GW_072

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1823 (1116 + / 707 −)

genes with fdr < 0.1 = 1535 (988 + / 547 −)

genes with fdr < 0.05 = 1355 (901 + / 454 −)

genes with fdr < 0.01 = 992 (709 + / 283 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.08

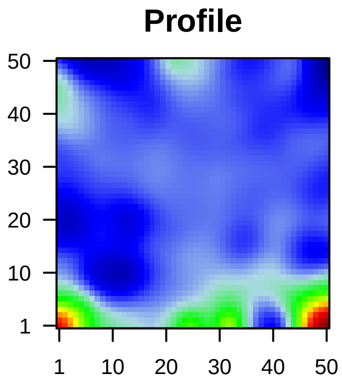
<fdr> = 0.85

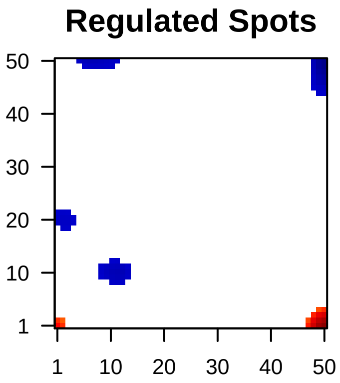
Global Genelist

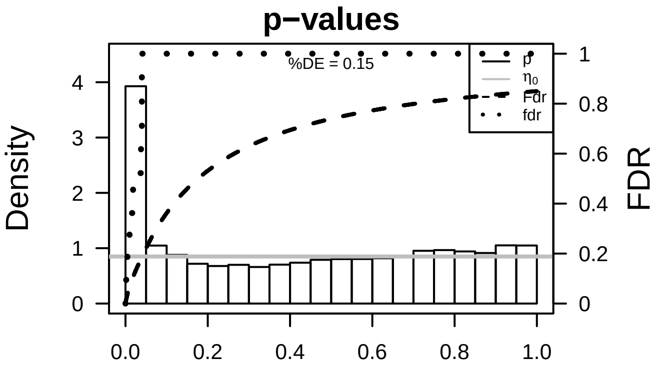
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	2.9	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	1.99	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	8728	1.29	2e−16	2e−14	50 x 3	ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
4	154	1.27	2e−16	2e−14	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:28
5	218	−1.58	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
6	241	1.4	2e−16	2e−14	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HG
7	401138	1.77	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
8	347	1.38	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
9	366	1.61	2e−16	2e−14	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
10	8412	1.47	2e−16	2e−14	1 x 5	breast cancer anti−estrogen resistance 3 [Source:HGNC Sy
11	590	1.4	2e−16	2e−14	16 x 50	butyrylcholinesterase [Source:HGNC Symbol;Acc:983]
12	650	1.27	2e−16	2e−14	1 x 4	bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1
13	387695	1.4	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Sym
14	92747	2.08	2e−16	2e−14	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
15	260436	1.84	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
16	92291	1.41	2e−16	2e−14	50 x 11	calpain 13 [Source:HGNC Symbol;Acc:16663]
17	875	−1.35	2e−16	2e−14	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
18	6364	1.26	2e−16	2e−14	46 x 1	chemokine (C−C motif) ligand 20 [Source:HGNC Symbol;Acc
19	6366	1.37	2e−16	2e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
20	6348	1.62	2e−16	2e−14	4 x 4	chemokine (C−C motif) ligand 3 [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	28.36	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	22.55	NULL	312	BP	immune response
3	19.01	NULL	417	H.Tiss	WIRTH_Immune system
4	18.3	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	18.3	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	18.3	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	18.3	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	16.49	NULL	572	Disease	GUDJ_psoriasis up
9	16.02	NULL	683	CC	extracellular space
10	15.72	NULL	269	BP	inflammatory response
11	15.67	NULL	43	MF	chemokine activity
12	15.29	NULL	1182	CC	extracellular region
13	14.31	NULL	274	Lymphoma	SPANG_IL21 DN
14	14.13	NULL	111	BP	chemotaxis
15	14.12	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
16	13.42	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
17	13.12	NULL	316	Cancer	SPANG_BCL6−index2
18	13.07	NULL	36	BP	muscle filament sliding
19	12.98	NULL	51	BP	type I interferon signaling pathway
20	12.88	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
Underexpressed					
1	−9.52	NULL	504	Chr	Chr 15
2	−7	NULL	1318	CC	mitochondrion
3	−6.7	NULL	1253	BP	small molecule metabolic process
4	−6.63	NULL	940	MF	nucleic acid binding
5	−6.61	NULL	7	MMML CGS	MACIEJ_MMML 5
6	−6.57	NULL	8	GSEA C2	RUNNE_GENDER_EFFECT_UP
7	−5.85	NULL	390	BP	metabolic process
8	−5.68	NULL	253	BP	translation
9	−5.66	NULL	153	MF	structural constituent of ribosome
10	−5.58	NULL	1135	Chr	Chr 19
11	−5.58	NULL	434	BP	oxidation−reduction process
12	−5.54	NULL	20	Lymphoma	ROSOLOWSKI_red UP
13	−5.53	NULL	296	MF	oxidoreductase activity
14	−5.32	NULL	92	BP	viral life cycle
15	−5.19	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
16	−5.15	NULL	167	CC	ribosome
17	−5.13	NULL	87	BP	translational termination
18	−5.12	NULL	81	BP	viral transcription
19	−5.09	NULL	13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
20	−5.07	NULL	92	BP	translational elongation







GW_072

Local Summary

%DE = 0.95

metagenes = 4

genes = 76

genes in genesets = 76

genes with fdr < 0.1 = 65 (64 + / 1 −)

genes with fdr < 0.05 = 65 (64 + / 1 −)

genes with fdr < 0.01 = 59 (58 + / 1 −)

<r> metagenes = 1

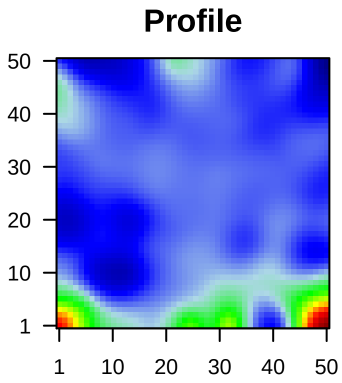
<r> genes = 0.46

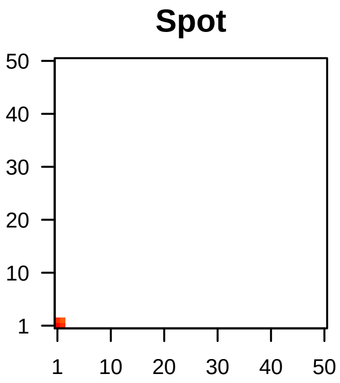
<FC> = 0.89

<shrinkage−t> = 31.33

<p−value> = 0

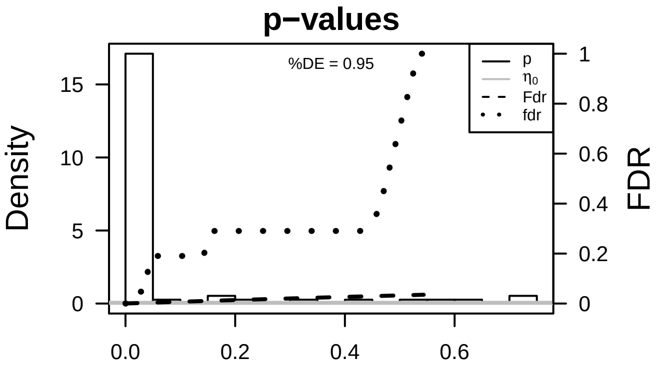
<fdr> = 0.19





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	366	1.61	2e−16	4e−17	1 x 1	aquaporin 9 [Source:HGNC Symbol;Acc:643]
2	414062	2.68	2e−16	4e−17	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
3	1289	1.27	2e−16	4e−17	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
4	2920	2.28	2e−16	4e−17	1 x 1	chemokine (C−X−C motif) ligand 2 [Source:HGNC Symbol;Ac
5	3491	2.02	2e−16	4e−17	2 x 1	cysteine−rich, angiogenic inducer, 61 [Source:HGNC Symbol
6	3553	2.22	2e−16	4e−17	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
7	3569	2.3	2e−16	4e−17	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:
8	3576	2.38	2e−16	4e−17	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
9	4312	1.53	2e−16	4e−17	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
10	4322	1.82	2e−16	4e−17	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
11	4316	1.27	2e−16	4e−17	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
12	4973	1.89	2e−16	4e−17	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
13	5008	1.29	2e−16	4e−17	1 x 1	oncostatin M [Source:HGNC Symbol;Acc:8506]
14	60675	1.63	2e−16	4e−17	1 x 1	prokineticin 2 [Source:HGNC Symbol;Acc:18455]
15	5054	1.57	2e−16	4e−17	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
16	7057	1.28	2e−16	4e−17	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
17	7078	1.36	2e−16	4e−17	2 x 1	TIMP metallopeptidase inhibitor 3 [Source:HGNC Symbol;Acc
18	7128	2	2e−16	4e−17	1 x 1	tumor necrosis factor, alpha−induced protein 3 [Source:HGNC
19	8406	1.23	4e−16	4e−15	2 x 1	sushi−repeat containing protein, X−linked [Source:HGNC Syr
20	163782	1.2	3e−15	4e−15	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	33.63	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
2	33.03	NULL	2 / 6	GSEA C2	BIOCARTA_IL5_PATHWAY
3	32.8	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	29.63	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
5	29.11	NULL	17 / 64	BP	collagen catabolic process
6	28.29	NULL	18 / 69	BP	extracellular matrix disassembly
7	27.57	NULL	2 / 8	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_UP
8	27.52	NULL	6 / 11	MF	platelet−derived growth factor binding
9	27.45	NULL	9 / 16	MMML CGS	MACIEJ_MMML 1
10	26.08	NULL	2 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
11	26	NULL	2 / 9	GSEA C2	HEDVAT_ELF4_TARGETS_UP
12	25.68	NULL	4 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
13	24.92	NULL	4 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
14	24.56	NULL	28 / 190	CC	extracellular matrix
15	24.52	NULL	4 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
16	24.43	NULL	7 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
17	23.64	NULL	4 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
18	23.18	NULL	4 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
19	22.97	NULL	2 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
20	22.84	NULL	2 / 6	Glio	Martinez_Glio_hypometh
21	22.51	NULL	1 / 4	GSEA C2	BIOCARTA_CYTOKINE_PATHWAY
22	22.22	NULL	6 / 12	miRNA target	miR−29c
23	22.05	NULL	30 / 242	BP	extracellular matrix organization
24	21.98	NULL	3 / 14	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP
25	21.79	NULL	1 / 4	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_DN
26	21.79	NULL	5 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
27	21.7	NULL	4 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_MCF10A
28	21.7	NULL	4 / 16	GSEA C2	AMIT_SERUM_RESPONSE_60_MCF10A
29	21.5	NULL	2 / 8	GSEA C2	OSAWA_TNF_TARGETS
30	20.71	NULL	2 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
31	20.6	NULL	4 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
32	20.19	NULL	3 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
33	19.9	NULL	4 / 11	Glio	Phillips MES up vs Prolif & PN
34	19.69	NULL	1 / 5	GSEA C2	DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCO
35	19.61	NULL	1 / 4	MMML CGS	MACIEJ_MMML 40
36	19.27	NULL	3 / 16	GSEA C2	TIAN_TNF_SIGNALING_VIA_NFKB
37	18.76	NULL	5 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
38	18.35	NULL	2 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
39	18.14	NULL	3 / 19	BP	defense response to Gram−negative bacterium
40	18.09	NULL	4 / 16	GSEA C2	BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN

GW_072

Local Summary

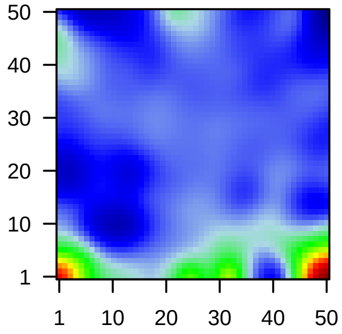
%DE = 0.88
metagenes = 13
genes = 245
genes in genesets = 243

genes with fdr < 0.1 = 203 (201 + / 2 −)
genes with fdr < 0.05 = 203 (201 + / 2 −)
genes with fdr < 0.01 = 192 (191 + / 1 −)

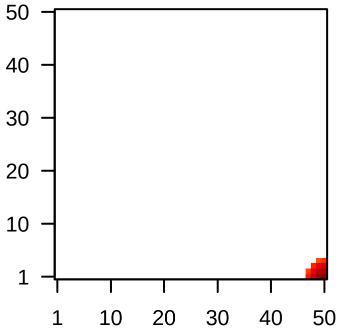
<r> metagenes = 0.99
<r> genes = 0.6

<FC> = 0.73
<shrinkage−t> = 25.64
<p−value> = 0
<fdr> = 0.18

Profile



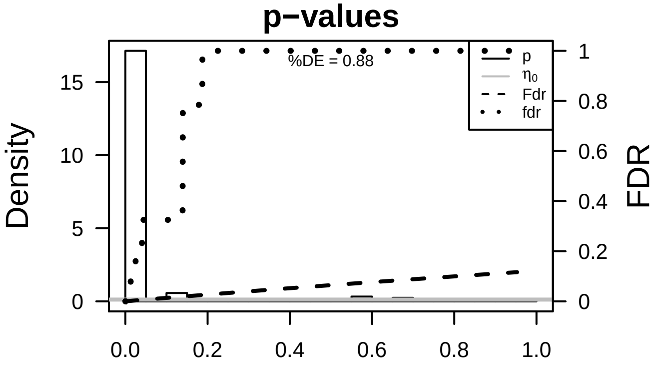
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8728	1.29	2e−16	2e−16	50 x 3	ADAM metallopeptidase domain 19 [Source:HGNC Symbol;A
2	241	1.4	2e−16	2e−16	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
3	260436	1.84	2e−16	2e−16	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
4	6366	1.37	2e−16	2e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
5	6352	1.47	2e−16	2e−16	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
6	1236	1.75	2e−16	2e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
7	914	1.35	2e−16	2e−16	49 x 1	CD2 molecule [Source:HGNC Symbol;Acc:1639]
8	919	1.39	2e−16	2e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
9	915	1.35	2e−16	2e−16	49 x 1	CD3d molecule, delta (CD3−TCR complex) [Source:HGNC S
10	962	1.35	2e−16	2e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
11	969	2.12	2e−16	2e−16	50 x 1	CD69 molecule [Source:HGNC Symbol;Acc:1694]
12	9308	1.48	2e−16	2e−16	50 x 3	CD83 molecule [Source:HGNC Symbol;Acc:1703]
13	10563	1.56	2e−16	2e−16	50 x 1	chemokine (C−X−C motif) ligand 13 [Source:HGNC Symbol;
14	4283	1.98	2e−16	2e−16	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;A
15	115361	1.38	2e−16	2e−16	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
16	3001	1.26	2e−16	2e−16	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
17	3002	1.8	2e−16	2e−16	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
18	3003	1.28	2e−16	2e−16	49 x 1	granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol
19	3119	1.35	2e−16	2e−16	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
20	3128	1.48	2e−16	2e−16	50 x 1	major histocompatibility complex, class II, DR beta 6 (pseudo

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	34.37	NULL	86 / 417	H.Tiss	WIRTH_Immune system
2	27.1	NULL	86 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.23	NULL	47 / 312	BP	immune response
4	21.22	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	20.89	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
6	20.49	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
7	19.72	NULL	6 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
8	19.55	NULL	12 / 15	CC	MHC class II protein complex
9	18.64	NULL	39 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	18.64	NULL	39 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	18.64	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	18.64	NULL	39 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	18.26	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
14	18.12	NULL	8 / 16	GSEA C2	SU_THYMUS
15	17.71	NULL	5 / 12	BP	dendritic cell chemotaxis
16	17.61	NULL	5 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
17	17.12	NULL	5 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
18	16.91	NULL	5 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
19	16.68	NULL	23 / 162	CC	external side of plasma membrane
20	16.49	NULL	4 / 14	BP	ruffle organization
21	16.46	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
22	15.71	NULL	17 / 74	BP	regulation of immune response
23	15.36	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
24	14.95	NULL	5 / 13	Cancer	GENTLES_modul18
25	14.84	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
26	14.62	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
27	14.56	NULL	4 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
28	14.46	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
29	13.77	NULL	4 / 10	GSEA C2	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
30	13.16	NULL	4 / 16	BP	cytolysis
31	12.81	NULL	8 / 45	BP	T cell activation
32	12.63	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
33	12.61	NULL	2 / 10	BP	negative regulation of G−protein coupled receptor protein signaling
34	12.56	NULL	3 / 10	BP	negative thymic T cell selection
35	12.49	NULL	15 / 47	BP	antigen processing and presentation
36	12.44	NULL	3 / 10	GSEA C2	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP
37	12.36	NULL	6 / 24	CC	immunological synapse
38	12.33	NULL	13 / 60	BP	T cell costimulation
39	12.18	NULL	7 / 43	MF	chemokine activity
40	12.15	NULL	2 / 6	GSEA C2	BUDHU_LIVER_CANCER_METASTASIS_UP

GW_072

Local Summary

%DE = 0.89

metagenes = 23

genes = 161

genes in genesets = 142

genes with fdr < 0.1 = 124 (4 + / 120 −)

genes with fdr < 0.05 = 92 (2 + / 90 −)

genes with fdr < 0.01 = 57 (1 + / 56 −)

<r> metagenes = 0.9

<r> genes = 0.23

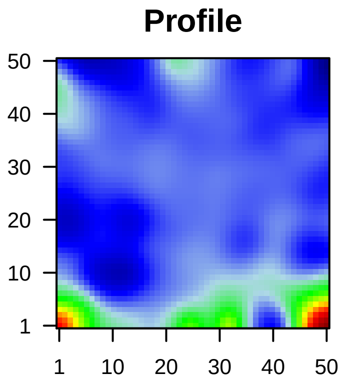
<FC> = −0.3

<shrinkage−t> = −10.67

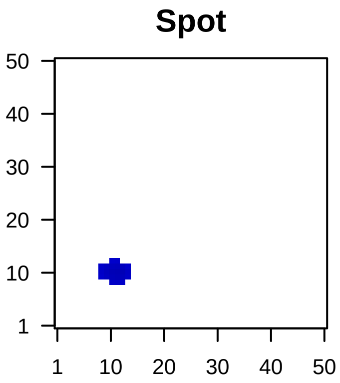
<p−value> = 0.02

<fdr> = 0.61

Profile



Spot



Local Genelist

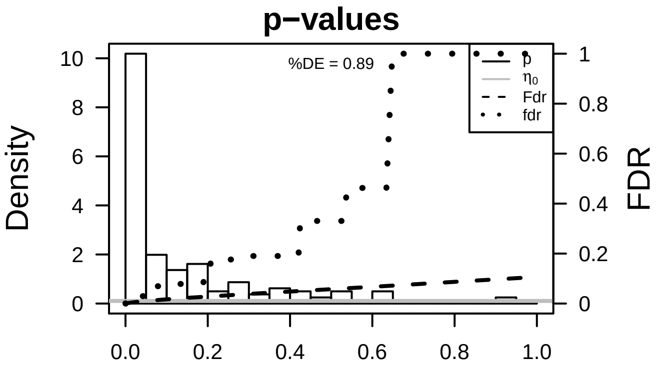
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	4103	−0.85	2e−08	3e−06	14 x 10	melanoma antigen family A, 4 [Source:HGNC Symbol;Acc:68
2	5792	−0.78	3e−07	3e−06	11 x 13	protein tyrosine phosphatase, receptor type, F [Source:HGNC
3	8408	−0.78	3e−07	2e−05	11 x 12	unc−51 like autophagy activating kinase 1 [Source:HGNC Sy
4	22859	−0.73	2e−06	2e−05	12 x 10	latrophilin 1 [Source:HGNC Symbol;Acc:20973]
5	441520	−0.71	3e−06	4e−05	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
6	4109	−0.7	5e−06	6e−05	14 x 11	melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
7	100128927	−0.68	9e−06	6e−05	11 x 11	zinc finger and BTB domain containing 42 [Source:HGNC Sy
8	4088	−0.67	1e−05	9e−05	12 x 13	SMAD family member 3 [Source:HGNC Symbol;Acc:6769]
9	64710	−0.65	2e−05	9e−05	9 x 11	nuclear casein kinase and cyclin−dependent kinase substrate
10	729422	−0.64	3e−05	9e−05	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
11	645037	−0.63	3e−05	9e−05	14 x 11	G antigen 2C [Source:HGNC Symbol;Acc:31958]
12	54938	−0.63	4e−05	9e−05	10 x 12	seryl−tRNA synthetase 2, mitochondrial [Source:HGNC Symb
13	729442	−0.62	4e−05	9e−05	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	3303	0.61	4e−05	3e−04	11 x 12	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
15	147968	−0.6	8e−05	3e−04	12 x 12	calpain 12 [Source:HGNC Symbol;Acc:13249]
16	23368	−0.58	1e−04	3e−04	10 x 12	protein phosphatase 1, regulatory subunit 13B [Source:HGNC
17	2577	−0.58	1e−04	3e−04	14 x 11	G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	729428	−0.58	1e−04	3e−04	14 x 11	G antigen 12C [Source:HGNC Symbol;Acc:28402]
19	24150	−0.58	1e−04	3e−04	14 x 11	TP53 target 3D [Source:HGNC Symbol;Acc:44657]
20	5446	−0.58	2e−04	7e−04	13 x 10	paraoxonase 3 [Source:HGNC Symbol;Acc:9206]

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−10.24	NULL	2 / 15	GSEA C2 BROWNE_HCMV_INFECTION_8HR_DN
2	−9.79	NULL	2 / 14	GSEA C2 DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN
3	−9.54	NULL	1 / 6	GSEA C2 TRAYNOR_RETT_SYNDROM_DN
4	−9.5	NULL	2 / 14	GSEA C2 NUYTTEN_NIPP1_TARGETS_DN
5	−8.57	NULL	2 / 13	GSEA C2 ENK_UV_RESPONSE_KERATINOCYTE_UP
6	−8.38	NULL	19 / 630	Chr Chr X
7	−8.01	NULL	2 / 17	BP osteoblast development
8	−7.99	NULL	1 / 4	GSEA C2 WEBER_METHYLATED_ICP_IN_SPERM_DN
9	−7.6	NULL	1 / 9	GSEA C2 GOZGIT_ESR1_TARGETS_DN
10	−7.28	NULL	1 / 4	GSEA C2 NIELSEN_LEIOMYOSARCOMA_DN
11	−7.2	NULL	1 / 10	GSEA C2 MURAKAMI_UV_RESPONSE_1HR_UP
12	−7.17	NULL	1 / 10	BP positive regulation of macroautophagy
13	−7.17	NULL	1 / 10	GSEA C2 STEIN_ESRRA_TARGETS
14	−7.17	NULL	1 / 10	GSEA C2 KEGG_REGULATION_OF_AUTOPHAGY
15	−7.07	NULL	2 / 15	GSEA C2 OLSSON_E2F3_TARGETS_DN
16	−6.91	NULL	2 / 8	GSEA C2 WEBER_METHYLATED_ICP_IN_FIBROBLAST
17	−6.8	NULL	1 / 11	CC pre−autophagosomal structure membrane
18	−6.8	NULL	1 / 11	GSEA C2 CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP
19	−6.8	NULL	1 / 11	GSEA C2 FUJII_YBX1_TARGETS_UP
20	−6.61	NULL	5 / 69	miRNA 3UTR AGCT−28
21	−6.52	NULL	1 / 14	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_B
22	−6.49	NULL	1 / 9	GSEA C2 BIOCARTA_NTHI_PATHWAY
23	−6.48	NULL	1 / 12	GSEA C2 PEREZ_TP53_TARGETS
24	−6.48	NULL	1 / 12	GSEA C2 BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
25	−6.48	NULL	1 / 12	GSEA C2 NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON
26	−6.48	NULL	1 / 12	GSEA C2 ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN
27	−6.38	NULL	1 / 11	BP positive regulation of synapse maturation
28	−6.38	NULL	1 / 6	GSEA C2 NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
29	−6.36	NULL	3 / 15	BP semaphorin−plexin signaling pathway
30	−6.31	NULL	2 / 26	BP negative regulation of osteoblast differentiation
31	−6.22	NULL	1 / 13	H.Tiss WIRTH_Sec. lymphoid organs
32	−6.22	NULL	1 / 13	H.Tiss WIRTH_Tonsil
33	−6.21	NULL	1 / 8	GSEA C2 HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER
34	−6.19	NULL	1 / 13	BP axon extension
35	−6.19	NULL	1 / 13	GSEA C2 CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_
36	−6.19	NULL	1 / 13	GSEA C2 DOUGLAS_BMI1_TARGETS_UP
37	−6.19	NULL	1 / 13	GSEA C2 MOOTHA_PGC
38	−6.17	NULL	2 / 27	CC receptor complex
39	−6.16	NULL	2 / 16	GSEA C2 LANDEMAINE_LUNG_METASTASIS
40	−6.12	NULL	1 / 10	MF co−SMAD binding

p−values



GW_072

Local Summary

%DE = 0.53

metagenes = 13

genes = 140

genes in genesets = 139

genes with fdr < 0.1 = 33 (0 + / 33 −)

genes with fdr < 0.05 = 27 (0 + / 27 −)

genes with fdr < 0.01 = 22 (0 + / 22 −)

<r> metagenes = 0.98

<r> genes = 0.31

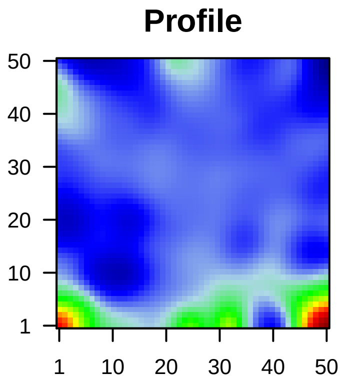
<FC> = −0.22

<shrinkage−t> = −7.83

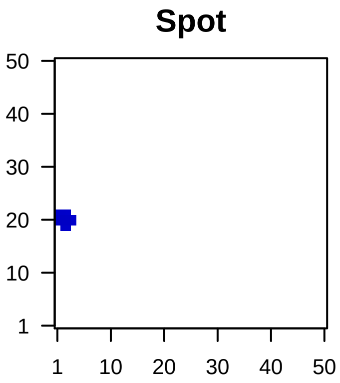
<p−value> = 0.05

<fdr> = 0.75

Profile



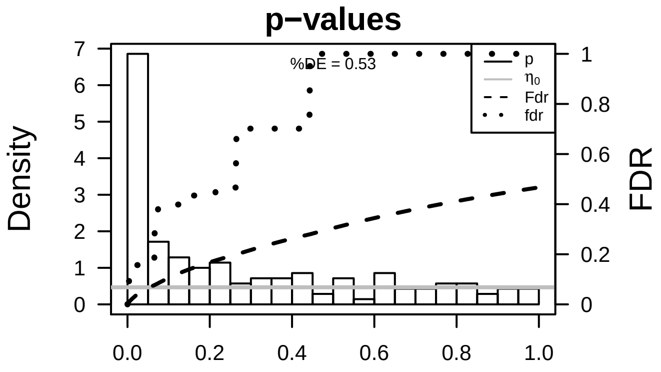
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	6884	−0.79	2e−07	8e−06	1 x 22	TAF13 RNA polymerase II, TATA box binding protein (TBP)−a
2	8045	−0.78	3e−07	5e−04	2 x 22	Ras association (RalGDS/AF−6) domain family (N−terminal)
3	58477	−0.68	7e−06	1e−03	2 x 21	signal recognition particle receptor, B subunit [Source:HGNC
4	5639	−0.64	3e−05	1e−03	1 x 22	proline rich Gla (G−carboxyglutamic acid) 2 [Source:HGNC S
5	645233	−0.62	5e−05	2e−03	1 x 21	
6	8214	−0.59	1e−04	2e−03	2 x 21	DiGeorge syndrome critical region gene 6 [Source:HGNC Sy
7	85359	−0.58	2e−04	2e−03	2 x 20	DiGeorge syndrome critical region gene 6−like [Source:HGN
8	51181	−0.57	2e−04	2e−03	2 x 21	dicarbonyl/L−xylulose reductase [Source:HGNC Symbol;Acc:
9	8570	−0.56	2e−04	2e−03	2 x 19	KH−type splicing regulatory protein [Source:HGNC Symbol;A
10	550	−0.55	3e−04	2e−03	1 x 20	ancient ubiquitous protein 1 [Source:HGNC Symbol;Acc:891]
11	118881	−0.55	3e−04	2e−03	1 x 22	catechol−O−methyltransferase domain containing 1 [Source:
12	56954	−0.55	3e−04	4e−03	3 x 19	nitrilase family, member 2 [Source:HGNC Symbol;Acc:29878]
13	6510	−0.54	3e−04	5e−03	2 x 19	solute carrier family 1 (neutral amino acid transporter), memb
14	374291	−0.53	5e−04	5e−03	3 x 21	NADH dehydrogenase (ubiquinone) Fe−S protein 7, 20kDa (
15	29763	−0.53	5e−04	5e−03	1 x 20	protein kinase C and casein kinase substrate in neurons 3 [S
16	85014	−0.52	6e−04	9e−03	1 x 21	transmembrane protein 141 [Source:HGNC Symbol;Acc:2821
17	6603	−0.5	9e−04	9e−03	4 x 21	SWI/SNF related, matrix associated, actin dependent regulat
18	83715	−0.49	1e−03	9e−03	2 x 22	espin [Source:HGNC Symbol;Acc:13281]
19	23464	−0.49	1e−03	9e−03	3 x 21	glycine C−acetyltransferase [Source:HGNC Symbol;Acc:418
20	1892	−0.49	1e−03	9e−03	2 x 22	enoyl CoA hydratase, short chain, 1, mitochondrial [Source:H

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−8.72	NULL	3 / 10	MF	NADH dehydrogenase activity
2	−8.68	NULL	3 / 16	GSEA C2	JIANG_HYPOXIA_VIA_VHL
3	−8.55	NULL	1 / 10	GSEA C2	REACTOME_HIV1_TRANSCRIPTION_INITIATION
4	−8.44	NULL	2 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
5	−8.27	NULL	2 / 10	GSEA C2	KEGG_LIMONENE_AND_PINENE_DEGRADATION
6	−8.27	NULL	2 / 10	GSEA C2	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
7	−8.14	NULL	1 / 11	GSEA C2	KEGG_BASAL_TRANSCRIPTION_FACTORS
8	−7.77	NULL	1 / 12	GSEA C2	CAMPS_COLON_CANCER_COPY_NUMBER_DN
9	−7.51	NULL	2 / 12	GSEA C2	KEGG_LYSINE_DEGRADATION
10	−7.49	NULL	2 / 23	CC	brush border
11	−7.45	NULL	1 / 13	GSEA C2	HOFMANN_CELL_LYMPHOMA_UP
12	−7.2	NULL	2 / 13	GSEA C2	KEGG_TRYPTOPHAN_METABOLISM
13	−7.2	NULL	2 / 13	GSEA C2	KEGG_BUTANOATE_METABOLISM
14	−7.19	NULL	3 / 16	GSEA C2	MOOTHA_FFA_OXYDATION
15	−7.17	NULL	2 / 15	GSEA C2	DAIRKEE_CANCER_PRONE_RESPONSE_E2
16	−7.15	NULL	2 / 15	GSEA C2	VANTVEER_BREAST_CANCER_BRCA1_UP
17	−7.08	NULL	1 / 6	miRNA target−starBase	hsa−miR−1281
18	−6.78	NULL	3 / 15	GSEA C2	ZHANG_RESPONSE_TO_CANTHARIDIN_DN
19	−6.71	NULL	1 / 14	Cancer	LIU_PROSTATE_CANCER_UP
20	−6.71	NULL	1 / 12	GSEA C2	SHEPARD_CRUSH_AND_BURN_MUTANT_UP
21	−6.71	NULL	1 / 12	GSEA C2	REACTOME_INSULIN_SYNTHESIS_AND_SECRETION
22	−6.67	NULL	2 / 15	GSEA C2	KEGG_BETA_ALANINE_METABOLISM
23	−6.67	NULL	2 / 15	GSEA C2	KEGG_PROPANOATE_METABOLISM
24	−6.66	NULL	2 / 16	GSEA C2	SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP
25	−6.61	NULL	36 / 1318	CC	mitochondrion
26	−6.54	NULL	2 / 16	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
27	−6.54	NULL	2 / 16	GSEA C2	MOOTHA_MITOCHONDRIA
28	−6.53	NULL	2 / 16	GSEA C2	BIOCARTA_PTDINS_PATHWAY
29	−6.44	NULL	2 / 16	GSEA C2	KEGG_FATTY_ACID_METABOLISM
30	−6.44	NULL	2 / 16	GSEA C2	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
31	−6.07	NULL	1 / 10	GSEA C2	OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN
32	−6	NULL	3 / 16	GSEA C2	GRATIAS_RETINOBLASTOMA_16Q24
33	−5.92	NULL	2 / 48	CC	cytoplasmic microtubule
34	−5.88	NULL	2 / 47	miRNA target−starBase	hsa−miR−302b*
35	−5.87	NULL	1 / 10	MF	neutral amino acid transmembrane transporter activity
36	−5.85	NULL	2 / 36	CC	microvillus
37	−5.81	NULL	1 / 11	GSEA C2	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS
38	−5.77	NULL	1 / 11	GSEA C2	LAIHO_COLORECTAL_CANCER_SERRATED_DN
39	−5.75	NULL	1 / 21	CC	transcription factor TFIID complex
40	−5.75	NULL	1 / 16	GSEA C2	CHOI_ATL_STAGE_PREDICTOR

GW_072

Local Summary

%DE = 0.74

metagenes = 20

genes = 244

genes in genesets = 242

genes with fdr < 0.1 = 132 (12 + / 120 −)

genes with fdr < 0.05 = 103 (11 + / 92 −)

genes with fdr < 0.01 = 75 (9 + / 66 −)

<r> metagenes = 0.95

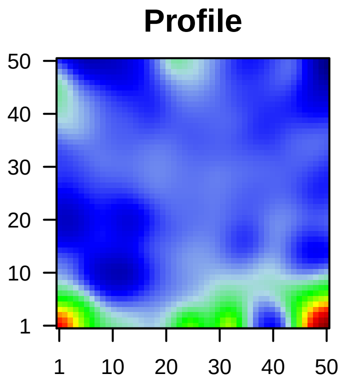
<r> genes = 0.26

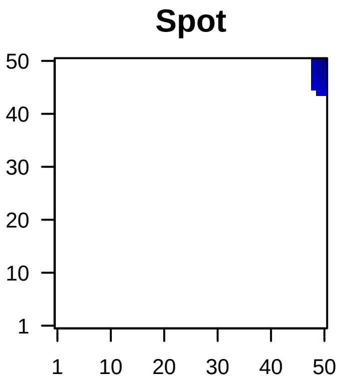
<FC> = −0.3

<shrinkage−t> = −10.63

<p−value> = 0

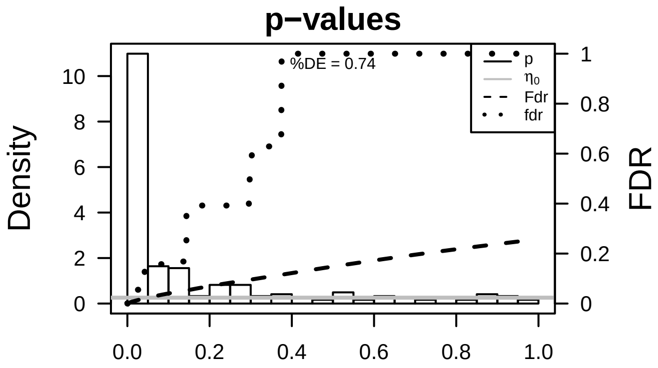
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	875	−1.35	2e−16	3e−15	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
2	2944	−1.27	2e−16	3e−15	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
3	2946	−1.25	2e−16	3e−15	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
4	3880	−1.27	2e−16	3e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
5	5625	−1.22	9e−16	8e−14	50 x 48	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;A
6	3866	−1.2	3e−15	8e−14	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
7	7546	−1.2	4e−15	3e−13	48 x 50	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
8	139728	−1.18	8e−15	2e−12	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
9	4922	−1.15	4e−14	1e−10	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
10	11166	−1.07	2e−12	5e−10	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
11	200634	−1.04	9e−12	1e−09	50 x 49	keratinocyte associated protein 3 [Source:HGNC Symbol;Acc
12	79844	−1.01	3e−11	3e−08	50 x 50	zinc finger, DHHC−type containing 11 [Source:HGNC Symbo
13	1056	−0.94	7e−10	3e−08	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
14	400916	−0.93	9e−10	3e−07	50 x 47	coiled−coil−helix−coiled−coil−helix domain containing 10 [So
15	3304	0.82	5e−09	9e−07	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
16	94234	0.85	2e−08	1e−06	50 x 50	forkhead box Q1 [Source:HGNC Symbol;Acc:20951]
17	440	−0.84	4e−08	2e−06	50 x 46	asparagine synthetase (glutamine−hydrolyzing) [Source:HG
18	25975	0.81	9e−08	2e−06	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
19	3790	−0.8	1e−07	2e−06	50 x 50	potassium voltage−gated channel, delayed−rectifier, subfami
20	4953	−0.8	1e−07	2e−06	50 x 50	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−19.87	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−18.2	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
3	−17.89	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
4	−17.59	NULL	3 / 11	MF	glutathione binding
5	−17.59	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
6	−14.69	NULL	5 / 20	MF	glutathione transferase activity
7	−13.51	NULL	9 / 34	BP	glutathione metabolic process
8	−13.35	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
9	−13.26	NULL	4 / 13	BP	regulation of blood vessel size
10	−12.94	NULL	6 / 25	BP	glutathione derivative biosynthetic process
11	−12.36	NULL	3 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
12	−12.34	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
13	−12.03	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
14	−11.62	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_UP
15	−11.62	NULL	2 / 15	GSEA C2	LEE_LIVER_CANCER_E2F1_UP
16	−11.39	NULL	2 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
17	−10.9	NULL	2 / 13	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
18	−10.49	NULL	4 / 19	BP	cellular amino acid biosynthetic process
19	−10.25	NULL	1 / 6	GSEA C2	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
20	−10.06	NULL	2 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
21	−9.71	NULL	2 / 16	GSEA C2	IGARASHI_ATF4_TARGETS_DN
22	−9.71	NULL	2 / 16	GSEA C2	GAJATE_RESPONSE_TO_TRABECTEDIN_UP
23	−9.53	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
24	−8.9	NULL	12 / 167	BP	cellular nitrogen compound metabolic process
25	−8.72	NULL	1 / 8	GSEA C2	BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
26	−8.64	NULL	2 / 14	GSEA C2	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM
27	−8.62	NULL	46 / 1253	BP	small molecule metabolic process
28	−8.33	NULL	3 / 31	BP	response to nutrient levels
29	−8.23	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
30	−8.13	NULL	3 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_DN
31	−8.09	NULL	2 / 14	MF	calmodulin−dependent protein kinase activity
32	−7.71	NULL	2 / 13	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT
33	−7.71	NULL	2 / 12	GSEA C2	ONDER_CDH1_TARGETS_1_UP
34	−7.7	NULL	2 / 18	BP	superoxide metabolic process
35	−7.65	NULL	2 / 10	BP	biotin metabolic process
36	−7.64	NULL	1 / 9	GSEA C2	GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
37	−7.59	NULL	4 / 15	GSEA C2	REACTOME_GLUTATHIONE_CONJUGATION
38	−7.55	NULL	2 / 15	BP	retinal ganglion cell axon guidance
39	−7.55	NULL	4 / 48	MF	pyridoxal phosphate binding
40	−7.36	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN

GW_072

Local Summary

%DE = 0.69

metagenes = 14

genes = 238

genes in genesets = 237

genes with fdr < 0.1 = 121 (13 + / 108 −)

genes with fdr < 0.05 = 97 (9 + / 88 −)

genes with fdr < 0.01 = 53 (6 + / 47 −)

<r> metagenes = 0.91

<r> genes = 0.28

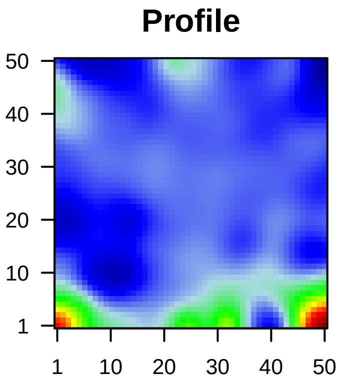
<FC> = −0.27

<shrinkage−t> = −9.47

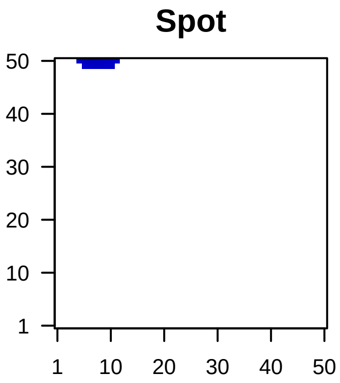
<p−value> = 0.01

<fdr> = 0.58

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1525	−1.55	2e−16	8e−15	10 x 50	coxsackie virus and adenovirus receptor [Source:HGNC Sym
2	6319	−1.42	2e−16	8e−15	12 x 50	stearoyl−CoA desaturase (delta−9−desaturase) [Source:HGN
3	57568	−1.2	3e−15	3e−10	11 x 50	signal−induced proliferation−associated 1 like 2 [Source:HGN
4	51195	−1.04	8e−12	3e−10	5 x 50	Rap guanine nucleotide exchange factor (GEF)−like 1 [Sourc
5	1718	−1.04	9e−12	2e−09	8 x 50	24−dehydrocholesterol reductase [Source:HGNC Symbol;Ac
6	5226	−1.01	3e−11	9e−09	6 x 50	phosphogluconate dehydrogenase [Source:HGNC Symbol;A
7	58489	−0.97	2e−10	5e−08	7 x 50	abhydrolase domain containing 17C [Source:HGNC Symbol;
8	100134938	−0.93	9e−10	5e−08	6 x 50	polymerase (RNA) II (DNA directed) polypeptide J3 [Source:
9	4258	−0.92	2e−09	3e−07	6 x 50	microsomal glutathione S−transferase 2 [Source:HGNC Sym
10	406988	−0.89	5e−09	3e−07	12 x 50	MIR205 host gene (non−protein coding) [Source:HGNC Sym
11	2064	−0.87	1e−08	3e−07	6 x 50	v−erb−b2 avian erythroblastic leukemia viral oncogene homo
12	1159	−0.86	1e−08	3e−07	5 x 50	creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Ac
13	1366	−0.86	2e−08	4e−07	6 x 50	claudin 7 [Source:HGNC Symbol;Acc:2049]
14	3485	0.84	3e−08	4e−07	11 x 50	insulin−like growth factor binding protein 2, 36kDa [Source:H
15	5627	−0.84	3e−08	1e−06	7 x 50	protein S (alpha) [Source:HGNC Symbol;Acc:9456]
16	3157	−0.83	5e−08	1e−06	7 x 50	3−hydroxy−3−methylglutaryl−CoA synthase 1 (soluble) [Sour
17	79977	−0.82	6e−08	2e−05	11 x 50	grainyhead−like 2 (Drosophila) [Source:HGNC Symbol;Acc:2
18	4582	−0.78	3e−07	8e−05	7 x 50	mucin 1, cell surface associated [Source:HGNC Symbol;Acc:
19	26355	−0.73	1e−06	8e−05	9 x 50	family with sequence similarity 162, member A [Source:HGN
20	7263	−0.72	2e−06	1e−04	5 x 50	thiosulfate sulfurtransferase (rhodanese) [Source:HGNC Sym

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−18.16	NULL	2 / 2	Cancer	GENTLES_modul8
2	−16.51	NULL	6 / 13	H.Tiss	WIRTH_Tonsil
3	−14.6	NULL	4 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
4	−11.94	NULL	2 / 16	GSEA C2	NELSON_RESPONSE_TO_ANDROGEN_UP
5	−11.51	NULL	2 / 13	GSEA C2	BAELDE_DIABETIC_NEPHROPATHY_DN
6	−11.18	NULL	3 / 15	GSEA C2	REACTOME_CHOLESTEROL_BIOSYNTHESIS
7	−11.09	NULL	3 / 14	GSEA C2	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
8	−11.06	NULL	2 / 6	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_8
9	−10.43	NULL	2 / 16	GSEA C2	MENSE_HYPOXIA_UP
10	−10.36	NULL	2 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
11	−9.77	NULL	2 / 15	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_7
12	−9.62	NULL	1 / 10	BP	germ cell migration
13	−9.32	NULL	1 / 2	miRNA target	miR−124a
14	−8.93	NULL	2 / 15	GSEA C2	PODAR_RESPONSE_TO_ADAPHOSTIN_DN
15	−8.91	NULL	2 / 13	miRNA 3UTR	TGCA−517A−−517C
16	−8.88	NULL	2 / 6	miRNA target	miR−125a
17	−8.73	NULL	2 / 15	GSEA C2	REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PER
18	−8.66	NULL	2 / 10	GSEA C2	REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHO
19	−8.53	NULL	2 / 16	GSEA C2	TOMLINS_PROSTATE_CANCER_UP
20	−8.47	NULL	2 / 14	GSEA C2	SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE
21	−8.46	NULL	2 / 16	GSEA C2	SESTO_RESPONSE_TO_UV_C2
22	−8.39	NULL	1 / 8	GSEA C2	WILLIAMS_ESR2_TARGETS_DN
23	−8.35	NULL	1 / 11	GSEA C2	AMIT_EGF_RESPONSE_20_MCF10A
24	−8.02	NULL	2 / 15	BP	pentose−phosphate shunt
25	−8.02	NULL	2 / 15	GSEA C2	KEGG_PENTOSE_PHOSPHATE_PATHWAY
26	−7.88	NULL	1 / 5	GSEA C2	WILLIAMS_ESR1_TARGETS_DN
27	−7.82	NULL	2 / 12	BP	sterol metabolic process
28	−7.75	NULL	3 / 15	GSEA C2	REACTOME_TIGHT_JUNCTION_INTERACTIONS
29	−7.65	NULL	3 / 13	BP	leukotriene biosynthetic process
30	−7.62	NULL	3 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
31	−7.5	NULL	1 / 5	GSEA C2	KERLEY_RESPONSE_TO_CISPLATIN_DN
32	−7.48	NULL	2 / 13	GSEA C2	REACTOME_STEROID_METABOLISM
33	−7.41	NULL	1 / 16	GSEA C2	KANNAN_TP53_TARGETS_DN
34	−7.38	NULL	8 / 137	CC	basolateral plasma membrane
35	−7.36	NULL	4 / 48	CC	cell body
36	−7.22	NULL	2 / 12	GSEA C2	REACTOME_PHASE_1_FUNCTIONALIZATION
37	−7.2	NULL	3 / 33	BP	cholesterol biosynthetic process
38	−7.16	NULL	26 / 614	CC	endoplasmic reticulum membrane
39	−7.15	NULL	3 / 15	GSEA C2	WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN
40	−7.08	NULL	2 / 9	miRNA target	miR−125b

p−values