

GW_203

Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1718 (1030 + / 688 -)
 # genes with fdr < 0.1 = 1270 (796 + / 474 -)
 # genes with fdr < 0.05 = 921 (609 + / 312 -)
 # genes with fdr < 0.01 = 701 (494 + / 207 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.86

Global Genelist

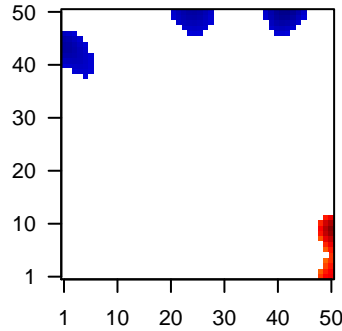
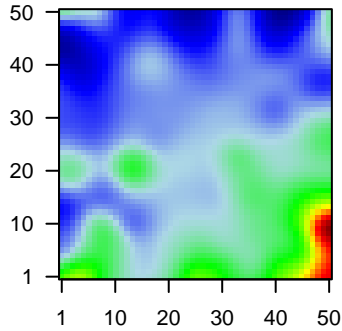
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	154664	1.46	2e-16 4e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:154664]
2	25890	1.33	2e-16 4e-14	50 x 4 ABI family, member 3 (NESH) binding protein [Source:HGNC Symbol;Acc:25890]
3	58	2.93	2e-16 4e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:154664]
4	10551	2.13	2e-16 4e-14	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
5	347	2.31	2e-16 4e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
6	525	1.7	2e-16 4e-14	12 x 8 ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 [Source:HGNC Symbol;Acc:525]
7	563	1.52	2e-16 4e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol;Acc:563]
8	80341	2.05	2e-16 4e-14	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symbol;Acc:80341]
9	92747	4.1	2e-16 4e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbol;Acc:92747]
10	260436	3.45	2e-16 4e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:260436]
11	352999	1.48	2e-16 4e-14	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbol;Acc:352999]
12	56892	1.29	2e-16 4e-14	50 x 7 chromosome 8 open reading frame 4 [Source:HGNC Symbol;Acc:56892]
13	6363	1.37	2e-16 4e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:6363]
14	6347	1.7	2e-16 4e-14	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:6347]
15	4680	1.4	2e-16 4e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (integrin alpha 5) [Source:HGNC Symbol;Acc:4680]
16	629	1.63	2e-16 4e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
17	1158	1.45	2e-16 4e-14	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
18	54544	-1.53	2e-16 4e-14	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
19	49860	1.62	2e-16 4e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
20	92196	1.46	2e-16 4e-14	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:292196]

Global Geneset Analysis

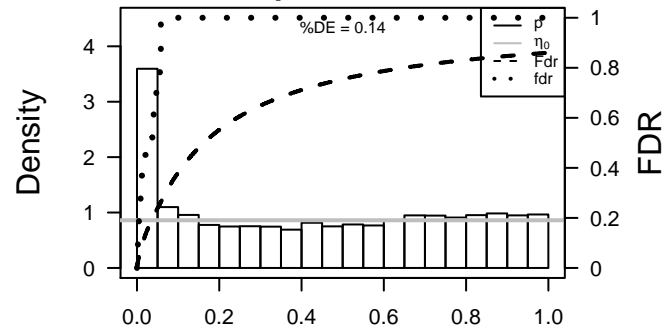
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	23.3	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	15.32	NULL	1182	CC extracellular region
3	14.05	NULL	553	Cancer Lembcke_Colonc Inflammation
4	12.97	NULL	683	CC extracellular space
5	11.21	NULL	250	LymphomaTENZ_Stromal signature 1
6	10.26	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
7	9.23	NULL	190	CC extracellular matrix
8	9.15	NULL	16	H.Tiss WIRTH_Hippocampus
9	9.14	NULL	13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
10	8.18	NULL	7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
11	7.97	NULL	16	GSEA C2TURASHVILLI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_UP
12	7.76	NULL	10	Glio wilscher_GBM_LTSwt_proteomics-G_UP
13	7.54	NULL	127	H.Tiss WIRTH_Muscle
14	7.5	NULL	9	GSEA C2GOUYER_TATI_TARGETS_UP
15	7.41	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
16	7.41	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
17	7.41	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
18	7.41	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
19	7.36	NULL	312	BP immune response
20	7.24	NULL	36	BP muscle filament sliding
<i>Underexpressed</i>				
1	-10.37	NULL	4640	CC nucleus
2	-9.27	NULL	1720	Chr Chr 1
3	-9.17	NULL	519	Chr Chr 14
4	-7.99	NULL	949	CC nucleoplasm
5	-7.82	NULL	262	miRNA target-miR-34c-3p
6	-7.41	NULL	436	miRNA target-miR-34c-3p
7	-6.84	NULL	302	miRNA target-miR-34c-3p
8	-6.65	NULL	321	miRNA target-miR-34c-3p
9	-6.62	NULL	307	miRNA target-miR-34c-3p
10	-6.46	NULL	313	miRNA target-miR-34c-3p
11	-6.32	NULL	42	BP keratinization
12	-6.28	NULL	313	Glio wilscher_GBM_Verhaak-CL_expression_D_up
13	-6.28	NULL	313	Glio wilscher_GBM_Verhaak-MES_expression_D_down
14	-6.28	NULL	313	Glio wilscher_GBM_Verhaak-PNwt_expression_D_up
15	-6.26	NULL	271	miRNA target-miR-34c-3p
16	-6.25	NULL	15	GSEA C2PRAMOONJAGO_SOX4_TARGETS_UP
17	-6.23	NULL	318	miRNA target-miR-34c-3p
18	-6.15	NULL	315	miRNA target-miR-34c-3p
19	-6.09	NULL	224	miRNA target-miR-34c-3p
20	-6.08	NULL	336	miRNA target-miR-34c-3p

Profile

Regulated Spots



p-values



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Local Summary

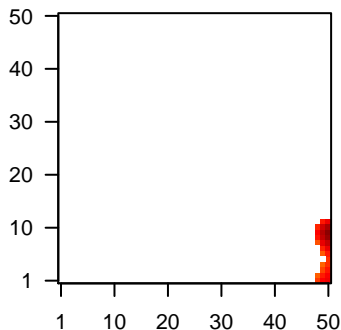
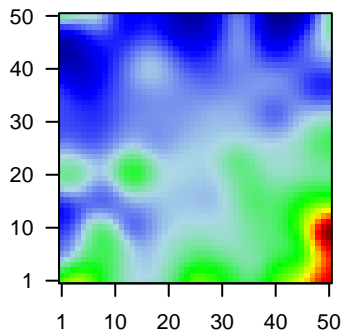
%DE = 0.75
 # metagenes = 29
 # genes = 466
 # genes in genesets = 463
 # genes with $fdr < 0.1 = 273$ (271 + / 2 -)
 # genes with $fdr < 0.05 = 256$ (254 + / 2 -)
 # genes with $fdr < 0.01 = 220$ (219 + / 1 -)

<r> metagenes = 0.81
 <r> genes = 0.32

<FC> = 0.56
 <shrinkage-t> = 19.47
 <p-value> = 0
 <fdr> = 0.41

Profile

Spot



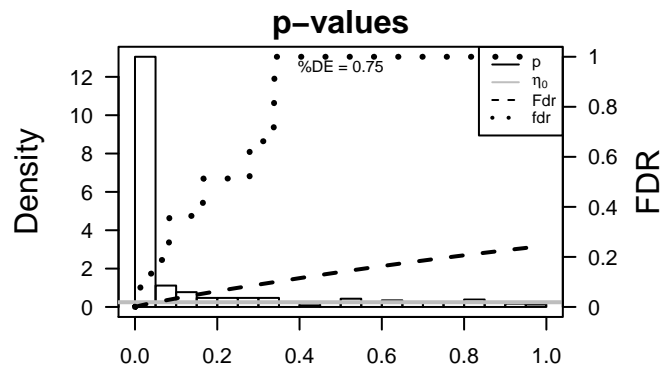
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	25890	1.33	2e-16	7e-16	50 x 4 ABI family, member 3 (NESH) binding protein [Source:HGNC
2	10551	2.13	2e-16	7e-16	50 x 10 anterior gradient 2 [Source:HGNC Symbol;Acc:328]
3	347	2.31	2e-16	7e-16	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
4	563	1.52	2e-16	7e-16	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol
5	80341	2.05	2e-16	7e-16	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symb
6	92747	4.1	2e-16	7e-16	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symb
7	260436	3.45	2e-16	7e-16	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symb
8	352999	1.48	2e-16	7e-16	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symb
9	56892	1.29	2e-16	7e-16	50 x 7 chromosome 8 open reading frame 4 [Source:HGNC Symbol
10	6363	1.37	2e-16	7e-16	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
11	6347	1.7	2e-16	7e-16	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:
12	1755	1.53	2e-16	7e-16	50 x 10 deleted in malignant brain tumors 1 [Source:HGNC Symbol;A
13	2327	1.56	2e-16	7e-16	50 x 11 flavin containing monooxygenase 2 (non-functional) [Source:
14	3512	1.44	2e-16	7e-16	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglo
15	57535	1.57	2e-16	7e-16	50 x 10 KIAA1324 [Source:HGNC Symbol;Acc:29618]
16	3855	1.26	2e-16	7e-16	50 x 11 keratin 7 [Source:HGNC Symbol;Acc:6445]
17	124220	2.41	2e-16	7e-16	50 x 10 zymogen granule protein 16B [Source:HGNC Symbol;Acc:30
18	389816	2.17	2e-16	7e-16	50 x 10 leucine rich repeat containing 26 [Source:HGNC Symbol;Acc
19	4057	1.85	2e-16	7e-16	50 x 10 lactotransferrin [Source:HGNC Symbol;Acc:6720]
20	4069	2.22	2e-16	7e-16	50 x 2 lysozyme [Source:HGNC Symbol;Acc:6740]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	46.89	NULL	14 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
2	17.63	NULL	4 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
3	13.74	NULL	97 / 1182	CC extracellular region
4	12.23	NULL	2 / 9	GSEA C2GOUYER_TATL_TARGETS_UP
5	11.97	NULL	93 / 553	Cancer Lembcke_Colonic Inflammation
6	11.82	NULL	3 / 10	Glio willscher_GBM_LTSwt_proteomics-G_UP
7	11.75	NULL	3 / 10	GSEA C2LUI_THYROID_CANCER_CLUSTER_5
8	11.62	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
9	11.32	NULL	67 / 683	CC extracellular space
10	10.88	NULL	3 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
11	10.87	NULL	3 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
12	10.65	NULL	6 / 12	GSEA C2BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_D
13	10.58	NULL	75 / 417	H.Tiss WIRTH_Immune system
14	10.08	NULL	3 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
15	9.85	NULL	4 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
16	9.8	NULL	6 / 14	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
17	9.66	NULL	3 / 15	GSEA C2LOPES_METHYLATED_IN_COLON_CANCER_UP
18	9.6	NULL	5 / 7	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN
19	9.31	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
20	9.29	NULL	5 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
21	9.01	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
22	8.63	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS
23	8.6	NULL	7 / 27	MF antigen binding
24	8.46	NULL	50 / 312	BP immune response
25	8.25	NULL	4 / 11	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
26	8.2	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
27	8.19	NULL	7 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
28	8.17	NULL	4 / 14	GSEA C2CHEOK_RESPONSE_TO_HD_MTX_UP
29	7.84	NULL	4 / 13	BP positive regulation of endocytosis
30	7.82	NULL	3 / 12	GSEA C2LIU_CDX2_TARGETS_UP
31	7.82	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
32	7.74	NULL	5 / 7	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
33	7.45	NULL	3 / 13	GSEA C2BOYVAULT_LIVER_CANCER_SUBCLASS_G3_DN
34	7.36	NULL	11 / 15	CC MHC class II protein complex
35	7.27	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
36	7.19	NULL	4 / 12	GSEA C2HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
37	7.09	NULL	2 / 8	GSEA C2ZHAN_MULTIPLE_MYELOMA_SPIKED
38	7.06	NULL	10 / 43	MF chemokine activity
39	6.97	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
40	6.96	NULL	4 / 21	BP chemokine-mediated signaling pathway



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Local Summary

%DE = 0.64
 # metagenes = 40
 # genes = 384
 # genes in genesets = 378

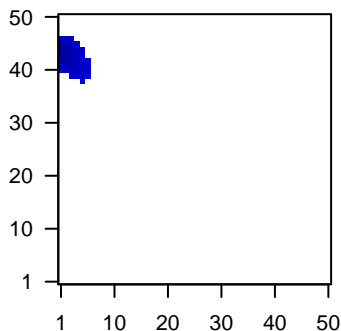
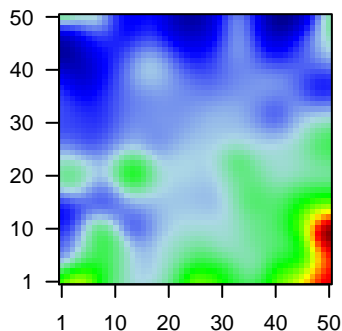
genes with $fdr < 0.1$ = 168 (17 + / 151 -)
 # genes with $fdr < 0.05$ = 139 (9 + / 130 -)
 # genes with $fdr < 0.01$ = 74 (6 + / 68 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.33

$\langle FC \rangle = -0.26$
 $\langle \text{shrinkage-t} \rangle = -9$
 $\langle p\text{-value} \rangle = 0.01$
 $\langle fdr \rangle = 0.61$

Profile

Spot



Local Genelist

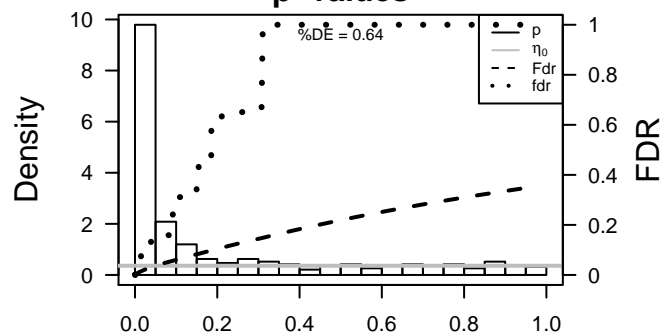
Rank	ID	log(FC)	fdr	p-value	Description
1	2167	2.64	2e-16	5e-15	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
2	3306	-1.5	2e-16	5e-15	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235]
3	10397	-1.48	2e-16	5e-15	1 x 42 N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:11279]
4	56901	-1.65	2e-16	5e-15	1 x 44 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-li
5	5947	1.57	2e-16	5e-15	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:11279]
6	6513	-1.62	2e-16	5e-15	1 x 43 solute carrier family 2 (facilitated glucose transporter), membr
7	53833	-1.19	1e-14	1e-10	1 x 46 interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004]
8	29923	-1.09	2e-12	1e-10	4 x 44 hypoxia inducible lipid droplet-associated [Source:HGNC Syr
9	6713	-1.09	2e-12	2e-10	2 x 43 squalene epoxidase [Source:HGNC Symbol;Acc:11279]
10	664	-1.07	3e-12	2e-09	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:HK
11	116211	-1.04	2e-11	5e-09	1 x 43 Transmembrane 4 L6 family member 19 [Source:UniProtKB/A
12	338382	1.01	5e-11	4e-08	1 x 40
13	5317	-0.95	5e-10	4e-08	1 x 46 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) [S
14	7286	-0.95	6e-10	4e-08	3 x 46 tuftelin 1 [Source:HGNC Symbol;Acc:12422]
15	51200	-0.94	1e-09	4e-08	1 x 44 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
16	133	-0.86	1e-09	6e-08	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
17	760	-0.92	2e-09	6e-08	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	56169	-0.92	2e-09	6e-08	1 x 46 gasdermin C [Source:HGNC Symbol;Acc:7151]
19	1825	-0.92	2e-09	9e-08	1 x 45 desmocollin 3 [Source:HGNC Symbol;Acc:3037]
20	6665	-0.91	3e-09	2e-07	1 x 45 SRY (sex determining region Y)-box 15 [Source:HGNC Synt

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-14.86	NULL	8 / 21	CC desmosome
2	-13.48	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
3	-12.94	NULL	3 / 15	GSEA C2PRAMOONJAGO_SOX4_TARGETS_UP
4	-11.91	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
5	-11.52	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
6	-11.04	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
7	-10.87	NULL	1 / 5	GSEA C2RODRIGUES_DCC_TARGETS_UP
8	-10.8	NULL	1 / 5	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NC
9	-10.23	NULL	2 / 9	GSEA C2KYNG_DNA_DAMAGE_UP
10	-10.23	NULL	2 / 9	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
11	-9.81	NULL	3 / 16	GSEA C2LEONARD_HYPOXIA
12	-9.75	NULL	1 / 6	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV
13	-9.69	NULL	6 / 22	MF cadherin binding
14	-9.65	NULL	2 / 10	GSEA C2RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
15	-9.65	NULL	2 / 10	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
16	-9.61	NULL	3 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
17	-9.27	NULL	2 / 8	GSEA C2REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TR
18	-9.09	NULL	26 / 135	H.Tiss WIRTH_Mucosa
19	-9.08	NULL	3 / 10	BP negative regulation of interleukin-2 production
20	-8.62	NULL	2 / 15	BP response to osmotic stress
21	-8.56	NULL	2 / 10	GSEA C2CAFFAREL_RESPONSE_TO_THC_8HR_5_DN
22	-8.44	NULL	2 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_F
23	-8.38	NULL	3 / 14	GSEA C2SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYN
24	-8.36	NULL	15 / 82	CC intermediate filament
25	-8.07	NULL	3 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
26	-8.06	NULL	3 / 15	GSEA C2SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B
27	-7.95	NULL	5 / 20	MF scaffold protein binding
28	-7.81	NULL	9 / 44	BP skin development
29	-7.78	NULL	3 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
30	-7.77	NULL	1 / 9	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM
31	-7.75	NULL	2 / 11	MF substrate-specific transmembrane transporter activity
32	-7.74	NULL	3 / 14	GSEA C2MAINA_VHL_TARGETS_DN
33	-7.46	NULL	3 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
34	-7.43	NULL	14 / 76	BP epidermis development
35	-7.41	NULL	4 / 12	BP keratinocyte proliferation
36	-7.32	NULL	1 / 10	GSEA C2PARK_TRETINOIN_RESPONSE
37	-7.24	NULL	2 / 15	GSEA C2PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION
38	-7.19	NULL	2 / 14	GSEA C2SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE
39	-7.08	NULL	3 / 16	GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP
40	-6.98	NULL	2 / 14	GSEA C2REACTOME_GENES_INVOLVED_IN_APOPTOTIC_CLEAVAGE_

p-values



GW_203

Local Summary

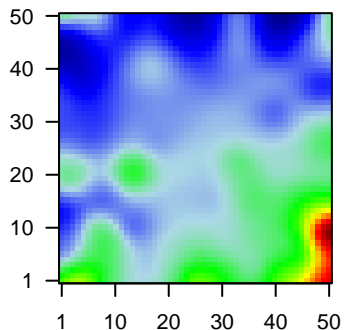
%DE = 0.7
 # metagenes = 31
 # genes = 382
 # genes in genesets = 376

genes with $fdr < 0.1 = 143$ (5 + / 138 -)
 # genes with $fdr < 0.05 = 96$ (4 + / 92 -)
 # genes with $fdr < 0.01 = 61$ (3 + / 58 -)

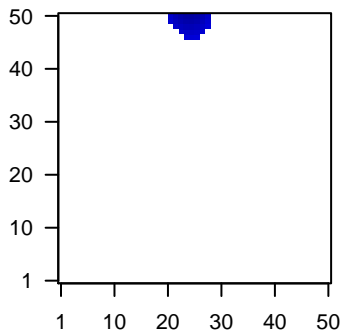
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.26

$\langle FC \rangle = -0.25$
 $\langle \text{shrinkage-t} \rangle = -8.66$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.69$

Profile



Spot



Local Genelist

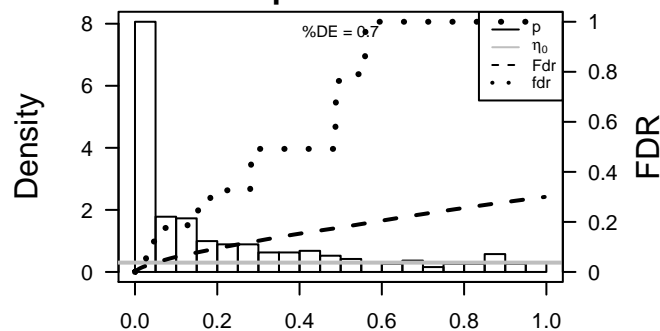
Rank	ID	log(FC)	fdr	p-value	Description
1	2354	1.08	1e-12	9e-10	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:12862]
2	7538	-1.04	9e-12	4e-07	22 x 50 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
3	23645	-0.91	4e-09	7e-06	22 x 50 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:12862]
4	3725	-0.83	6e-08	2e-05	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
5	51377	-0.8	2e-07	3e-05	28 x 50 ubiquitin carboxyl-terminal hydrolase L5 [Source:HGNC Symbol;Acc:12862]
6	91612	0.76	7e-07	3e-05	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:20000]
7	4609	-0.76	7e-07	6e-05	22 x 50 v-myc avian myelocytomatosis viral oncogene homolog [Source:HGNC Symbol;Acc:12862]
8	1647	-0.74	1e-06	1e-04	22 x 50 growth arrest and DNA-damage-inducible, alpha [Source:HGNC Symbol;Acc:12862]
9	57162	-0.72	3e-06	1e-04	23 x 50 pellino E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:12862]
10	678	-0.72	3e-06	1e-04	23 x 50 ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:12862]
11	8349	-0.71	4e-06	6e-04	21 x 50 histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760]
12	150094	-0.67	1e-05	6e-04	22 x 50 salt-inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
13	5782	-0.67	1e-05	1e-03	25 x 50 protein tyrosine phosphatase, non-receptor type 12 [Source:HGNC Symbol;Acc:12862]
14	55970	-0.62	5e-05	1e-03	25 x 50 guanine nucleotide binding protein (G protein), gamma 12 [Source:HGNC Symbol;Acc:12862]
15	6622	0.62	6e-05	1e-03	27 x 50 synuclein, alpha (non A4 component of amyloid precursor) [Source:HGNC Symbol;Acc:12862]
16	3799	-0.61	7e-05	1e-03	25 x 50 kinesin family member 5B [Source:HGNC Symbol;Acc:6324]
17	11260	-0.61	7e-05	1e-03	25 x 50 exportin, tRNA [Source:HGNC Symbol;Acc:12826]
18	2353	-0.56	8e-05	1e-03	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:12862]
19	50640	-0.6	9e-05	1e-03	22 x 50 patatin-like phospholipase domain containing 8 [Source:HGNC Symbol;Acc:12862]
20	10787	-0.6	1e-04	1e-03	25 x 50 NCK-associated protein 1 [Source:HGNC Symbol;Acc:7666]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-17.14	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
2	-15.91	NULL	7 / 16	GSEA C2AMIT_DELAYED_EARLY_GENES
3	-15.67	NULL	6 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
4	-14.02	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
5	-13.94	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
6	-12.95	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
7	-12.36	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
8	-11.72	NULL	4 / 15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
9	-11.68	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
10	-11.55	NULL	3 / 11	MF AU-rich element binding
11	-11.31	NULL	55 / 436	miRNA target site 59
12	-11.02	NULL	1 / 2	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
13	-10.93	NULL	4 / 8	MML C2OCIEJ_MMML_50
14	-10.84	NULL	3 / 12	GSEA C2BIOCARTA_ARENR2_PATHWAY
15	-10.82	NULL	4 / 11	miRNA target site 399-5p
16	-10.57	NULL	5 / 14	GSEA C2CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN
17	-10.27	NULL	25 / 189	miRNA target site 548a-3p
18	-10.21	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
19	-9.97	NULL	3 / 16	MF 14-3-3 protein binding
20	-9.93	NULL	2 / 12	BP regulation of mRNA stability
21	-9.91	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY
22	-9.91	NULL	3 / 15	GSEA C2BIOCARTA_TPO_PATHWAY
23	-9.88	NULL	39 / 269	miRNA target site 344
24	-9.81	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
25	-9.73	NULL	21 / 157	miRNA target site 340
26	-9.56	NULL	3 / 16	GSEA C2BIOCARTA_EPO_PATHWAY
27	-9.56	NULL	3 / 16	GSEA C2BIOCARTA_IGF1_PATHWAY
28	-9.56	NULL	3 / 16	GSEA C2BIOCARTA_GLEEVEC_PATHWAY
29	-9.56	NULL	3 / 16	GSEA C2BIOCARTA_NGF_PATHWAY
30	-9.5	NULL	2 / 13	BP mRNA catabolic process
31	-9.47	NULL	3 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_API_FAMILY_OF_TRANSC
32	-9.38	NULL	26 / 167	miRNA target site 548g
33	-9.38	NULL	39 / 310	miRNA target site 340
34	-9.38	NULL	2 / 15	GSEA C2KORKOLA_TERATOMA
35	-9.32	NULL	3 / 15	GSEA C2BIOCARTA_IL6_PATHWAY
36	-9.3	NULL	34 / 318	miRNA target site 590-3p
37	-9.15	NULL	24 / 151	miRNA target site 340
38	-9.12	NULL	2 / 14	GSEA C2DASU_IL6_SIGNALING_SCAR_UP
39	-9	NULL	4 / 16	GSEA C2I_RESPONSE_TO_FSH_DN
40	-8.99	NULL	3 / 16	GSEA C2BIOCARTA_EGF_PATHWAY

p-values



GW_203

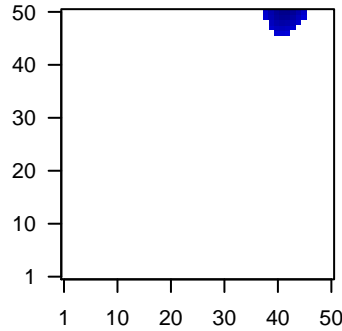
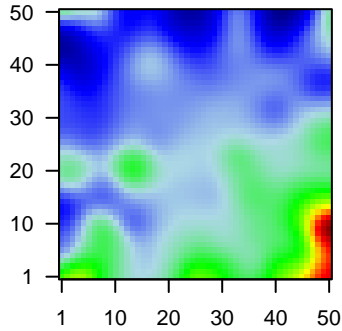
Local Summary

%DE = 0.75
 # metagenes = 30
 # genes = 418
 # genes in genesets = 413
 # genes with $fdr < 0.1$ = 213 (4 + / 209 -)
 # genes with $fdr < 0.05$ = 148 (4 + / 144 -)
 # genes with $fdr < 0.01$ = 82 (2 + / 80 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.34
 $\langle FC \rangle = -0.28$
 $\langle \text{shrinkage-t} \rangle = -9.78$
 $\langle p\text{-value} \rangle = 0.03$
 $\langle fdr \rangle = 0.64$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	29028	-1.03	2e-11	1e-09	44 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Sym
2	81831	-1.03	2e-11	5e-07	42 x 50 neuroligin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Sym
3	8500	-0.89	6e-09	5e-07	42 x 50 protein tyrosine phosphatase, receptor type, f polypeptide (P1
4	7027	-0.88	1e-08	6e-05	43 x 50 transcription factor Dp-1 [Source:HGNC Symbol;Acc:11749]
5	7913	-0.77	6e-07	7e-05	45 x 49 DEK oncogene [Source:HGNC Symbol;Acc:2768]
6	93081	-0.73	2e-06	7e-05	43 x 49 testis expressed 30 [Source:HGNC Symbol;Acc:25188]
7	10728	-0.72	3e-06	7e-05	45 x 50 prostaglandin E synthase 3 (cytosolic) [Source:HGNC Symbc
8	9972	-0.72	3e-06	8e-05	42 x 48 nucleoporin 153kDa [Source:HGNC Symbol;Acc:8062]
9	154807	-0.71	3e-06	1e-04	40 x 50 vitamin K epoxide reductase complex, subunit 1-like 1 [Sourc
10	51319	-0.69	7e-06	1e-04	43 x 50 arginine/serine-rich coiled-coil 1 [Source:HGNC Symbol;Acc
11	54888	-0.68	8e-06	1e-04	40 x 50 NOP2/Sun RNA methyltransferase family, member 2 [Source:
12	7083	0.68	8e-06	1e-04	45 x 49 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:1183
13	26774	-0.68	9e-06	2e-04	41 x 50 growth arrest-specific 5 (non-protein coding) [Source:HGNC
14	6873	-0.68	1e-05	2e-04	41 x 50 TAF2 RNA polymerase II, TATA box binding protein (TBP)-as
15	51571	-0.67	1e-05	4e-04	40 x 50 family with sequence similarity 49, member B [Source:HGNC
16	54802	-0.66	2e-05	4e-04	38 x 50 tRNA isopentenyltransferase 1 [Source:HGNC Symbol;Acc:21
17	29899	-0.65	2e-05	8e-04	41 x 50 G-protein signaling modulator 2 [Source:HGNC Symbol;Acc:
18	9928	-0.64	3e-05	8e-04	44 x 50 kinesin family member 14 [Source:HGNC Symbol;Acc:19181]
19	55646	-0.63	4e-05	8e-04	40 x 50 Ly1 antibody reactive [Source:HGNC Symbol;Acc:26021]
20	125228	-0.63	4e-05	1e-03	40 x 50 family with sequence similarity 210, member A [Source:HGNC

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.49	NULL	72 / 142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
2	-19.49	NULL	72 / 142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
3	-14.84	NULL	80 / 370	BP mitotic cell cycle
4	-12.76	NULL	76 / 530	Cancer Lemcke_Normal vs Adenoma
5	-12.55	NULL	6 / 16	Cancer WOLFER_overlap genes
6	-12.39	NULL	8 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
7	-12.21	NULL	13 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
8	-12.17	NULL	9 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
9	-11.96	NULL	9 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
10	-11.19	NULL	12 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
11	-10.72	NULL	7 / 18	LymphomaDAVE_c-myc_BL_UP
12	-10.69	NULL	46 / 232	BP mitosis
13	-10.62	NULL	21 / 56	CC chromosome, centromeric region
14	-10.57	NULL	15 / 59	CC nuclear pore
15	-10.49	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
16	-10.37	NULL	13 / 35	BP mitotic nuclear envelope disassembly
17	-10.12	NULL	7 / 15	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
18	-10.03	NULL	5 / 14	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA
19	-9.87	NULL	6 / 15	Cancer GENTLES_modul6
20	-9.8	NULL	11 / 18	BP spindle organization
21	-9.65	NULL	86 / 949	CC nucleoplasm
22	-9.6	NULL	11 / 14	MMML C2CIEJ_MMML_4
23	-9.44	NULL	9 / 29	BP regulation of glucose transport
24	-9.22	NULL	8 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
25	-9.19	NULL	5 / 9	GSEA C2BIOCARTA_RANMS_PATHWAY
26	-9.1	NULL	10 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
27	-8.87	NULL	19 / 57	Glio developing astrocytes
28	-8.82	NULL	16 / 68	Cancer SHAUGHNESSY_MM_high_risk
29	-8.75	NULL	9 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
30	-8.68	NULL	5 / 16	GSEA C2REACTOME_REV_MEDIATED_NUCLEAR_EXPORT_OF_HIV1_P
31	-8.61	NULL	15 / 83	CC spindle pole
32	-8.56	NULL	7 / 11	BP mitotic metaphase plate congression
33	-8.43	NULL	9 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
34	-8.41	NULL	3 / 12	BP regulation of double-strand break repair via homologous recomb
35	-8.37	NULL	6 / 15	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_UP
36	-8.26	NULL	7 / 48	miRNA target-miR-34c
37	-8.24	NULL	10 / 13	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_UP
38	-8.23	NULL	5 / 11	GSEA C2DODONELL_TFRC_TARGETS_DN
39	-8.2	NULL	5 / 14	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_48HR_DN
40	-8.18	NULL	9 / 37	BP hexose transport

p-values

