GW_009

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1840 (955 + / 885 −)

genes with fdr < 0.1 = 1460 (764 + / 696 −)

genes with fdr < 0.05 = 1110 (575 + / 535 −)

genes with fdr < 0.01 = 765 (403 + / 362 −)

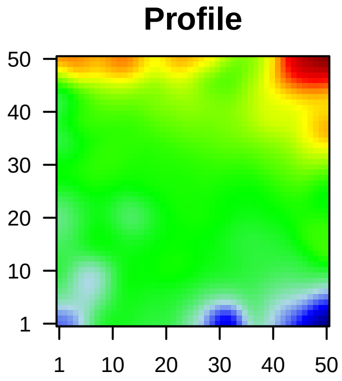
genes in genesets = 16332

<FC> = 0

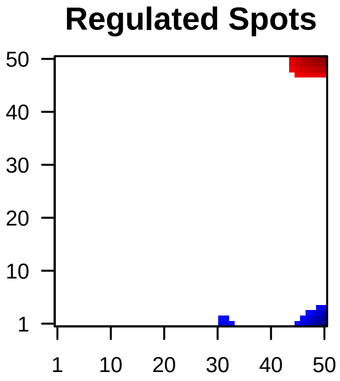
<shrinkage−t> = 0

<p−value> = 0.11

<fdr> = 0.85



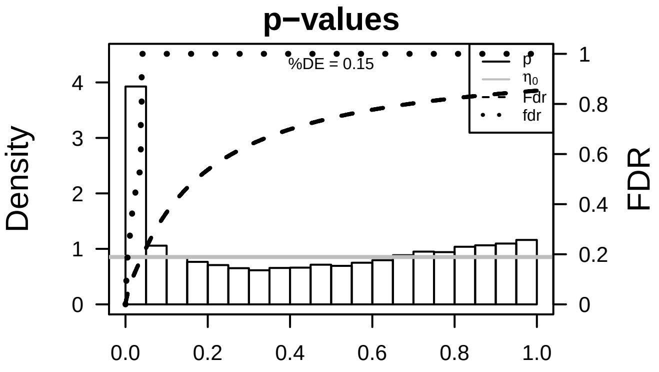
Profile



Regulated Spots

Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.89	2e−16	5e−14	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	131	2.78	2e−16	5e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	8644	2.61	2e−16	5e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
4	1109	2.09	2e−16	5e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Sy
5	216	2.35	2e−16	5e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
6	479	1.65	2e−16	5e−14	7 x 50	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
7	8702	1.86	2e−16	5e−14	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
8	10409	−1.85	2e−16	5e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
9	684	−2.4	2e−16	5e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	260436	−1.73	2e−16	5e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbo
11	51806	1.89	2e−16	5e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
12	595	−2.16	2e−16	5e−14	1 x 6	cyclin D1 [Source:HGNC Symbol;Acc:1582]
13	629	−1.93	2e−16	5e−14	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
14	56548	1.66	2e−16	5e−14	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7 [
15	441520	2.36	2e−16	5e−14	14 x 11	cancer/testis antigen family 45, member A2 [Source:HGNC S
16	3627	−1.67	2e−16	5e−14	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
17	1592	1.67	2e−16	5e−14	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sour
18	92196	1.75	2e−16	5e−14	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	1673	−1.71	2e−16	5e−14	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	1749	1.99	2e−16	5e−14	13 x 50	distal−less homeobox 5 [Source:HGNC Symbol;Acc:2918]



p−values

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	18.04	NULL	914	Chr	Chr 3
2	13.38	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
3	13.38	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
4	11.68	NULL	633	Chr	Chr 9
5	10.56	NULL	370	BP	mitotic cell cycle
6	9.46	NULL	4640	CC	nucleus
7	8.95	NULL	313	miRNA target−starBase	hsa−miR−559
8	8.87	NULL	436	miRNA target−starBase	hsa−miR−548n
9	8.42	NULL	135	H.Tiss	WIRTH_Mucosa
10	8.21	NULL	321	miRNA target−starBase	hsa−miR−548a−5p
11	8.17	NULL	336	miRNA target−starBase	hsa−miR−548d−5p
12	8.08	NULL	302	miRNA target−starBase	hsa−miR−548i
13	8.02	NULL	336	miRNA target−starBase	hsa−miR−548b−5p
14	7.96	NULL	307	miRNA target−starBase	hsa−miR−548c−5p
15	7.85	NULL	271	miRNA target−starBase	hsa−miR−548h
16	7.71	NULL	311	miRNA target−starBase	hsa−miR−302c
17	7.63	NULL	949	CC	nucleoplasm
18	7.58	NULL	16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
19	7.47	NULL	335	miRNA target−starBase	hsa−miR−520d−3p
20	7.42	NULL	316	miRNA target−starBase	hsa−miR−302a
Underexpressed					
1	−16.94	NULL	553	Cancer	Lembcke_Colonic Inflammation
2	−15.11	NULL	51	BP	type I interferon signaling pathway
3	−15.08	NULL	312	BP	immune response
4	−13.59	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	−13.59	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	−13.59	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	−13.59	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	−12.31	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
9	−11.38	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
10	−11.15	NULL	683	CC	extracellular space
11	−11.08	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
12	−11.01	NULL	957	Chr	Chr 11
13	−10.94	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
14	−10.78	NULL	417	H.Tiss	WIRTH_Immune system
15	−10.57	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
16	−10.5	NULL	1182	CC	extracellular region
17	−10.21	NULL	1135	Chr	Chr 19
18	−9.97	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
19	−9.94	NULL	23	CC	integral to lumenal side of endoplasmic reticulum membrane
20	−9.88	NULL	109	BP	response to virus

GW_009

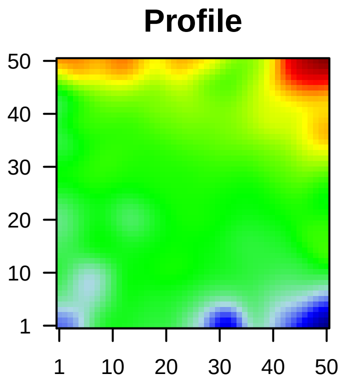
Local Summary

%DE = 0.91
metagenes = 27
genes = 374
genes in genesets = 370

genes with fdr < 0.1 = 292 (282 + / 10 −)
genes with fdr < 0.05 = 292 (282 + / 10 −)
genes with fdr < 0.01 = 229 (223 + / 6 −)

<r> metagenes = 0.89
<r> genes = 0.28

<FC> = 0.64
<shrinkage−t> = 22.26
<p−value> = 0
<fdr> = 0.35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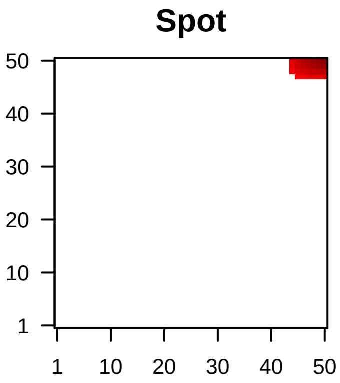

Spot

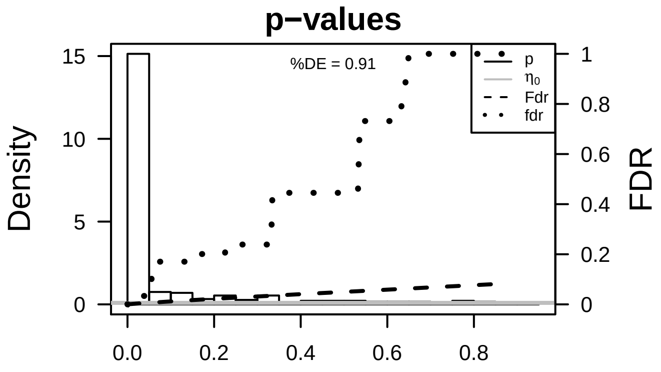
Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154664	1.89	2e−16	5e−16	50 x 50	ATP−binding cassette, sub−family A (ABC1), member 13 [Sou
2	216	2.35	2e−16	5e−16	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	8702	1.86	2e−16	5e−16	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp
4	56548	1.66	2e−16	5e−16	50 x 50	carbohydrate (N−acetylglucosamine 6−O) sulfotransferase 7 [
5	1592	1.67	2e−16	5e−16	50 x 50	cytochrome P450, family 26, subfamily A, polypeptide 1 [Sour
6	2938	2.51	2e−16	5e−16	50 x 50	glutathione S−transferase alpha 2 [Source:HGNC Symbol;Ac
7	2944	1.92	2e−16	5e−16	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:4
8	3880	1.8	2e−16	5e−16	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
9	4915	1.92	2e−16	5e−16	50 x 50	neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
10	4922	3.42	2e−16	5e−16	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
11	6657	1.86	2e−16	5e−16	50 x 50	SRY (sex determining region Y)−box 2 [Source:HGNC Symb
12	11166	1.84	2e−16	5e−16	50 x 50	SRY (sex determining region Y)−box 21 [Source:HGNC Sym
13	7348	2.14	2e−16	5e−16	50 x 50	uroplakin 1B [Source:HGNC Symbol;Acc:12578]
14	256764	1.67	2e−16	5e−16	50 x 50	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
15	214	1.62	9e−16	1e−13	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC S
16	1894	1.57	7e−15	1e−13	45 x 50	epithelial cell transforming sequence 2 oncogene [Source:HG
17	7358	1.56	9e−15	1e−13	50 x 50	UDP−glucose 6−dehydrogenase [Source:HGNC Symbol;Acc
18	54800	1.56	1e−14	7e−13	50 x 48	kelch−like family member 24 [Source:HGNC Symbol;Acc:259
19	10643	1.52	4e−14	7e−13	48 x 50	insulin−like growth factor 2 mRNA binding protein 3 [Source:
20	4171	1.52	5e−14	4e−11	46 x 48	minichromosome maintenance complex component 2 [Sourc

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.96	NULL	70 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	28.96	NULL	70 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	19.75	NULL	22 / 57	Glio	developing astrocytes
4	17.94	NULL	11 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
5	17.61	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
6	17.33	NULL	7 / 11	GSEA C2	KALMA_E2F1_TARGETS
7	17.17	NULL	12 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
8	16.49	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
9	16.01	NULL	11 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
10	14.84	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	14.66	NULL	66 / 370	BP	mitotic cell cycle
12	14.09	NULL	72 / 914	Chr	Chr 3
13	14.05	NULL	8 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
14	13.82	NULL	7 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
15	13.47	NULL	8 / 15	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G23_UP
16	13.36	NULL	12 / 30	BP	DNA strand elongation involved in DNA replication
17	13.34	NULL	4 / 13	BP	regulation of blood vessel size
18	13.12	NULL	9 / 14	MMML CGS	MACIEJ_MMML 4
19	13.07	NULL	8 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
20	12.99	NULL	8 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
21	12.98	NULL	5 / 20	MF	glutathione transferase activity
22	12.95	NULL	6 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
23	12.54	NULL	6 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
24	12.45	NULL	8 / 34	BP	glutathione metabolic process
25	12.35	NULL	9 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
26	12.33	NULL	4 / 8	GSEA C2	REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
27	12.18	NULL	7 / 16	Cancer	WOLFER_overlap genes
28	12.14	NULL	31 / 149	BP	DNA replication
29	12.08	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
30	12.04	NULL	6 / 25	BP	glutathione derivative biosynthetic process
31	12.01	NULL	8 / 15	GSEA C2	ODONNELL_TARGETS_OF_MYC_AND_TFRC_DN
32	12	NULL	7 / 16	GSEA C2	REACTOME_DNA_STRAND_ELONGATION
33	11.8	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
34	11.73	NULL	6 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
35	11.71	NULL	4 / 12	GSEA C2	REACTOME_CELL_CYCLE_MITOTIC
36	11.7	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
37	11.36	NULL	7 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
38	11.28	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
39	11.26	NULL	7 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
40	11.15	NULL	67 / 530	Cancer	Lembcke_Normal vs Adenoma


p−values

GW_009

Local Summary

%DE = 0.93

metagenes = 5

genes = 111

genes in genesets = 109

genes with fdr < 0.1 = 97 (1 + / 96 −)

genes with fdr < 0.05 = 87 (1 + / 86 −)

genes with fdr < 0.01 = 71 (0 + / 71 −)

<r> metagenes = 1

<r> genes = 0.48

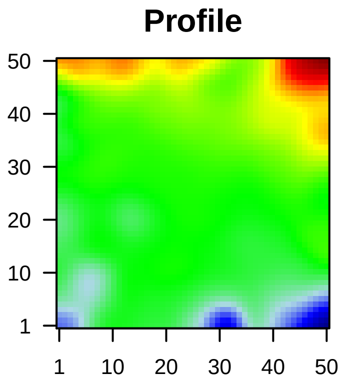
<FC> = −0.84

<shrinkage−t> = −29.69

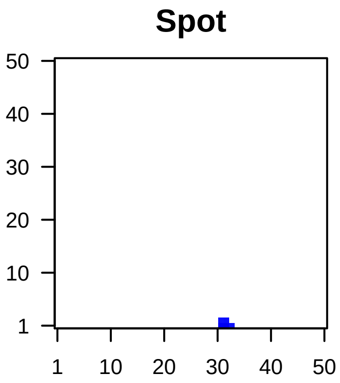
<p−value> = 0

<fdr> = 0.3

Profile



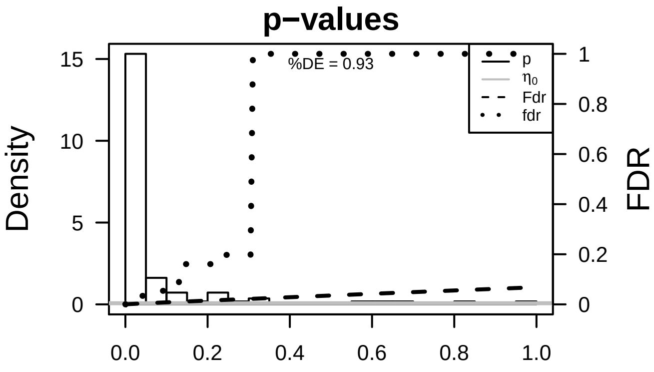
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	−2.4	2e−16	1e−16	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	629	−1.93	2e−16	1e−16	32 x 1	complement factor B [Source:HGNC Symbol;Acc:1037]
3	3627	−1.67	2e−16	1e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;
4	94240	−2.03	2e−16	1e−16	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symb
5	10866	−1.76	2e−16	1e−16	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symb
6	3106	−1.9	2e−16	1e−16	32 x 1	major histocompatibility complex, class I, B [Source:HGNC S
7	10561	−1.87	2e−16	1e−16	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
8	10964	−2.07	2e−16	1e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
9	2537	−2.04	2e−16	1e−16	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;
10	8519	−2.05	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC
11	10581	−1.87	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 2 [Source:HGNC
12	10410	−1.92	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 3 [Source:HGNC
13	9636	−2.29	2e−16	1e−16	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:40
14	4061	−1.83	2e−16	1e−16	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
15	6890	−1.63	7e−16	2e−13	32 x 1	transporter 1, ATP−binding cassette, sub−family B (MDR/TAP
16	85441	−1.52	5e−14	2e−13	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
17	54739	−1.51	6e−14	1e−12	32 x 1	XIAP associated factor 1 [Source:HGNC Symbol;Acc:30932]
18	4600	−1.48	3e−13	4e−12	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
19	6772	−1.44	8e−13	9e−12	32 x 1	signal transducer and activator of transcription 1, 91kDa [Sou
20	3430	−1.42	2e−12	5e−11	32 x 1	interferon−induced protein 35 [Source:HGNC Symbol;Acc:53

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−60.43	NULL	29 / 51	BP	type I interferon signaling pathway
2	−52.46	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	−52.03	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
4	−50.29	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
5	−45.74	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	−42.86	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
7	−42.65	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
8	−41.58	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
9	−40.78	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
10	−40.63	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
11	−38.17	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
12	−36.42	NULL	13 / 31	BP	negative regulation of viral genome replication
13	−34.52	NULL	7 / 10	CC	MHC class I protein complex
14	−33.65	NULL	27 / 109	BP	response to virus
15	−33.63	NULL	31 / 123	BP	defense response to virus
16	−31.07	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
17	−30.87	NULL	34 / 204	BP	cytokine−mediated signaling pathway
18	−30.74	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
19	−30.42	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
20	−30.24	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
21	−29.66	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
22	−29.4	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
23	−29.3	NULL	8 / 18	BP	positive regulation of T cell mediated cytotoxicity
24	−28.08	NULL	5 / 18	BP	response to interferon−gamma
25	−27.04	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
26	−26.9	NULL	7 / 18	MF	peptide antigen binding
27	−26.26	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
28	−25.38	NULL	5 / 16	GSEA C2	ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
29	−25.11	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
30	−24.77	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
31	−23.78	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
32	−23.32	NULL	31 / 274	Lymphoma	SPANG_IL21 DN
33	−23.29	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
34	−23.12	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
35	−22.79	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
36	−22.08	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
37	−22.08	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
38	−22.02	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
39	−21.11	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
40	−21.09	NULL	5 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_LB_DN

GW_009

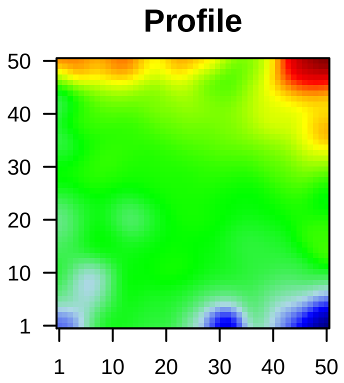
Local Summary

%DE = 0.93
metagenes = 17
genes = 281
genes in genesets = 278

genes with fdr < 0.1 = 247 (5 + / 242 −)
genes with fdr < 0.05 = 240 (3 + / 237 −)
genes with fdr < 0.01 = 180 (0 + / 180 −)

<r> metagenes = 0.99
<r> genes = 0.58

<FC> = −0.69
<shrinkage−t> = −24.3
<p−value> = 0
<fdr> = 0.28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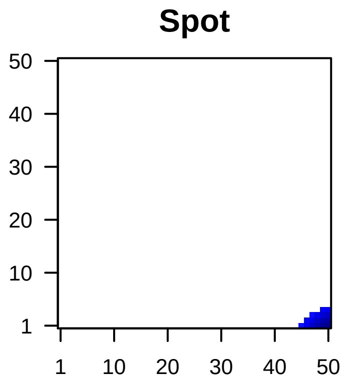
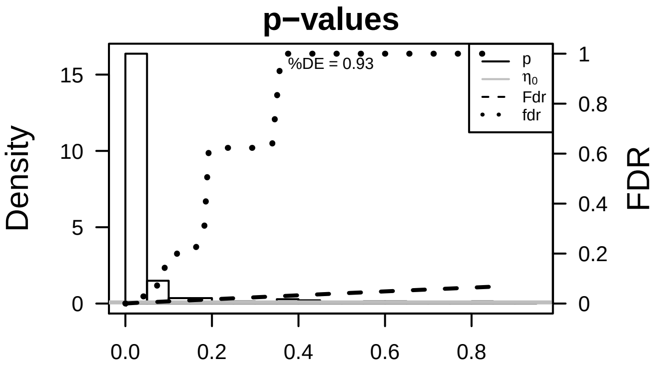

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	260436	−1.73	2e−16	5e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
2	5880	−1.6	2e−15	4e−14	50 x 1	ras−related C3 botulinum toxin substrate 2 (rho family, small (
3	894	−1.58	4e−15	5e−13	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
4	713	−1.53	3e−14	2e−12	50 x 1	complement component 1, q subcomponent, B chain [Source
5	5920	−1.5	1e−13	2e−12	48 x 1	retinoic acid receptor responder (tazarotene induced) 3 [Sour
6	3108	−1.48	2e−13	6e−12	50 x 1	major histocompatibility complex, class II, DM alpha [Source:I
7	3109	−1.46	5e−13	8e−12	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
8	10537	−1.44	1e−12	8e−12	50 x 1	ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	6363	−1.43	1e−12	3e−11	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
10	3122	−1.32	3e−12	3e−11	50 x 1	major histocompatibility complex, class II, DR alpha [Source:I
11	348	−1.4	4e−12	3e−11	50 x 1	apolipoprotein E [Source:HGNC Symbol;Acc:613]
12	241	−1.39	5e−12	3e−10	50 x 1	arachidonate 5−lipoxygenase−activating protein [Source:HGN
13	6352	−1.33	4e−11	3e−10	48 x 1	chemokine (C−C motif) ligand 5 [Source:HGNC Symbol;Acc:
14	3936	−1.33	4e−11	3e−10	50 x 1	lymphocyte cytosolic protein 1 (L−plastin) [Source:HGNC Syr
15	3123	−1.33	5e−11	3e−10	45 x 1	major histocompatibility complex, class II, DR beta 1 [Source:
16	6347	−1.32	5e−11	6e−10	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:
17	397	−1.29	9e−11	6e−10	50 x 1	Rho GDP dissociation inhibitor (GDI) beta [Source:HGNC Syı
18	83641	−1.3	1e−10	6e−10	50 x 1	family with sequence similarity 107, member B [Source:HGN(
19	3059	−1.29	2e−10	6e−10	50 x 1	hematopoietic cell−specific Lyn substrate 1 [Source:HGNC Sy
20	3113	−1.29	2e−10	7e−10	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source


p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−32.33	NULL	13 / 15	CC	MHC class II protein complex
2	−29.57	NULL	92 / 417	H.Tiss	WIRTH_Immune system
3	−24.14	NULL	95 / 553	Cancer	Lembcke_Colonic Inflammation
4	−22.22	NULL	54 / 312	BP	immune response
5	−19.54	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
6	−19.54	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
7	−19.54	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
8	−19.54	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
9	−19.29	NULL	16 / 47	BP	antigen processing and presentation
10	−18.67	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
11	−18.53	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
12	−18.48	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
13	−18.01	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
14	−17.98	NULL	3 / 3	MMML CGS	MACIEJ_MMML 7
15	−17.91	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
16	−17.59	NULL	17 / 60	BP	T cell costimulation
17	−17.28	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
18	−17.11	NULL	18 / 74	BP	regulation of immune response
19	−17.1	NULL	8 / 21	CC	clathrin−coated endocytic vesicle membrane
20	−16.77	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
21	−16.33	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
22	−16.25	NULL	8 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
23	−16.05	NULL	2 / 4	MMML CGS	MACIEJ_MMML 2
24	−15.4	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
25	−15.07	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
26	−14.62	NULL	5 / 12	BP	immunoglobulin mediated immune response
27	−14.54	NULL	8 / 28	CC	transport vesicle membrane
28	−14.31	NULL	9 / 35	CC	trans−Golgi network membrane
29	−14.3	NULL	5 / 12	GSEA C2	ZHAN_MULTIPLE_MYELOMA_DN
30	−14.24	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
31	−13.65	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
32	−13.54	NULL	5 / 12	BP	dendritic cell chemotaxis
33	−13.47	NULL	8 / 32	CC	ER to Golgi transport vesicle membrane
34	−13.47	NULL	14 / 87	BP	antigen processing and presentation of exogenous peptide antigen
35	−13.46	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
36	−13.44	NULL	7 / 13	Cancer	GENTLES_modul18
37	−13.16	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
38	−13.06	NULL	17 / 84	BP	T cell receptor signaling pathway
39	−12.95	NULL	4 / 8	Lymphoma	MASCQUE_ABC UP
40	−12.75	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS