

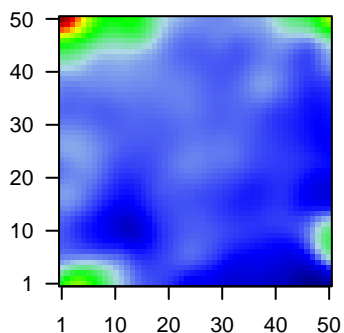
GW_302

Global Summary

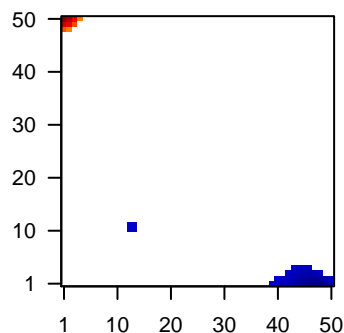
%DE = 0.12
 # genes with fdr < 0.2 = 1435 (911 + / 524 -)
 # genes with fdr < 0.1 = 1121 (742 + / 379 -)
 # genes with fdr < 0.05 = 885 (620 + / 265 -)
 # genes with fdr < 0.01 = 636 (471 + / 165 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.88

Profile



Regulated Spots



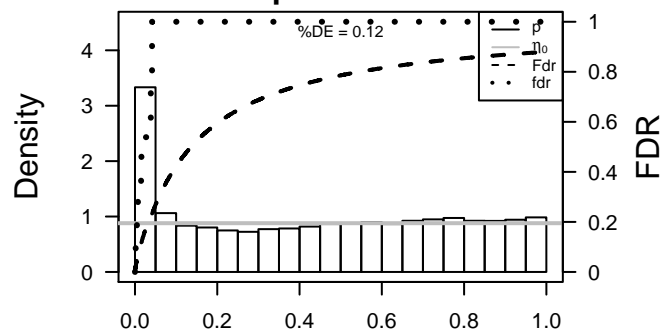
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description
1	8745	1.28	2e-16 3e-14	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
2	131	2.17	2e-16 3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	84803	1.03	2e-16 3e-14	8 x 47 1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC
4	10551	1.29	2e-16 3e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	57016	1.87	2e-16 3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
6	441282	1.38	2e-16 3e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
7	1646	1.69	2e-16 3e-14	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Sy
8	8644	2.8	2e-16 3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
9	1109	3.11	2e-16 3e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy
10	216	1.83	2e-16 3e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
11	218	1.4	2e-16 3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
12	353322	1.04	2e-16 3e-14	6 x 48 ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:29593]
13	11199	1.11	2e-16 3e-14	15 x 50 annexin A10 [Source:HGNC Symbol;Acc:534]
14	360	1.58	2e-16 3e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
15	445328	1.15	2e-16 3e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:Hi
16	80115	-1.19	2e-16 3e-14	1 x 43 BAI1-associated protein 2-like 2 [Source:HGNC Symbol;Acc
17	586	1.52	2e-16 3e-14	6 x 1 branched chain amino-acid transaminase 1, cytosolic [Sourc
18	92747	1.74	2e-16 3e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
19	260436	-1.32	2e-16 3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symb
20	394263	1.03	2e-16 3e-14	3 x 50

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.6	NULL	135	H.Tiss WIRTH_Mucosa
2	11	NULL	190	CC extracellular matrix
3	10.24	NULL	250	Lymphoid ENZ_Stromal signature 1
4	10.13	NULL	572	Disease GUDJ_poriasis up
5	10.07	NULL	38	BP epithelial cell differentiation
6	8.77	NULL	19	BP peptide cross-linking
7	8.6	NULL	242	BP extracellular matrix organization
8	8.53	NULL	16	MMML C63CIEJ_MMML 1
9	8.53	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
10	8.01	NULL	11	MF platelet-derived growth factor binding
11	7.86	NULL	39	BP retinoid metabolic process
12	7.72	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	7.68	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
14	7.64	NULL	57	MF extracellular matrix structural constituent
15	7.59	NULL	76	BP wound healing
16	7.43	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
17	7.4	NULL	13	BP negative regulation of peptidase activity
18	7.34	NULL	534	Chr Chr 8
19	7.14	NULL	51	BP osteoblast differentiation
20	7.06	NULL	11	BP prostaglandin metabolic process
<i>Underexpressed</i>				
1	-11.93	NULL	717	Chr Chr 16
2	-7.52	NULL	417	H.Tiss WIRTH_Immune system
3	-6.28	NULL	15	CC MHC class II protein complex
4	-6.25	NULL	1720	Chr Chr 1
5	-6.07	NULL	60	BP interferon-gamma-mediated signaling pathway
6	-6.06	NULL	10	BP cellular response to zinc ion
7	-6	NULL	7	MMML C63CIEJ_MMML 13
8	-5.56	NULL	127	H.Tiss WIRTH_Muscle
9	-5.35	NULL	316	Cancer SPANG_BCL6-index2
10	-5.02	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
11	-4.92	NULL	47	BP antigen processing and presentation
12	-4.89	NULL	15	BP negative regulation of growth
13	-4.89	NULL	3	MMML C63CIEJ_MMML 7
14	-4.87	NULL	36	BP muscle filament sliding
15	-4.77	NULL	16	H.Tiss WIRTH_Hippocampus
16	-4.77	NULL	699	Chr Chr 5
17	-4.75	NULL	449	Chr Chr 20
18	-4.7	NULL	204	BP cytokine-mediated signaling pathway
19	-4.62	NULL	312	BP immune response
20	-4.52	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F

p-values



GW_302

Local Summary

%DE = 0.83
 # metagenes = 9
 # genes = 159
 # genes in genesets = 156

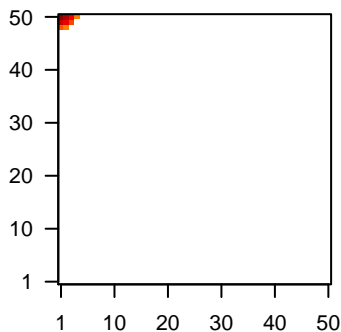
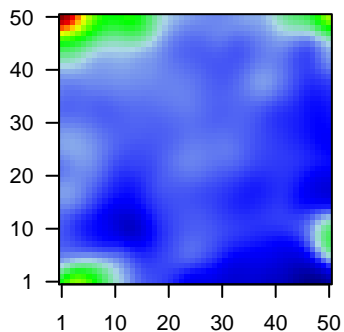
genes with $fdr < 0.1$ = 126 (112 + / 14 -)
 # genes with $fdr < 0.05$ = 119 (106 + / 13 -)
 # genes with $fdr < 0.01$ = 106 (96 + / 10 -)

<r> metagenes = 0.99
 <r> genes = 0.5

<FC> = 0.62
 <shrinkage-t> = 21.92
 <p-value> = 0
 <fdr> = 0.25

Profile

Spot



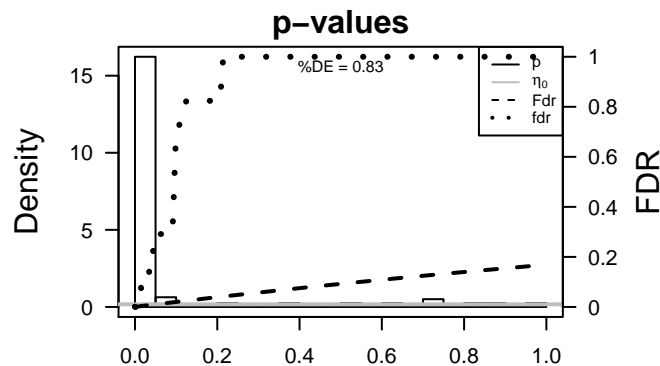
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	2.17	2e-16	1e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	1.87	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	1.38	2e-16	1e-16	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	2.8	2e-16	1e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
5	218	1.4	2e-16	1e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	360	1.58	2e-16	1e-16	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
7	394263	1.03	2e-16	1e-16	3 x 50
8	375791	1.44	2e-16	1e-16	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
9	51806	-1.36	2e-16	1e-16	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
10	22802	1.88	2e-16	1e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	9022	1.18	2e-16	1e-16	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2l
12	49860	3.34	2e-16	1e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
13	163351	1.42	2e-16	1e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
14	2877	2.57	2e-16	1e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syr
15	43849	1.05	2e-16	1e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6i
16	26085	1.28	2e-16	1e-16	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6i
17	5653	1.19	2e-16	1e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63l
18	3860	1.89	2e-16	1e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
19	192666	2.02	2e-16	1e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
20	3851	3.31	2e-16	1e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	50.35	NULL	67 / 135	H.Tiss WIRTH_Mucosa
2	18.25	NULL	8 / 19	BP peptide cross-linking
3	16.86	NULL	6 / 13	BP negative regulation of peptidase activity
4	16.59	NULL	19 / 53	BP keratinocyte differentiation
5	16.38	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
6	16.17	NULL	70 / 572	Disease GUDJ_poriasis up
7	16.14	NULL	4 / 15	MF retinol dehydrogenase activity
8	15.21	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
9	14.84	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	14.42	NULL	14 / 21	CC cornified envelope
11	13.24	NULL	6 / 38	BP epithelial cell differentiation
12	12.96	NULL	16 / 42	BP keratinization
13	11.76	NULL	5 / 29	BP regulation of proteolysis
14	11.44	NULL	4 / 39	BP retinoid metabolic process
15	11.36	NULL	1 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
16	10.61	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
17	10.55	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
18	10.28	NULL	4 / 44	CC keratin filament
19	10.27	NULL	8 / 52	BP negative regulation of endopeptidase activity
20	10.14	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
21	10.1	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
22	10.06	NULL	1 / 10	BP positive regulation of endothelial cell apoptotic process
23	10.06	NULL	1 / 10	BP retinal metabolic process
24	9.95	NULL	6 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
25	9.9	NULL	3 / 12	BP cellular aldehyde metabolic process
26	9.86	NULL	18 / 76	BP epidermis development
27	9.65	NULL	1 / 11	Glio VERHAAK_Brain
28	9.5	NULL	1 / 11	BP prostaglandin metabolic process
29	9.44	NULL	2 / 12	MF retinol binding
30	9.36	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
31	9.33	NULL	10 / 122	MF serine-type endopeptidase activity
32	9.19	NULL	1 / 7	GSEA C2DASU_IL6_SIGNALING_DN
33	9.16	NULL	1 / 12	MF channel activity
34	9.11	NULL	2 / 14	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN
35	9.05	NULL	4 / 13	H.Tiss WIRTH_Tonsil
36	9	NULL	2 / 13	BP retinoic acid metabolic process
37	8.92	NULL	13 / 186	MF structural molecule activity
38	8.85	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
39	8.82	NULL	6 / 82	CC intermediate filament
40	8.73	NULL	1 / 13	GSEA C2HASLINGER_B_CLL_WITH_MUTATED_VH_GENES



GW_302

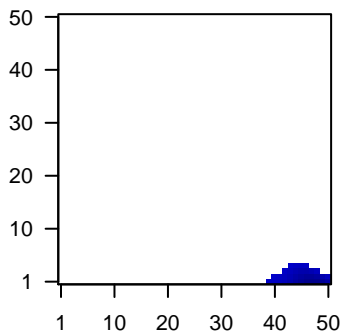
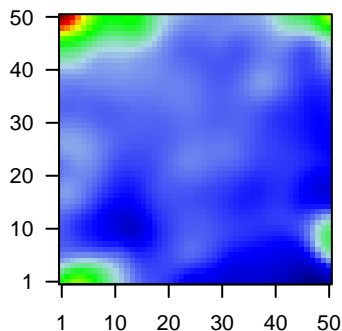
Local Summary

%DE = 0.69
 # metagenes = 34
 # genes = 525
 # genes in genesets = 497
 # genes with $fdr < 0.1$ = 169 (9 + / 160 -)
 # genes with $fdr < 0.05$ = 102 (5 + / 97 -)
 # genes with $fdr < 0.01$ = 50 (4 + / 46 -)

$\langle r \rangle$ metagenes = 0.89
 $\langle r \rangle$ genes = 0.42
 $\langle FC \rangle = -0.19$
 $\langle \text{shrinkage-t} \rangle = -6.5$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.78$

Profile

Spot



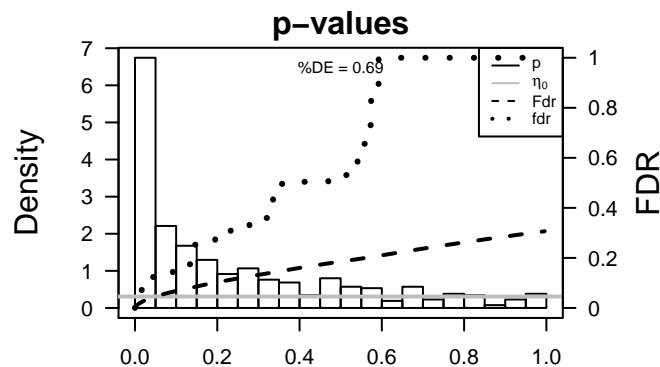
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	260436	-1.32	2e-16	7e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
2	6364	-1.03	2e-16	7e-15	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
3	3123	-1.27	2e-16	7e-15	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
4	125050	1.33	2e-16	7e-15	40 x 1 RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
5	10628	-1.28	2e-16	7e-15	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16
6	3120	-1.01	9e-16	2e-07	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:
7	5880	-0.76	1e-09	4e-07	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small (
8	23466	0.74	4e-09	6e-06	41 x 1 chromobox homolog 6 [Source:HGNC Symbol;Acc:1556]
9	89932	-0.69	4e-08	6e-06	45 x 4 papilin, proteoglycan-like sulfated glycoprotein [Source:HGNC
10	126306	-0.66	1e-07	6e-06	49 x 1 junctional sarcoplasmic reticulum protein 1 [Source:HGNC Sy
11	5336	-0.66	1e-07	6e-06	48 x 3 phospholipase C, gamma 2 (phosphatidylinositol-specific) [S
12	3620	-0.66	1e-07	9e-06	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:f
13	440353	-0.65	3e-07	9e-06	40 x 1
14	51326	0.65	3e-07	3e-05	42 x 1 ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc
15	3512	0.63	6e-07	3e-05	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobu
16	10537	-0.62	7e-07	9e-05	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
17	4815	-0.6	2e-06	9e-05	45 x 4 ninjurin 2 [Source:HGNC Symbol;Acc:7825]
18	255231	-0.6	2e-06	2e-04	49 x 1 mucolinpin 2 [Source:HGNC Symbol;Acc:13357]
19	389289	-0.59	3e-06	3e-04	45 x 2 annexin A2 receptor [Source:HGNC Symbol;Acc:33463]
20	613037	-0.57	5e-06	1e-03	40 x 2 nuclear pore complex interacting protein family, member B5 [

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-29.98	NULL	14 / 15	CC MHC class II protein complex
2	-24.64	NULL	3 / 3	MMML C6ACIEJ_MMML 7
3	-23.51	NULL	115 / 417	H Tiss WIRTH_Immune system
4	-19.88	NULL	9 / 21	CC clathrin-coated endocytic vesicle membrane
5	-18.94	NULL	9 / 23	CC integral to luminal side of endoplasmic reticulum membrane
6	-18.42	NULL	102 / 553	Cancer Lembecke_Colonc Inflammation
7	-18.01	NULL	16 / 47	BP antigen processing and presentation
8	-17.03	NULL	9 / 28	CC transport vesicle membrane
9	-16.69	NULL	24 / 84	BP T cell receptor signaling pathway
10	-16.04	NULL	25 / 60	BP T cell costimulation
11	-15.84	NULL	9 / 32	CC ER to Golgi transport vesicle membrane
12	-15.08	NULL	9 / 35	CC trans-Golgi network membrane
13	-13.03	NULL	9 / 52	Chr HSCR6_MHC_QBL
14	-12.95	NULL	9 / 46	CC endocytic vesicle membrane
15	-12.9	NULL	69 / 312	BP immune response
16	-12.6	NULL	16 / 87	BP antigen processing and presentation of exogenous peptide antigen
17	-11.96	NULL	15 / 60	BP interferon-gamma-mediated signaling pathway
18	-11.52	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPD_SIGNATURE
19	-11.36	NULL	8 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
20	-11.27	NULL	9 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
21	-11.11	NULL	8 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
22	-10.8	NULL	10 / 13	Cancer GENTLES_modul18
23	-10.65	NULL	12 / 28	BP B cell receptor signaling pathway
24	-9.47	NULL	7 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
25	-9.46	NULL	41 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
26	-9.46	NULL	41 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
27	-9.46	NULL	41 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
28	-9.46	NULL	41 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
29	-9.31	NULL	3 / 15	GSEA C2SHIPP_DLCL_VS_FOLLICULAR_LYMPHOMA_DN
30	-9.05	NULL	19 / 74	BP regulation of immune response
31	-9.02	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
32	-8.7	NULL	5 / 8	GSEA C2BIOCARTA_TCAPOPTOSIS_PATHWAY
33	-8.7	NULL	5 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
34	-8.67	NULL	3 / 18	miRNA target sites
35	-8.43	NULL	19 / 215	CC lysosomal membrane
36	-8.41	NULL	3 / 14	GSEA C2WINPENNINGKX_MELANOMA_METASTASIS_DN
37	-8.4	NULL	5 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE
38	-8.33	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
39	-8.28	NULL	26 / 204	BP cytokine-mediated signaling pathway
40	-8.25	NULL	31 / 162	CC external side of plasma membrane



GW_302

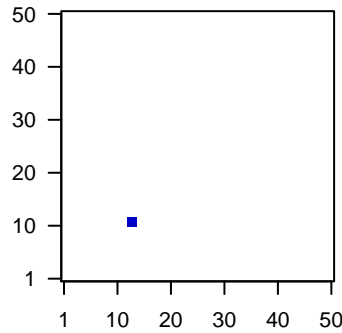
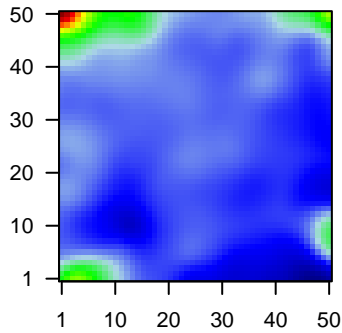
Local Summary

%DE = 0.95
 # metagenes = 4
 # genes = 35
 # genes in genesets = 20
 # genes with $fdr < 0.1$ = 32 (0 + / 32 -)
 # genes with $fdr < 0.05$ = 27 (0 + / 27 -)
 # genes with $fdr < 0.01$ = 23 (0 + / 23 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.57
 $\langle FC \rangle = -0.35$
 $\langle \text{shrinkage-t} \rangle = -12.42$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.42$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	4109	-0.63	5e-07	2e-06	14 x 11 melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6
2	645037	-0.59	3e-06	2e-06	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
3	121355	-0.59	3e-06	2e-06	14 x 11 gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
4	441520	-0.58	4e-06	6e-06	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
5	24150	-0.56	8e-06	1e-05	14 x 11 TP53 target 3D [Source:HGNC Symbol;Acc:44657]
6	729422	-0.55	1e-05	6e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	-0.48	1e-04	6e-05	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729442	-0.47	2e-04	6e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	2577	-0.47	2e-04	6e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	729428	-0.46	2e-04	6e-05	14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402]
11	2576	-0.46	2e-04	6e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
12	4100	-0.46	2e-04	2e-04	14 x 11 melanoma antigen family A, 1 (directs expression of antigen I
13	100008586	-0.45	3e-04	3e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
14	645073	-0.43	5e-04	3e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	2579	-0.43	7e-04	3e-04	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
16	26749	-0.42	8e-04	2e-03	14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960]
17	729396	-0.39	2e-03	3e-03	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
18	729447	-0.37	4e-03	9e-03	14 x 11 G antigen 2A [Source:HGNC Symbol;Acc:4099]
19	402381	-0.31	1e-02	9e-03	13 x 11 spermatogenesis and oogenesis specific basic helix-loop-he
20	4105	-0.3	2e-02	9e-03	14 x 11 melanoma antigen family A, 6 [Source:HGNC Symbol;Acc:68

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-18.72	NULL	1 / 11	GSEA C2S0_PLACENTA
2	-15.96	NULL	1 / 14	GSEA C2NIELSEN_GIST
3	-15.85	NULL	1 / 5	GSEA C2CHOI_ATL_ACUTE_STAGE
4	-15.73	NULL	16 / 630	Chr Chr X
5	-15.26	NULL	1 / 15	GSEA C2BROWNE_HCMV_INFECTION_8HR_DN
6	-12.64	NULL	1 / 12	GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
7	-12.37	NULL	2 / 15	GSEA C2MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
8	-9.28	NULL	1 / 10	GSEA C2TSUNODA_CISPLATIN_RESISTANCE_DN
9	-9.01	NULL	1 / 21	BP negative regulation of Notch signaling pathway
10	-7.06	NULL	1 / 15	GSEA C2LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
11	-7.06	NULL	1 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
12	-6.77	NULL	1 / 16	GSEA C2JAEGER_METASTASIS_UP
13	-6.43	NULL	1 / 19	BP oogenesis
14	-6.06	NULL	2 / 48	Cancer KUIPER_MM poor survival
15	-5.84	NULL	1 / 6	GSEA C2NIELSEN_LEIOMYOSARCOMA_UP
16	-4.95	NULL	1 / 16	GSEA C2MID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
17	-4.41	NULL	1 / 68	MF histone deacetylase binding
18	-4.24	NULL	1 / 37	BP ovarian follicle development
19	-4.01	NULL	1 / 120	H.Tiss WIRTH_Testis
20	-3.69	NULL	3 / 419	CC cellular_component
21	-3.35	NULL	3 / 481	BP biological_process
22	-3.11	NULL	1 / 21	BP chromatin organization
23	-3.04	NULL	3 / 549	MF molecular_function
24	-2.49	NULL	1 / 16	GSEA C2ROZANOV_MMP14_TARGETS_DN
25	-1.85	NULL	2 / 259	BP spermatogenesis
26	-1.61	NULL	1 / 156	MF protein dimerization activity
27	-1.57	NULL	1 / 68	CC collagen
28	-1.4	NULL	1 / 79	MF serine-type endopeptidase inhibitor activity
29	-1.35	NULL	1 / 83	CC basement membrane
30	-0.9	NULL	1 / 504	BP negative regulation of transcription from RNA polymerase II promot
31	-0.78	NULL	1 / 153	CC endoplasmic reticulum lumen
32	-0.78	NULL	1 / 717	Chr Chr 16
33	-0.73	NULL	1 / 346	BP cell differentiation
34	-0.64	NULL	3 / 579	CC nucleolus
35	-0.62	NULL	7 / 4640	CC nucleus
36	-0.61	NULL	1 / 866	Chr Chr 12
37	-0.42	NULL	1 / 242	BP extracellular matrix organization
38	-0.36	NULL	1 / 504	BP positive regulation of transcription, DNA-dependent
39	-0.24	NULL	2 / 1574	BP transcription, DNA-templated
40	-0.2	NULL	1 / 188	BP brain development

p-values

