

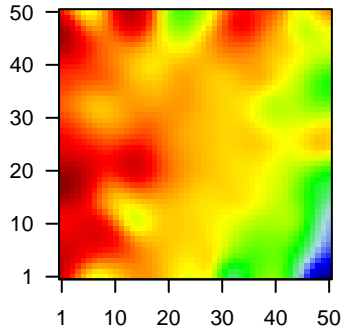
GW_065

Global Summary

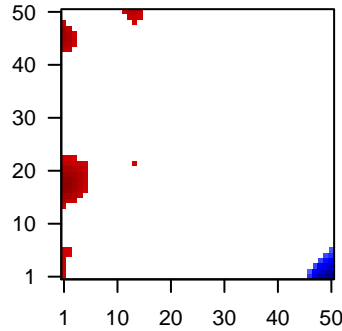
%DE = 0.13
 # genes with fdr < 0.2 = 1522 (754 + / 768 -)
 # genes with fdr < 0.1 = 1176 (579 + / 597 -)
 # genes with fdr < 0.05 = 920 (451 + / 469 -)
 # genes with fdr < 0.01 = 651 (321 + / 330 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.13
 <fdr> = 0.87

Profile



Regulated Spots



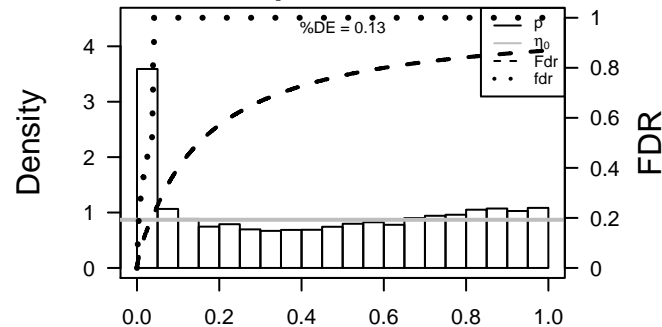
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	24	1.91	2e-16	6e-14	16 x 50 ATP-binding cassette, sub-family A (ABC1), member 4 [Sou
2	131	1.8	2e-16	6e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	1.89	2e-16	6e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	1.83	2e-16	6e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Sy
5	8644	2.19	2e-16	6e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	1109	2.36	2e-16	6e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
7	218	2.63	2e-16	6e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	479	2.22	2e-16	6e-14	7 x 50 ATPase, H+/K+ transporting, nongastric, alpha polypeptide [S
9	684	-1.71	2e-16	6e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	339512	2.09	2e-16	6e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
11	29113	3.12	2e-16	6e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
12	8900	1.95	2e-16	6e-14	1 x 42 cyclin A1 [Source:HGNC Symbol;Acc:1577]
13	972	-2.02	2e-16	6e-14	50 x 1 CD74 molecule, major histocompatibility complex, class II inv
14	1066	2.28	2e-16	6e-14	14 x 50 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
15	629	-2.03	2e-16	6e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
16	22802	-1.92	2e-16	6e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	49860	-1.85	2e-16	6e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1437	1.7	2e-16	6e-14	1 x 4 colony stimulating factor 2 (granulocyte-macrophage) [Source
19	3627	-1.79	2e-16	6e-14	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;f
20	4283	-1.9	2e-16	6e-14	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.23	NULL	633	Chr Chr 9
2	10.67	NULL	957	Chr Chr 11
3	7.94	NULL	918	Chr Chr 17
4	6.31	NULL	253	BP translation
5	6.19	NULL	743	Chr Chr 7
6	6.07	NULL	153	MF structural constituent of ribosome
7	5.86	NULL	16	GSEA C2ZONDER_CDH1_TARGETS_3_DN
8	5.59	NULL	167	CC ribosome
9	5.58	NULL	1233	TF KIM_MYC targets
10	5.48	NULL	13	GSEA C2SINGH_NFE2L2_TARGETS
11	5.46	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	5.45	NULL	34	BP glutathione metabolic process
13	5.42	NULL	96	BP rRNA processing
14	5.4	NULL	434	BP oxidation-reduction process
15	5.19	NULL	15	GSEA C2BILD_HRAS_ONCOGENIC_SIGNATURE
16	5.19	NULL	1253	BP small molecule metabolic process
17	5.14	NULL	39	BP retinoid metabolic process
18	4.96	NULL	482	BP cellular protein metabolic process
19	4.89	NULL	21	CC cornified envelope
20	4.84	NULL	9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
<i>Underexpressed</i>				
1	-14.24	NULL	15	CC MHC class II protein complex
2	-13.46	NULL	717	Chr Chr 16
3	-12.15	NULL	417	H.Tiss WIRTH_Immune system
4	-11.62	NULL	47	BP antigen processing and presentation
5	-11.09	NULL	618	Chr Chr 4
6	-11.01	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
7	-10.74	NULL	32	CC ER to Golgi transport vesicle membrane
8	-10.19	NULL	60	BP interferon-gamma-mediated signaling pathway
9	-9.83	NULL	602	Chr Chr 10
10	-9.79	NULL	312	BP immune response
11	-8.59	NULL	386	Chr Chr 22
12	-8.53	NULL	52	Chr Chr HSCHR6_MHC_QBL
13	-8.34	NULL	28	CC transport vesicle membrane
14	-7.89	NULL	316	Cancer SPANG_BCL6-index2
15	-7.88	NULL	185	Cancer SPANG_LPS-index2
16	-7.6	NULL	274	Lymphom SPANG_IL21 DN
17	-7.57	NULL	553	Cancer Lemcke_Colonc Inflammation
18	-7.43	NULL	74	BP regulation of immune response
19	-7.36	NULL	6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
20	-7.33	NULL	51	BP type I interferon signaling pathway

p-values



GW_065

Local Summary

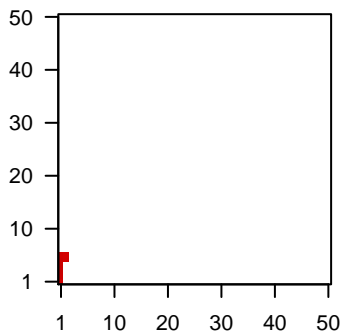
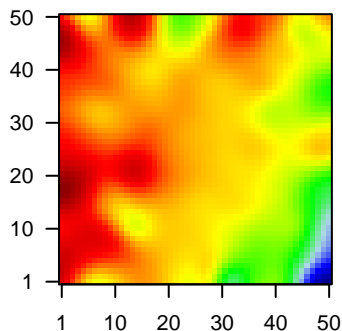
%DE = 0.62
 # metagenes = 8
 # genes = 165
 # genes in genesets = 163
 # genes with $fdr < 0.1$ = 72 (60 + / 12 -)
 # genes with $fdr < 0.05$ = 68 (56 + / 12 -)
 # genes with $fdr < 0.01$ = 50 (43 + / 7 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.37

$\langle FC \rangle = 0.34$
 $\langle \text{shrinkage-t} \rangle = 11.78$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.55$

Profile

Spot



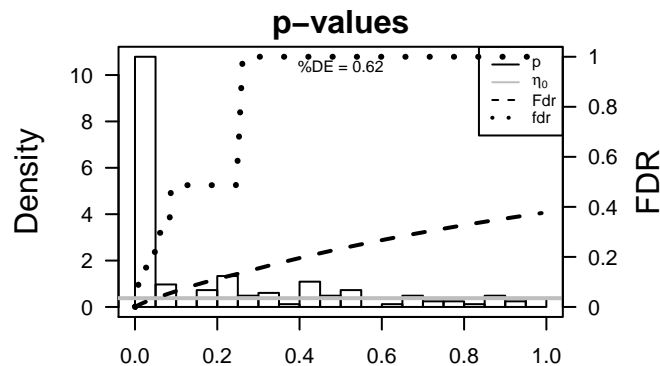
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	1437	1.7	2e-16	3e-15	1 x 4 colony stimulating factor 2 (granulocyte-macrophage) [Source:HGNC Symbol;Acc:10242]
2	4312	1.76	2e-16	3e-15	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:10242]
3	4319	2.14	2e-16	3e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:10242]
4	10630	2.01	2e-16	3e-15	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]
5	3918	1.64	7e-16	2e-14	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
6	3553	1.63	9e-16	6e-14	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
7	5008	1.61	2e-15	1e-12	1 x 1 oncostatin M [Source:HGNC Symbol;Acc:8506]
8	60675	1.55	2e-14	2e-12	1 x 1 prokineticin 2 [Source:HGNC Symbol;Acc:18455]
9	366	1.53	5e-14	3e-11	1 x 1 aquaporin 9 [Source:HGNC Symbol;Acc:643]
10	12	1.45	8e-13	3e-11	1 x 1
11	3576	1.44	1e-12	3e-11	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
12	55107	-1.44	1e-12	3e-11	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:11374]
13	2195	-1.43	2e-12	3e-11	1 x 5 FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
14	8614	1.42	2e-12	6e-11	1 x 6 stanniocalcin 2 [Source:HGNC Symbol;Acc:11374]
15	169611	-1.41	4e-12	6e-11	1 x 5 olfactomedin-like 2A [Source:HGNC Symbol;Acc:27270]
16	3909	1.41	4e-12	6e-10	1 x 5 laminin, alpha 3 [Source:HGNC Symbol;Acc:6483]
17	25907	1.37	1e-11	6e-10	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:10242]
18	285761	1.36	2e-11	1e-09	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC Symbol;Acc:10242]
19	4628	1.32	7e-11	1e-09	1 x 5 myosin, heavy chain 10, non-muscle [Source:HGNC Symbol;Acc:10242]
20	3569	1.32	7e-11	3e-09	1 x 1 interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:10242]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.69	NULL	8 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
2	20.14	NULL	3 / 11	GSEA C2BIOCARTA_STEM_PATHWAY
3	19.86	NULL	3 / 15	GSEA C2TRAYNOR_RETT_SYNDROM_UP
4	19.77	NULL	6 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
5	19.61	NULL	2 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
6	18.83	NULL	2 / 6	GSEA C2BIOCARTA_IL5_PATHWAY
7	15.53	NULL	3 / 12	BP hemidesmosome assembly
8	15.47	NULL	9 / 35	Glio Colman_survival_associated
9	15.38	NULL	2 / 12	GSEA C2Y_AGING_MIDDLE_UP
10	15.03	NULL	4 / 9	GSEA C2ERBINI_RESPONSE_TO_SULINDAC_UP
11	13.99	NULL	1 / 3	GSEA C2REN_MIF_TARGETS_DN
12	13.78	NULL	1 / 3	GSEA C2ICENT_METASTASIS_DN
13	13.39	NULL	5 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
14	13.21	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
15	13.2	NULL	2 / 12	GSEA C2WU_HBX_TARGETS_2_DN
16	13.19	NULL	2 / 11	BP negative regulation of hormone secretion
17	13.05	NULL	3 / 11	Glio Phillips MES up vs Prolif & PN
18	12.92	NULL	2 / 12	GSEA C2BIOCARTA_ERYTH_PATHWAY
19	12.67	NULL	2 / 12	GSEA C2SEISS_RESPONSE_TO_DSRNA_DN
20	12.61	NULL	2 / 11	CC filopodium membrane
21	12.46	NULL	1 / 5	GSEA C2OXFORD_RALA_AND_RALB_TARGETS_UP
22	12.41	NULL	3 / 15	GSEA C2WU_HBX_TARGETS_1_UP
23	12.36	NULL	4 / 16	GSEA C2I_PROSTATE_CANCER_EPIGENETIC
24	12.13	NULL	4 / 16	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_UP
25	12.01	NULL	4 / 37	Glio Christensen_hypomethylated_in_ependymoma
26	11.65	NULL	2 / 11	BP prostaglandin metabolic process
27	11.58	NULL	4 / 13	GSEA C2CHIN_BREAST_CANCER_COPY_NUMBER_UP
28	11.29	NULL	2 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
29	11.23	NULL	4 / 14	GSEA C2SIBULAN_UV_RESPONSE_IMMORTALIZED_DN
30	11.2	NULL	3 / 17	BP calcium ion homeostasis
31	11.19	NULL	2 / 16	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
32	11.09	NULL	5 / 51	BP regulation of cell migration
33	11.09	NULL	2 / 10	BP regulation of receptor activity
34	11.09	NULL	2 / 10	GSEA C2BIOCARTA_FIBRINOLYSIS_PATHWAY
35	10.94	NULL	2 / 11	GSEA C2VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1
36	10.88	NULL	3 / 27	BP negative regulation of extrinsic apoptotic signaling pathway in absence of ligand
37	10.73	NULL	2 / 12	GSEA C2SHI_SPARC_TARGETS_UP
38	10.7	NULL	2 / 13	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_UP
39	10.69	NULL	1 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
40	10.64	NULL	3 / 15	BP fibrinolysis



GW_065

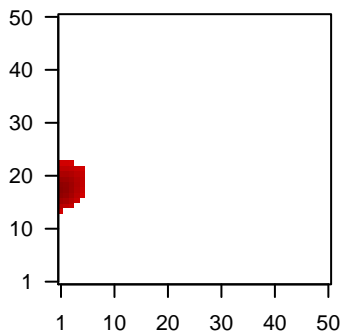
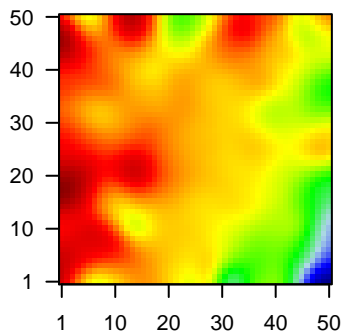
Local Summary

%DE = 0.54
 # metagenes = 41
 # genes = 435
 # genes in genesets = 430
 # genes with $fdr < 0.1$ = 127 (116 + / 11 -)
 # genes with $fdr < 0.05$ = 97 (89 + / 8 -)
 # genes with $fdr < 0.01$ = 32 (30 + / 2 -)

$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.26
 $\langle FC \rangle = 0.27$
 $\langle \text{shrinkage-t} \rangle = 9.33$
 $\langle p\text{-value} \rangle = 0.05$
 $\langle fdr \rangle = 0.73$

Profile

Spot



Local Genelist

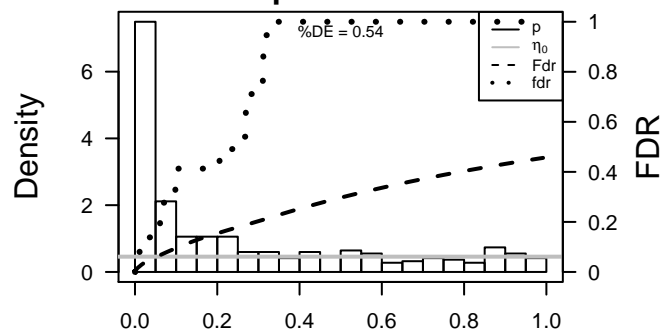
Rank	ID	log(FC)	fdr	p-value	Description
1	51083	1.39	8e-12	1e-07	1 x 15 galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:417
2	230	1.24	9e-10	1e-07	2 x 17 aldolase C, fructose-bisphosphate [Source:HGNC Symbol;A
3	286016	1.23	1e-09	2e-06	1 x 19
4	131076	1.16	1e-08	5e-06	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
5	388581	1.11	4e-08	5e-06	1 x 15 family with sequence similarity 132, member A [Source:HGNC
6	51042	1.1	6e-08	1e-05	1 x 19 zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
7	6884	1.07	1e-07	1e-05	1 x 22 TAF13 RNA polymerase II, TATA box binding protein (TBP)-a
8	6227	1.06	2e-07	2e-04	1 x 17 ribosomal protein S21 [Source:HGNC Symbol;Acc:10409]
9	79763	-0.97	2e-06	2e-04	3 x 19 isochorismatase domain containing 2 [Source:HGNC Symbol
10	3217	0.95	3e-06	7e-04	1 x 15 homeobox B7 [Source:HGNC Symbol;Acc:5118]
11	30968	0.92	6e-06	7e-04	2 x 20 stomatin (EPB72)-like 2 [Source:HGNC Symbol;Acc:14559]
12	51367	0.88	2e-05	7e-04	1 x 17 processing of precursor 5, ribonuclease P/MRP subunit (S. ce
13	84791	0.87	2e-05	7e-04	5 x 17 long intergenic non-protein coding RNA 467 [Source:HGNC :
14	56954	0.87	2e-05	7e-04	3 x 19 nitrilase family, member 2 [Source:HGNC Symbol;Acc:29878]
15	220064	-0.87	2e-05	1e-03	1 x 14 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
16	57820	0.85	3e-05	1e-03	4 x 17 cyclin B1 interacting protein 1, E3 ubiquitin protein ligase [Sou
17	27294	0.84	4e-05	1e-03	1 x 16 dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;
18	10436	0.84	4e-05	1e-03	1 x 17 Ribosomal RNA small subunit methyltransferase NEP1 [Sou
19	85014	0.83	5e-05	3e-03	1 x 21 transmembrane protein 141 [Source:HGNC Symbol;Acc:2821
20	51400	0.8	8e-05	3e-03	1 x 18 protein phosphatase methylesterase 1 [Source:HGNC Symbc

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	12.35	NULL	4 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
2	10.47	NULL	4 / 13	BP ribosomal small subunit biogenesis
3	10.28	NULL	18 / 96	BP rRNA processing
4	10.12	NULL	4 / 13	GSEA C2REACTOME_GLYCOLYSIS
5	8.9	NULL	25 / 153	MF structural constituent of ribosome
6	8.87	NULL	2 / 8	GSEA C2REACTOME_G_ALPHA_1_SIGNALLING_EVENTS
7	8.75	NULL	2 / 10	GSEA C2ZHU_CMV_24_HR_UP
8	8.75	NULL	2 / 10	GSEA C2ZHU_CMV_ALL_UP
9	8.32	NULL	5 / 39	BP glycolysis
10	8.3	NULL	1 / 6	GSEA C2REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS
11	8.3	NULL	1 / 6	GSEA C2REACTOME_GPCR_LIGAND_BINDING
12	8.18	NULL	3 / 10	MF monosaccharide binding
13	7.9	NULL	94 / 1318	CC mitochondrion
14	7.77	NULL	3 / 13	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN
15	7.63	NULL	1 / 7	GSEA C2REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
16	7.55	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
17	7.51	NULL	3 / 14	BP mitochondrial ATP synthesis coupled proton transport
18	7.5	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
19	7.36	NULL	4 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
20	7.34	NULL	5 / 15	CC mitochondrial large ribosomal subunit
21	7.33	NULL	3 / 16	Cancer GENTLES_modul7
22	7.3	NULL	42 / 579	CC nucleolus
23	7.17	NULL	29 / 253	BP translation
24	7.15	NULL	21 / 167	CC ribosome
25	7.12	NULL	4 / 15	Cancer GENTLES_modul1
26	7.08	NULL	1 / 8	GSEA C2SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP
27	6.96	NULL	3 / 15	GSEA C2REACTOME_GLYCOLYSIS
28	6.95	NULL	5 / 15	GSEA C2ZHANG_RESPONSE_TO_CANTHARIDIN_DN
29	6.94	NULL	2 / 7	GSEA C2REACTOME_SIGNALING_BY_WNT
30	6.93	NULL	2 / 14	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_DN
31	6.85	NULL	4 / 39	BP gluconeogenesis
32	6.65	NULL	2 / 7	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_5_UP
33	6.64	NULL	8 / 63	TF MYC_Targets UP
34	6.51	NULL	3 / 15	GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY
35	6.47	NULL	2 / 6	GSEA C2KORKOLA_CHORIOCARCINOMA_UP
36	6.46	NULL	3 / 9	GSEA C2MOREIRA_RESPONSE_TO_TSA_UP
37	6.42	NULL	3 / 7	GSEA C2PARK_HSC_MARKERS
38	6.25	NULL	1 / 10	GSEA C2WELCSH_BRCA1_TARGETS_1_DN
39	6.25	NULL	1 / 10	GSEA C2TAKAO_RESPONSE_TO_UVB_RADIATION_UP
40	6.23	NULL	1 / 2	miRNA 3183-371

p-values



GW_065

Local Summary

%DE = 0.71
 # metagenes = 1
 # genes = 29
 # genes in genesets = 28
 # genes with fdr < 0.1 = 12 (12 + / 0 -)
 # genes with fdr < 0.05 = 11 (11 + / 0 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)

<r> metagenes = NA

<r> genes = 0.31

<FC> = 0.3

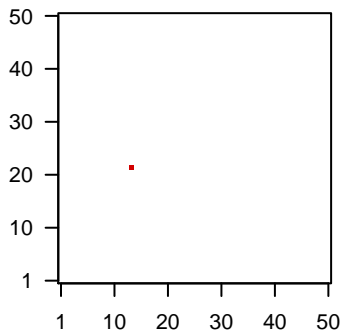
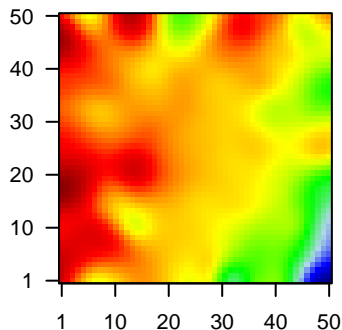
<shrinkage-t> = 10.34

<p-value> = 0.09

<fdr> = 0.81

Profile

Spot



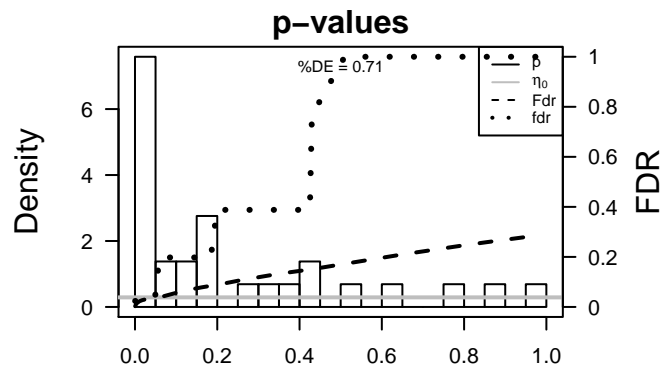
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	140823	0.72	4e-04	0.02	14 x 22 reactive oxygen species modulator 1 [Source:HGNC Symbol;]
2	4708	0.6	3e-03	0.02	14 x 22 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8k
3	126003	0.56	6e-03	0.04	14 x 22 trafficking protein particle complex 5 [Source:HGNC Symbol;]
4	125988	0.52	1e-02	0.04	14 x 22 chromosome 19 open reading frame 70 [Source:HGNC Symt
5	23378	0.48	2e-02	0.04	14 x 22 ribosomal RNA processing 8, methyltransferase, homolog (ye
6	51024	0.47	2e-02	0.04	14 x 22 fission 1 (mitochondrial outer membrane) homolog (S. cerevis
7	29099	0.44	3e-02	0.04	14 x 22 COMM domain containing 9 [Source:HGNC Symbol;Acc:250
8	138716	0.42	4e-02	0.04	14 x 22 ribonuclease P/MRP 25kDa subunit-like [Source:HGNC Sym
9	131474	0.41	4e-02	0.04	14 x 22 coiled-coil-helix-coiled-coil-helix domain containing 4 [Sour
10	5558	0.41	5e-02	0.04	14 x 22 primase, DNA, polypeptide 2 (58kDa) [Source:HGNC Symbol
11	116541	0.4	5e-02	0.04	14 x 22 mitochondrial ribosomal protein L54 [Source:HGNC Symbol;]
12	25873	0.39	5e-02	0.06	14 x 22 ribosomal protein L36 [Source:HGNC Symbol;Acc:13631]
13	83443	0.38	6e-02	0.20	14 x 22 splicing factor 3b, subunit 5, 10kDa [Source:HGNC Symbol;A
14	1939	0.32	1e-01	0.20	14 x 22 eukaryotic translation initiation factor 2D [Source:HGNC Syml
15	327	0.3	1e-01	0.20	14 x 22 acylaminoacyl-peptidase [Source:HGNC Symbol;Acc
16	55651	0.28	2e-01	0.20	14 x 22 NHP2 ribonucleoprotein [Source:HGNC Symbol;Acc:14377]
17	84967	0.28	2e-01	0.20	14 x 22 LSM10, U7 small nuclear RNA associated [Source:HGNC Sy
18	51647	-0.27	2e-01	0.20	14 x 22 family with sequence similarity 96, member B [Source:HGNC
19	51499	0.26	2e-01	0.39	14 x 22 TP53 regulated inhibitor of apoptosis 1 [Source:HGNC Symb
20	8802	0.23	3e-01	0.39	14 x 22 succinate-CoA ligase, alpha subunit [Source:HGNC Symbol;]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	12.45	NULL	1 / 15	BP cellular response to reactive oxygen species
2	11.86	NULL	2 / 15	GSEA C2REACTOME_EXTENSION_OF_TELOMERES
3	11.47	NULL	2 / 16	GSEA C2REACTOME_TELOMERE_MAINTENANCE
4	10.59	NULL	1 / 14	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA
5	9.97	NULL	1 / 10	BP peroxisome fission
6	9.69	NULL	1 / 11	MF S-adenosylmethionine-dependent methyltransferase activity
7	9.61	NULL	1 / 8	GSEA C2HOEGERKORP_CD44_TARGETS_TEMPORAL_UP
8	9.49	NULL	1 / 11	BP positive regulation of protein targeting to membrane
9	9.34	NULL	1 / 26	BP positive regulation of reactive oxygen species metabolic process
10	9.06	NULL	1 / 12	BP calcium-mediated signaling using intracellular calcium source
11	9.06	NULL	1 / 12	BP mitochondrial fission
12	8.69	NULL	1 / 13	CC integral to peroxisomal membrane
13	8.54	NULL	1 / 14	H.Tiss WIRTH_Globus pallidus
14	8.39	NULL	2 / 47	BP protein targeting to mitochondrion
15	8.36	NULL	1 / 14	CC integral to mitochondrial outer membrane
16	8.36	NULL	1 / 14	BP mitochondrion morphogenesis
17	8.24	NULL	1 / 15	BP positive regulation of cell cycle arrest
18	8.14	NULL	1 / 11	GSEA C2REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLIC
19	8.06	NULL	1 / 15	GSEA C2AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
20	7.71	NULL	1 / 17	BP cellular response to glucose starvation
21	7.36	NULL	1 / 12	GSEA C2KEGG_SPLICEOSOME
22	7.36	NULL	1 / 12	GSEA C2REACTOME_ELONGATION_AND_PROCESSING_OF_CAPPED
23	7.25	NULL	1 / 13	GSEA C2CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP
24	7.17	NULL	1 / 14	GSEA C2REACTOME_POLYMERASE_SWITCHING
25	7.17	NULL	1 / 14	GSEA C2REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE
26	7.05	NULL	1 / 13	GSEA C2REACTOME_FORMATION_AND_MATURATION_OF_MRNA_TRA
27	6.91	NULL	1 / 15	GSEA C2BROWNE_HCMV_INFECTION_2HR_DN
28	6.91	NULL	1 / 15	GSEA C2KEGG_DNA_REPLICATION
29	6.78	NULL	1 / 14	GSEA C2SENESE_HDAC2_TARGETS_UP
30	6.78	NULL	1 / 14	GSEA C2REACTOME_MRNA_SPLICING
31	6.78	NULL	1 / 14	GSEA C2REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAININ
32	6.73	NULL	1 / 15	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN
33	6.73	NULL	1 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
34	6.73	NULL	1 / 15	GSEA C2LEE_LIVER_CANCER_DENA_UP
35	6.68	NULL	1 / 16	GSEA C2BROWNE_HCMV_INFECTION_12HR_DN
36	6.68	NULL	1 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
37	6.68	NULL	1 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
38	6.68	NULL	1 / 16	GSEA C2REACTOME_LAGGING_STRAND_SYNTHESIS
39	6.63	NULL	1 / 34	MF NADH dehydrogenase (ubiquinone) activity
40	6.58	NULL	1 / 22	BP release of cytochrome c from mitochondria



GW_065

Local Summary

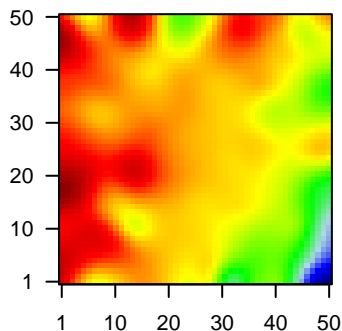
%DE = 0.64
 # metagenes = 14
 # genes = 184
 # genes in genesets = 179

genes with $fdr < 0.1 = 95$ (77 + / 18 -)
 # genes with $fdr < 0.05 = 76$ (64 + / 12 -)
 # genes with $fdr < 0.01 = 54$ (48 + / 6 -)

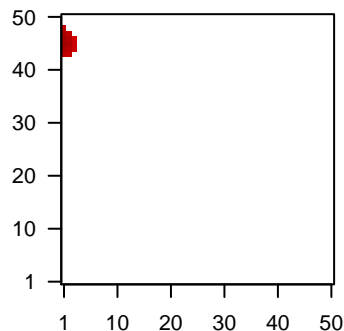
<r> metagenes = 0.95
 <r> genes = 0.42

<FC> = 0.36
 <shrinkage-t> = 12.56
 <p-value> = 0
 <fdr> = 0.52

Profile



Spot



Local Genelist

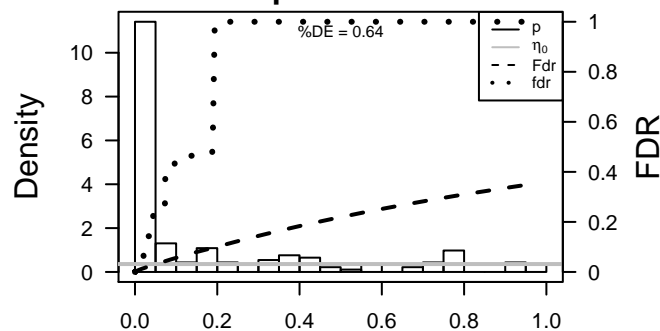
Rank	ID	log(FC)	fdr	p-value	Description
1	29113	3.12	2e-16	2e-15	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
2	6785	1.71	2e-16	2e-15	2 x 46 ELOVL fatty acid elongase 4 [Source:HGNC Symbol;Acc:144
3	2167	2.86	2e-16	2e-15	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
4	118430	3.06	2e-16	2e-15	2 x 44 mucin-like 1 [Source:HGNC Symbol;Acc:30588]
5	4747	1.81	2e-16	2e-15	1 x 43
6	338324	1.73	2e-16	2e-15	1 x 48 S100 calcium binding protein A7A [Source:HGNC Symbol;Ac
7	1474	1.59	5e-15	6e-12	1 x 47 cystatin E/M [Source:HGNC Symbol;Acc:2478]
8	6706	1.5	2e-13	6e-12	1 x 48 small proline-rich protein 2G [Source:HGNC Symbol;Acc:112
9	4753	1.49	2e-13	3e-11	1 x 44 NEL-like 2 (chicken) [Source:HGNC Symbol;Acc:7751]
10	3963	1.46	7e-13	2e-10	1 x 47 lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol
11	1515	1.41	3e-12	5e-10	1 x 44 cathepsin V [Source:HGNC Symbol;Acc:2538]
12	8601	1.36	2e-11	5e-10	1 x 44 regulator of G-protein signaling 20 [Source:HGNC Symbol;A
13	55612	1.36	2e-11	5e-10	1 x 43 feritin family member 1 [Source:HGNC Symbol;Acc:15889]
14	147495	-1.35	3e-11	3e-09	2 x 44 adenomatosis polyposis coli down-regulated 1 [Source:HGNC
15	84648	1.31	1e-10	3e-09	1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
16	2810	1.2	1e-10	6e-09	1 x 45 stratifin [Source:HGNC Symbol;Acc:10773]
17	6273	1.29	2e-10	3e-08	1 x 44 S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
18	1382	-1.23	1e-09	3e-08	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
19	10804	1.23	2e-09	3e-08	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
20	6339	1.22	2e-09	6e-08	1 x 45 sodium channel, non-voltage-gated 1, delta subunit [Source:

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	16.9	NULL	32 / 135	H.Tiss WIRTH_Mucosa
2	15.14	NULL	4 / 16	GSEA C2XCOLDREN_GEFITINIB_RESISTANCE_DN
3	14.61	NULL	2 / 12	MF fatty acid binding
4	13.62	NULL	10 / 21	CC desmosome
5	13.1	NULL	59 / 572	Disease GUDJ_poriasis up
6	12.56	NULL	5 / 21	CC cornified envelope
7	12.38	NULL	1 / 10	BP white fat cell differentiation
8	11.73	NULL	1 / 11	GSEA C2REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED
9	10.74	NULL	1 / 15	CC interstitial matrix
10	10.67	NULL	1 / 13	BP cellular response to lithium ion
11	10.36	NULL	2 / 12	BP keratinocyte proliferation
12	10.35	NULL	1 / 16	MF fibronectin binding
13	9.84	NULL	1 / 15	BP triglyceride catabolic process
14	9.78	NULL	2 / 23	Chr Chr HSCHR6_MHC_DBB
15	9.49	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
16	9.4	NULL	1 / 19	MF hyaluronic acid binding
17	9.4	NULL	1 / 19	MF laminin binding
18	9.32	NULL	3 / 11	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
19	9.17	NULL	1 / 6	GSEA C2Y_AGING_OLD_UP
20	9.1	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
21	9.08	NULL	6 / 42	BP keratinization
22	9	NULL	2 / 10	GSEA C2KIM_MYCL1_AMPLIFICATION_TARGETS_UP
23	8.88	NULL	2 / 15	GSEA C2KARAKAS_TGFB1_SIGNALING
24	8.81	NULL	2 / 25	BP brown fat cell differentiation
25	8.8	NULL	4 / 21	CC gap junction
26	8.59	NULL	2 / 15	GSEA C2DOANE_BREAST_CANCER_CLASSES_DN
27	8.52	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
28	8.48	NULL	2 / 15	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION
29	8.42	NULL	1 / 4	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_DN
30	8.37	NULL	1 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
31	8.36	NULL	3 / 15	CC connexon complex
32	8.09	NULL	6 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
33	8.05	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
34	7.97	NULL	13 / 76	BP epidermis development
35	7.74	NULL	1 / 8	GSEA C2ZHAN_MULTIPLE_MYELOMA_SPIKED
36	7.4	NULL	1 / 6	Glio Martinez_Glio_hypometh
37	7.37	NULL	1 / 25	BP cytokine production
38	7.09	NULL	3 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C1
39	7.05	NULL	3 / 16	GSEA C2ANDEMAINE_LUNG_METASTASIS
40	7.03	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP

p-values



GW_065

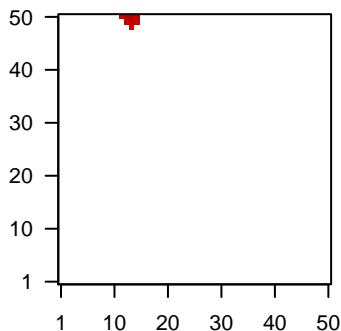
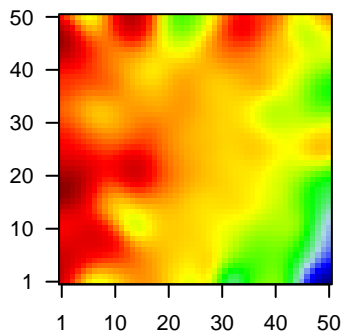
Local Summary

%DE = 0.7
 # metagenes = 8
 # genes = 115
 # genes in genesets = 114
 # genes with $fdr < 0.1$ = 54 (48 + / 6 -)
 # genes with $fdr < 0.05$ = 41 (39 + / 2 -)
 # genes with $fdr < 0.01$ = 37 (35 + / 2 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.28
 $\langle FC \rangle = 0.4$
 $\langle \text{shrinkage-t} \rangle = 14.13$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.57$

Profile

Spot



Local Genelist

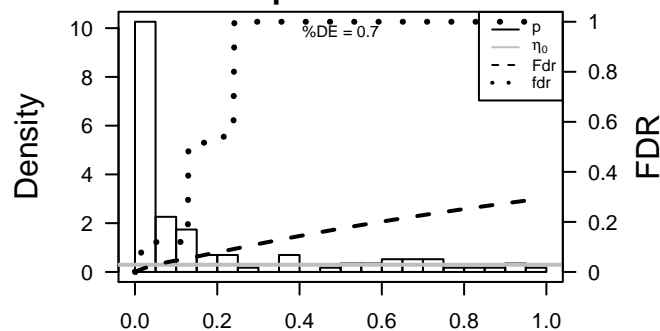
Rank	ID	log(FC)	fdr	p-value	Description
1	1109	2.36	2e-16	3e-15	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Sy]
2	1066	2.28	2e-16	3e-15	14 x 50 carboxylesterase 1 [Source:HGNC Symbol;Acc:1863]
3	57834	1.88	2e-16	3e-15	13 x 50 cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
4	140809	1.59	4e-15	3e-12	13 x 50 sulfiredoxin 1 [Source:HGNC Symbol;Acc:16132]
5	100288413	1.51	1e-13	1e-09	14 x 50 endogenous retrovirus group MER34, member 1 [Source:HG
6	29948	1.34	4e-11	2e-09	13 x 50 oxidative stress induced growth inhibitor 1 [Source:HGNC Sy]
7	7102	1.31	1e-10	7e-09	15 x 50 tetraspanin 7 [Source:HGNC Symbol;Acc:11854]
8	2539	1.28	3e-10	5e-08	13 x 50 glucose-6-phosphate dehydrogenase [Source:HGNC Symb
9	9048	1.22	2e-09	6e-08	14 x 50 artemin [Source:HGNC Symbol;Acc:727]
10	5217	1.2	4e-09	9e-07	14 x 50 profilin 2 [Source:HGNC Symbol;Acc:8882]
11	4051	1.12	3e-08	2e-06	12 x 50 cytochrome P450, family 4, subfamily F, polypeptide 3 [Sour
12	873	1.07	1e-07	2e-06	12 x 50 carbonyl reductase 1 [Source:HGNC Symbol;Acc:1548]
13	1646	1.06	2e-07	2e-06	13 x 50 aldo-keto reductase family 1, member C2 [Source:HGNC Sy]
14	65997	1.05	2e-07	2e-06	15 x 50 RAS-like, family 11, member B [Source:HGNC Symbol;Acc:2
15	4071	0.96	3e-07	9e-06	12 x 50 transmembrane 4 L six family member 1 [Source:HGNC Sym
16	11199	1.02	5e-07	1e-05	15 x 50 annexin A10 [Source:HGNC Symbol;Acc:534]
17	57007	0.99	1e-06	1e-05	14 x 50 atypical chemokine receptor 3 [Source:HGNC Symbol;Acc:23
18	1399	-0.98	1e-06	1e-05	14 x 50 v-cr avian sarcoma virus CT10 oncogene homolog-like [So
19	406988	0.97	2e-06	9e-05	12 x 50 MIR205 host gene (non-protein coding) [Source:HGNC Sym]
20	5909	0.92	5e-06	9e-05	14 x 50 RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.93	NULL	1 / 7	Glo Donson-cytotoxic effectors-associated with LTS in HGA
2	12.82	NULL	1 / 12	BP androgen metabolic process
3	11.73	NULL	1 / 14	BP bile acid and bile salt transport
4	11.32	NULL	3 / 13	GSEA C2SINGH_NFE2L2_TARGETS
5	10.19	NULL	2 / 15	BP pentose-phosphate shunt
6	10.16	NULL	1 / 18	BP bile acid biosynthetic process
7	9.85	NULL	3 / 39	BP retinoid metabolic process
8	9.76	NULL	2 / 10	BP response to food
9	8.98	NULL	2 / 44	BP steroid metabolic process
10	8.91	NULL	13 / 434	BP oxidation-reduction process
11	8.9	NULL	2 / 35	MF monooxygenase activity
12	8.77	NULL	3 / 32	MF NADP binding
13	8.68	NULL	5 / 69	BP response to toxic substance
14	8.58	NULL	1 / 16	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G1_DN
15	8.45	NULL	2 / 12	BP nitric oxide biosynthetic process
16	8.33	NULL	2 / 15	GSEA C2COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOMASTOMA_UP
17	8.02	NULL	1 / 18	MF aromatase activity
18	7.83	NULL	1 / 10	GSEA C2AMUNDSON_GAMMA_RADIATION_RESISTANCE
19	7.7	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
20	7.64	NULL	3 / 31	BP positive regulation of actin filament polymerization
21	7.63	NULL	1 / 10	BP erythrocyte maturation
22	7.5	NULL	3 / 63	BP phototransduction, visible light
23	7.45	NULL	1 / 31	BP bile acid metabolic process
24	7.33	NULL	2 / 15	GSEA C2KANG_FLUOROURACIL_RESISTANCE_UP
25	7.23	NULL	4 / 63	MF oxidoreductase activity, acting on paired donors, with incorporation
26	7.04	NULL	3 / 34	BP glutathione metabolic process
27	7	NULL	2 / 12	BP head development
28	6.61	NULL	5 / 119	BP xenobiotic metabolic process
29	6.54	NULL	4 / 110	MF heme binding
30	6.42	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
31	6.22	NULL	1 / 13	BP induction of positive chemotaxis
32	6.17	NULL	1 / 15	Cancer GENTLES_modul13
33	6.17	NULL	1 / 15	GSEA C2ALK_AML_CLUSTER_4
34	6.01	NULL	1 / 15	GSEA C2MELLMAN_TUT1_TARGETS_UP
35	5.98	NULL	1 / 11	BP prostaglandin metabolic process
36	5.94	NULL	1 / 16	GSEA C2DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN
37	5.94	NULL	1 / 16	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP
38	5.89	NULL	1 / 6	GSEA C2ZAIID_OSTEOBLAST_TRANSCRIPTION_FACTORS
39	5.89	NULL	1 / 6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
40	5.88	NULL	2 / 79	MF electron carrier activity

p-values



GW_065

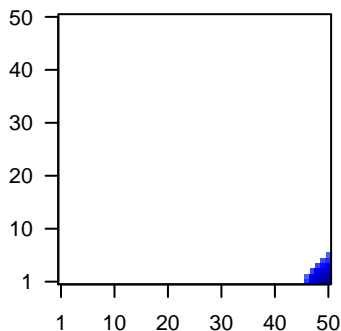
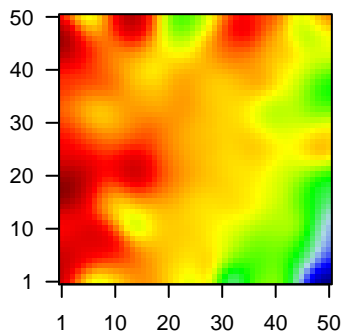
Local Summary

%DE = 0.88
 # metagenes = 20
 # genes = 323
 # genes in genesets = 321
 # genes with $fdr < 0.1$ = 271 (15 + / 256 -)
 # genes with $fdr < 0.05$ = 233 (8 + / 225 -)
 # genes with $fdr < 0.01$ = 184 (5 + / 179 -)

<r> metagenes = 0.97
 <r> genes = 0.53
 <FC> = -0.64
 <shrinkage-t> = -22.55
 <p-value> = 0
 <fdr> = 0.34

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	972	-2.02	2e-16	1e-15	50 x 1 CD74 molecule, major histocompatibility complex, class II inv.
2	4283	-1.9	2e-16	1e-15	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:18795]
3	3108	-2	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DM alpha [Source:HGNC Symbol;Acc:18795]
4	3109	-2.09	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DM beta [Source:HGNC Symbol;Acc:18795]
5	3113	-2.03	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:18795]
6	3122	-2.15	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:18795]
7	3512	-1.78	2e-16	1e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
8	3543	-1.88	2e-16	1e-15	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:18795]
9	10537	-1.89	2e-16	1e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
10	9806	-1.59	5e-15	4e-13	50 x 1 sparco/osteonectin, cwcv and kazal-like domains proteoglycan
11	260436	-1.56	2e-14	4e-13	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:18795]
12	894	-1.55	2e-14	4e-13	50 x 4 cyclin D2 [Source:HGNC Symbol;Acc:1583]
13	6347	-1.54	3e-14	5e-13	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:1677]
14	919	-1.53	5e-14	9e-13	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
15	915	-1.52	7e-14	3e-12	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC Symbol;Acc:1677]
16	6352	-1.49	2e-13	3e-12	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:1677]
17	54855	-1.49	2e-13	3e-11	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:1677]
18	2532	-1.44	1e-12	2e-10	50 x 5 Duffy blood group, atypical chemokine receptor [Source:HGNC Symbol;Acc:1677]
19	1396	1.39	8e-12	2e-10	50 x 5 cysteine-rich protein 1 (intestinal) [Source:HGNC Symbol;Acc:1677]
20	57172	-1.38	1e-11	2e-10	49 x 1 calcium/calmodulin-dependent protein kinase I gamma [Source:HGNC Symbol;Acc:1677]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-39.55	NULL	12 / 15	CC MHC class II protein complex
2	-24.47	NULL	15 / 47	BP antigen processing and presentation
3	-23.61	NULL	55 / 312	BP immune response
4	-22.32	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
5	-21.9	NULL	92 / 417	H.Tiss WIRTH_Immune system
6	-20.57	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
7	-20.53	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
8	-20.18	NULL	103 / 553	Cancer Lembecke_Colonc Inflammation
9	-19.52	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
10	-19.49	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
11	-19.14	NULL	17 / 60	BP T cell costimulation
12	-18.49	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
13	-18.41	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
14	-17.5	NULL	7 / 28	CC transport vesicle membrane
15	-17.13	NULL	6 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
16	-17.02	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
17	-16.82	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
18	-16.79	NULL	9 / 35	CC trans-Golgi network membrane
19	-16.72	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
20	-16.24	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
21	-15.94	NULL	14 / 87	BP antigen processing and presentation of exogenous peptide antigen
22	-15.69	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
23	-15.68	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
24	-15.37	NULL	2 / 4	MMML C6B3CIEJ_MMML_2
25	-15.34	NULL	5 / 12	BP immunoglobulin mediated immune response
26	-15.11	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIIS_DN
27	-15.09	NULL	6 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
28	-15.01	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
29	-14.96	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
30	-14.76	NULL	1 / 2	GSEA C2KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
31	-14.76	NULL	1 / 2	GSEA C2KEGG_AUTOIMMUNE_THYROID_DISEASE
32	-14.76	NULL	1 / 2	GSEA C2KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
33	-14.57	NULL	9 / 46	CC endocytic vesicle membrane
34	-14.34	NULL	17 / 84	BP T cell receptor signaling pathway
35	-14.34	NULL	2 / 4	GSEA C2KEGG_LEISHMANIA_INFECTION
36	-13.91	NULL	11 / 60	BP interferon-gamma-mediated signaling pathway
37	-13.63	NULL	2 / 5	GSEA C2WEST_ADRENOCORICAL_CARCINOMA_VS_ADENOMA_DN
38	-13.33	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
39	-13.2	NULL	8 / 52	Chr HSCR6_MHC_QBL
40	-13.19	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN

p-values

