GW_157

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1905 (1110 + / 795 −)

genes with fdr < 0.1 = 1536 (919 + / 617 −)

genes with fdr < 0.05 = 1319 (798 + / 521 −)

genes with fdr < 0.01 = 862 (557 + / 305 −)

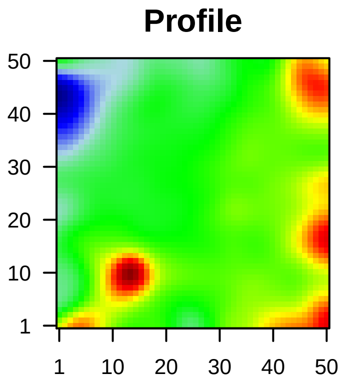
genes in genesets = 16332

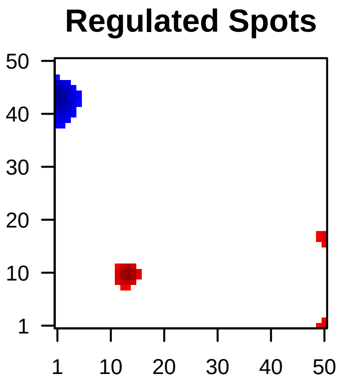
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

<fdr> = 0.85



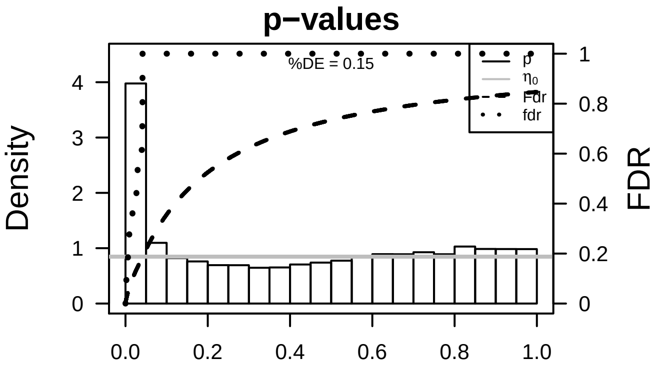


Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.46	2e−16	3e−14	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	72	1.43	2e−16	3e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	56892	1.47	2e−16	3e−14	50 x 7	chromosome 8 open reading frame 4 [Source:HGNC Symbol
4	23705	1.6	2e−16	3e−14	50 x 7	cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
5	6352	1.68	2e−16	3e−14	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
6	1063	1.43	2e−16	3e−14	46 x 48	centromere protein F, 350/400kDa [Source:HGNC Symbol;Ac
7	1116	1.79	2e−16	3e−14	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
8	9071	1.7	2e−16	3e−14	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]
9	5010	1.67	2e−16	3e−14	50 x 7	claudin 11 [Source:HGNC Symbol;Acc:8514]
10	26047	1.59	2e−16	3e−14	50 x 50	contactin associated protein−like 2 [Source:HGNC Symbol;Ac
11	1277	1.48	2e−16	3e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
12	169044	1.96	2e−16	3e−14	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
13	1298	1.51	2e−16	3e−14	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
14	49860	2.43	2e−16	3e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
15	441520	2.42	2e−16	3e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
16	57007	−1.79	2e−16	3e−14	14 x 50	atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
17	1591	1.64	2e−16	3e−14	33 x 2	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
18	92196	2.85	2e−16	3e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	1673	1.63	2e−16	3e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	8632	1.83	2e−16	3e−14	1 x 8	dynein, axonemal, heavy chain 17 [Source:HGNC Symbol;Ac

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	12.18	NULL	15	CC	MHC class II protein complex
2	11.67	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
3	8.63	NULL	21	CC	clathrin−coated endocytic vesicle membrane
4	8.17	NULL	250	Lymphoma	LENZ_Stromal signature 1
5	7.96	NULL	16	MMML CGS	MACIEJ_MMML 1
6	7.77	NULL	15	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_UP
7	7.75	NULL	1033	Chr	Chr 2
8	7.72	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
9	7.72	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
10	7.7	NULL	866	Chr	Chr 12
11	7.5	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
12	7.42	NULL	914	Chr	Chr 3
13	7.27	NULL	57	Glio	developing astrocytes
14	7.25	NULL	47	BP	antigen processing and presentation
15	7.22	NULL	3	MMML CGS	MACIEJ_MMML 7
16	6.92	NULL	190	CC	extracellular matrix
17	6.67	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
18	6.63	NULL	15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
19	6.57	NULL	153	CC	endoplasmic reticulum lumen
20	6.53	NULL	64	BP	collagen catabolic process
Underexpressed					
1	−12.57	NULL	717	Chr	Chr 16
2	−7.27	NULL	957	Chr	Chr 11
3	−7.13	NULL	7	MMML CGS	MACIEJ_MMML 9
4	−6.81	NULL	16	GSEA C2	GRATIAS_RETINOBLASTOMA_16Q24
5	−6.39	NULL	519	Chr	Chr 14
6	−6.15	NULL	572	Disease	GUDJ_psoriasis up
7	−5.72	NULL	127	H.Tiss	WIRTH_Muscle
8	−5.63	NULL	511	miRNA target−starBase	hsa−miR−106b
9	−5.29	NULL	15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
10	−5.22	NULL	603	miRNA target−starBase	hsa−miR−20a
11	−5.12	NULL	187	Chr	Chr 21
12	−4.9	NULL	13	GSEA C2	NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON
13	−4.72	NULL	47	CC	nucleosome
14	−4.71	NULL	14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
15	−4.7	NULL	565	miRNA target−starBase	hsa−miR−20b
16	−4.7	NULL	8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
17	−4.7	NULL	412	miRNA target−starBase	hsa−miR−372
18	−4.58	NULL	426	miRNA target−starBase	hsa−miR−519d
19	−4.56	NULL	15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
20	−4.49	NULL	538	miRNA target−starBase	hsa−miR−17



GW_157

Local Summary

%DE = 0.64

metagenes = 3

genes = 123

genes in genesets = 122

genes with fdr < 0.1 = 53 (50 + / 3 −)

genes with fdr < 0.05 = 51 (48 + / 3 −)

genes with fdr < 0.01 = 42 (40 + / 2 −)

<r> metagenes = 1

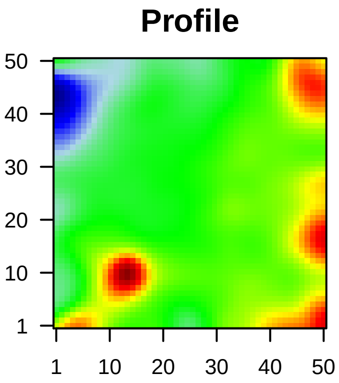
<r> genes = 0.68

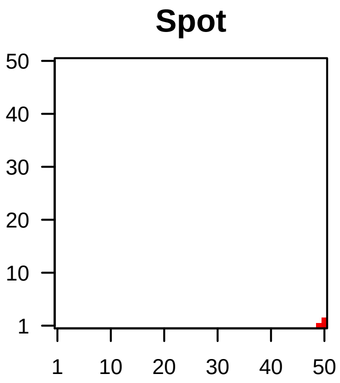
<FC> = 0.4

<shrinkage−t> = 14.09

<p−value> = 0

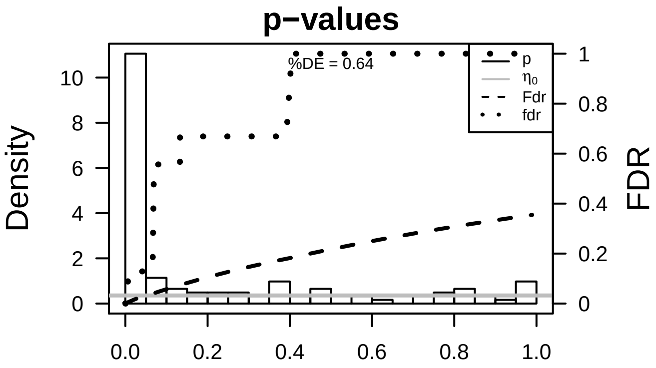
<fdr> = 0.53





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3512	1.68	2e−16	2e−15	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
2	3543	1.37	2e−16	2e−15	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC Sy
3	25849	1.82	2e−16	2e−15	50 x 2	prostate androgen−regulated mucin−like protein 1 [Source:H
4	57484	1.76	2e−16	2e−15	50 x 2	ring finger protein 150 [Source:HGNC Symbol;Acc:23138]
5	9806	1.78	2e−16	2e−15	50 x 1	sparc/osteonectin, cwcv and kazal−like domains proteoglyca
6	10537	2.28	2e−16	2e−15	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
7	3111	1.38	3e−15	1e−10	50 x 1	major histocompatibility complex, class II, DO alpha [Source:
8	260436	1.22	3e−12	7e−10	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
9	969	1.17	2e−11	7e−10	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
10	3113	1.15	4e−11	7e−10	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Sourc
11	3109	1.15	5e−11	2e−09	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
12	5996	1.13	8e−11	2e−09	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
13	3122	1.05	1e−10	8e−09	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
14	348	1.08	6e−10	8e−09	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
15	3128	1.08	6e−10	8e−09	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo
16	972	1.08	7e−10	8e−09	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
17	3108	1.07	9e−10	1e−08	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
18	713	1.06	1e−09	2e−08	50 x 1	complement component 1, q subcomponent, B chain [Source
19	4283	1.05	2e−09	4e−07	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
20	51755	0.98	2e−08	4e−07	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	45.54	NULL	10 / 15	CC	MHC class II protein complex
2	30.26	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
3	27.74	NULL	2 / 3	MMML CGS	MACIEJ_MMML 7
4	24.8	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
5	24.35	NULL	10 / 47	BP	antigen processing and presentation
6	23.37	NULL	1 / 4	MMML CGS	MACIEJ_MMML 2
7	21.48	NULL	6 / 21	CC	clathrin−coated endocytic vesicle membrane
8	20.95	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEME
9	20.53	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
10	20.42	NULL	6 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
11	18.32	NULL	6 / 28	CC	transport vesicle membrane
12	18.18	NULL	10 / 87	BP	antigen processing and presentation of exogenous peptide antigen
13	17.82	NULL	4 / 12	BP	immunoglobulin mediated immune response
14	17.76	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
15	17.71	NULL	2 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
16	17.63	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
17	17.63	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
18	17.63	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
19	17.3	NULL	31 / 312	BP	immune response
20	17.08	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
21	17.01	NULL	6 / 32	CC	ER to Golgi transport vesicle membrane
22	16.8	NULL	4 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
23	16.79	NULL	7 / 52	Chr	Chr HSCHR6_MHC_QBL
24	16.19	NULL	6 / 35	CC	trans−Golgi network membrane
25	16.19	NULL	3 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
26	14.98	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
27	14.82	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
28	13.92	NULL	6 / 46	CC	endocytic vesicle membrane
29	13.78	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
30	13.68	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
31	13.68	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
32	13.68	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
33	13.41	NULL	2 / 8	GSEA C2	KEGG_CELL_ADHESION_MOLECULES_CAMS
34	13.21	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
35	12.3	NULL	7 / 60	BP	interferon−gamma−mediated signaling pathway
36	11.95	NULL	2 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
37	11.93	NULL	2 / 11	BP	chaperone mediated protein folding requiring cofactor
38	11.93	NULL	2 / 11	BP	positive regulation of T cell differentiation
39	11.93	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP
40	11.89	NULL	1 / 6	H.Tiss	WIRTH_Bone marrow

GW_157

Local Summary

%DE = 0.74

metagenes = 20

genes = 101

genes in genesets = 78

genes with fdr < 0.1 = 66 (65 + / 1 −)

genes with fdr < 0.05 = 66 (65 + / 1 −)

genes with fdr < 0.01 = 61 (60 + / 1 −)

<r> metagenes = 0.96

<r> genes = 0.28

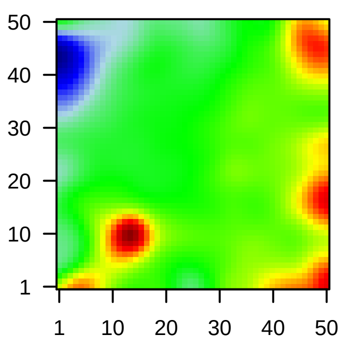
<FC> = 0.92

<shrinkage−t> = 32.1

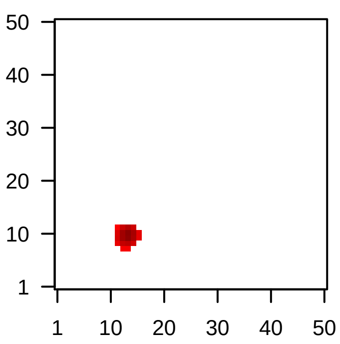
<p−value> = 0

<fdr> = 0.35

Profile



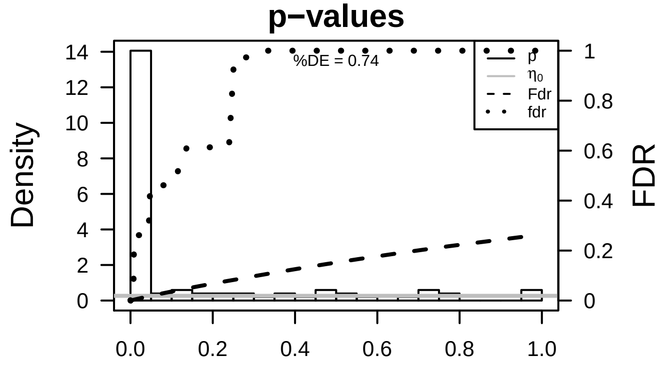
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	441520	2.42	2e−16	2e−16	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
2	729428	3.03	2e−16	2e−16	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
3	729422	3.41	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
4	100008586	2.63	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	645073	2.41	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
6	729442	3.15	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	2.79	2e−16	2e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729396	1.55	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	729447	2.26	2e−16	2e−16	14 x 11	G antigen 2A [Source:HGNC Symbol;Acc:4099]
10	645037	3.1	2e−16	2e−16	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
11	26749	2.38	2e−16	2e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	2576	2.58	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	2577	2.86	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	2578	1.78	2e−16	2e−16	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	2.32	2e−16	2e−16	14 x 11	G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	100101629	1.87	2e−16	2e−16	14 x 11	G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	121355	1.75	2e−16	2e−16	14 x 11	gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
18	547	2.54	2e−16	2e−16	12 x 9	kinesin family member 1A [Source:HGNC Symbol;Acc:888]
19	4100	1.49	2e−16	2e−16	14 x 11	melanoma antigen family A, 1 (directs expression of antigen
20	4103	1.87	2e−16	2e−16	14 x 10	melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	15.59	NULL	30 / 630	Chr	Chr X
2	13.08	NULL	1 / 4	GSEA C2	WEBER_METHYLATED_ICP_IN_SPERM_DN
3	11.84	NULL	1 / 12	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
4	11.09	NULL	1 / 6	GSEA C2	NIELSEN_LEIOMYOSARCOMA_UP
5	10	NULL	1 / 11	BP	dopamine metabolic process
6	10	NULL	1 / 11	BP	regulation of neurotransmitter secretion
7	10	NULL	1 / 11	GSEA C2	BIOCARTA_PARKIN_PATHWAY
8	9.77	NULL	2 / 23	BP	calcium−dependent cell−cell adhesion
9	9.74	NULL	1 / 6	GSEA C2	NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
10	9.09	NULL	2 / 27	Glio	WIRTH_PN subtype
11	8.76	NULL	1 / 7	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_UP
12	8.37	NULL	1 / 21	BP	anterograde axon cargo transport
13	7.81	NULL	1 / 14	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_B
14	7.62	NULL	2 / 8	GSEA C2	WEBER_METHYLATED_ICP_IN_FIBROBLAST
15	7.38	NULL	2 / 37	BP	synapse assembly
16	6.4	NULL	1 / 17	BP	positive regulation of interleukin−1 beta secretion
17	6.23	NULL	1 / 2	miRNA target	miR−107
18	5.86	NULL	1 / 13	GSEA C2	HATADA_METHYLATED_IN_LUNG_CANCER_DN
19	5.86	NULL	1 / 13	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP
20	5.59	NULL	1 / 14	BP	negative regulation of retinoic acid receptor signaling pathway
21	5.59	NULL	1 / 14	GSEA C2	KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_DN
22	5.36	NULL	10 / 481	BP	biological_process
23	5.35	NULL	1 / 15	GSEA C2	LI_WILMS_TUMOR
24	5.34	NULL	7 / 419	CC	cellular_component
25	5.3	NULL	1 / 45	CC	kinesin complex
26	5.21	NULL	3 / 15	GSEA C2	MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
27	5.15	NULL	1 / 4	GSEA C2	NIELSEN_LEIOMYOSARCOMA_DN
28	5.14	NULL	1 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
29	5.13	NULL	3 / 99	BP	homophilic cell adhesion
30	5.12	NULL	1 / 12	GSEA C2	HO_LIVER_CANCER_VASCULAR_INVASION
31	5.06	NULL	2 / 44	CC	presynaptic membrane
32	4.8	NULL	1 / 21	BP	negative regulation of Notch signaling pathway
33	4.64	NULL	2 / 68	BP	microtubule−based movement
34	4.63	NULL	1 / 56	MF	motor activity
35	4.62	NULL	1 / 19	MF	retinoic acid receptor binding
36	4.53	NULL	1 / 7	GSEA C2	KONDO_PROSTATE_CANCER_WITH_H3K27ME3
37	4.52	NULL	2 / 164	BP	cell death
38	4.51	NULL	2 / 71	MF	microtubule motor activity
39	4.48	NULL	10 / 549	MF	molecular_function
40	4.48	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN

GW_157

Local Summary

%DE = 0.9

metagenes = 5

genes = 105

genes in genesets = 105

genes with fdr < 0.1 = 86 (77 + / 9 −)

genes with fdr < 0.05 = 67 (64 + / 3 −)

genes with fdr < 0.01 = 56 (55 + / 1 −)

<r> metagenes = 0.99

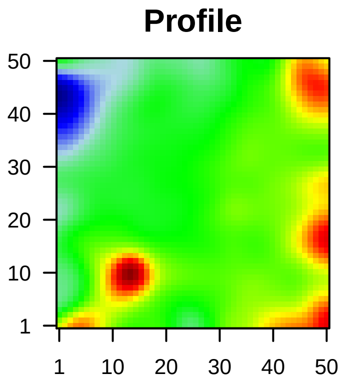
<r> genes = 0.38

<FC> = 0.56

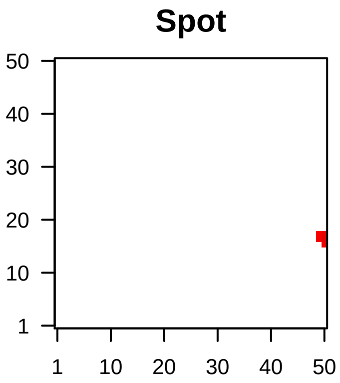
<shrinkage−t> = 19.57

<p−value> = 0

<fdr> = 0.4



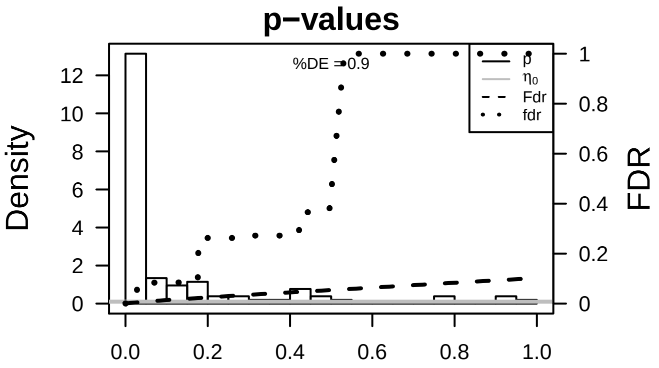
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	21	1.46	2e−16	3e−16	50 x 17	ATP−binding cassette, sub−family A (ABC1), member 3 [Sour
2	1298	1.51	2e−16	3e−16	50 x 17	collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
3	728715	1.94	2e−16	3e−16	50 x 18	
4	26002	1.6	2e−16	3e−16	50 x 16	monooxygenase, DBH−like 1 [Source:HGNC Symbol;Acc:21
5	4602	1.97	2e−16	3e−16	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
6	9603	2.1	2e−16	3e−16	50 x 18	nuclear factor, erythroid 2−like 3 [Source:HGNC Symbol;Acc:
7	10439	1.49	2e−16	3e−16	50 x 17	olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
8	162494	1.6	2e−16	3e−16	50 x 17	rhomboid, veinlet−like 3 (Drosophila) [Source:HGNC Symbol;
9	4948	1.39	2e−15	7e−14	50 x 17	oculocutaneous albinism II [Source:HGNC Symbol;Acc:8101]
10	51768	1.35	1e−14	7e−14	50 x 16	transmembrane 7 superfamily member 3 [Source:HGNC Sym
11	83988	1.34	1e−14	3e−13	50 x 17	neurocalcin delta [Source:HGNC Symbol;Acc:7655]
12	9915	1.32	4e−14	2e−12	50 x 17	aryl−hydrocarbon receptor nuclear translocator 2 [Source:HG
13	6096	1.28	2e−13	4e−11	50 x 16	RAR−related orphan receptor B [Source:HGNC Symbol;Acc:
14	221061	1.21	4e−12	1e−09	50 x 16	family with sequence similarity 171, member A1 [Source:HG
15	56994	1.1	3e−10	1e−09	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
16	56997	1.1	3e−10	1e−09	50 x 16	aarF domain containing kinase 3 [Source:HGNC Symbol;Acc
17	89876	1.1	3e−10	2e−09	50 x 16	MYCBP−associated, testis expressed 1 [Source:HGNC Sym
18	4613	1.09	5e−10	2e−08	50 x 17	v−myc avian myelocytomatosis viral oncogene neuroblastom
19	3670	1.05	2e−09	7e−08	50 x 17	ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
20	60436	0.99	2e−08	7e−08	50 x 18	TGFB−induced factor homeobox 2 [Source:HGNC Symbol;A



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	27.05	NULL	4 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
2	18.77	NULL	3 / 15	GSEA C2	MASSARWEH_RESPONSE_TO_ESTRADIOL
3	15.85	NULL	3 / 16	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
4	14.81	NULL	2 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
5	14.38	NULL	2 / 14	GSEA C2	CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
6	14.33	NULL	1 / 2	miRNA target	miR−153
7	13.74	NULL	1 / 8	GSEA C2	BENPORATH_ES_CORE_NINE
8	12.86	NULL	1 / 8	GSEA C2	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
9	12.44	NULL	2 / 15	BP	embryonic digestive tract development
10	12.22	NULL	1 / 3	miRNA target	miR−148a
11	11.97	NULL	1 / 9	GSEA C2	BASSO_CD40_SIGNALING_UP
12	11.97	NULL	1 / 9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
13	11.82	NULL	2 / 9	GSEA C2	GOZGIT_ESR1_TARGETS_DN
14	11.04	NULL	3 / 15	GSEA C2	DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
15	10.95	NULL	2 / 13	BP	developmental pigmentation
16	10.69	NULL	1 / 7	GSEA C2	KANG_CISPLATIN_RESISTANCE_DN
17	10.6	NULL	1 / 11	BP	homeostasis of number of cells
18	10.6	NULL	1 / 11	Pathw Act	BENTINK_e2f3.2
19	10.6	NULL	1 / 11	GSEA C2	DOANE_BREAST_CANCER_ESR1_UP
20	10.6	NULL	1 / 11	GSEA C2	TURJANSKI_MAPK1_AND_MAPK2_TARGETS
21	10.47	NULL	2 / 16	GSEA C2	SASAKI_ADULT_T_CELL_LEUKEMIA
22	10.45	NULL	1 / 3	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
23	10.11	NULL	2 / 10	BP	positive regulation of histone H3−K4 methylation
24	10.06	NULL	1 / 12	GSEA C2	DING_LUNG_CANCER_BY_MUTATION_RATE
25	9.7	NULL	1 / 9	GSEA C2	RODWELL_AGING_KIDNEY_UP
26	9.59	NULL	1 / 13	GSEA C2	OSADA_ASCL1_TARGETS_UP
27	9.59	NULL	1 / 13	GSEA C2	ALONSO_METASTASIS_UP
28	9.59	NULL	1 / 13	GSEA C2	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
29	9.47	NULL	1 / 5	TF	MYC_TFs
30	9.47	NULL	1 / 5	miRNA target	miR−101
31	9.41	NULL	2 / 13	miRNA target	miR−34a
32	9.18	NULL	1 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
33	9.18	NULL	1 / 14	GSEA C2	GOTTWEIN_TARGETS_OF_KSHV_MIR_K12_11
34	9.18	NULL	1 / 14	GSEA C2	TENEDINI_MEGAKARYOCYTE_MARKERS
35	9.18	NULL	1 / 14	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_UP
36	9.18	NULL	1 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
37	9.1	NULL	1 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
38	8.99	NULL	3 / 42	BP	B cell differentiation
39	8.93	NULL	2 / 15	GSEA C2	DELYS_THYROID_CANCER_DN
40	8.85	NULL	2 / 16	GSEA C2	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN

GW_157

Local Summary

%DE = 0.9

metagenes = 36

genes = 380

genes in genesets = 372

genes with fdr < 0.1 = 307 (9 + / 298 −)

genes with fdr < 0.05 = 290 (9 + / 281 −)

genes with fdr < 0.01 = 236 (7 + / 229 −)

<r> metagenes = 0.94

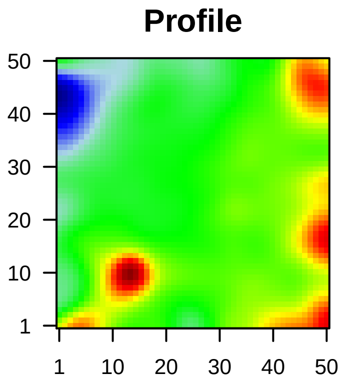
<r> genes = 0.33

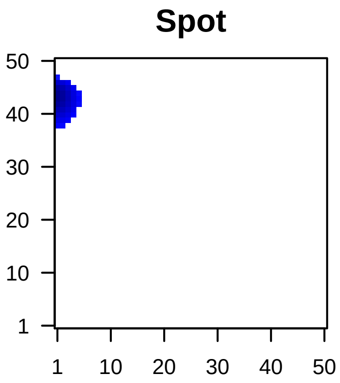
<FC> = −0.53

<shrinkage−t> = −18.68

<p−value> = 0

<fdr> = 0.34





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	9982	−1.43	2e−16	1e−15	1 x 47	fibroblast growth factor binding protein 1 [Source:HGNC Syml
2	3857	1.64	2e−16	1e−15	3 x 42	keratin 9 [Source:HGNC Symbol;Acc:6447]
3	55214	−1.64	2e−16	1e−15	1 x 42	leprecan−like 1 [Source:HGNC Symbol;Acc:19317]
4	3963	−1.45	2e−16	1e−15	1 x 47	lectin, galactoside−binding, soluble, 7 [Source:HGNC Symbol
5	5744	−1.75	2e−16	1e−15	1 x 43	parathyroid hormone−like hormone [Source:HGNC Symbol;A
6	6273	−1.61	2e−16	1e−15	1 x 44	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
7	8140	−1.54	2e−16	1e−15	1 x 43	solute carrier family 7 (amino acid transporter light chain, L sy
8	780854	−1.51	2e−16	1e−15	2 x 39	small nucleolar RNA, C/D box 3D [Source:HGNC Symbol;Acc
9	6665	−1.46	2e−16	1e−15	1 x 45	SRY (sex determining region Y)−box 15 [Source:HGNC Symb
10	723790	−1.42	4e−16	3e−14	2 x 38	histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
11	2167	−1.39	1e−15	6e−14	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
12	113146	−1.38	3e−15	2e−13	1 x 44	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
13	1001	−1.36	7e−15	3e−12	1 x 43	cadherin 3, type 1, P−cadherin (placental) [Source:HGNC Sy
14	6274	−1.3	1e−13	2e−11	1 x 43	S100 calcium binding protein A3 [Source:HGNC Symbol;Acc:
15	348938	−1.23	2e−12	2e−11	1 x 46	NIPA−like domain containing 4 [Source:HGNC Symbol;Acc:2
16	10804	−1.23	2e−12	2e−11	1 x 47	gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
17	8337	−1.23	2e−12	1e−10	2 x 38	histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
18	3489	−1.2	7e−12	1e−10	1 x 44	insulin−like growth factor binding protein 6 [Source:HGNC Sy
19	23682	−1.2	8e−12	1e−10	1 x 46	RAB38, member RAS oncogene family [Source:HGNC Symb
20	116211	−1.19	9e−12	1e−09	1 x 43	Transmembrane 4 L6 family member 19 [Source:UniProtKB/

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.24	NULL	79 / 572	Disease	GUDJ_psoriasis up
2	−14.77	NULL	30 / 135	H.Tiss	WIRTH_Mucosa
3	−12.76	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
4	−9.22	NULL	4 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_3
5	−9.1	NULL	3 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
6	−8.88	NULL	4 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_4
7	−8.78	NULL	3 / 10	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G3
8	−8.75	NULL	8 / 21	CC	desmosome
9	−8.65	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
10	−8.13	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
11	−8.06	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
12	−7.7	NULL	1 / 2	miRNA target	miR−346
13	−7.52	NULL	5 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
14	−7.49	NULL	5 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
15	−7.48	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
16	−7.43	NULL	2 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	−7.32	NULL	3 / 13	GSEA C2	HASINA_NOL7_TARGETS_UP
18	−7.28	NULL	3 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
19	−7.25	NULL	4 / 16	GSEA C2	COLDREN_GEFITINIB_RESISTANCE_DN
20	−7.25	NULL	2 / 12	MF	fatty acid binding
21	−7.1	NULL	2 / 12	GSEA C2	ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN
22	−7	NULL	2 / 10	GSEA C2	HOEBEKE_LYMPHOID_STEM_CELL_DN
23	−6.97	NULL	2 / 9	GSEA C2	KORKOLA_CORRELATED_WITH_POU5F1
24	−6.95	NULL	5 / 12	BP	hemidesmosome assembly
25	−6.95	NULL	3 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
26	−6.91	NULL	1 / 6	Glio	Martinez_Glio_hypometh
27	−6.91	NULL	3 / 15	Pathw Act	GUSTAFSON_PI3K_DN
28	−6.89	NULL	1 / 7	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
29	−6.84	NULL	2 / 8	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
30	−6.82	NULL	3 / 17	MF	amino acid transmembrane transporter activity
31	−6.7	NULL	16 / 76	BP	epidermis development
32	−6.7	NULL	3 / 10	BP	negative regulation of interleukin−2 production
33	−6.61	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
34	−6.61	NULL	1 / 6	miRNA target−starBase	hsa−miR−126
35	−6.59	NULL	2 / 15	GSEA C2	KANG_CISPLATIN_RESISTANCE_UP
36	−6.57	NULL	2 / 8	GSEA C2	WILLIAMS_ESR2_TARGETS_DN
37	−6.55	NULL	2 / 10	MF	neutral amino acid transmembrane transporter activity
38	−6.55	NULL	5 / 15	CC	connexon complex
39	−6.49	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
40	−6.44	NULL	2 / 11	BP	response to metal ion