GW_244

Global Summary

%DE = 0.14

genes with fdr < 0.2 = 1564 (850 + / 714 −)

genes with fdr < 0.1 = 1297 (723 + / 574 −)

genes with fdr < 0.05 = 1117 (623 + / 494 −)

genes with fdr < 0.01 = 787 (460 + / 327 −)

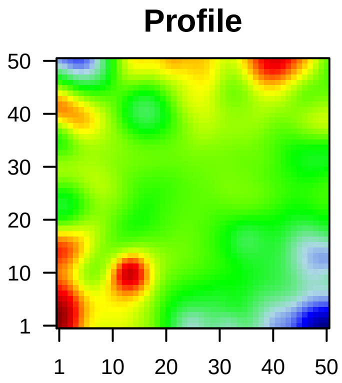
genes in genesets = 16332

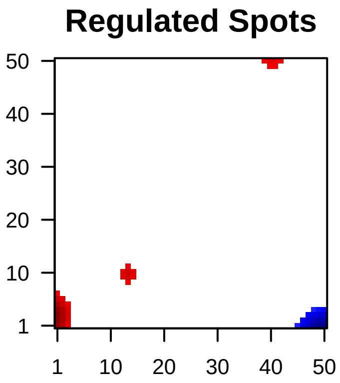
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.12

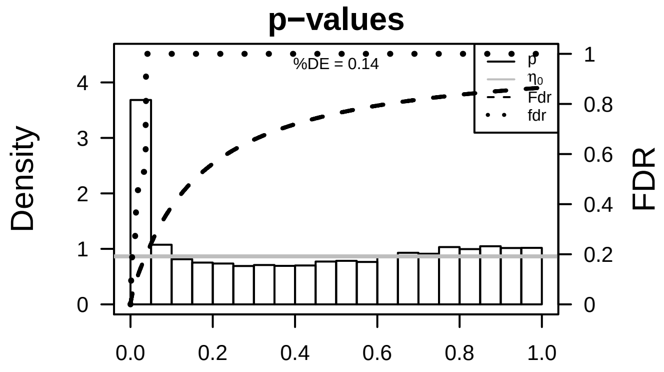
<fdr> = 0.86





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	131	−2.09	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	220	2.14	2e−16	5e−14	4 x 46	aldehyde dehydrogenase 1 family, member A3 [Source:HGN
3	218	−2.18	2e−16	5e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
4	55107	1.56	2e−16	5e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
5	445328	−2.3	2e−16	5e−14	4 x 46	Rho guanine nucleotide exchange factor (GEF) 35 [Source:H
6	590	1.65	2e−16	5e−14	16 x 50	butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
7	387695	−1.79	2e−16	5e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
8	51806	−1.58	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
9	857	1.62	2e−16	5e−14	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;
10	858	1.79	2e−16	5e−14	1 x 42	caveolin 2 [Source:HGNC Symbol;Acc:1528]
11	595	1.51	2e−16	5e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
12	1675	−1.62	2e−16	5e−14	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
13	2920	1.89	2e−16	5e−14	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;A
14	6372	1.67	2e−16	5e−14	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;A
15	131566	1.63	2e−16	5e−14	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
16	729428	3.39	2e−16	5e−14	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
17	729422	3.74	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	729431	1.62	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
19	100008586	2.81	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
20	645073	3.13	2e−16	5e−14	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	10.52	NULL	743	Chr	Chr 7
2	9.95	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
3	9.74	NULL	15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
4	9.34	NULL	242	BP	extracellular matrix organization
5	9.08	NULL	64	BP	collagen catabolic process
6	8.81	NULL	69	BP	extracellular matrix disassembly
7	8.73	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
8	7.76	NULL	1720	Chr	Chr 1
9	7.49	NULL	16	GSEA C2	TIAN_TNF_SIGNALING_VIA_NFKB
10	7.41	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
11	7.1	NULL	15	GSEA C2	HOOI_ST7_TARGETS_UP
12	7.08	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
13	7.02	NULL	15	GSEA C2	NAGASHIMA_NRG1_SIGNALING_UP
14	6.95	NULL	11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
15	6.84	NULL	9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
16	6.83	NULL	530	Cancer	Lembcke_Normal vs Adenoma
17	6.73	NULL	11	GSEA C2	MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
18	6.66	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
19	6.62	NULL	153	CC	endoplasmic reticulum lumen
20	6.55	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
Underexpressed					
1	−10.85	NULL	417	H.Tiss	WIRTH_Immune system
2	−10.73	NULL	15	CC	MHC class II protein complex
3	−10.5	NULL	633	Chr	Chr 9
4	−7.8	NULL	47	BP	antigen processing and presentation
5	−7.71	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
6	−7.64	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
7	−7.31	NULL	7	MMML CGS	MACIEJ_MMML 5
8	−7.3	NULL	135	H.Tiss	WIRTH_Mucosa
9	−7.23	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
10	−6.72	NULL	504	Chr	Chr 15
11	−6.54	NULL	6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
12	−6.51	NULL	21	CC	clathrin−coated endocytic vesicle membrane
13	−6.16	NULL	60	BP	T cell costimulation
14	−6.13	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
15	−6.06	NULL	74	BP	regulation of immune response
16	−5.9	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
17	−5.6	NULL	12	BP	cellular aldehyde metabolic process
18	−5.59	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
19	−5.56	NULL	5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
20	−5.45	NULL	127	H.Tiss	WIRTH_Muscle

GW_244

Local Summary

%DE = 0.72

metagenes = 18

genes = 296

genes in genesets = 294

genes with fdr < 0.1 = 159 (152 + / 7 −)

genes with fdr < 0.05 = 143 (137 + / 6 −)

genes with fdr < 0.01 = 121 (119 + / 2 −)

<r> metagenes = 0.95

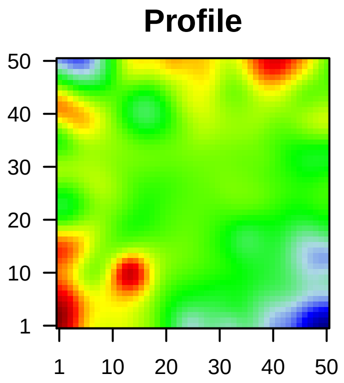
<r> genes = 0.34

<FC> = 0.5

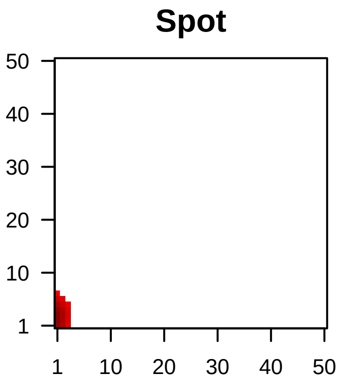
<shrinkage−t> = 17.38

<p−value> = 0

<fdr> = 0.5



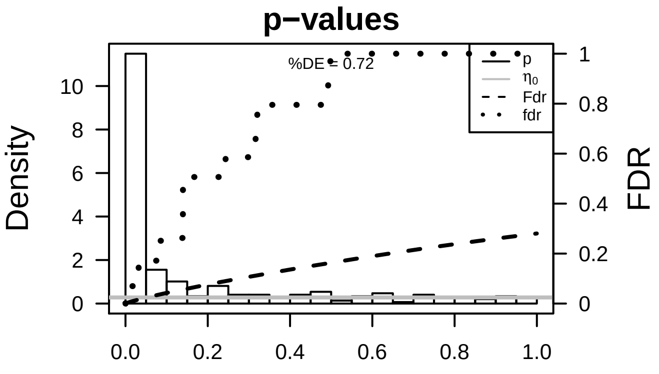
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	1.56	2e−16	1e−15	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	857	1.62	2e−16	1e−15	1 x 4	caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
3	595	1.51	2e−16	1e−15	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
4	2920	1.89	2e−16	1e−15	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
5	6372	1.67	2e−16	1e−15	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
6	131566	1.63	2e−16	1e−15	1 x 4	discoidin, CUB and LCCL domain containing 2 [Source:HGN
7	8870	1.86	2e−16	1e−15	1 x 3	immediate early response 3 [Source:HGNC Symbol;Acc:539
8	3576	1.56	2e−16	1e−15	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
9	3918	1.67	2e−16	1e−15	1 x 4	laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
10	4319	1.93	2e−16	1e−15	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
11	4314	1.87	2e−16	1e−15	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
12	4316	2.2	2e−16	1e−15	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
13	55714	1.86	2e−16	1e−15	1 x 1	teneurin transmembrane protein 3 [Source:HGNC Symbol;Ac
14	56034	1.78	2e−16	1e−15	1 x 4	platelet derived growth factor C [Source:HGNC Symbol;Acc:8
15	5328	1.6	2e−16	1e−15	1 x 3	plasminogen activator, urokinase [Source:HGNC Symbol;Acc
16	5054	1.75	2e−16	1e−15	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	7980	1.59	2e−16	1e−15	3 x 5	tissue factor pathway inhibitor 2 [Source:HGNC Symbol;Acc:1
18	7128	1.81	2e−16	1e−15	1 x 1	tumor necrosis factor, alpha−induced protein 3 [Source:HGN
19	84141	1.48	5e−15	2e−12	1 x 2	eva−1 homolog A (C. elegans) [Source:HGNC Symbol;Acc:2
20	4907	1.44	3e−14	2e−12	1 x 3	5'−nucleotidase, ecto (CD73) [Source:HGNC Symbol;Acc:80



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.15	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	21.59	NULL	60 / 242	BP	extracellular matrix organization
3	21.37	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN
4	20.69	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
5	20.67	NULL	24 / 64	BP	collagen catabolic process
6	20.44	NULL	25 / 69	BP	extracellular matrix disassembly
7	19.33	NULL	47 / 190	CC	extracellular matrix
8	18.95	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
9	18.27	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
10	17.7	NULL	7 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
11	17.43	NULL	7 / 11	MF	platelet−derived growth factor binding
12	17.11	NULL	71 / 683	CC	extracellular space
13	16.94	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
14	16.94	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
15	16.35	NULL	14 / 37	BP	collagen fibril organization
16	16.22	NULL	59 / 250	Lymphoma	LENZ_Stromal signature 1
17	16.22	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
18	16.17	NULL	10 / 40	BP	cellular response to amino acid stimulus
19	15.94	NULL	14 / 16	MMML CGS	MACIEJ_MMML 1
20	15.33	NULL	5 / 11	GSEA C2	BIOCARTA_PLATELETAPP_PATHWAY
21	15.06	NULL	3 / 7	GSEA C2	TSUNODA_CISPLATIN_RESISTANCE_UP
22	15.02	NULL	6 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
23	14.95	NULL	7 / 14	GSEA C2	VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
24	14.84	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
25	14.32	NULL	100 / 1182	CC	extracellular region
26	14.24	NULL	7 / 12	miRNA target	miR−29c
27	14.09	NULL	32 / 183	CC	proteinaceous extracellular matrix
28	14.02	NULL	4 / 7	GSEA C2	WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
29	13.95	NULL	4 / 15	GSEA C2	SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS
30	13.93	NULL	3 / 13	GSEA C2	SUZUKI_AMPLIFIED_IN_ORAL_CANCER
31	13.87	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
32	13.84	NULL	1 / 2	miRNA target	miR−16−1
33	13.84	NULL	6 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
34	13.6	NULL	7 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
35	13.52	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
36	13.4	NULL	5 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
37	13.35	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
38	13.28	NULL	55 / 403	BP	cell adhesion
39	13.22	NULL	3 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
40	13.19	NULL	8 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH

GW_244

Local Summary

%DE = 0.61

metagenes = 8

genes = 62

genes in genesets = 46

genes with fdr < 0.1 = 35 (32 + / 3 −)

genes with fdr < 0.05 = 30 (30 + / 0 −)

genes with fdr < 0.01 = 29 (29 + / 0 −)

<r> metagenes = 0.99

<r> genes = 0.38

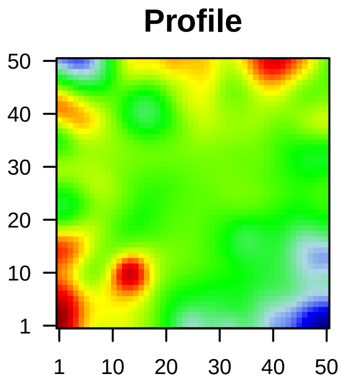
<FC> = 1.01

<shrinkage−t> = 35.4

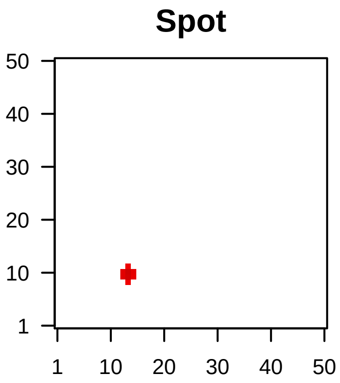
<p−value> = 0

<fdr> = 0.45

Profile



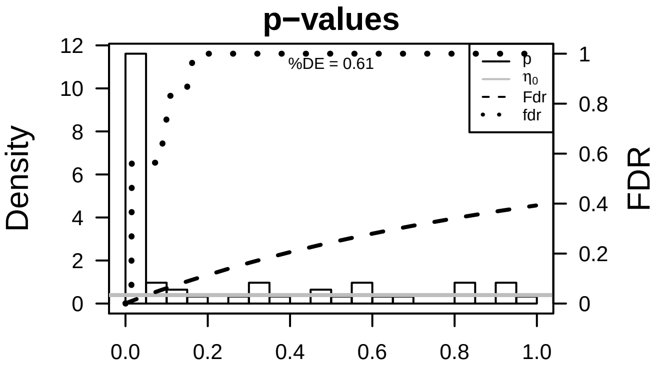
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	729428	3.39	2e−16	3e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
2	729422	3.74	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	729431	1.62	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	2.81	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	3.13	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.51	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	3.41	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	2.57	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.86	2e−16	3e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	3.6	2e−16	3e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.92	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	3.27	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	3.48	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2578	1.9	2e−16	3e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	2.9	2e−16	3e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	100101629	2.38	2e−16	3e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	4109	1.63	2e−16	3e−16	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
18	4103	1.57	2e−16	3e−16	14 x 10	melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
19	5446	1.77	2e−16	3e−16	13 x 10	paraoxonase 3 [Source:HGNC Symbol;Acc:9206]
20	402381	1.57	2e−16	3e−16	13 x 11	spermatogenesis and oogenesis specific basic helix−loop−he

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	29.25	NULL	1 / 2	miRNA target	miR−107
2	17.57	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
3	11.98	NULL	25 / 630	Chr	Chr X
4	11.14	NULL	1 / 10	GSEA C2	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
5	10.62	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
6	10.42	NULL	1 / 11	GSEA C2	NIKOLSKY_BREAST_CANCER_7Q21_Q22_AMPLICON
7	9.82	NULL	1 / 12	GSEA C2	HSIAO_LIVER_SPECIFIC_GENES
8	9.55	NULL	1 / 11	GSEA C2	SU_PLACENTA
9	9.53	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
10	9.31	NULL	1 / 13	GSEA C2	HOSHIDA_LIVER_CANCER_SURVIVAL_DN
11	9.31	NULL	1 / 10	GSEA C2	XU_RESPONSE_TO_TRETINOIN_DN
12	8.47	NULL	1 / 15	GSEA C2	WHITEFORD_PEDIATRIC_CANCER_MARKERS
13	8.47	NULL	1 / 15	GSEA C2	AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
14	8.47	NULL	1 / 15	GSEA C2	SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4
15	8.47	NULL	1 / 15	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S3
16	8.13	NULL	1 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
17	8.13	NULL	1 / 16	GSEA C2	JI_METASTASIS_REPRESSED_BY_STK11
18	8.12	NULL	1 / 14	GSEA C2	NIELSEN_GIST
19	7.97	NULL	1 / 5	miRNA target	miR−181a
20	7.83	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
21	7.76	NULL	1 / 15	GSEA C2	BROWNE_HCMV_INFECTION_8HR_DN
22	7.33	NULL	1 / 10	GSEA C2	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1
23	7.33	NULL	1 / 10	GSEA C2	CONRAD_STEM_CELL
24	7.31	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
25	6.85	NULL	1 / 11	GSEA C2	ODONNELL_TFRC_TARGETS_DN
26	6.81	NULL	1 / 6	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16
27	6.81	NULL	1 / 6	miRNA target	miR−181b
28	6.45	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
29	6.45	NULL	1 / 19	BP	oogenesis
30	6.01	NULL	1 / 7	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9
31	5.82	NULL	1 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
32	5.56	NULL	1 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
33	5.56	NULL	1 / 15	miRNA 3UTR	GTTCT−379
34	5.42	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
35	4.98	NULL	1 / 26	MF	cyclin−dependent protein serine/threonine kinase activity
36	4.61	NULL	1 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_DN
37	4.61	NULL	1 / 10	miRNA target	hsa−miR−933
38	4.47	NULL	1 / 17	BP	positive regulation of interleukin−1 beta secretion
39	4.3	NULL	6 / 419	CC	cellular_component
40	4.26	NULL	1 / 37	BP	ovarian follicle development

GW_244

Local Summary

%DE = 0.73

metagenes = 6

genes = 168

genes in genesets = 167

genes with fdr < 0.1 = 84 (81 + / 3 −)

genes with fdr < 0.05 = 73 (70 + / 3 −)

genes with fdr < 0.01 = 46 (46 + / 0 −)

<r> metagenes = 0.99

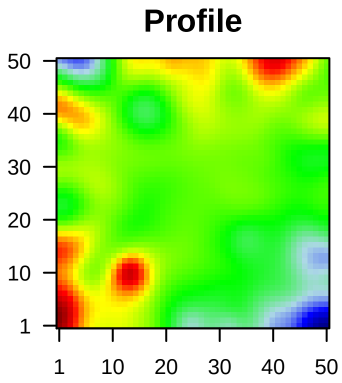
<r> genes = 0.36

<FC> = 0.4

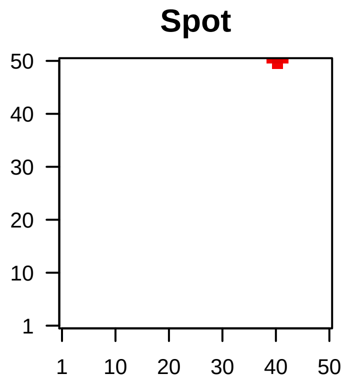
<shrinkage−t> = 14.03

<p−value> = 0.01

<fdr> = 0.59



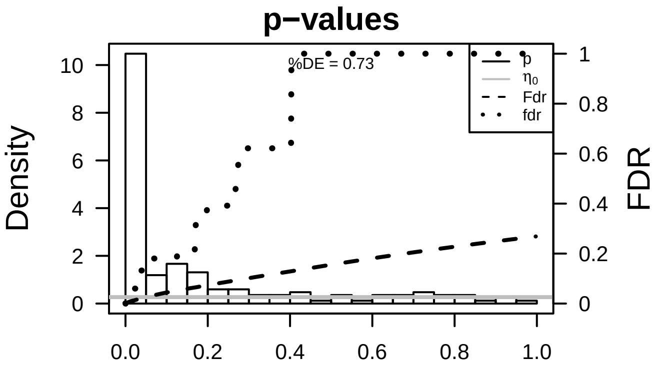
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8500	1.67	2e−16	5e−15	42 x 50	protein tyrosine phosphatase, receptor type, f polypeptide (PT
2	26872	1.76	2e−16	5e−15	40 x 50	six transmembrane epithelial antigen of the prostate 1 [Sourc
3	136	1.33	2e−12	4e−10	41 x 50	adenosine A2b receptor [Source:HGNC Symbol;Acc:264]
4	54517	1.29	1e−11	3e−09	41 x 50	pseudouridylate synthase 7 homolog (S. cerevisiae) [Source:
5	4904	1.13	7e−11	3e−08	41 x 49	Y box binding protein 1 [Source:HGNC Symbol;Acc:8014]
6	51678	1.16	1e−09	3e−08	40 x 50	membrane protein, palmitoylated 6 (MAGUK p55 subfamily m
7	10165	1.15	1e−09	4e−07	40 x 50	solute carrier family 25 (aspartate/glutamate carrier), membe
8	28969	1.09	1e−08	8e−07	39 x 50	basic leucine zipper and W2 domains 2 [Source:HGNC Symb
9	10026	1.04	4e−08	8e−07	40 x 49	phosphatidylinositol glycan anchor biosynthesis, class K [Sou
10	55536	1.04	5e−08	2e−06	42 x 50	cell division cycle associated 7−like [Source:HGNC Symbol;A
11	83787	1.01	9e−08	2e−05	39 x 50	armadillo repeat containing 10 [Source:HGNC Symbol;Acc:2
12	55127	0.95	5e−07	3e−05	40 x 50	HEAT repeat containing 1 [Source:HGNC Symbol;Acc:25517]
13	23161	0.92	1e−06	3e−05	39 x 50	sorting nexin 13 [Source:HGNC Symbol;Acc:21335]
14	3251	0.9	2e−06	4e−05	42 x 50	hypoxanthine phosphoribosyltransferase 1 [Source:HGNC Sy
15	1503	0.89	3e−06	4e−05	41 x 50	CTP synthase 1 [Source:HGNC Symbol;Acc:2519]
16	55706	0.88	4e−06	9e−05	40 x 50	NDC1 transmembrane nucleoporin [Source:HGNC Symbol;A
17	388962	0.84	1e−05	9e−05	41 x 50	bolA family member 3 [Source:HGNC Symbol;Acc:24415]
18	26774	0.83	1e−05	9e−05	41 x 50	growth arrest−specific 5 (non−protein coding) [Source:HGNC
19	9793	0.83	1e−05	9e−05	42 x 50	cytoskeleton associated protein 5 [Source:HGNC Symbol;Ac
20	23279	0.82	1e−05	9e−05	42 x 50	nucleoporin 160kDa [Source:HGNC Symbol;Acc:18017]



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	12.19	NULL	4 / 13	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
2	11.03	NULL	3 / 14	GSEA C2	MAYBURD_RESPONSE_TO_L663536_DN
3	9.8	NULL	3 / 10	CC	nuclear pore outer ring
4	9.77	NULL	2 / 16	GSEA C2	GALE_APL_WITH_FLT3_MUTATED_UP
5	9.63	NULL	3 / 16	GSEA C2	REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MA
6	9.61	NULL	1 / 12	MF	channel activity
7	9.61	NULL	1 / 12	GSEA C2	ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION
8	9.18	NULL	1 / 13	GSEA C2	ZUCCHI_METASTASIS_UP
9	8.99	NULL	2 / 15	GSEA C2	YAGI_AML_WITH_11Q23_REARRANGED
10	8.95	NULL	3 / 14	GSEA C2	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN
11	8.61	NULL	3 / 15	GSEA C2	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_
12	8.61	NULL	3 / 15	GSEA C2	REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_E
13	8.59	NULL	6 / 29	BP	regulation of glucose transport
14	8.57	NULL	8 / 59	CC	nuclear pore
15	8.48	NULL	2 / 9	GSEA C2	REACTOME_RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL_
16	8.46	NULL	1 / 15	GSEA C2	NEWMAN_ERCC6_TARGETS_UP
17	8.46	NULL	1 / 15	GSEA C2	WANG_SMARCE1_TARGETS_UP
18	8.37	NULL	2 / 15	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
19	8.3	NULL	3 / 16	GSEA C2	REACTOME_REV_MEDIATED_NUCLEAR_EXPORT_OF_HIV1_F
20	8.3	NULL	3 / 16	GSEA C2	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKI
21	8.3	NULL	2 / 15	GSEA C2	TIEN_INTESTINE_PROBIOTICS_24HR_UP
22	8.22	NULL	2 / 11	BP	mitotic metaphase plate congression
23	8.08	NULL	4 / 18	Lymphoma	DAVE_c−myc BL UP
24	7.99	NULL	1 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
25	7.7	NULL	6 / 35	BP	mitotic nuclear envelope disassembly
26	7.59	NULL	2 / 10	Cancer	GENTLES_modul3
27	7.48	NULL	2 / 14	Pathw Act	BENTINK_src.2
28	7.46	NULL	6 / 37	BP	hexose transport
29	7.42	NULL	2 / 14	GSEA C2	REACTOME_GLUCOSE_TRANSPORT
30	7.38	NULL	2 / 18	BP	glutamine metabolic process
31	7.29	NULL	1 / 9	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_
32	7.29	NULL	1 / 9	GSEA C2	BROWNE_HCMV_INFECTION_18HR_UP
33	7.2	NULL	2 / 10	CC	microtubule plus−end
34	7.15	NULL	2 / 14	MF	pseudouridine synthase activity
35	7.11	NULL	3 / 16	GSEA C2	BIDUS_METASTASIS_UP
36	6.98	NULL	1 / 21	BP	iron ion homeostasis
37	6.89	NULL	2 / 8	GSEA C2	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS
38	6.88	NULL	2 / 14	GSEA C2	REACTOME_TRNA_AMINOACYLATION
39	6.87	NULL	2 / 16	GSEA C2	REACTOME_VPR_MEDIATED_NUCLEAR_IMPORT_OF_PICS
40	6.86	NULL	2 / 14	BP	purine nucleotide biosynthetic process

GW_244

Local Summary

%DE = 0.94

metagenes = 18

genes = 289

genes in genesets = 286

genes with fdr < 0.1 = 242 (10 + / 232 −)

genes with fdr < 0.05 = 234 (7 + / 227 −)

genes with fdr < 0.01 = 189 (5 + / 184 −)

<r> metagenes = 0.99

<r> genes = 0.57

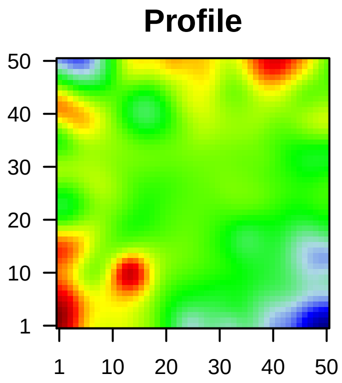
<FC> = −0.55

<shrinkage−t> = −19.09

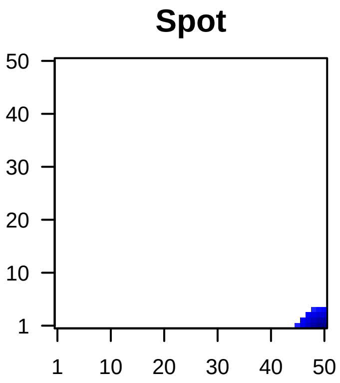
<p−value> = 0

<fdr> = 0.35

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3122	−1.47	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
2	3512	−1.87	2e−16	1e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
3	5920	−1.57	2e−16	1e−15	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
4	54855	−1.51	2e−15	5e−13	49 x 1	family with sequence similarity 46, member C [Source:HGNC
5	3113	−1.44	3e−14	5e−13	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
6	3109	−1.43	6e−14	2e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
7	3108	−1.4	2e−13	1e−11	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
8	3123	−1.36	7e−13	8e−11	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
9	10628	−1.27	9e−12	8e−11	48 x 1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
10	6352	−1.29	1e−11	8e−11	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
11	8635	−1.28	1e−11	1e−09	46 x 1	ribonuclease T2 [Source:HGNC Symbol;Acc:21686]
12	23643	−1.2	2e−10	1e−09	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
13	972	−1.2	2e−10	1e−09	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
14	919	−1.2	3e−10	1e−09	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
15	692084	−1.19	3e−10	3e−09	48 x 4	small nucleolar RNA, C/D box 13 [Source:HGNC Symbol;Acc
16	3059	−1.18	4e−10	1e−08	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC S
17	55303	−1.14	2e−09	1e−08	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
18	3120	−1.14	2e−09	2e−08	47 x 1	major histocompatibility complex, class II, DQ beta 2 [Source:
19	6347	1.13	3e−09	3e−08	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
20	57172	−1.1	6e−09	3e−08	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−40.43	NULL	13 / 15	CC	MHC class II protein complex
2	−28.79	NULL	93 / 417	H.Tiss	WIRTH_Immune system
3	−25.43	NULL	16 / 47	BP	antigen processing and presentation
4	−23.07	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
5	−22.74	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
6	−22.02	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
7	−22.02	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
8	−21.63	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
9	−20.92	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−20.89	NULL	97 / 553	Cancer	Lembcke_Colonic Inflammation
11	−20.82	NULL	18 / 60	BP	T cell costimulation
12	−19.83	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
13	−19.41	NULL	8 / 28	CC	transport vesicle membrane
14	−19.09	NULL	54 / 312	BP	immune response
15	−18.58	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
16	−18.14	NULL	9 / 35	CC	trans−Golgi network membrane
17	−18.03	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
18	−18.01	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
19	−17.29	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
20	−15.74	NULL	18 / 84	BP	T cell receptor signaling pathway
21	−15.47	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
22	−15.3	NULL	9 / 46	CC	endocytic vesicle membrane
23	−15.19	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
24	−14.99	NULL	18 / 74	BP	regulation of immune response
25	−14.62	NULL	5 / 12	BP	immunoglobulin mediated immune response
26	−14.53	NULL	5 / 12	BP	dendritic cell chemotaxis
27	−14.35	NULL	44 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
28	−14.35	NULL	44 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
29	−14.35	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
30	−14.35	NULL	44 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
31	−14.22	NULL	12 / 60	BP	interferon−gamma−mediated signaling pathway
32	−14.16	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
33	−14.03	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
34	−13.97	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
35	−13.94	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
36	−13.92	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
37	−13.87	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
38	−13.78	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
39	−13.61	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
40	−13.38	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis

p−values