

GW_082

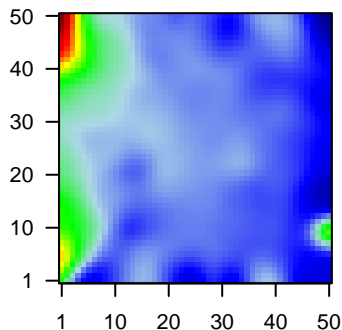
Global Summary

%DE = 0.12
 # genes with $fdr < 0.2$ = 1356 (821 + / 535 -)
 # genes with $fdr < 0.1$ = 1143 (729 + / 414 -)
 # genes with $fdr < 0.05$ = 873 (591 + / 282 -)
 # genes with $fdr < 0.01$ = 653 (482 + / 171 -)

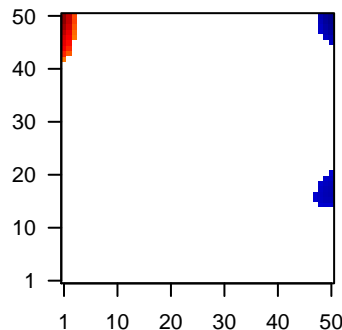
genes in genesets = 16332

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

Profile



Regulated Spots



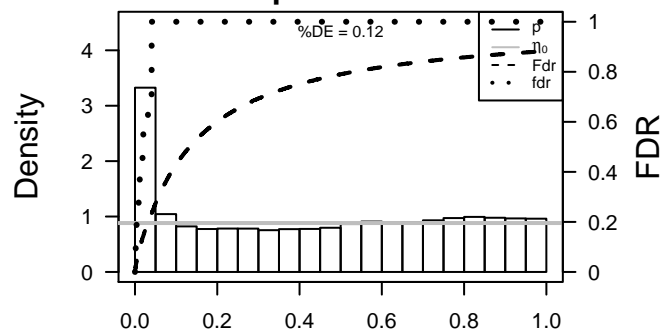
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	79852	1.15	2e-16	2e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	10551	1.28	2e-16	2e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	220	1.52	2e-16	2e-14	4 x 46 aldehyde dehydrogenase 1 family, member A3 [Source:HGNC]
4	222	1.95	2e-16	2e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC]
5	55107	2.19	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
6	360	1.22	2e-16	2e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63]
7	84707	-1.18	2e-16	2e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
8	79703	1.33	2e-16	2e-14	1 x 23 chromosome 11 open reading frame 80 [Source:HGNC Synt]
9	92747	4.75	2e-16	2e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb]
10	260436	1.22	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc]
11	352999	1.94	2e-16	2e-14	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbc]
12	760	1.3	2e-16	2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	51806	1.42	2e-16	2e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
14	595	1.19	2e-16	2e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
15	1021	1.21	2e-16	2e-14	1 x 6 cyclin-dependent kinase 6 [Source:HGNC Symbol;Acc:1777]
16	4680	1.35	2e-16	2e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
17	1308	1.21	2e-16	2e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
18	169044	1.49	2e-16	2e-14	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298]
19	49860	2.59	2e-16	2e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
20	1464	1.15	2e-16	2e-14	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.62	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	21.35	NULL	135	H.Tiss WIRTH_Mucosa
3	17.09	NULL	572	Disease GUDJ_pсориазис up
4	13.66	NULL	42	BP keratinization
5	12.53	NULL	76	BP epidermis development
6	11.93	NULL	21	CC cornified envelope
7	10.05	NULL	1182	CC extracellular region
8	9.83	NULL	53	BP keratinocyte differentiation
9	8.85	NULL	14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
10	8.61	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	8.42	NULL	519	Chr Chr 14
12	8.32	NULL	13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
13	7.79	NULL	5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
14	7.61	NULL	16	GSEA C2JAEGER_METASTASIS_DN
15	7.56	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
16	7.43	NULL	386	Chr Chr 22
17	7.09	NULL	16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
18	6.95	NULL	12	BP hemidesmosome assembly
19	6.93	NULL	19	BP peptide cross-linking
20	6.93	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
<i>Underexpressed</i>				
1	-9.64	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
2	-8.6	NULL	914	Chr Chr 3
3	-8.18	NULL	630	Chr Chr X
4	-7.05	NULL	4	MMML C2CACIEJ_MMML_23
5	-6.86	NULL	14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
6	-6.08	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
7	-5.74	NULL	51	BP type I interferon signaling pathway
8	-5.67	NULL	20	TF Tissue/AQUERIZAS_Adrenal cortex
9	-5.36	NULL	9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
10	-5.2	NULL	204	BP cytokine-mediated signaling pathway
11	-5.18	NULL	15	CC MHC class II protein complex
12	-5.16	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HEL4
13	-5.06	NULL	16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
14	-4.97	NULL	280	Chr Chr 13
15	-4.92	NULL	24	TF Tissue/AQUERIZAS_Trachea
16	-4.78	NULL	60	BP interferon-gamma-mediated signaling pathway
17	-4.76	NULL	1581	BP regulation of transcription, DNA-dependent
18	-4.69	NULL	32	CC ER to Golgi transport vesicle membrane
19	-4.67	NULL	1749	MF DNA binding
20	-4.62	NULL	127	H.Tiss WIRTH_Muscle

p-values



GW_082

Local Summary

%DE = 0.85
 # metagenes = 22
 # genes = 325
 # genes in genesets = 318

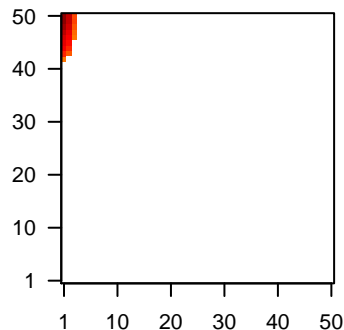
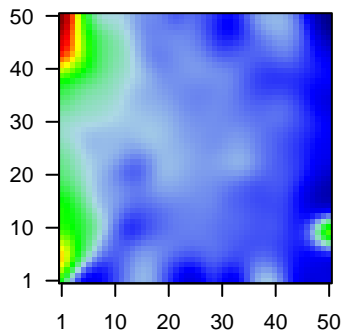
genes with $fdr < 0.1$ = 249 (228 + / 21 -)
 # genes with $fdr < 0.05$ = 243 (222 + / 21 -)
 # genes with $fdr < 0.01$ = 208 (197 + / 11 -)

<r> metagenes = 0.88
 <r> genes = 0.36

<FC> = 0.57
 <shrinkage-t> = 19.96
 <p-value> = 0
 <fdr> = 0.29

Profile

Spot



Local Genelist

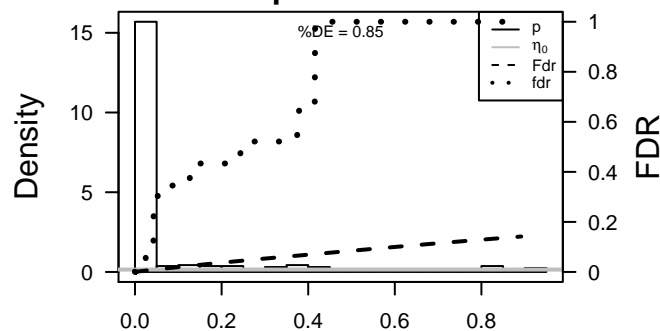
Rank	ID	log(FC)	fdr	p-value	Description
1	79852	1.15	2e-16	2e-16	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	222	1.95	2e-16	2e-16	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	360	1.22	2e-16	2e-16	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63
4	760	1.3	2e-16	2e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
5	4680	1.35	2e-16	2e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
6	1308	1.21	2e-16	2e-16	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
7	49860	2.59	2e-16	2e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
8	1672	1.3	2e-16	2e-16	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
9	55894	1.71	2e-16	2e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	414325	2.27	2e-16	2e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1673	2.37	2e-16	2e-16	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
12	2167	1.29	2e-16	2e-16	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
13	131177	1.24	2e-16	2e-16	3 x 50 family with sequence similarity 3, member D [Source:HGNC
14	2697	1.29	2e-16	2e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol,
15	10804	1.29	2e-16	2e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
16	3306	1.18	2e-16	2e-16	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
17	56300	1.37	2e-16	2e-16	1 x 47 interleukin 36, gamma [Source:HGNC Symbol;Acc:15741]
18	50805	1.26	2e-16	2e-16	1 x 43 iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
19	26085	1.2	2e-16	2e-16	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6:
20	5653	2.06	2e-16	2e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	46.13	NULL	88 / 135	H.Tiss WIRTH_Mucosa
2	30.48	NULL	116 / 572	Disease GUDJ_psooriasis up
3	29.1	NULL	18 / 21	CC cornified envelope
4	28.32	NULL	20 / 42	BP keratinization
5	26.56	NULL	28 / 76	BP epidermis development
6	21.68	NULL	24 / 53	BP keratinocyte differentiation
7	17.29	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
8	16.99	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
9	15.97	NULL	10 / 19	BP peptide cross-linking
10	15.49	NULL	10 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
11	13.73	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
12	13.25	NULL	13 / 44	CC keratin filament
13	12.93	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
14	12.69	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
15	12.55	NULL	21 / 82	CC intermediate filament
16	12.33	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
17	11.69	NULL	4 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
18	11.57	NULL	4 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
19	11.49	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
20	11.47	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
21	11.38	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
22	11.24	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
23	11.13	NULL	5 / 10	MF RAGE receptor binding
24	11.06	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
25	10.81	NULL	4 / 12	H.Tiss WIRTH_Prim. lymphoid organs
26	10.75	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
27	10.67	NULL	70 / 1182	CC extracellular region
28	10.63	NULL	12 / 21	CC desmosome
29	10.6	NULL	29 / 186	MF structural molecule activity
30	10.37	NULL	4 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
31	10.36	NULL	3 / 15	GSEA C2STOSSI_RESPONSE_TO ESTRADIOL
32	10.2	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
33	10.11	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
34	9.6	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
35	9.34	NULL	4 / 12	BP hemidesmosome assembly
36	9.28	NULL	5 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
37	9.16	NULL	3 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
38	9.1	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
39	9.06	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
40	8.81	NULL	8 / 73	BP defense response to bacterium

p-values



GW_082

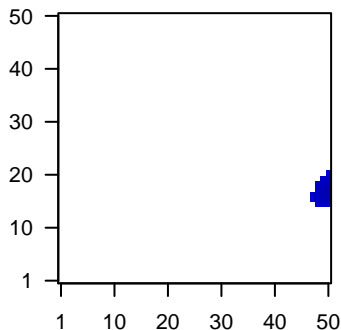
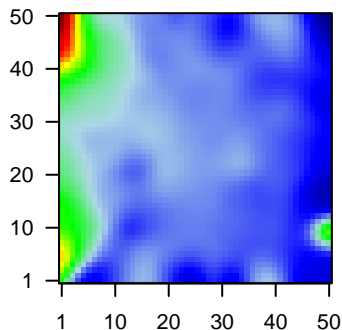
Local Summary

%DE = 0.66
 # metagenes = 20
 # genes = 234
 # genes in genesets = 231
 # genes with $fdr < 0.1$ = 85 (6 + / 79 -)
 # genes with $fdr < 0.05$ = 55 (4 + / 51 -)
 # genes with $fdr < 0.01$ = 24 (2 + / 22 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.32
 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -7.02$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.72$

Profile

Spot



Local Genelist

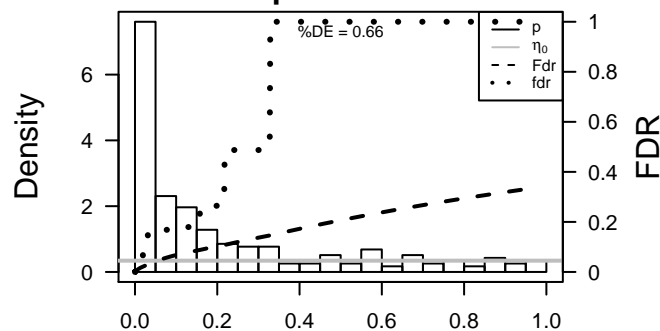
Rank	ID	log(FC)	fdr	p-value	Description
1	293	-0.77	1e-08	5e-07	50 x 15 solute carrier family 25 (mitochondrial carrier; adenine nucleo
2	9189	-0.77	1e-08	4e-06	50 x 18 zinc finger, BED-type containing 1 [Source:HGNC Symbol;Ac
3	54959	0.74	6e-08	5e-05	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;
4	4255	-0.67	7e-07	1e-04	48 x 15 O-6-methylguanine-DNA methyltransferase [Source:HGNC
5	1959	-0.62	5e-06	1e-04	50 x 19 early growth response 2 [Source:HGNC Symbol;Acc:3239]
6	26002	-0.62	5e-06	1e-04	50 x 16 monooxygenase, DBH-like 1 [Source:HGNC Symbol;Acc:216
7	9204	-0.61	6e-06	4e-04	50 x 19
8	56987	-0.59	1e-05	4e-04	50 x 20 bobby sox homolog (Drosophila) [Source:HGNC Symbol;Acc:
9	4602	-0.59	2e-05	8e-04	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source
10	26018	-0.57	3e-05	9e-04	50 x 16 leucine-rich repeats and immunoglobulin-like domains 1 [So
11	6263	-0.55	5e-05	9e-04	50 x 18 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
12	7915	-0.55	5e-05	2e-03	50 x 16 aldehyde dehydrogenase 5 family, member A1 [Source:HGNC
13	51101	-0.52	1e-04	2e-03	50 x 16 zinc finger, C2HC-type containing 1A [Source:HGNC Symbol
14	694	-0.47	2e-04	2e-03	50 x 18 B-cell translocation gene 1, anti-proliferative [Source:HGNC
15	9603	-0.51	2e-04	2e-03	50 x 18 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:
16	221061	-0.51	2e-04	2e-03	50 x 16 family with sequence similarity 171, member A1 [Source:HG
17	79621	-0.51	2e-04	2e-03	50 x 21 ribonuclease H2, subunit B [Source:HGNC Symbol;Acc:2567
18	57556	-0.51	2e-04	2e-03	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic
19	79191	0.5	2e-04	2e-03	50 x 15 iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
20	727	-0.5	2e-04	5e-03	50 x 16 complement component 5 [Source:HGNC Symbol;Acc:1331]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.52	NULL	5 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
2	-10.68	NULL	2 / 11	GSEA C2BIOCARTA_ETC_PATHWAY
3	-9.46	NULL	3 / 15	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
4	-8.69	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30
5	-8.56	NULL	6 / 64	miRNA target set miR-398-5p
6	-8.02	NULL	1 / 5	GSEA C2STAEGE_EWING_FAMILY_TUMOR
7	-7.76	NULL	3 / 10	CC nBAF complex
8	-7.72	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
9	-7.71	NULL	2 / 12	GSEA C2PROVENZANI_METASTASIS_UP
10	-7.53	NULL	4 / 40	miRNA target set miR-375
11	-7.37	NULL	3 / 11	CC npBAF complex
12	-7.03	NULL	3 / 12	CC SWI/SNF complex
13	-7.02	NULL	1 / 2	miRNA target set miR-153
14	-6.93	NULL	2 / 15	GSEA C2NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON
15	-6.9	NULL	2 / 12	CC TCTN-B9D complex
16	-6.85	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
17	-6.84	NULL	4 / 34	BP thymus development
18	-6.75	NULL	1 / 8	GSEA C2SCHLESINGER_METHYLATED_IN_COLON_CANCER
19	-6.6	NULL	3 / 15	GSEA C2FAELT_B_CLL_WITH_VH3_21_DN
20	-6.58	NULL	2 / 13	Cancer GENTLES_modul12
21	-6.53	NULL	2 / 8	GSEA C2BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
22	-6.44	NULL	1 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
23	-6.41	NULL	10 / 81	miRNA target set miR-3188-5p
24	-6.38	NULL	2 / 14	BP regulation of cysteine-type endopeptidase activity involved in apop
25	-6.35	NULL	2 / 11	MF poly(A)-specific ribonuclease activity
26	-6.24	NULL	2 / 16	GSEA C2NAKAYAMA_FRA2_TARGETS
27	-5.97	NULL	1 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
28	-5.88	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_DN
29	-5.87	NULL	2 / 16	GSEA C2DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
30	-5.83	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
31	-5.82	NULL	1 / 9	GSEA C2ABE_VEGFA_TARGETS_30MIN
32	-5.79	NULL	1 / 9	GSEA C2RODWELL_AGING_KIDNEY_UP
33	-5.77	NULL	3 / 36	miRNA target set miR-324-5P
34	-5.76	NULL	2 / 9	GSEA C2GOZGIT_ESR1_TARGETS_DN
35	-5.75	NULL	3 / 30	BP negative regulation of cell death
36	-5.67	NULL	2 / 11	miRNA target set miR-3140
37	-5.63	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
38	-5.63	NULL	3 / 22	CC heterochromatin
39	-5.63	NULL	2 / 16	GSEA C2SASAKI_ADULT_T_CELL_LEUKEMIA
40	-5.55	NULL	2 / 16	GSEA C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53

p-values



GW_082

Local Summary

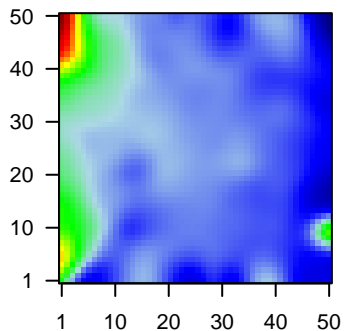
%DE = 0.67
 # metagenes = 15
 # genes = 215
 # genes in genesets = 214

 # genes with $fdr < 0.1$ = 98 (7 + / 91 -)
 # genes with $fdr < 0.05$ = 60 (6 + / 54 -)
 # genes with $fdr < 0.01$ = 41 (5 + / 36 -)

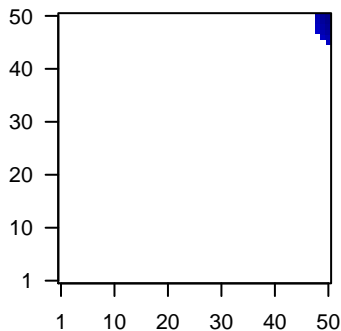
 $\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle = -0.24$
 $\langle \text{shrinkage-t} \rangle = -8.44$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.64$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84707	-1.18	2e-16	8e-15	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
2	4922	-1.62	2e-16	8e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
3	4953	1.04	2e-14	1e-12	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
4	200810	-1.03	3e-14	7e-10	49 x 50 ALG1, chitobiosylidiphosphodolichol beta-mannosyltransferase
5	400916	-0.91	2e-11	7e-10	50 x 47 coiled-coil-helix-coiled-coil-helix domain containing 10 [Source:HGNC Symbol;Acc:100916]
6	5096	-0.91	2e-11	4e-09	49 x 50 propionyl CoA carboxylase, beta polypeptide [Source:HGNC Symbol;Acc:5096]
7	11166	-0.88	7e-11	4e-08	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symbol;Acc:11166]
8	1056	-0.84	6e-10	2e-07	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
9	139728	-0.8	3e-09	5e-07	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:HGNC Symbol;Acc:139728]
10	286676	-0.78	1e-08	8e-07	50 x 49 immunoglobulin-like domain containing receptor 1 [Source:HGNC Symbol;Acc:286676]
11	79844	-0.76	2e-08	1e-06	50 x 50 zinc finger, DHHC-type containing 11 [Source:HGNC Symbol;Acc:79844]
12	205428	-0.74	4e-08	2e-06	50 x 50 chromosome 3 open reading frame 58 [Source:HGNC Symbol;Acc:205428]
13	5625	-0.73	8e-08	2e-06	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Acc:5625]
14	3202	-0.72	1e-07	7e-06	49 x 47 homeobox A5 [Source:HGNC Symbol;Acc:5106]
15	90161	-0.7	3e-07	7e-06	48 x 50 heparan sulfate 6-O-sulfotransferase 2 [Source:HGNC Symbol;Acc:90161]
16	4690	-0.69	3e-07	3e-05	49 x 50 NCK adaptor protein 1 [Source:HGNC Symbol;Acc:7664]
17	10643	-0.67	8e-07	3e-05	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:HGNC Symbol;Acc:10643]
18	339512	0.66	1e-06	3e-05	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:339512]
19	3866	-0.65	2e-06	3e-05	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
20	3880	-0.65	2e-06	9e-05	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.89	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	-16.99	NULL	4 / 13	BP regulation of blood vessel size
3	-15.66	NULL	3 / 8	GSEA C2LJU_CDX2_TARGETS_DN
4	-12.24	NULL	3 / 16	GSEA C2MEINHOLD_OVARIAN_CANCER_LOW_GRADE_DN
5	-11.59	NULL	1 / 11	Glio neurons_glio
6	-10.86	NULL	2 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
7	-9.76	NULL	1 / 15	MF neuropeptide hormone activity
8	-9.29	NULL	2 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
9	-8.78	NULL	2 / 10	BP biotin metabolic process
10	-8.74	NULL	2 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
11	-8.63	NULL	1 / 4	GSEA C2LJ_TUMOR_ENDOTHELIAL_MARKERS_DN
12	-8.56	NULL	8 / 34	BP glutathione metabolic process
13	-8.52	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
14	-8.24	NULL	6 / 25	BP glutathione derivative biosynthetic process
15	-8.14	NULL	2 / 13	BP epithelial tube branching involved in lung morphogenesis
16	-8.12	NULL	44 / 914	Chr Chr 3
17	-7.52	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
18	-7.02	NULL	1 / 8	GSEA C2KEGG_GLYCEROLIPID_METABOLISM
19	-6.82	NULL	2 / 15	BP retinal ganglion cell axon guidance
20	-6.74	NULL	2 / 16	GSEA C2KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
21	-6.7	NULL	2 / 23	BP stem cell differentiation
22	-6.67	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
23	-6.66	NULL	5 / 20	MF glutathione transferase activity
24	-6.65	NULL	3 / 11	MF glutathione binding
25	-6.65	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
26	-6.45	NULL	12 / 119	BP xenobiotic metabolic process
27	-6.45	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
28	-6.27	NULL	1 / 7	miRNA target sites 3p
29	-6.22	NULL	2 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
30	-6.22	NULL	2 / 13	GSEA C2HOFMANN_CELL_LYMPHOMA_UP
31	-6.17	NULL	2 / 14	MF calmodulin-dependent protein kinase activity
32	-6.12	NULL	2 / 16	GSEA C2KEGG_STEROID_BIOSYNTHESIS
33	-6.11	NULL	3 / 16	GSEA C2KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
34	-6.1	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
35	-6.1	NULL	1 / 12	BP oxidative phosphorylation
36	-6.08	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY
37	-6.08	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
38	-6.08	NULL	1 / 12	GSEA C2LEE_LIVER_CANCER_SURVIVAL_UP
39	-6.01	NULL	3 / 15	BP lipid glycosylation
40	-5.98	NULL	2 / 16	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS

p-values

