

GW_006

Global Summary

%DE = 0.13
 # genes with fdr < 0.2 = 1719 (966 + / 753 -)
 # genes with fdr < 0.1 = 1280 (725 + / 555 -)
 # genes with fdr < 0.05 = 1108 (634 + / 474 -)
 # genes with fdr < 0.01 = 747 (430 + / 317 -)

 # genes in genesets = 16332

 <FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.87

Global Genelist

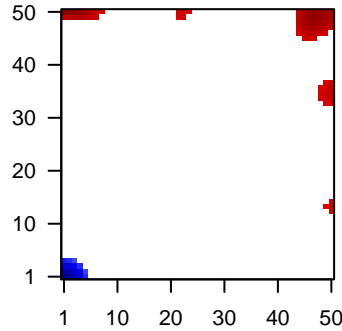
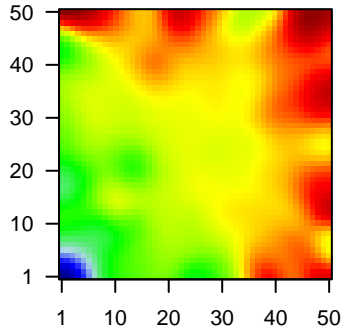
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	154664	1.43	2e-16 4e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:23760]
2	79852	1.67	2e-16 4e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
3	58	-1.3	2e-16 4e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12]
4	55107	1.32	2e-16 4e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:23760]
5	360	1.3	2e-16 4e-14	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63]
6	445328	-2.31	2e-16 4e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:HGNC Symbol;Acc:23760]
7	23120	1.36	2e-16 4e-14	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543]
8	339512	1.84	2e-16 4e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:23760]
9	343990	1.35	2e-16 4e-14	50 x 12 KIAA1211-like [Source:HGNC Symbol;Acc:33454]
10	6363	1.74	2e-16 4e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:23760]
11	414062	-1.27	2e-16 4e-14	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:23760]
12	6355	-1.34	2e-16 4e-14	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:23760]
13	1236	1.31	2e-16 4e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:23760]
14	1048	1.83	2e-16 4e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [Source:HGNC Symbol;Acc:23760]
15	22802	3.04	2e-16 4e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20760]
16	9076	1.3	2e-16 4e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
17	1207	1.52	2e-16 4e-14	31 x 49 chloride channel, nucleotide-sensitive, 1A [Source:HGNC Symbol;Acc:23760]
18	1308	-1.28	2e-16 4e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194]
19	1277	-1.52	2e-16 4e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
20	1278	-1.38	2e-16 4e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]

Global Geneset Analysis

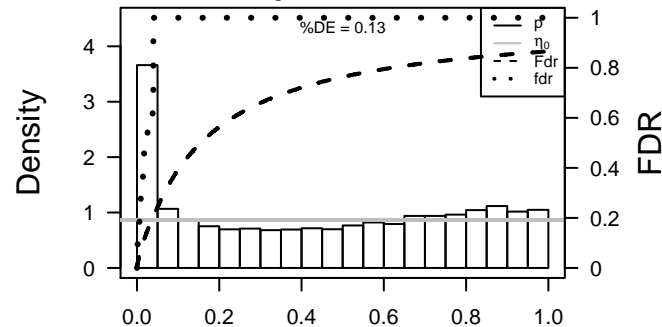
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.84	NULL	135	H.Tiss WIRTH_Mucosa
2	12.7	NULL	417	H.Tiss WIRTH_Immune system
3	10.39	NULL	914	Chr Chr 3
4	9.19	NULL	4640	CC nucleus
5	8.39	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
6	8.39	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
7	8.3	NULL	370	BP mitotic cell cycle
8	8.3	NULL	316	miRNA target:miR-332a
9	8.1	NULL	949	CC nucleoplasm
10	7.99	NULL	303	miRNA target:miR-332b
11	7.92	NULL	13	GSEA C2_SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
12	7.91	NULL	545	miRNA target:miR-332c
13	7.89	NULL	15	GSEA C2_RICKMAN_HEAD_AND_NECK_CANCER_E
14	7.81	NULL	314	miRNA target:miR-550c-3p
15	7.8	NULL	311	miRNA target:miR-332c
16	7.68	NULL	412	miRNA target:miR-332e
17	7.63	NULL	271	miRNA target:miR-332b
18	7.56	NULL	325	miRNA target:miR-332d
19	7.42	NULL	368	miRNA target:miR-332f
20	7.31	NULL	376	miRNA target:miR-332g
<i>Underexpressed</i>				
1	-16.91	NULL	190	CC extracellular matrix
2	-14.2	NULL	250	Lymphoma_TENZ_Stromal signature 1
3	-13.97	NULL	242	BP extracellular matrix organization
4	-12.87	NULL	69	BP extracellular matrix disassembly
5	-12.65	NULL	683	CC extracellular space
6	-12.49	NULL	1182	CC extracellular region
7	-11.89	NULL	64	BP collagen catabolic process
8	-11.57	NULL	16	GSEA C2_FARMER_BREAST_CANCER_CLUSTER_5
9	-11.2	NULL	183	CC proteinaceous extracellular matrix
10	-10.3	NULL	11	MF platelet-derived growth factor binding
11	-10.01	NULL	16	MMML C63_CIEJ_MMML 1
12	-9.49	NULL	35	Glio Colman_survival_associated
13	-9.35	NULL	12	miRNA target:miR-29c
14	-9.2	NULL	83	CC basement membrane
15	-9.15	NULL	57	MF extracellular matrix structural constituent
16	-8.6	NULL	13	GSEA C2_REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT
17	-8.51	NULL	403	BP cell adhesion
18	-8.5	NULL	12	GSEA C2_Y_AGING_MIDDLE_UP
19	-8.44	NULL	37	BP collagen fibril organization
20	-8.35	NULL	68	CC collagen

Profile

Regulated Spots



p-values



GW_006

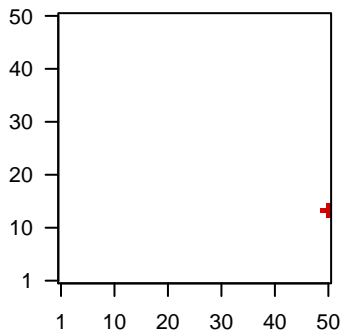
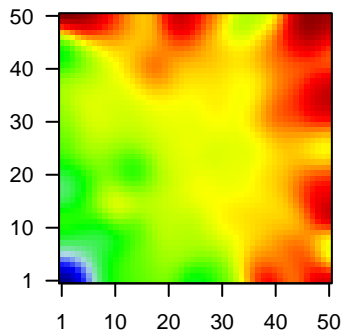
Local Summary

%DE = 0.79
 # metagenes = 4
 # genes = 58
 # genes in genesets = 58
 # genes with $fdr < 0.1$ = 31 (29 + / 2 -)
 # genes with $fdr < 0.05$ = 23 (23 + / 0 -)
 # genes with $fdr < 0.01$ = 19 (19 + / 0 -)

<r> metagenes = 0.98
 <r> genes = 0.36
 <FC> = 0.39
 <shrinkage-t> = 13.59
 <p-value> = 0
 <fdr> = 0.57

Profile

Spot



Local Genelist

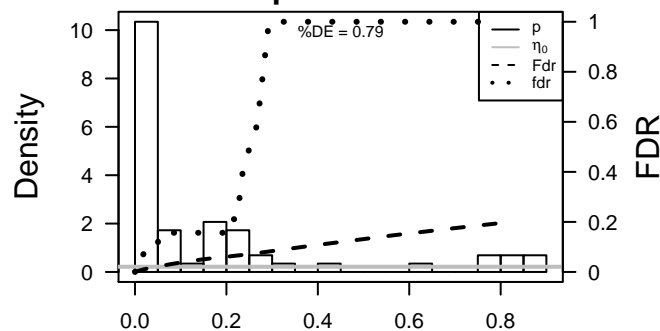
Rank	ID	log(FC)	fdr	p-value	Description
1	2568	2.79	2e-16	1e-15	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:14360]
2	51316	1.8	2e-16	1e-15	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
3	79191	0.96	4e-10	7e-08	50 x 15 iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360]
4	6920	0.9	6e-09	7e-08	50 x 13 transcription elongation factor A (SII), 3 [Source:HGNC Symbol;Acc:14360]
5	135112	0.88	1e-08	2e-07	50 x 13 nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21436]
6	260293	0.86	3e-08	6e-07	50 x 14 cytochrome P450, family 4, subfamily X, polypeptide 1 [Source:HGNC Symbol;Acc:14360]
7	2139	0.83	7e-08	6e-06	50 x 13 eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:14360]
8	3033	0.77	6e-07	6e-06	50 x 14 hydroxycytopl CoA dehydrogenase [Source:HGNC Symbol;Acc:14360]
9	4211	0.75	1e-06	6e-06	50 x 13 Meis homeobox 1 [Source:HGNC Symbol;Acc:7000]
10	57189	0.74	2e-06	6e-06	50 x 15 KIAA1147 [Source:HGNC Symbol;Acc:29472]
11	2205	0.73	2e-06	2e-05	50 x 13 Fc fragment of IgE, high affinity I, receptor for; alpha polypept
12	79085	0.7	6e-06	2e-05	50 x 13 solute carrier family 25 (mitochondrial carrier; phosphate carr
13	8543	0.69	7e-06	2e-05	50 x 15 LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
14	55268	0.69	7e-06	1e-04	50 x 14 enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:14360]
15	9249	0.66	2e-05	2e-04	50 x 13 dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:14360]
16	55930	0.64	3e-05	4e-04	50 x 13 myosin VC [Source:HGNC Symbol;Acc:7604]
17	391267	0.61	7e-05	2e-03	50 x 13 ankyrin repeat domain 20 family, member A11, pseudogene [Source:HGNC Symbol;Acc:14360]
18	4585	0.57	2e-04	2e-03	50 x 13 mucin 4, cell surface associated [Source:HGNC Symbol;Acc:14360]
19	6228	0.55	3e-04	9e-03	50 x 14 ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
20	143	0.51	1e-03	1e-02	50 x 14 poly (ADP-ribose) polymerase family, member 4 [Source:HGNC Symbol;Acc:14360]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	45.44	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
2	44.26	NULL	2 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	32.96	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
4	28.57	NULL	1 / 10	MF GABA-A receptor activity
5	26.92	NULL	1 / 11	GSEA C2JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
6	24.49	NULL	2 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_DN
7	23.23	NULL	1 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN
8	23.23	NULL	1 / 14	GSEA C2TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
9	23.23	NULL	1 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
10	22.29	NULL	1 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
11	22.29	NULL	1 / 15	GSEA C2JIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
12	21.44	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_DN
13	21.44	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_UP
14	21.44	NULL	1 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
15	21.44	NULL	1 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
16	21.44	NULL	1 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
17	21.44	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
18	17.36	NULL	1 / 11	BP negative regulation of multicellular organism growth
19	17.32	NULL	1 / 23	MF extracellular ligand-gated ion channel activity
20	14.29	NULL	1 / 4	miRNA target-204
21	13.83	NULL	1 / 34	CC chloride channel complex
22	13.23	NULL	1 / 4	GSEA C2NICK_RESPONSE_TO_PROC_TREATMENT_UP
23	12.61	NULL	1 / 40	MF chloride channel activity
24	11.32	NULL	2 / 12	MF NAD+ binding
25	10.6	NULL	1 / 25	BP brown fat cell differentiation
26	10.08	NULL	2 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_DN
27	9.58	NULL	2 / 15	GSEA C2NAKAJIMA_MAST_CELL
28	9.53	NULL	1 / 7	TF Tissue/AQUERIZAS_Appendix
29	9.51	NULL	1 / 3	miRNA target-223
30	9.41	NULL	2 / 30	BP response to cold
31	9.39	NULL	1 / 7	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED
32	8.92	NULL	1 / 10	GSEA C2NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
33	8.4	NULL	1 / 11	BP cell wall macromolecule catabolic process
34	8.4	NULL	1 / 11	MF nuclear hormone receptor binding
35	8.15	NULL	1 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL QUIESCENT_DN
36	8.09	NULL	1 / 12	BP regulation of DNA-dependent transcription, elongation
37	7.79	NULL	1 / 10	GSEA C2REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION
38	7.56	NULL	1 / 13	GSEA C2WANG_LMO4_TARGETS_DN
39	7.56	NULL	1 / 13	GSEA C2ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP
40	7.52	NULL	2 / 16	GSEA C2BOYALTY_LIVER_CANCER_SUBCLASS_G1_UP

p-values



GW_006

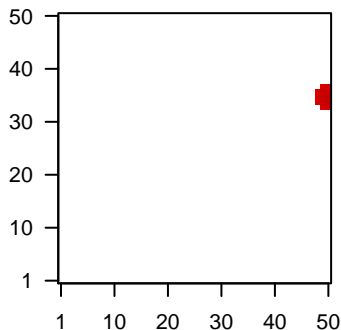
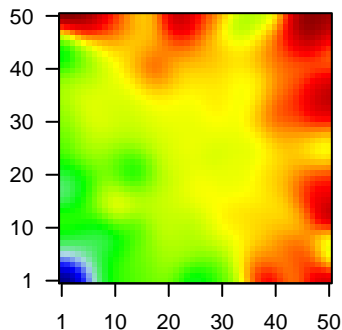
Local Summary

%DE = 0.63
 # metagenes = 13
 # genes = 217
 # genes in genesets = 217
 # genes with $fdr < 0.1 = 74$ (72 + / 2 -)
 # genes with $fdr < 0.05 = 48$ (47 + / 1 -)
 # genes with $fdr < 0.01 = 19$ (19 + / 0 -)

<r> metagenes = 0.98
 <r> genes = 0.32
 <FC> = 0.24
 <shrinkage-t> = 8.47
 <p-value> = 0.04
 <fdr> = 0.73

Profile

Spot



Local Genelist

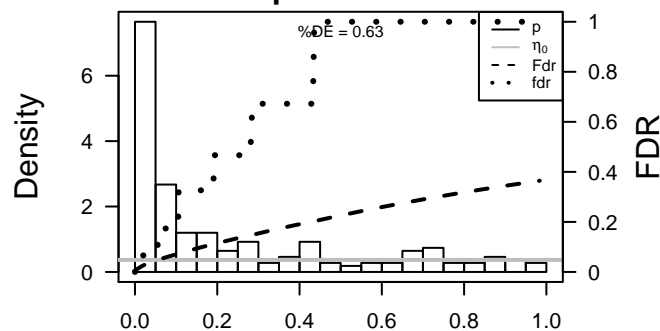
Rank	ID	log(FC)	fdr	p-value	Description
1	57088	1.04	2e-11	1e-06	50 x 36 phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649]
2	1968	0.87	1e-08	5e-06	49 x 33 eukaryotic translation initiation factor 2, subunit 3 gamma, 52l
3	57092	0.83	8e-08	5e-06	50 x 35 PEST proteolytic signal containing nuclear protein [Source:HK
4	5934	0.81	1e-07	5e-05	50 x 36 retinoblastoma-like 2 (p130) [Source:HGNC Symbol;Acc:989
5	64747	0.74	2e-06	5e-05	50 x 34 major facilitator superfamily domain containing 1 [Source:HGI
6	6041	0.74	2e-06	5e-05	48 x 34 ribonuclease L (2',5'-oligoadenylate synthetase-depender
7	80209	0.73	2e-06	7e-05	50 x 36 proline and serine rich 1 [Source:HGNC Symbol;Acc:20291]
8	8723	0.72	3e-06	2e-04	50 x 36 sorting nexin 4 [Source:HGNC Symbol;Acc:11175]
9	9685	0.7	6e-06	2e-03	50 x 34 clathrin interactor 1 [Source:HGNC Symbol;Acc:23186]
10	64393	0.64	3e-05	3e-03	50 x 37 zinc finger, matrin-type 3 [Source:HGNC Symbol;Acc:29983]
11	56947	0.62	6e-05	3e-03	50 x 33 mitochondrial fission factor [Source:HGNC Symbol;Acc:2485f
12	34	0.59	1e-04	3e-03	50 x 34 acyl-CoA dehydrogenase, C-4 to C-12 straight chain [Sourc
13	728026	0.58	2e-04	3e-03	50 x 35 prothymosin, alpha [Source:HGNC Symbol;Acc:9623]
14	167153	0.57	2e-04	3e-03	50 x 34 PAP associated domain containing 4 [Source:HGNC Symbol;
15	55252	0.57	2e-04	5e-03	50 x 37 additional sex combs like 2 (Drosophila) [Source:HGNC Syml
16	80208	0.55	3e-04	5e-03	50 x 35 spastic paraplegia 11 (autosomal recessive) [Source:HGNC s
17	51455	0.55	4e-04	5e-03	50 x 35 REV1, polymerase (DNA directed) [Source:HGNC Symbol;Ac
18	4154	0.54	4e-04	6e-03	48 x 34 muscleblind-like splicing regulator 1 [Source:HGNC Symbol;
19	7520	0.54	5e-04	6e-03	50 x 35 X-ray repair complementing defective repair in Chinese hams
20	221154	0.53	6e-04	1e-02	50 x 33 mitochondrial calcium uptake 2 [Source:HGNC Symbol;Acc:3

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	11.39	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
2	10.2	NULL	2 / 11	GSEA C2BIOCARTA_EIF2_PATHWAY
3	9.55	NULL	2 / 15	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_UP
4	9.28	NULL	4 / 14	GSEA C2REACTOME_MRNA_3_END_PROCESSING
5	8.99	NULL	12 / 171	miRNA target star0369-3p
6	8.88	NULL	3 / 16	Cancer GENTLES_modul14
7	8.86	NULL	12 / 121	miRNA target star0393
8	8.64	NULL	18 / 314	miRNA target star0520-3p
9	8.2	NULL	6 / 41	BP mRNA 3-end processing
10	8.12	NULL	8 / 90	miRNA target star046a
11	8.11	NULL	3 / 21	BP regulation of RNA splicing
12	7.95	NULL	17 / 303	miRNA target star0302b
13	7.88	NULL	6 / 44	BP termination of RNA polymerase II transcription
14	7.81	NULL	1 / 12	Pathw AcBENTINK_e2f3.1
15	7.79	NULL	6 / 49	miRNA target star0115-487
16	7.66	NULL	1 / 9	GSEA C2DISTECHE_ESCAPED_FROM_X_INACTIVATION
17	7.65	NULL	6 / 51	miRNA target star0566-3p
18	7.64	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C5
19	7.62	NULL	16 / 271	miRNA target star0520b
20	7.55	NULL	18 / 325	miRNA target star0302d
21	7.52	NULL	9 / 93	miRNA target star046b
22	7.49	NULL	19 / 376	miRNA target star0393
23	7.46	NULL	9 / 114	miRNA target star0397
24	7.36	NULL	16 / 316	miRNA target star0302a
25	7.26	NULL	9 / 142	miRNA target star0469-3p
26	7.24	NULL	13 / 181	miRNA target star0391
27	7.05	NULL	6 / 45	miRNA target star046d
28	7.03	NULL	10 / 134	miRNA target star0468
29	7.03	NULL	24 / 603	miRNA target star0320a
30	7.03	NULL	16 / 318	miRNA target star0590-3p
31	7.02	NULL	22 / 479	miRNA target star046e
32	6.98	NULL	12 / 163	BP mRNA splicing, via spliceosome
33	6.98	NULL	31 / 595	MF RNA binding
34	6.87	NULL	3 / 11	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
35	6.86	NULL	10 / 159	miRNA target star0562-3p
36	6.84	NULL	12 / 186	miRNA target star0302
37	6.82	NULL	16 / 311	miRNA target star0302c
38	6.81	NULL	3 / 16	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G6
39	6.77	NULL	2 / 15	GSEA C2DAIRKEE_TERT_TARGETS_DN
40	6.74	NULL	5 / 49	miRNA target star0461

p-values



GW_006

Local Summary

%DE = 0.63
 # metagenes = 37
 # genes = 464
 # genes in genesets = 460

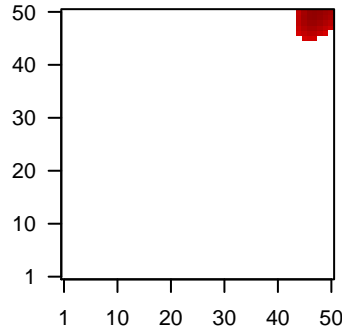
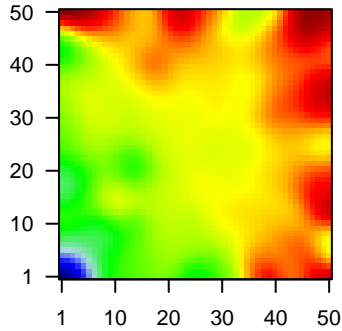
genes with $fdr < 0.1$ = 208 (195 + / 13 -)
 # genes with $fdr < 0.05$ = 175 (163 + / 12 -)
 # genes with $fdr < 0.01$ = 115 (108 + / 7 -)

$\langle r \rangle$ metagenes = 0.89
 $\langle r \rangle$ genes = 0.27

$\langle FC \rangle = 0.29$
 $\langle \text{shrinkage-t} \rangle = 10.24$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.58$

Profile

Spot



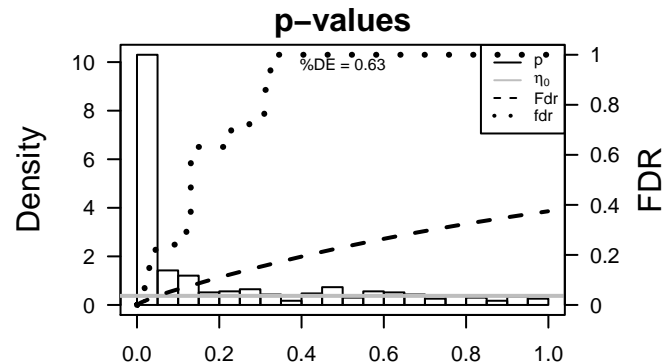
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.43	2e-16	6e-15	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:21488]
2	339512	1.84	2e-16	6e-15	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt
3	9076	1.3	2e-16	6e-15	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
4	3787	1.38	2e-16	6e-15	46 x 45 potassium voltage-gated channel, delayed-rectifier, subfamil
5	3880	1.31	2e-16	6e-15	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
6	84171	1.63	2e-16	6e-15	50 x 49 lysyl oxidase-like 4 [Source:HGNC Symbol;Acc:17171]
7	387103	1.25	4e-16	8e-14	45 x 49 centromere protein W [Source:HGNC Symbol;Acc:21488]
8	4953	-1.24	9e-16	1e-11	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
9	10388	1.15	1e-13	1e-11	47 x 46 synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
10	84223	1.14	1e-13	1e-11	47 x 46 IQ motif containing G [Source:HGNC Symbol;Acc:25251]
11	200810	1.13	2e-13	1e-11	49 x 50 ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferas
12	4690	1.13	2e-13	5e-10	49 x 50 NCK adaptor protein 1 [Source:HGNC Symbol;Acc:7664]
13	115749	1.08	3e-12	7e-10	50 x 50 chromosome 12 open reading frame 56 [Source:HGNC Symt
14	256764	-1.05	9e-12	7e-10	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
15	51087	1.05	1e-11	8e-09	47 x 46 Y box binding protein 2 [Source:HGNC Symbol;Acc:17948]
16	11166	1.01	6e-11	1e-08	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symt
17	84707	0.98	2e-10	1e-08	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
18	5357	0.98	2e-10	1e-08	50 x 50 plastin 1 [Source:HGNC Symbol;Acc:9090]
19	4171	0.98	2e-10	2e-08	46 x 48 minichromosome maintenance complex component 2 [Sourc
20	27094	0.97	3e-10	4e-08	49 x 47 potassium large conductance calcium-activated channel, sub

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	26.92	NULL	79 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	26.92	NULL	79 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	21.91	NULL	15 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
4	18.81	NULL	9 / 11	GSEA C2KALMA_E2F1_TARGETS
5	18.05	NULL	84 / 370	BP mitotic cell cycle
6	17.86	NULL	5 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
7	16.49	NULL	17 / 30	BP DNA strand elongation involved in DNA replication
8	16.31	NULL	78 / 914	Chr Chr 3
9	16.08	NULL	43 / 149	BP DNA replication
10	15.84	NULL	8 / 11	GSEA C2REACTOME_UNWINDING_OF_DNA
11	14.88	NULL	11 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
12	14.11	NULL	12 / 22	BP DNA replication initiation
13	14.1	NULL	25 / 57	Glio developing astrocytes
14	14.04	NULL	8 / 14	GSEA C2PUJANA_BRCA_CENTERED_NETWORK
15	13.76	NULL	7 / 13	GSEA C2PUJANA_XPRSS_INT_NETWORK
16	13.62	NULL	10 / 22	BP CENP-A containing nucleosome assembly at centromere
17	13.51	NULL	7 / 16	Cancer WOLFER_overlap genes
18	13.5	NULL	8 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
19	13.5	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
20	13.18	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
21	13.13	NULL	8 / 15	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G23_UP
22	12.68	NULL	11 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
23	12.63	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
24	12.55	NULL	6 / 14	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP
25	11.88	NULL	10 / 16	GSEA C2REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMP
26	11.73	NULL	8 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
27	11.63	NULL	9 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
28	11.41	NULL	10 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
29	11.34	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
30	11.15	NULL	90 / 530	Cancer Lembecke_Normal vs Adenoma
31	11.08	NULL	10 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
32	10.85	NULL	9 / 16	GSEA C2REACTOME_G2_M_CHECKPOINTS
33	10.84	NULL	6 / 15	GSEA C2STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_DN
34	10.82	NULL	12 / 24	BP telomere maintenance via recombination
35	10.75	NULL	6 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
36	10.69	NULL	5 / 9	GSEA C2REACTOME_MITOTIC_M_M_G1_PHASES
37	10.68	NULL	9 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
38	10.52	NULL	6 / 15	GSEA C2KAUFFMANN_DNA_REPLICATION_GENES
39	10.52	NULL	5 / 7	GSEA C2REACTOME_G1_S_TRANSITION
40	10.39	NULL	6 / 15	GSEA C2BASAKI_YBX1_TARGETS_UP



GW_006

Local Summary

%DE = 0.77
 # metagenes = 15
 # genes = 276
 # genes in genesets = 272
 # genes with $fdr < 0.1$ = 163 (142 + / 21 -)
 # genes with $fdr < 0.05$ = 146 (126 + / 20 -)
 # genes with $fdr < 0.01$ = 128 (109 + / 19 -)

$\langle r \rangle$ metagenes = 0.97

$\langle r \rangle$ genes = 0.41

$\langle FC \rangle = 0.4$

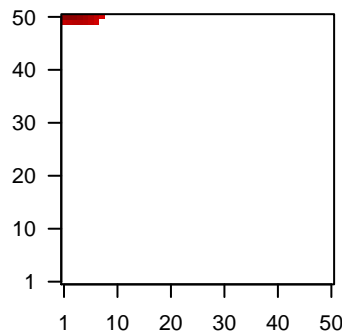
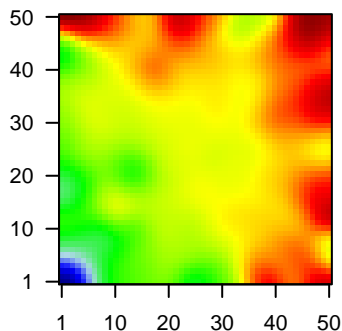
$\langle \text{shrinkage-t} \rangle = 14.19$

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

$\langle fdr \rangle = 0.44$

Profile

Spot



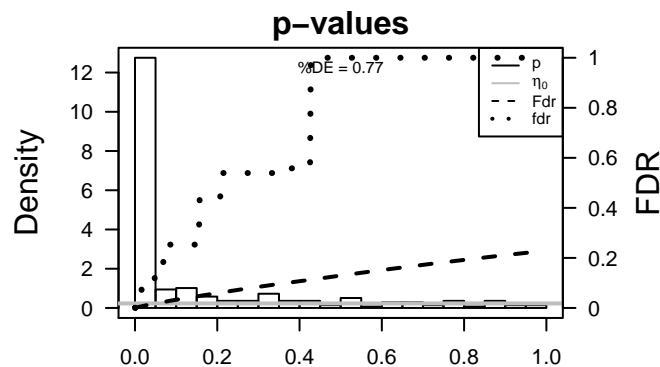
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	79852	1.67	2e-16	6e-16	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	360	1.3	2e-16	6e-16	1 x 50 aquaporin 3 (Gill blood group) [Source:HGNC Symbol;Acc:63]
3	23120	1.36	2e-16	6e-16	1 x 50 ATPase, class V, type 10B [Source:HGNC Symbol;Acc:13543]
4	1048	1.83	2e-16	6e-16	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [S
5	22802	3.04	2e-16	6e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20-
6	49860	2.17	2e-16	6e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
7	1475	1.47	2e-16	6e-16	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
8	1999	1.28	2e-16	6e-16	5 x 50 E74-like factor 3 (ets domain transcription factor, epithelial-s
9	3860	1.81	2e-16	6e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
10	192666	1.63	2e-16	6e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
11	3851	2.41	2e-16	6e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
12	388533	-2.16	2e-16	6e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
13	4118	1.66	2e-16	6e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
14	200958	1.63	2e-16	6e-16	6 x 50 mucin 20, cell surface associated [Source:HGNC Symbol;Acc
15	5627	1.32	2e-16	6e-16	7 x 50 protein S (alpha) [Source:HGNC Symbol;Acc:9456]
16	51458	1.44	2e-16	6e-16	1 x 50 Rh family, C glycoprotein [Source:HGNC Symbol;Acc:18140]
17	8796	1.28	2e-16	6e-16	1 x 50 sciellin [Source:HGNC Symbol;Acc:10573]
18	5275	1.28	2e-16	6e-16	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 13 [S
19	6317	1.76	2e-16	6e-16	1 x 49 serpin peptidase inhibitor, clade B (ovalbumin), member 3 [Sc
20	6707	1.59	2e-16	6e-16	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	42.84	NULL	68 / 135	H.Tiss WIRTH_Mucosa
2	19.47	NULL	12 / 21	CC cornified envelope
3	16.49	NULL	7 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
4	16.16	NULL	16 / 53	BP keratinocyte differentiation
5	15.36	NULL	7 / 19	BP peptide cross-linking
6	15.08	NULL	17 / 76	BP epidermis development
7	14.74	NULL	13 / 42	BP keratinization
8	12.48	NULL	7 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
9	12.41	NULL	67 / 572	Disease GUDJ_psooriasis up
10	12.35	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
11	12.25	NULL	5 / 13	H.Tiss WIRTH_Tonsil
12	10.95	NULL	5 / 13	BP negative regulation of peptidase activity
13	10.08	NULL	8 / 38	BP epithelial cell differentiation
14	9.89	NULL	2 / 10	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
15	9.85	NULL	10 / 52	BP negative regulation of endopeptidase activity
16	9.3	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
17	9.24	NULL	5 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
18	9.03	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
19	8.92	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
20	8.9	NULL	14 / 186	MF structural molecule activity
21	8.87	NULL	2 / 8	TF Tissue/AQUERIZAS_Tongue
22	8.84	NULL	17 / 201	CC apical plasma membrane
23	8.81	NULL	4 / 10	MF RAGE receptor binding
24	8.52	NULL	5 / 29	BP regulation of proteolysis
25	8.27	NULL	2 / 8	GSEA C2SCHURINGA_STAT5A_TARGETS_UP
26	8.22	NULL	5 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
27	7.97	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_T
28	7.8	NULL	4 / 44	CC keratin filament
29	7.39	NULL	5 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
30	7.38	NULL	2 / 8	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
31	7.32	NULL	3 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_UP
32	7.21	NULL	6 / 82	CC intermediate filament
33	7.1	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER
34	7.1	NULL	1 / 5	GSEA C2NAKAMURA_LUNG_CANCER_MARKERS
35	6.91	NULL	3 / 13	GSEA C2WONG_ENDMETRIUM_CANCER_UP
36	6.9	NULL	1 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
37	6.89	NULL	3 / 16	CC microvillus membrane
38	6.89	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
39	6.82	NULL	4 / 15	GSEA C2AIGNER_ZEB1_TARGETS
40	6.76	NULL	4 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN



GW_006

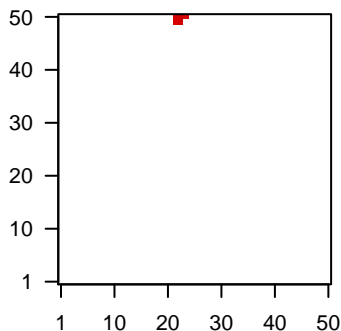
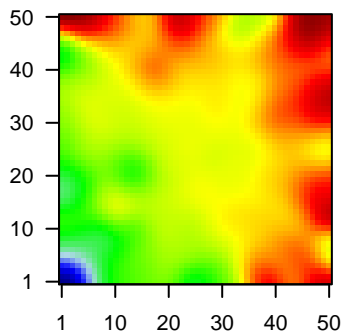
Local Summary

%DE = 0.94
 # metagenes = 5
 # genes = 86
 # genes in genesets = 84
 # genes with $fdr < 0.1 = 72$ (70 + / 2 -)
 # genes with $fdr < 0.05 = 48$ (47 + / 1 -)
 # genes with $fdr < 0.01 = 34$ (34 + / 0 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.28
 $\langle FC \rangle = 0.4$
 $\langle \text{shrinkage-t} \rangle = 14.15$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.57$

Profile

Spot



Local Genelist

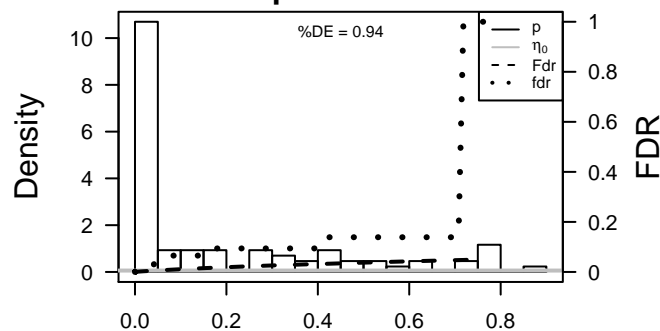
Rank	ID	log(FC)	fdr	p-value	Description
1	1843	1.22	2e-16	4e-16	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:30215]
2	2354	1.47	2e-16	4e-16	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:37659]
3	100008589	1.72	2e-16	4e-16	23 x 50 RNA, 28S ribosomal 5 [Source:HGNC Symbol;Acc:37659]
4	1806	1.21	4e-15	1e-13	24 x 50 dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Acc:32338]
5	1958	1.17	3e-14	1e-13	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:32338]
6	2353	1.07	5e-14	2e-12	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:32338]
7	7538	1.11	4e-13	5e-11	22 x 50 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
8	7465	1.05	1e-11	1e-09	23 x 50 WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:12704]
9	57018	0.98	2e-10	9e-07	22 x 50 cyclin L1 [Source:HGNC Symbol;Acc:20569]
10	523	0.8	2e-07	1e-06	24 x 50 ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A [Source:HGNC Symbol;Acc:32338]
11	8553	0.71	4e-07	1e-06	22 x 50 basic helix-loop-helix family, member e40 [Source:HGNC Symbol;Acc:32338]
12	1654	0.76	8e-07	1e-06	23 x 50 DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked [Source:HGNC Symbol;Acc:32338]
13	407006	0.76	8e-07	5e-06	22 x 50 microRNA 221 [Source:HGNC Symbol;Acc:31601]
14	55773	0.73	2e-06	5e-06	24 x 50 TBC1 domain family, member 23 [Source:HGNC Symbol;Acc:32338]
15	467	0.72	3e-06	7e-06	22 x 50 activating transcription factor 3 [Source:HGNC Symbol;Acc:7104]
16	2117	0.7	5e-06	7e-06	22 x 50 ets variant 3 [Source:HGNC Symbol;Acc:3492]
17	5573	0.7	5e-06	1e-05	24 x 50 protein kinase, cAMP-dependent, regulatory, type I, alpha [Source:HGNC Symbol;Acc:32338]
18	4609	0.69	8e-06	1e-05	22 x 50 v-myc avian myelocytomatosis viral oncogene homolog [Source:HGNC Symbol;Acc:32338]
19	3725	0.68	1e-05	1e-05	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
20	1316	0.67	2e-05	1e-05	22 x 50 Kruppel-like factor 6 [Source:HGNC Symbol;Acc:2235]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	44.04	NULL	5 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	40.19	NULL	6 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
3	39.11	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
4	34.93	NULL	6 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HEL4
5	33.44	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
6	29.98	NULL	4 / 14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
7	29.56	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
8	27.27	NULL	2 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
9	26.94	NULL	4 / 14	BP response to light stimulus
10	26.65	NULL	5 / 16	GSEA C2UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
11	24.79	NULL	5 / 16	TF Tissue/AQUERIZAS_Pancreas
12	24.16	NULL	3 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
13	22.19	NULL	2 / 5	miRNA target-101
14	21.71	NULL	6 / 16	GSEA C2AMIT_DELAYED_EARLY_GENES
15	21.7	NULL	3 / 12	GSEA C2SESTO_RESPONSE_TO_UV_C3
16	21.58	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HEL4
17	21.36	NULL	3 / 15	BP response to corticosterone
18	21.06	NULL	5 / 39	BP response to cAMP
19	20.99	NULL	4 / 30	BP cellular response to hormone stimulus
20	20.87	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
21	20.81	NULL	3 / 12	GSEA C2BIOCARTA_DREAM_PATHWAY
22	20.75	NULL	2 / 12	GSEA C2BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN
23	20.34	NULL	1 / 2	miRNA target-101
24	20.34	NULL	1 / 2	miRNA target-101
25	20.16	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
26	19.89	NULL	4 / 16	GSEA C2BIOCARTA_ETS_PATHWAY
27	19.88	NULL	3 / 15	GSEA C2BROWNE_HCMV_INFECTION_30MIN_UP
28	19.21	NULL	2 / 8	GSEA C2YEMELYANOV_GR_TARGETS_DN
29	18.87	NULL	1 / 4	GSEA C2GARASHI_ATF4_TARGETS_UP
30	18.84	NULL	3 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_DN
31	18.42	NULL	1 / 2	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14
32	18.27	NULL	2 / 14	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G4
33	18.22	NULL	4 / 15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
34	17.77	NULL	4 / 30	BP cellular response to calcium ion
35	17.44	NULL	3 / 16	GSEA C2DAUER_STAT3_TARGETS_UP
36	17.06	NULL	2 / 15	GSEA C2BENTILE_UV_RESPONSE_CLUSTER_D1
37	16.86	NULL	1 / 4	miRNA target-195
38	16.79	NULL	3 / 16	GSEA C2LEONARD_HYPOXIA
39	16.71	NULL	2 / 9	GSEA C2BIOCARTA_NTHL_PATHWAY
40	16.71	NULL	2 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_API_FAMILY_OF_TRANSC

p-values



GW_006

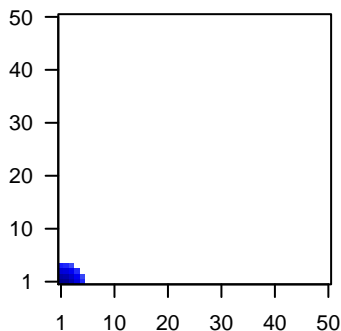
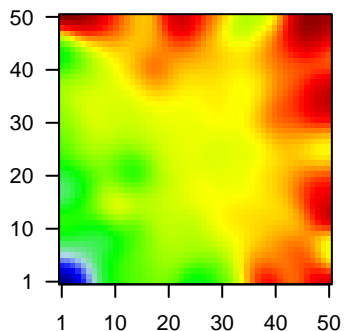
Local Summary

%DE = 0.93
 # metagenes = 17
 # genes = 263
 # genes in genesets = 262
 # genes with $fdr < 0.1$ = 225 (3 + / 222 -)
 # genes with $fdr < 0.05$ = 224 (3 + / 221 -)
 # genes with $fdr < 0.01$ = 200 (3 + / 197 -)

<r> metagenes = 0.96
 <r> genes = 0.4
 <FC> = -0.63
 <shrinkage-t> = -21.98
 <p-value> = 0
 <fdr> = 0.24

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	414062	-1.27	2e-16	2e-16	1 x 1 chemokine (C-C motif) ligand 3-like 3 [Source:HGNC Symbol;Acc:2197]
2	1277	-1.52	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	-1.38	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1282	-1.66	2e-16	2e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
5	1290	-1.41	2e-16	2e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
6	1291	-1.27	2e-16	2e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
7	3040	-1.82	2e-16	2e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	3043	-1.61	2e-16	2e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
9	3553	-1.46	2e-16	2e-16	1 x 1 interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
10	3576	-1.83	2e-16	2e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	3956	-1.4	2e-16	2e-16	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6025]
12	4312	-2.57	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:6025]
13	4319	-1.37	2e-16	2e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:6025]
14	4314	-2.05	2e-16	2e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:6025]
15	5743	-1.28	2e-16	2e-16	1 x 1 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H/synthase) [Source:HGNC Symbol;Acc:6025]
16	7045	-1.43	2e-16	2e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:6025]
17	7058	-1.51	2e-16	2e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
18	25907	-1.66	2e-16	2e-16	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:6025]
19	7130	-1.33	2e-16	2e-16	1 x 1 tumor necrosis factor, alpha-induced protein 6 [Source:HGNC Symbol;Acc:6025]
20	1462	-1.33	2e-16	2e-16	3 x 1 versican [Source:HGNC Symbol;Acc:2464]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-40.37	NULL	63 / 190	CC extracellular matrix
2	-35.57	NULL	31 / 69	BP extracellular matrix disassembly
3	-34.66	NULL	28 / 64	BP collagen catabolic process
4	-34.24	NULL	67 / 242	BP extracellular matrix organization
5	-33.46	NULL	15 / 16	MMML C2G3CIEJ_MMML 1
6	-33.42	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
7	-32.77	NULL	8 / 11	MF platelet-derived growth factor binding
8	-32.23	NULL	72 / 250	Lymphoma ENZ_Stromal signature 1
9	-28.94	NULL	8 / 12	miRNA target-29c
10	-28.38	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
11	-25.81	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
12	-23.68	NULL	15 / 37	BP collagen fibril organization
13	-23.65	NULL	20 / 57	MF extracellular matrix structural constituent
14	-23.12	NULL	37 / 183	CC proteinaceous extracellular matrix
15	-22.69	NULL	12 / 35	Glio Colman_survival_associated
16	-22.53	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
17	-21.68	NULL	5 / 12	GSEA C2Y_AGING_MIDDLE_UP
18	-21.41	NULL	103 / 1182	CC extracellular region
19	-21.18	NULL	11 / 19	MF extracellular matrix binding
20	-20.95	NULL	76 / 683	CC extracellular space
21	-20.85	NULL	12 / 40	BP cellular response to amino acid stimulus
22	-20.68	NULL	39 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
23	-20.68	NULL	39 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
24	-20.68	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
25	-20.68	NULL	39 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
26	-20.2	NULL	62 / 553	Cancer Lembcke_Colonc Inflammation
27	-19.87	NULL	22 / 83	CC basement membrane
28	-19.51	NULL	7 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
29	-19.28	NULL	6 / 11	Glio Phillips MES up vs Prolif & PN
30	-19.26	NULL	2 / 4	MMML C2G3CIEJ_MMML 23
31	-18.48	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
32	-18.03	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
33	-17.46	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
34	-17.26	NULL	18 / 68	CC collagen
35	-17.04	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
36	-16.9	NULL	6 / 10	GSEA C2JEON_SMAD6_TARGETS_UP
37	-16.78	NULL	6 / 13	GSEA C2TSAI_RESPONSE_TO_RADIATION_THERAPY
38	-16.62	NULL	4 / 10	BP protein heterotrimerization
39	-16.55	NULL	7 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
40	-16.09	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL

p-values

