

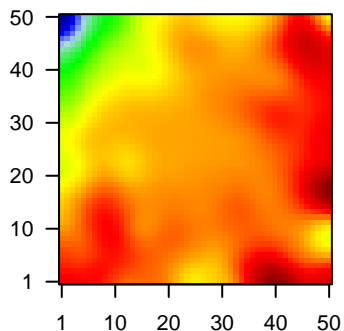
GW_031

Global Summary

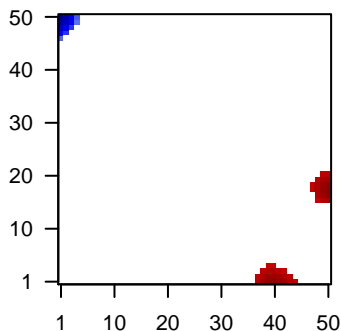
%DE = 0.16
 # genes with $fdr < 0.2$ = 2261 (1209 + / 1052 -)
 # genes with $fdr < 0.1$ = 1778 (956 + / 822 -)
 # genes with $fdr < 0.05$ = 1429 (757 + / 672 -)
 # genes with $fdr < 0.01$ = 1051 (546 + / 505 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = -0.01
 <p-value> = 0.08
 <fdr> = 0.84

Profile



Regulated Spots



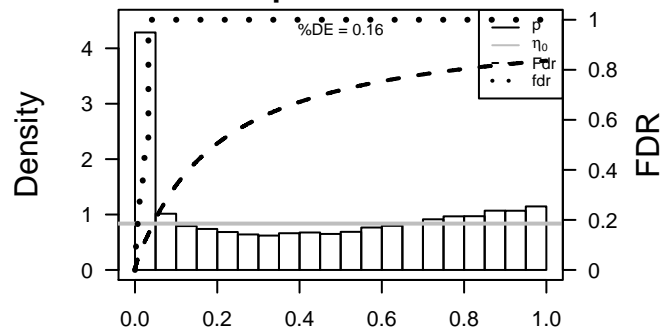
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	72	1.69	2e-16	2e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	131	-2.62	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	-2.7	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	-1.93	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	8644	-2.02	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	1109	-2.05	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
7	218	-3.66	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	55107	2.37	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
9	301	-1.54	2e-16	2e-14	4 x 48 annexin A1 [Source:HGNC Symbol;Acc:533]
10	244	-1.84	2e-16	2e-14	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]
11	25805	1.76	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S
12	633	1.67	2e-16	2e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
13	10974	-2.01	2e-16	2e-14	5 x 50 adipogenesis regulatory factor [Source:HGNC Symbol;Acc:24
14	387695	-2.47	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Syml
15	64207	1.94	2e-16	2e-14	50 x 40 interferon regulatory factor 2 binding protein-like [Source:HG
16	64073	-1.97	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Syml
17	260436	3.09	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
18	375791	-2.28	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Syml
19	84290	-1.7	2e-16	2e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
20	6363	2.49	2e-16	2e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	9.34	NULL	4640	CC nucleus
2	9.31	NULL	1749	MF DNA binding
3	9.06	NULL	630	Chr Chr X
4	7.98	NULL	1574	BP transcription, DNA-templated
5	7.96	NULL	949	CC nucleoplasm
6	7.64	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
7	7.64	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
8	7.54	NULL	15	CC MHC class II protein complex
9	7.53	NULL	370	BP mitotic cell cycle
10	7.37	NULL	318	MF chromatin binding
11	7.02	NULL	1581	BP regulation of transcription, DNA-dependent
12	6.97	NULL	504	BP positive regulation of transcription, DNA-dependent
13	6.7	NULL	149	BP DNA replication
14	6.11	NULL	423	BP negative regulation of transcription, DNA-dependent
15	6.08	NULL	16	GSEA C2L_U_TUMOR_ANGIOGENESIS_UP
16	6.02	NULL	8023	MF protein binding
17	5.96	NULL	823	MF sequence-specific DNA binding transcription factor activity
18	5.88	NULL	940	MF nucleic acid binding
19	5.61	NULL	171	miRNA target sites -3p
20	5.55	NULL	335	CC centrosome
<i>Underexpressed</i>				
1	-36.05	NULL	135	H.Tiss WIRTH_Mucosa
2	-21.5	NULL	572	Disease GUDJ_psooriasis up
3	-19.4	NULL	21	CC cornified envelope
4	-16.69	NULL	42	BP keratinization
5	-16	NULL	53	BP keratinocyte differentiation
6	-13.97	NULL	76	BP epidermis development
7	-13.48	NULL	19	BP peptide cross-linking
8	-10.68	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
9	-9.55	NULL	16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
10	-9.33	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	-9.07	NULL	15	GSEA C2AIGNER_ZEB1_TARGETS
12	-8.97	NULL	13	H.Tiss WIRTH_Tonsil
13	-8.82	NULL	8	GSEA C2LU_CDX2_TARGETS_DN
14	-8.48	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
15	-7.81	NULL	16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
16	-7.74	NULL	15	GSEA C2IN_SILENCED_BY_TUMOR_MICROENVIRONMENT
17	-7.69	NULL	186	MF structural molecule activity
18	-7.69	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
19	-7.61	NULL	15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
20	-7.55	NULL	52	BP negative regulation of endopeptidase activity

p-values



GW_031

Local Summary

%DE = 0.85
 # metagenes = 22
 # genes = 320
 # genes in genesets = 293
 # genes with $fdr < 0.1$ = 211 (207 + / 4 -)
 # genes with $fdr < 0.05$ = 174 (172 + / 2 -)
 # genes with $fdr < 0.01$ = 122 (121 + / 1 -)

$\langle r \rangle$ metagenes = 0.95

$\langle r \rangle$ genes = 0.43

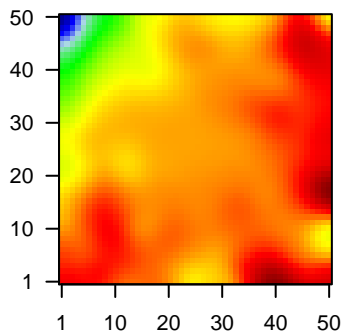
$\langle FC \rangle = 0.51$

$\langle \text{shrinkage-t} \rangle = 17.84$

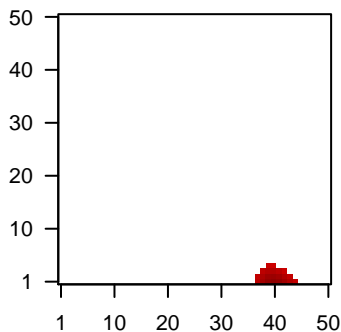
$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.51$

Profile



Spot



Local Genelist

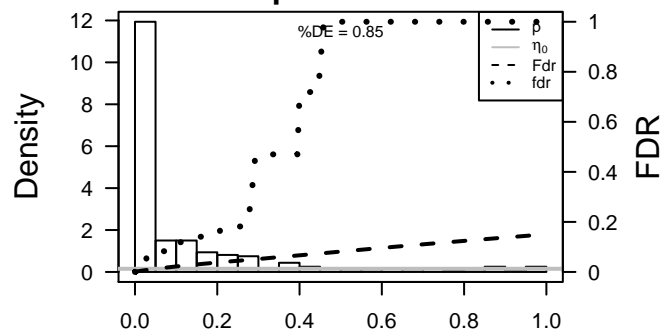
Rank	ID	log(FC)	fdr	p-value	Description
1	3127	2.94	2e-16	4e-15	43 x 1 major histocompatibility complex, class II, DR beta 5 [Source:HGNC Symbol;Acc:10037]
2	125050	2.53	2e-16	4e-15	40 x 1 RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
3	7127	1.66	2e-16	4e-15	43 x 1 tumor necrosis factor, alpha-induced protein 2 [Source:HGNC Symbol;Acc:10037]
4	4851	1.57	4e-15	2e-12	42 x 1 notch 1 [Source:HGNC Symbol;Acc:7881]
5	29944	1.51	5e-14	2e-12	42 x 1 paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:187]
6	22809	1.49	9e-14	5e-09	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:71]
7	641737	1.2	1e-10	5e-09	40 x 1
8	84446	1.27	2e-10	2e-08	43 x 1 BR serine/threonine kinase 1 [Source:HGNC Symbol;Acc:187]
9	442578	1.24	6e-10	2e-08	39 x 1
10	400818	1.23	9e-10	3e-08	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt]
11	65108	1.21	2e-09	3e-08	44 x 1 MARCKS-like 1 [Source:HGNC Symbol;Acc:7142]
12	440353	1.2	2e-09	1e-07	40 x 1
13	56127	1.17	5e-09	4e-07	40 x 1 protocadherin beta 10 [Source:HGNC Symbol;Acc:8681]
14	100132406	1.13	2e-08	4e-07	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC]
15	23015	1.12	2e-08	4e-07	39 x 1 golgin A8 family, member A [Source:HGNC Symbol;Acc:3197]
16	250	1.11	3e-08	8e-07	40 x 1 alkaline phosphatase, placental [Source:HGNC Symbol;Acc:4]
17	23468	1.09	6e-08	8e-07	40 x 1 chromobox homolog 5 [Source:HGNC Symbol;Acc:1555]
18	399900	1	6e-08	2e-06	39 x 1
19	84861	1.06	1e-07	2e-06	39 x 3 kelch-like family member 22 [Source:HGNC Symbol;Acc:258]
20	9612	1.06	1e-07	2e-06	38 x 1 nuclear receptor corepressor 2 [Source:HGNC Symbol;Acc:71]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.48	NULL	2 / 9	GSEA C2GOERING_BLOOD_HDL_CHOLESTEROL_QTL_CIS
2	11.72	NULL	3 / 16	BP negative regulation of neurogenesis
3	9.28	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
4	8.98	NULL	1 / 15	CC MHC class II protein complex
5	8.88	NULL	2 / 8	GSEA C2OSAWA_TNF_TARGETS
6	7.4	NULL	1 / 21	CC clathrin-coated endocytic vesicle membrane
7	7.26	NULL	2 / 16	GSEA C2KEGG_DORSO_VENTRAL_AXIS_FORMATION
8	7.23	NULL	1 / 7	GSEA C2BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS
9	7.01	NULL	1 / 23	CC integral to luminal side of endoplasmic reticulum membrane
10	6.99	NULL	3 / 14	MMML C2SCIEJ_MMML_8
11	6.69	NULL	1 / 8	GSEA C2KEGG_PRION_DISEASES
12	6.5	NULL	2 / 13	BP positive regulation of JAK-STAT cascade
13	6.4	NULL	2 / 28	CC transport vesicle membrane
14	6.25	NULL	1 / 9	GSEA C2REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES
15	6.25	NULL	1 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
16	5.92	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
17	5.92	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
18	5.87	NULL	1 / 10	BP anagen
19	5.87	NULL	1 / 10	BP cardiac epithelial to mesenchymal transition
20	5.87	NULL	1 / 10	BP inflammatory response to antigenic stimulus
21	5.87	NULL	1 / 10	BP negative regulation of cell-substrate adhesion
22	5.87	NULL	1 / 10	BP positive regulation of keratinocyte differentiation
23	5.87	NULL	1 / 10	BP prostate gland epithelium morphogenesis
24	5.87	NULL	1 / 10	BP somatic stem cell division
25	5.87	NULL	1 / 10	GSEA C2CAMP5_COLON_CANCER_COPY_NUMBER_UP
26	5.83	NULL	3 / 19	BP sprouting angiogenesis
27	5.74	NULL	1 / 32	CC ER to Golgi transport vesicle membrane
28	5.7	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
29	5.61	NULL	1 / 12	CC exocyst
30	5.58	NULL	2 / 11	GSEA C2KIM_GASTRIC_CANCER_CHEMOSENSITIVITY
31	5.55	NULL	1 / 11	BP cardiac muscle tissue morphogenesis
32	5.55	NULL	1 / 11	BP negative regulation of myoblast differentiation
33	5.55	NULL	1 / 11	BP negative regulation of oligodendrocyte differentiation
34	5.55	NULL	1 / 11	BP neuronal stem cell maintenance
35	5.55	NULL	1 / 11	BP regulation of epithelial cell proliferation
36	5.55	NULL	1 / 11	GSEA C2BIOCARTA_PS1_PATHWAY
37	5.55	NULL	1 / 11	GSEA C2REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY
38	5.43	NULL	1 / 35	CC trans-Golgi network membrane
39	5.4	NULL	2 / 26	BP negative regulation of catalytic activity
40	5.33	NULL	2 / 15	GSEA C2CAIRO_HEPATOBLASTOMA_UP

p-values



GW_031

Local Summary

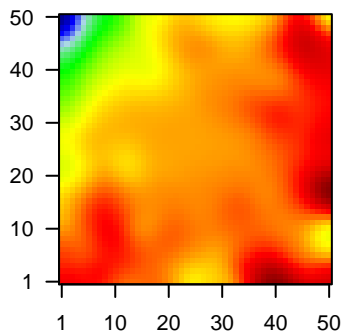
%DE = 0.81
 # metagenes = 19
 # genes = 216
 # genes in genesets = 212

genes with $fdr < 0.1 = 150$ (149 + / 1 -)
 # genes with $fdr < 0.05 = 144$ (143 + / 1 -)
 # genes with $fdr < 0.01 = 108$ (108 + / 0 -)

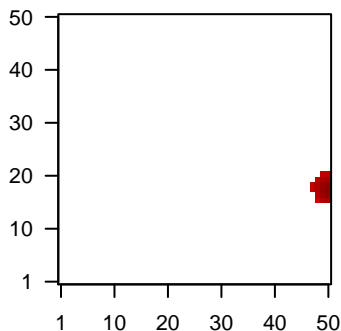
<r> metagenes = 0.98
 <r> genes = 0.33

<FC> = 0.63
 <shrinkage-t> = 22.09
 <p-value> = 0
 <fdr> = 0.4

Profile



Spot



Local Genelist

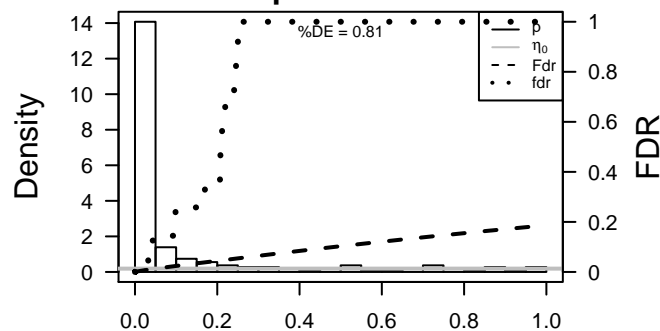
Rank	ID	log(FC)	fdr	p-value	Description
1	1298	2.01	2e-16	1e-15	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
2	1959	1.92	2e-16	1e-15	50 x 19 early growth response 2 [Source:HGNC Symbol;Acc:3239]
3	2248	2.07	2e-16	1e-15	50 x 19 fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
4	728715	2.18	2e-16	1e-15	50 x 18
5	4602	2.28	2e-16	1e-15	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:2218]
6	83988	2.09	2e-16	1e-15	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
7	494470	1.75	2e-16	1e-15	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
8	30812	1.83	2e-16	1e-15	50 x 18 SRY (sex determining region Y)-box 8 [Source:HGNC Symbol;Acc:2218]
9	57556	1.59	2e-15	1e-13	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic tail domain [Source:HGNC Symbol;Acc:2218]
10	54959	1.57	5e-15	1e-13	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:2218]
11	9686	1.56	8e-15	3e-13	50 x 19 vestigial like 4 (Drosophila) [Source:HGNC Symbol;Acc:2896]
12	285016	1.54	1e-14	1e-11	50 x 17 family with sequence similarity 150, member B [Source:HGNC Symbol;Acc:2218]
13	84532	1.44	7e-13	1e-11	50 x 17 acyl-CoA synthetase short-chain family member 1 [Source:HGNC Symbol;Acc:2218]
14	26018	1.43	9e-13	1e-11	50 x 16 leucine-rich repeats and immunoglobulin-like domains 1 [Source:HGNC Symbol;Acc:2218]
15	56994	1.43	1e-12	1e-10	50 x 16 choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17]
16	79805	1.39	4e-12	1e-10	50 x 18 vasohibin 2 [Source:HGNC Symbol;Acc:25723]
17	9603	1.37	7e-12	5e-10	50 x 18 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:2218]
18	6929	1.34	2e-11	1e-09	50 x 20 transcription factor 3 [Source:HGNC Symbol;Acc:11633]
19	55691	1.31	5e-11	5e-09	50 x 18 FERM domain containing 4A [Source:HGNC Symbol;Acc:254]
20	79924	1.27	2e-10	5e-09	50 x 18 adrenomedullin 2 [Source:HGNC Symbol;Acc:28898]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.98	NULL	5 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.5	NULL	2 / 7	GSEA C2KANG_CISPLATIN_RESISTANCE_DN
3	13.18	NULL	3 / 5	LymphomaMASCQUE_mBL_UP
4	12.71	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
5	11.03	NULL	2 / 10	BP positive regulation of histone H3-K4 methylation
6	10.73	NULL	1 / 5	GSEA C2STAGE_EWING_FAMILY_TUMOR
7	10.02	NULL	3 / 34	BP thymus development
8	9.93	NULL	3 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
9	9.81	NULL	2 / 12	GSEA C2PROVENZANI_METASTASIS_UP
10	9.76	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
11	9.76	NULL	4 / 42	BP B cell differentiation
12	9.12	NULL	1 / 9	GSEA C2BASSO_CD40_SIGNALING_UP
13	9.12	NULL	1 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
14	8.99	NULL	2 / 16	GSEA C2WU_HBX_TARGETS_3_UP
15	8.89	NULL	1 / 8	GSEA C2REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTOR
16	8.37	NULL	3 / 15	GSEA C2GOLUB_ALL_VS_AML_UP
17	8.35	NULL	1 / 2	miRNA target-153
18	8.17	NULL	2 / 15	BP embryonic digestive tract development
19	8.12	NULL	2 / 14	GSEA C2ONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
20	8.11	NULL	1 / 11	BP homeostasis of number of cells
21	8.11	NULL	1 / 11	Pathway AcBENTINK_e2f3.2
22	8.11	NULL	1 / 11	GSEA C2DOANE_BREAST_CANCER_ESR1_UP
23	8.11	NULL	1 / 11	GSEA C2TURJANSKI_MAPK1_AND_MAPK2_TARGETS
24	8.01	NULL	2 / 14	GSEA C2WATANABE_COLON_CANCER_MSI_VS_MSS_UP
25	7.79	NULL	2 / 15	GSEA C2DORSAM_HOXA9_TARGETS_UP
26	7.74	NULL	2 / 29	BP peripheral nervous system development
27	7.73	NULL	2 / 8	GSEA C2HOEGERKORP_CD44_TARGETS_TEMPORAL_UP
28	7.71	NULL	1 / 12	GSEA C2DING_LUNG_CANCER_BY_MUTATION_RATE
29	7.6	NULL	1 / 9	GSEA C2ABE_VEGFA_TARGETS_30MIN
30	7.49	NULL	2 / 16	BP post-anal tail morphogenesis
31	7.36	NULL	1 / 13	GSEA C2OSADA_ASCL1_TARGETS_UP
32	7.36	NULL	1 / 13	GSEA C2ALONSO_METASTASIS_UP
33	7.35	NULL	2 / 13	GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN
34	7.29	NULL	1 / 3	miRNA target-148a
35	7.24	NULL	4 / 41	TF Tissue/AQUERIZAS_Thymus
36	7.15	NULL	2 / 16	GSEA C2SASAKI_ADULT_T_CELL_LEUKEMIA
37	7.15	NULL	6 / 78	BP positive regulation of angiogenesis
38	7.14	NULL	1 / 10	BP cellular response to gonadotropin stimulus
39	7.14	NULL	1 / 10	BP regulation of ossification
40	7.14	NULL	1 / 10	GSEA C2CHASSOT_SKIN_WOUND

p-values



GW_031

Local Summary

%DE = 0.97
 # metagenes = 14
 # genes = 214
 # genes in genesets = 209

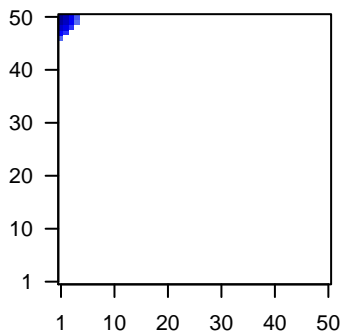
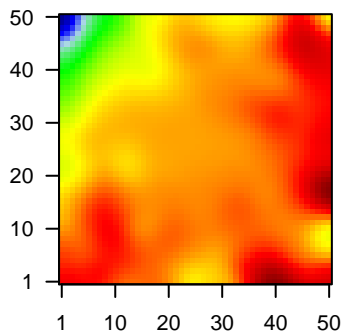
genes with $fdr < 0.1 = 204$ (1 + / 203 -)
 # genes with $fdr < 0.05 = 201$ (1 + / 200 -)
 # genes with $fdr < 0.01 = 198$ (1 + / 197 -)

<r> metagenes = 0.97
 <r> genes = 0.46

<FC> = -1.45
 <shrinkage-t> = -51.52
 <p-value> = 0
 <fdr> = 0.07

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.62	2e-16	2e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.7	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.93	2e-16	2e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
4	8644	-2.02	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
5	218	-3.66	2e-16	2e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC S]
6	387695	-2.47	2e-16	2e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt]
7	64073	-1.97	2e-16	2e-17	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt]
8	375791	-2.28	2e-16	2e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt]
9	84290	-1.7	2e-16	2e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	1048	-1.87	2e-16	2e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
11	4680	-2.68	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
12	548596	-1.84	2e-16	2e-17	4 x 50 creatine kinase, mitochondrial 1B [Source:HGNC Symbol;Acc:
13	9635	-2.52	2e-16	2e-17	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
14	22802	-2.1	2e-16	2e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	9022	-1.67	2e-16	2e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2l
16	84518	-2.63	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
17	49860	-3.04	2e-16	2e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
18	1475	-1.85	2e-16	2e-17	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
19	1476	-1.69	2e-16	2e-17	1 x 50 cystatin B (stefin B) [Source:HGNC Symbol;Acc:2482]
20	1672	-2.12	2e-16	2e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-66.8	NULL	84 / 135	H.Tiss WIRTH_Mucosa
2	-43.16	NULL	18 / 21	CC cornified envelope
3	-35.61	NULL	19 / 42	BP keratinization
4	-34.59	NULL	23 / 53	BP keratinocyte differentiation
5	-31.87	NULL	91 / 572	Disease GUDJ_pсориаз up
6	-28.87	NULL	10 / 19	BP peptide cross-linking
7	-28.78	NULL	24 / 76	BP epidermis development
8	-19.66	NULL	5 / 10	MF RAGE receptor binding
9	-18.25	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	-18.09	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
11	-16.89	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
12	-15.46	NULL	6 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
13	-15.42	NULL	6 / 13	BP negative regulation of peptidase activity
14	-15.28	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
15	-14.85	NULL	20 / 186	MF structural molecule activity
16	-14.84	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
17	-14.02	NULL	9 / 44	CC keratin filament
18	-13.97	NULL	10 / 52	BP negative regulation of endopeptidase activity
19	-13.61	NULL	4 / 15	GSEA C2ZHANG_IMMORTALIZED_BY_HPV31_DN
20	-13.15	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
21	-12.68	NULL	5 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
22	-12.65	NULL	12 / 79	MF serine-type endopeptidase inhibitor activity
23	-12.65	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
24	-12.56	NULL	3 / 12	BP cellular aldehyde metabolic process
25	-12.2	NULL	13 / 82	CC intermediate filament
26	-12.14	NULL	8 / 21	CC desmosome
27	-12.06	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
28	-11.95	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
29	-11.92	NULL	7 / 29	BP regulation of proteolysis
30	-11.64	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
31	-11.14	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
32	-11.09	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
33	-10.75	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
34	-10.59	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
35	-10.54	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE VS LUMINAL
36	-10.52	NULL	4 / 13	H.Tiss WIRTH_Tonsil
37	-10.38	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
38	-10.17	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
39	-10.05	NULL	8 / 38	BP epithelial cell differentiation
40	-9.99	NULL	54 / 1182	CC extracellular region

p-values

