 x 48	minichromosome maintenance complex component 2 [Source
18	9334	1.17	4e−11	9e−09	50 x 41	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
19	23462	1.16	5e−11	1e−08	50 x 45	hes−related family bHLH transcription factor with YRPW moti
20	26227	1.14	1e−10	1e−08	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.38	NULL	96 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	25.38	NULL	96 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	18.24	NULL	117 / 370	BP	mitotic cell cycle
4	17.11	NULL	9 / 11	GSEA C2	KALMA_E2F1_TARGETS
5	16.73	NULL	19 / 30	BP	DNA strand elongation involved in DNA replication
6	16.06	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
7	15.66	NULL	10 / 16	Cancer	WOLFER_overlap genes
8	15.28	NULL	8 / 16	GSEA C2	LY_AGING_PREMATURE_DN
9	14.57	NULL	13 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
10	14.57	NULL	27 / 57	Glio	developing astrocytes
11	14.48	NULL	53 / 149	BP	DNA replication
12	14.13	NULL	8 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
13	13.88	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
14	13.69	NULL	8 / 15	GSEA C2	LY_AGING_OLD_DN
15	13.63	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
16	13.6	NULL	12 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
17	13.56	NULL	9 / 11	GSEA C2	LIANG_SILENCED_BY_METHYLATION_DN
18	13.37	NULL	122 / 530	Cancer	Lembcke_Normal vs Adenoma
19	13.16	NULL	11 / 16	GSEA C2	SONG_TARGETS_OF_IE86_CMV_PROTEIN
20	12.64	NULL	154 / 949	CC	nucleoplasm
21	12.46	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
22	12.01	NULL	11 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
23	11.77	NULL	7 / 16	GSEA C2	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
24	11.55	NULL	12 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
25	11.37	NULL	13 / 22	BP	DNA replication initiation
26	11.36	NULL	10 / 14	GSEA C2	PUJANA_BRCA2_PCC_NETWORK
27	11.33	NULL	13 / 21	BP	telomere maintenance via semi−conservative replication
28	11.31	NULL	10 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
29	11.22	NULL	11 / 16	GSEA C2	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
30	11.21	NULL	13 / 14	MMML CGS	MACIEJ_MMML 4
31	11.19	NULL	62 / 298	BP	DNA repair
32	11.17	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
33	11.05	NULL	12 / 16	GSEA C2	SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
34	10.92	NULL	9 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
35	10.68	NULL	12 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
36	10.64	NULL	11 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
37	10.58	NULL	13 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
38	10.57	NULL	14 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
39	10.24	NULL	7 / 9	GSEA C2	REACTOME_CELL_CYCLE_CHECKPOINTS
40	10.23	NULL	2 / 8	GSEA C2	MUNSHI_MULTIPLE_MYELOMA_DN

GW_306

Local Summary

%DE = 0.96

metagenes = 18

genes = 257

genes in genesets = 251

genes with fdr < 0.1 = 240 (4 + / 236 −)

genes with fdr < 0.05 = 233 (2 + / 231 −)

genes with fdr < 0.01 = 228 (2 + / 226 −)

<r> metagenes = 0.94

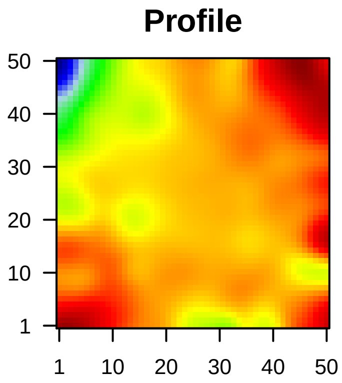
<r> genes = 0.43

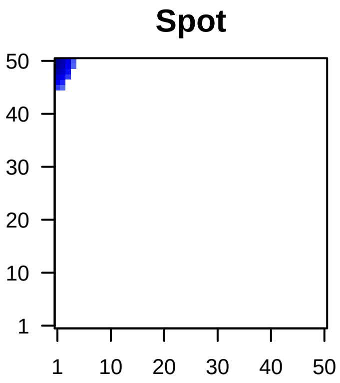
<FC> = −0.99

<shrinkage−t> = −35.11

<p−value> = 0

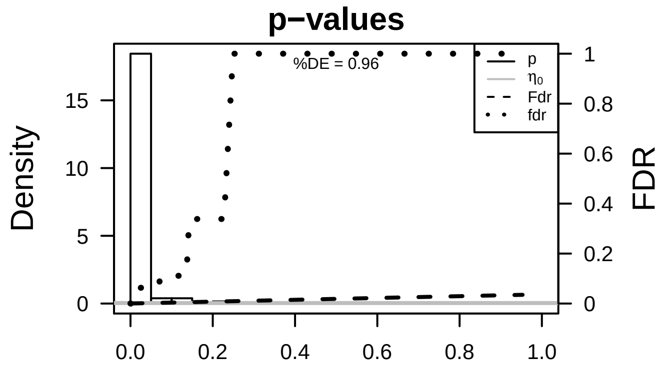
<fdr> = 0.12





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	−1.95	2e−16	4e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	441282	−1.51	2e−16	4e−17	1 x 49	aldo−keto reductase family 1, member B15 [Source:HGNC Sy
3	8644	−1.55	2e−16	4e−17	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	218	−2.92	2e−16	4e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	387695	−1.61	2e−16	4e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
6	64073	−1.71	2e−16	4e−17	1 x 46	chromosome 19 open reading frame 33 [Source:HGNC Sym
7	375791	−1.74	2e−16	4e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
8	810	−1.36	2e−16	4e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
9	84290	−1.7	2e−16	4e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	548596	−2.13	2e−16	4e−17	4 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Ac
11	9635	−1.72	2e−16	4e−17	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
12	22802	−1.9	2e−16	4e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
13	84518	−1.86	2e−16	4e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
14	49860	−2.14	2e−16	4e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	414325	−1.55	2e−16	4e−17	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	1673	−1.67	2e−16	4e−17	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
17	1825	−1.46	2e−16	4e−17	1 x 45	desmocollin 3 [Source:HGNC Symbol;Acc:3037]
18	1830	−1.69	2e−16	4e−17	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
19	9982	−1.43	2e−16	4e−17	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Sym
20	163351	−1.47	2e−16	4e−17	1 x 50	guanylate binding protein family, member 6 [Source:HGNC S



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all		Geneset
1	−71.15	NULL	90 / 135	H.Tiss	WIRTH_Mucosa
2	−31.71	NULL	18 / 21	CC	cornified envelope
3	−31.34	NULL	103 / 572	Disease	GUDJ_psoriasis up
4	−28.43	NULL	24 / 53	BP	keratinocyte differentiation
5	−25.36	NULL	19 / 42	BP	keratinization
6	−23.72	NULL	25 / 76	BP	epidermis development
7	−23.64	NULL	10 / 19	BP	peptide cross−linking
8	−19.48	NULL	12 / 21	CC	desmosome
9	−17.85	NULL	10 / 44	CC	keratin filament
10	−16.55	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
11	−16.52	NULL	16 / 82	CC	intermediate filament
12	−15.18	NULL	23 / 186	MF	structural molecule activity
13	−15.01	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
14	−14.12	NULL	9 / 38	BP	epithelial cell differentiation
15	−13.78	NULL	6 / 13	BP	negative regulation of peptidase activity
16	−13.76	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	−13.54	NULL	3 / 12	BP	cellular aldehyde metabolic process
18	−12.89	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
19	−12.17	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
20	−12.13	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
21	−11.98	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
22	−11.96	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
23	−11.74	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
24	−11.5	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
25	−11.29	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_
26	−10.89	NULL	6 / 16	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
27	−10.62	NULL	7 / 29	BP	regulation of proteolysis
28	−10.52	NULL	4 / 14	GSEA C2	CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
29	−10.36	NULL	3 / 13	BP	intermediate filament cytoskeleton organization
30	−10.34	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
31	−10.32	NULL	13 / 79	MF	serine−type endopeptidase inhibitor activity
32	−10.18	NULL	10 / 52	BP	negative regulation of endopeptidase activity
33	−10.04	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
34	−10.03	NULL	5 / 10	MF	RAGE receptor binding
35	−9.98	NULL	60 / 1182	CC	extracellular region
36	−9.85	NULL	5 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
37	−9.63	NULL	2 / 9	GSEA C2	NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
38	−9.58	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
39	−9.47	NULL	4 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
40	−9.06	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP