

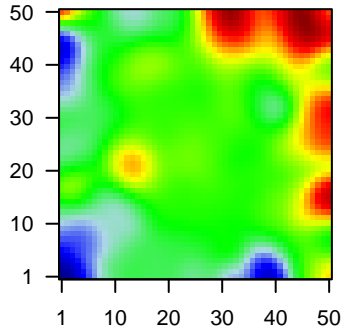
# GW\_248

## Global Summary

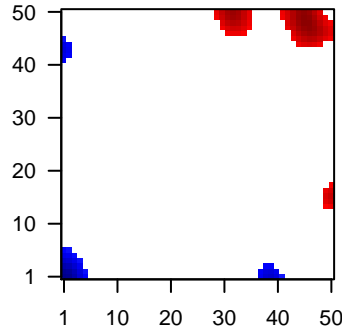
%DE = 0.14  
 # genes with fdr < 0.2 = 1791 ( 967 + / 824 - )  
 # genes with fdr < 0.1 = 1287 ( 711 + / 576 - )  
 # genes with fdr < 0.05 = 961 ( 536 + / 425 - )  
 # genes with fdr < 0.01 = 647 ( 356 + / 291 - )  
  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.13  
 <fdr> = 0.86

Profile



Regulated Spots



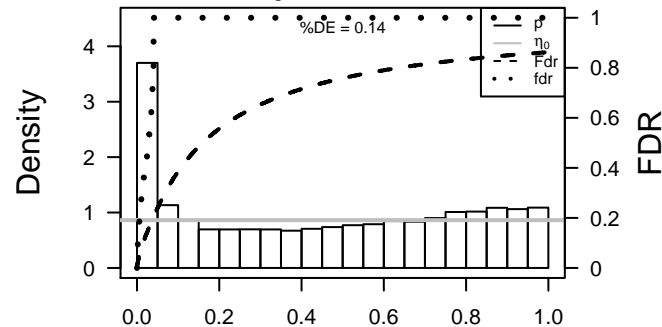
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	131	2.08	2e-16 9e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	260436	3.89	2e-16 9e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
3	6363	1.79	2e-16 9e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
4	9635	-2.22	2e-16 9e-14	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
5	9071	2.58	2e-16 9e-14	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
6	9022	1.86	2e-16 9e-14	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
7	54544	2.13	2e-16 9e-14	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
8	49860	3.5	2e-16 9e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
9	1591	2.19	2e-16 9e-14	33 x 2 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
10	55894	1.8	2e-16 9e-14	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	414325	2.23	2e-16 9e-14	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
12	10457	1.84	2e-16 9e-14	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
13	283120	-1.93	2e-16 9e-14	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
14	84223	2.16	2e-16 9e-14	47 x 46 IQ motif containing G [Source:HGNC Symbol;Acc:25251]
15	43849	1.89	2e-16 9e-14	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6
16	5653	1.84	2e-16 9e-14	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
17	196374	2.46	2e-16 9e-14	1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926]
18	137797	2.02	2e-16 9e-14	1 x 50 LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
19	4118	3.23	2e-16 9e-14	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
20	4312	-2.24	2e-16 9e-14	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.43	NULL	699	Chr Chr 5
2	12.82	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
3	12.82	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
4	12.15	NULL	153	MF structural constituent of ribosome
5	11.76	NULL	1318	CC mitochondrion
6	11.64	NULL	253	BP translation
7	10.97	NULL	167	CC ribosome
8	10.91	NULL	128	BP translational initiation
9	10.28	NULL	92	BP translational elongation
10	10.27	NULL	81	BP viral transcription
11	10.14	NULL	87	BP translational termination
12	9.49	NULL	92	BP viral life cycle
13	9.45	NULL	370	BP mitotic cell cycle
14	9.2	NULL	304	CC mitochondrial inner membrane
15	9.11	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
16	8.89	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
17	8.52	NULL	83	BP respiratory electron transport chain
18	8.39	NULL	287	BP viral process
19	8.16	NULL	51	CC cytosolic large ribosomal subunit
20	8.07	NULL	618	Chr Chr 4
<i>Underexpressed</i>				
1	-13.13	NULL	242	BP extracellular matrix organization
2	-12.38	NULL	190	CC extracellular matrix
3	-11.67	NULL	717	Chr Chr 16
4	-10.78	NULL	69	BP extracellular matrix disassembly
5	-10.21	NULL	64	BP collagen catabolic process
6	-9.6	NULL	2659	CC plasma membrane
7	-9.29	NULL	51	BP type I interferon signaling pathway
8	-9	NULL	683	CC extracellular space
9	-9	NULL	403	BP cell adhesion
10	-8.91	NULL	16	MMML C2orf107
11	-8.63	NULL	15	GSEA C2orf107_TUMORIGENESIS_UP
12	-8.44	NULL	16	GSEA C2orf107_BREAST_CANCER_CLUSTER_5
13	-8.27	NULL	250	Lymphoma ENZ_Stromal signature 1
14	-8.09	NULL	153	CC endoplasmic reticulum lumen
15	-7.82	NULL	37	BP collagen fibril organization
16	-7.8	NULL	183	CC proteinaceous extracellular matrix
17	-7.61	NULL	11	MF platelet-derived growth factor binding
18	-7.31	NULL	83	CC basement membrane
19	-7.15	NULL	57	MF extracellular matrix structural constituent
20	-7.05	NULL	1182	CC extracellular region

p-values



# GW\_248

## Local Summary

%DE = 0.83  
 # metagenes = 9  
 # genes = 150  
 # genes in genesets = 149

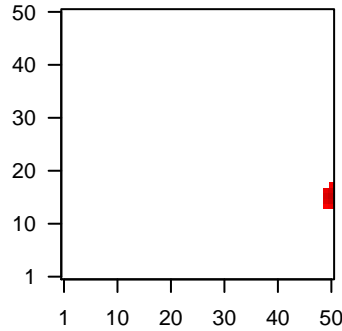
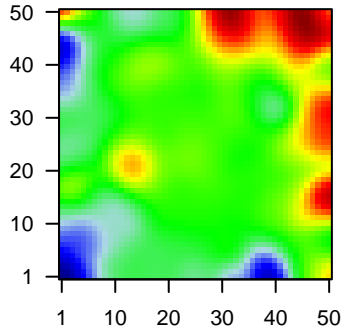
# genes with  $fdr < 0.1 = 100$  ( 98 + / 2 - )  
 # genes with  $fdr < 0.05 = 84$  ( 83 + / 1 - )  
 # genes with  $fdr < 0.01 = 62$  ( 62 + / 0 - )

<r> metagenes = 0.97  
 <r> genes = 0.35

<FC> = 0.58  
 <shrinkage-t> = 20.38  
 <p-value> = 0  
 <fdr> = 0.47

Profile

Spot



## Local Genelist

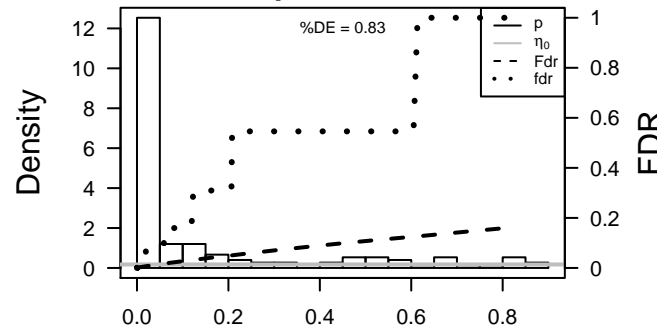
Rank	ID	log(FC)	fdr	p-value	Description
1	54959	2.28	2e-16	6e-15	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:10410]
2	3670	1.67	1e-14	4e-13	50 x 17 ISL LIM homeobox 1 [Source:HGNC Symbol;Acc:6132]
3	399948	1.65	3e-14	1e-12	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3122]
4	21	1.62	7e-14	1e-12	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Source:HGNC Symbol;Acc:10410]
5	57556	1.61	1e-13	8e-12	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic tail domain [Source:HGNC Symbol;Acc:10410]
6	10439	1.57	4e-13	2e-11	50 x 17 olfactomedin 1 [Source:HGNC Symbol;Acc:17187]
7	56994	1.54	1e-12	1e-10	50 x 16 choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17187]
8	26002	1.5	5e-12	5e-10	50 x 16 monooxygenase, DBH-like 1 [Source:HGNC Symbol;Acc:2161]
9	3977	1.45	3e-11	1e-09	50 x 17 leukemia inhibitory factor receptor alpha [Source:HGNC Symbol;Acc:10410]
10	9603	1.42	6e-11	4e-09	50 x 18 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:10410]
11	153579	1.38	2e-10	3e-08	50 x 17 butyrophilin-like 9 [Source:HGNC Symbol;Acc:24176]
12	909	1.3	2e-09	3e-08	50 x 16 CD1a molecule [Source:HGNC Symbol;Acc:1634]
13	6228	1.29	3e-09	2e-07	50 x 14 ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
14	4602	1.22	2e-08	2e-07	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:10410]
15	6263	1.21	3e-08	2e-07	50 x 18 ryanodine receptor 3 [Source:HGNC Symbol;Acc:10485]
16	1365	1.2	3e-08	2e-07	50 x 15 claudin 3 [Source:HGNC Symbol;Acc:2045]
17	10461	1.2	3e-08	3e-07	50 x 17 c-mer proto-oncogene tyrosine kinase [Source:HGNC Symbol;Acc:10410]
18	6096	1.18	5e-08	3e-07	50 x 16 RAR-related orphan receptor B [Source:HGNC Symbol;Acc:10410]
19	2628	1.18	5e-08	5e-07	50 x 14 glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Source:HGNC Symbol;Acc:10410]
20	641638	1.17	7e-08	1e-06	50 x 18 small nucleolar RNA host gene 6 (non-protein coding) [Source:HGNC Symbol;Acc:10410]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	16.91	NULL	4 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.69	NULL	2 / 6	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_UP
3	12.4	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
4	12	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
5	11.87	NULL	2 / 11	MF enhancer sequence-specific DNA binding
6	11.82	NULL	2 / 9	GSEA C2GOZGIT_ESR1_TARGETS_DN
7	10.93	NULL	2 / 11	GSEA C2RIGGI_EWING_SARCOMA_PROGENITOR_DN
8	10.7	NULL	1 / 2	TF MYC_Cell cycle DOWN
9	10.45	NULL	3 / 15	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMES_DN
10	9.85	NULL	1 / 2	miRNA target-153
11	9.53	NULL	2 / 16	GSEA C2ZHAN_MULTIPLE_MYELOMA_MF_DN
12	9.49	NULL	3 / 20	MF RNA polymerase II transcription coactivator activity
13	9.45	NULL	1 / 13	GSEA C2FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN
14	9.25	NULL	2 / 15	BP retinal ganglion cell axon guidance
15	9.05	NULL	1 / 14	BP biomineral tissue development
16	8.87	NULL	2 / 15	BP positive regulation vascular endothelial growth factor production
17	8.79	NULL	2 / 16	GSEA C2CHANDRAN_METASTASIS_DN
18	8.65	NULL	2 / 19	BP spinal cord motor neuron differentiation
19	8.62	NULL	2 / 15	GSEA C2GEORGES_TARGETS_OF_MIR192_AND_MIR215
20	8.6	NULL	2 / 12	GSEA C2PROVENZANI_METASTASIS_UP
21	8.37	NULL	2 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
22	8.16	NULL	2 / 16	GSEA C2DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN
23	8.04	NULL	2 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
24	7.84	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DIFFERENTIATED_DN
25	7.7	NULL	1 / 8	GSEA C2BENPORATH_ES_CORE_NINE
26	7.69	NULL	1 / 10	BP centrosome localization
27	7.69	NULL	2 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
28	7.59	NULL	1 / 9	GSEA C2RODWELL_AGING_KIDNEY_UP
29	7.59	NULL	4 / 32	miRNA target-510
30	7.55	NULL	1 / 11	BP innervation
31	7.55	NULL	1 / 11	BP negative regulation of intracellular estrogen receptor signaling pathway
32	7.5	NULL	1 / 10	GSEA C2BROWNE_HCMV_INFECTION_12HR_UP
33	7.5	NULL	1 / 10	GSEA C2XU_GH1_AUTOCRINE_TARGETS_DN
34	7.47	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18
35	7.37	NULL	1 / 4	GSEA C2CALVET_IRINOTECAN_SENSITIVE_VS_RESISTANT_UP
36	7.33	NULL	1 / 10	MF diacylglycerol binding
37	7.27	NULL	2 / 10	BP positive regulation of histone H3-K4 methylation
38	7.25	NULL	2 / 11	BP DNA integration
39	7.2	NULL	3 / 15	GSEA C2DELYS_THYROID_CANCER_DN
40	7.17	NULL	1 / 12	BP neuron fate specification

p-values

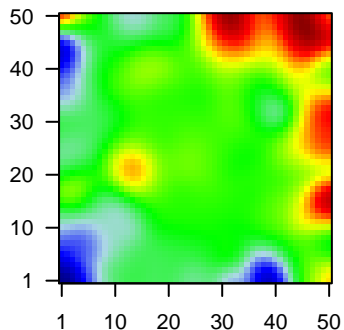


# GW\_248

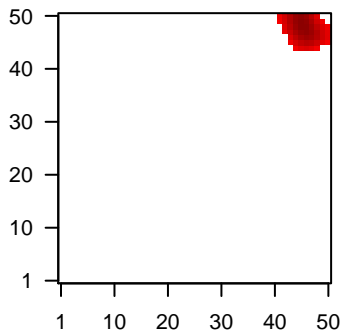
## Local Summary

%DE = 0.66  
 # metagenes = 56  
 # genes = 590  
 # genes in genesets = 587  
  
 # genes with  $fdr < 0.1$  = 246 ( 237 + / 9 - )  
 # genes with  $fdr < 0.05$  = 218 ( 209 + / 9 - )  
 # genes with  $fdr < 0.01$  = 149 ( 144 + / 5 - )  
  
 $\langle r \rangle$  metagenes = 0.86  
 $\langle r \rangle$  genes = 0.28  
  
 $\langle FC \rangle = 0.42$   
 $\langle \text{shrinkage-t} \rangle = 14.57$   
 $\langle p\text{-value} \rangle = 0.01$   
 $\langle fdr \rangle = 0.59$

Profile



Spot



## Local Genelist

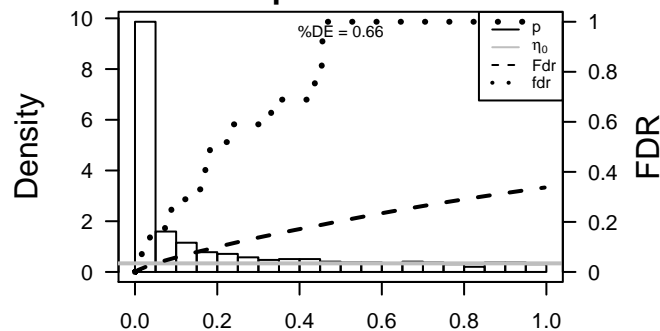
Rank	ID	log(FC)	fdr	p-value	Description
1	84223	2.16	2e-16	4e-14	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
2	84707	1.67	2e-14	2e-12	brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093]
3	7345	1.66	2e-14	1e-10	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesteras
4	10388	1.56	6e-13	2e-10	synaptonemal complex protein 2 [Source:HGNC Symbol;Acc:
5	445	1.53	2e-12	1e-09	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75]
6	3787	1.49	6e-12	1e-09	potassium voltage-gated channel, delayed-rectifier, subfamil
7	4897	1.47	1e-11	5e-09	neuronal cell adhesion molecule [Source:HGNC Symbol;Acc:
8	5984	1.43	4e-11	2e-08	replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn
9	79190	1.38	2e-10	2e-08	iroquois homeobox 6 [Source:HGNC Symbol;Acc:14675]
10	11013	1.37	2e-10	1e-07	thymosin beta 15a [Source:HGNC Symbol;Acc:30744]
11	26255	1.31	1e-09	1e-07	pituitary tumor-transforming 3, pseudogene [Source:HGNC S
12	139728	-1.31	2e-09	1e-07	pregnancy up-regulated nonubiquitous CaM kinase [Source:l
13	79682	1.3	2e-09	1e-07	centromere protein U [Source:HGNC Symbol;Acc:21348]
14	6596	1.3	2e-09	5e-07	helicase-like transcription factor [Source:HGNC Symbol;Acc:
15	1894	1.27	5e-09	5e-07	epithelial cell transforming sequence 2 oncogene [Source:HG
16	3304	-1.15	8e-09	5e-07	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52]
17	84303	1.24	1e-08	5e-07	coiled-coil-helix-coiled-coil-helix domain containing 6 [Sou
18	93081	1.23	1e-08	5e-07	testis expressed 30 [Source:HGNC Symbol;Acc:25188]
19	9582	1.23	1e-08	2e-06	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
20	283212	1.2	3e-08	2e-06	kelch-like family member 35 [Source:HGNC Symbol;Acc:265

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	37.62	NULL	96 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	37.62	NULL	96 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	24.3	NULL	113 / 370	BP mitotic cell cycle
4	24.15	NULL	16 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
5	19	NULL	114 / 530	Cancer Lembcke_Normal vs Adenoma
6	18.98	NULL	20 / 30	BP DNA strand elongation involved in DNA replication
7	18.96	NULL	13 / 14	MMLL C6SCIEJ_MMLL 4
8	18.86	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
9	17.65	NULL	14 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
10	17.43	NULL	9 / 11	GSEA C2KALMA_E2F1_TARGETS
11	17.21	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	16.96	NULL	11 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
13	16.96	NULL	53 / 149	BP DNA replication
14	16.64	NULL	10 / 16	Cancer WOLFER_overlap genes
15	16.58	NULL	10 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
16	16.1	NULL	13 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
17	15.84	NULL	8 / 12	GSEA C2LWILMS_TUMOR_VS_FETAL_KIDNEY_1_DN
18	15.39	NULL	9 / 11	GSEA C2JIANG_SILENCED_BY_METHYLATION_DN
19	15.37	NULL	14 / 21	BP telomere maintenance via semi-conservative replication
20	15.28	NULL	25 / 66	CC condensed chromosome kinetochore
21	15.05	NULL	26 / 57	Glio developing astrocytes
22	15.02	NULL	12 / 16	GSEA C2REACTOME_DNA_STRAND_ELONGATION
23	14.58	NULL	12 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
24	14.47	NULL	9 / 15	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G23_UP
25	14.36	NULL	8 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
26	14.36	NULL	61 / 232	BP mitosis
27	14.33	NULL	7 / 13	GSEA C2SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
28	14.22	NULL	15 / 24	BP telomere maintenance via recombination
29	14.11	NULL	24 / 56	CC chromosome, centromeric region
30	13.97	NULL	6 / 9	GSEA C2SEMBA_FHIT_TARGETS_DN
31	13.83	NULL	12 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
32	13.82	NULL	11 / 22	BP CENP-A containing nucleosome assembly at centromere
33	13.78	NULL	10 / 15	GSEA C2WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
34	13.69	NULL	11 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
35	13.54	NULL	4 / 6	GSEA C2ZERBINI_RESPONSE_TO_SULINDAC_DN
36	13.4	NULL	14 / 22	BP DNA replication initiation
37	13.38	NULL	131 / 949	CC nucleoplasm
38	13.36	NULL	11 / 16	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN
39	13.29	NULL	9 / 16	GSEA C2PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
40	13.17	NULL	12 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP

p-values



# GW\_248

## Local Summary

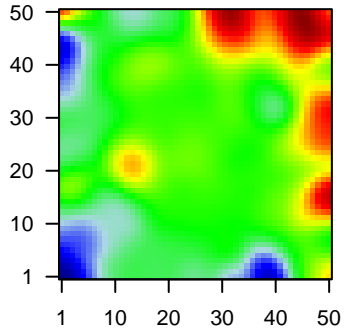
%DE = 0.75  
 # metagenes = 30  
 # genes = 364  
 # genes in genesets = 357

# genes with  $fdr < 0.1 = 172$  ( 170 + / 2 - )  
 # genes with  $fdr < 0.05 = 139$  ( 139 + / 0 - )  
 # genes with  $fdr < 0.01 = 86$  ( 86 + / 0 - )

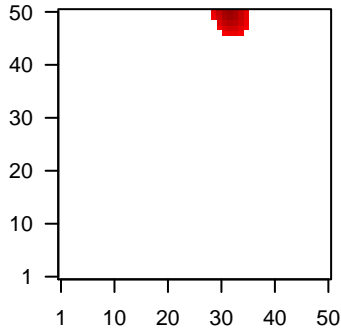
<r> metagenes = 0.94  
 <r> genes = 0.25

<FC> = 0.41  
 <shrinkage-t> = 14.55  
 <p-value> = 0.02  
 <fdr> = 0.62

Profile



Spot



## Local Genelist

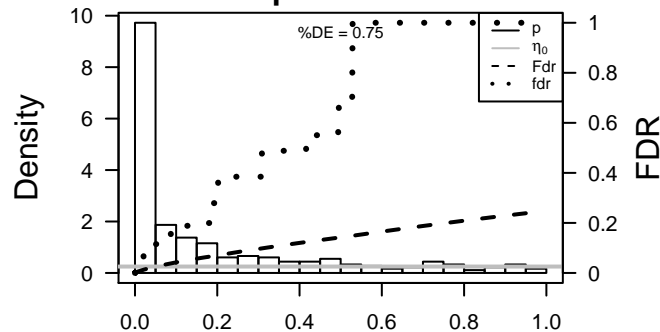
Rank	ID	log(FC)	fdr	p-value	Description
1	84833	1.34	7e-10	3e-05	33 x 50 up-regulated during skeletal muscle growth 5 homolog (mous
2	6165	1.1	4e-07	7e-05	33 x 49 ribosomal protein L35a [Source:HGNC Symbol;Acc:10345]
3	3094	0.95	2e-06	7e-05	32 x 50 histidine triad nucleotide binding protein 1 [Source:HGNC Syr
4	6152	1.02	3e-06	7e-05	32 x 49 ribosomal protein L24 [Source:HGNC Symbol;Acc:10325]
5	4724	1.01	3e-06	7e-05	33 x 50 NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (t
6	79752	1	4e-06	4e-04	31 x 49 zinc finger, AN1-type domain 1 [Source:HGNC Symbol;Acc:2
7	51397	0.92	2e-05	4e-04	29 x 50 COMM domain containing 10 [Source:HGNC Symbol;Acc:30;
8	54534	0.92	2e-05	4e-04	31 x 50 mitochondrial ribosomal protein L50 [Source:HGNC Symbol;/
9	23517	0.92	2e-05	4e-04	30 x 50 superkiller viralicidic activity 2-like 2 (S. cerevisiae) [Source;t
10	10412	0.91	2e-05	4e-04	31 x 49 NSA2 ribosome biogenesis homolog (S. cerevisiae) [Source:l
11	6164	0.91	2e-05	4e-04	32 x 50 ribosomal protein L34 [Source:HGNC Symbol;Acc:10340]
12	442454	0.9	3e-05	4e-04	32 x 50
13	6160	0.9	3e-05	4e-04	32 x 49 ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]
14	653147	0.89	4e-05	4e-04	34 x 50
15	51110	0.88	5e-05	4e-04	32 x 50 lactamase, beta 2 [Source:HGNC Symbol;Acc:18512]
16	6129	0.88	5e-05	4e-04	32 x 48 ribosomal protein L7 [Source:HGNC Symbol;Acc:10363]
17	157567	0.87	6e-05	4e-04	29 x 50 ankyrin repeat domain 46 [Source:HGNC Symbol;Acc:27229]
18	10190	0.87	6e-05	4e-04	31 x 50 thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:;
19	441951	0.86	7e-05	4e-04	33 x 49 ZNF1 antisense RNA 1 [Source:HGNC Symbol;Acc:33101]
20	1666	0.86	7e-05	4e-04	32 x 46 2,4-dienoyl CoA reductase 1, mitochondrial [Source:HGNC S

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	21.9	NULL	23 / 81	BP viral transcription
2	21.49	NULL	24 / 87	BP translational termination
3	21.26	NULL	24 / 92	BP translational elongation
4	21.01	NULL	34 / 153	BP structural constituent of ribosome
5	20.4	NULL	23 / 92	BP viral life cycle
6	19.9	NULL	15 / 51	CC cytosolic large ribosomal subunit
7	19.79	NULL	26 / 109	BP SRP-dependent cotranslational protein targeting to membrane
8	19.6	NULL	30 / 83	BP respiratory electron transport chain
9	19.41	NULL	26 / 128	BP translational initiation
10	18.12	NULL	40 / 253	BP translation
11	17.97	NULL	23 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
12	17.56	NULL	31 / 167	CC ribosome
13	15.15	NULL	9 / 19	CC mitochondrial proton-transporting ATP synthase complex
14	15.05	NULL	5 / 10	CC large ribosomal subunit
15	14.93	NULL	33 / 152	BP cellular metabolic process
16	14.64	NULL	30 / 219	BP mRNA metabolic process
17	14.52	NULL	4 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
18	14.05	NULL	43 / 304	CC mitochondrial inner membrane
19	14	NULL	31 / 242	BP RNA metabolic process
20	13.9	NULL	39 / 287	BP viral process
21	13.61	NULL	4 / 9	GSEA C2KEGG_RIBOSOME
22	13.61	NULL	4 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
23	13.61	NULL	4 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
24	13.61	NULL	4 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
25	13.61	NULL	4 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
26	13.61	NULL	4 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
27	13.61	NULL	4 / 9	GSEA C2REACTOME_VIRAL_MRNA_TRANSLATION
28	12.84	NULL	4 / 10	GSEA C2REACTOME_TRANSLATION
29	11.96	NULL	100 / 1318	CC mitochondrion
30	11.69	NULL	3 / 11	BP ribosomal large subunit biogenesis
31	11.47	NULL	6 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
32	11.1	NULL	7 / 15	BP ATP synthesis coupled proton transport
33	11.01	NULL	41 / 482	BP cellular protein metabolic process
34	11	NULL	6 / 14	BP mitochondrial ATP synthesis coupled proton transport
35	10.77	NULL	4 / 11	GSEA C2OSMAN_BLADDER_CANCER_DN
36	10.61	NULL	49 / 649	BP gene expression
37	9.68	NULL	12 / 36	CC mitochondrial respiratory chain complex I
38	9.56	NULL	11 / 34	MF NADH dehydrogenase (ubiquinone) activity
39	8.79	NULL	4 / 13	CC mitochondrial respiratory chain
40	8.55	NULL	11 / 35	BP mitochondrial electron transport, NADH to ubiquinone

p-values



# GW\_248

## Local Summary

%DE = 0.75  
 # metagenes = 23  
 # genes = 346  
 # genes in genesets = 343

# genes with  $fdr < 0.1$  = 199 ( 18 + / 181 - )  
 # genes with  $fdr < 0.05$  = 175 ( 16 + / 159 - )  
 # genes with  $fdr < 0.01$  = 128 ( 8 + / 120 - )

<r> metagenes = 0.93

<r> genes = 0.34

<FC> = -0.48

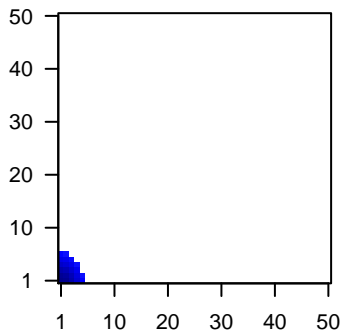
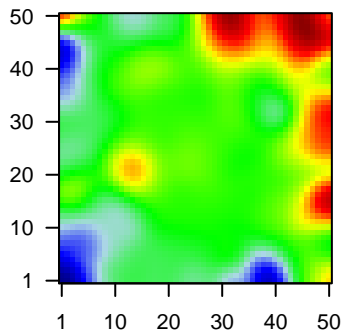
<shrinkage-t> = -16.81

<p-value> = 0

<fdr> = 0.49

Profile

Spot



## Local Genelist

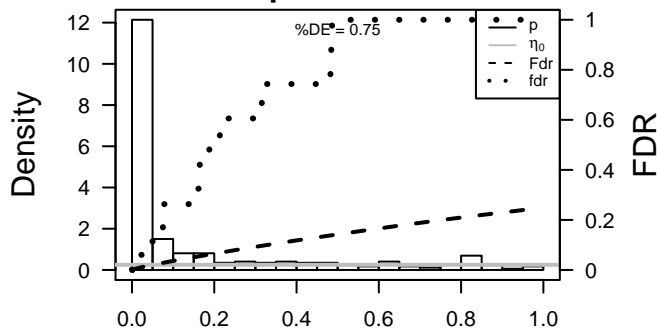
Rank	ID	log(FC)	fdr	p-value	Description
1	4312	-2.24	2e-16	1e-14	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:2197]
2	4314	-2.28	2e-16	1e-14	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:2197]
3	1277	-1.77	4e-16	4e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	25878	-1.74	9e-16	2e-13	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:2197]
5	3371	-1.71	3e-15	2e-11	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]
6	4502	-1.58	4e-13	2e-11	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
7	1293	-1.58	4e-13	5e-11	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	1290	-1.54	1e-12	5e-11	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
9	4319	-1.53	2e-12	1e-09	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:2197]
10	10644	-1.47	1e-11	1e-09	1 x 6 insulin-like growth factor 2 mRNA binding protein 2 [Source:HGNC Symbol;Acc:2464]
11	1462	-1.43	5e-11	1e-09	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
12	25907	-1.42	5e-11	1e-09	1 x 1 transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:2464]
13	1289	-1.41	7e-11	1e-09	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
14	4489	-1.29	1e-10	1e-09	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]
15	6423	-1.4	1e-10	1e-09	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:2197]
16	1278	-1.4	1e-10	7e-09	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
17	3486	-1.38	2e-10	1e-08	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Symbol;Acc:2197]
18	83716	-1.36	4e-10	1e-08	2 x 1 cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:2197]
19	7057	-1.36	4e-10	4e-08	1 x 1 thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
20	3678	-1.31	1e-09	4e-08	1 x 1 integrin, alpha 5 (fibronectin receptor, alpha polypeptide) [Source:HGNC Symbol;Acc:2197]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-34.84	NULL	15 / 16	MMML C6S1CIEJ_MMML_1
2	-34.16	NULL	75 / 242	BP extracellular matrix organization
3	-33.9	NULL	65 / 190	CC extracellular matrix
4	-32.93	NULL	33 / 69	BP extracellular matrix disassembly
5	-31.81	NULL	29 / 64	BP collagen catabolic process
6	-31.31	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
7	-28.2	NULL	77 / 250	LymphomaENZ_Stromal signature 1
8	-27.36	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
9	-26.68	NULL	8 / 11	MF platelet-derived growth factor binding
10	-23.08	NULL	22 / 57	MF extracellular matrix structural constituent
11	-22.56	NULL	16 / 37	BP collagen fibril organization
12	-20.95	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
13	-20.49	NULL	12 / 19	MF extracellular matrix binding
14	-20.08	NULL	8 / 12	miRNA target-29c
15	-19.2	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
16	-18.99	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
17	-18.74	NULL	40 / 183	CC proteinaceous extracellular matrix
18	-18.37	NULL	6 / 13	GSEA C2REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR
19	-18.01	NULL	121 / 1182	CC extracellular region
20	-17.98	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
21	-17.95	NULL	25 / 83	CC basement membrane
22	-17.82	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
23	-17.16	NULL	85 / 683	CC extracellular space
24	-16.88	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
25	-16.5	NULL	6 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
26	-16.44	NULL	12 / 40	BP cellular response to amino acid stimulus
27	-16.3	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
28	-16.06	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
29	-15.97	NULL	13 / 35	Glio Colman_survival_associated
30	-15.94	NULL	4 / 10	BP protein heterotrimerization
31	-15.51	NULL	6 / 16	GSEA C2LIEN_BREAST_CARCINOMA_METAPLASTIC
32	-15.44	NULL	7 / 16	MF fibronectin binding
33	-15.37	NULL	60 / 403	BP cell adhesion
34	-15.05	NULL	20 / 85	MF integrin binding
35	-14.92	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
36	-14.8	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
37	-14.7	NULL	46 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
38	-14.7	NULL	46 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
39	-14.7	NULL	46 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
40	-14.7	NULL	46 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down

p-values



# GW\_248

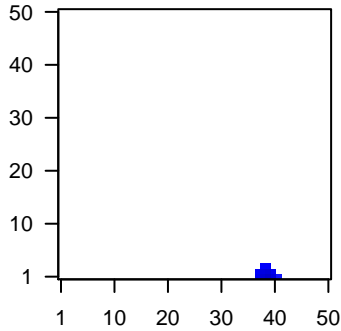
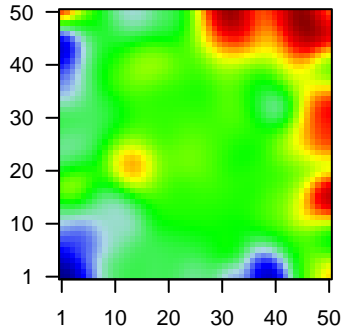
## Local Summary

%DE = 0.91  
 # metagenes = 11  
 # genes = 203  
 # genes in genesets = 177  
 # genes with  $fdr < 0.1 = 160$  ( 1 + / 159 - )  
 # genes with  $fdr < 0.05 = 159$  ( 1 + / 158 - )  
 # genes with  $fdr < 0.01 = 96$  ( 0 + / 96 - )

<r> metagenes = 0.99  
 <r> genes = 0.56  
 <FC> = -0.53  
 <shrinkage-t> = -18.57  
 <p-value> = 0.01  
 <fdr> = 0.51

Profile

Spot



## Local Genelist

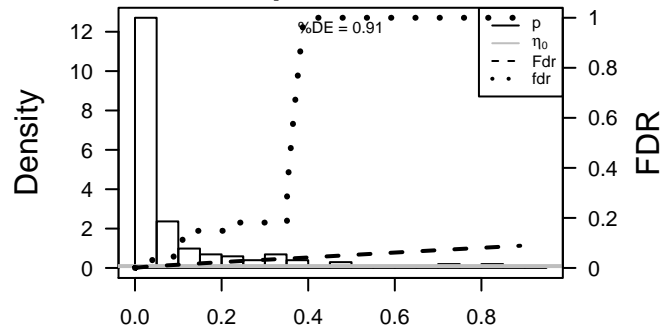
Rank	ID	log(FC)	fdr	p-value	Description
1	400818	-1.55	1e-12	5e-11	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
2	100132406	-1.51	4e-12	2e-07	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
3	91368	-1.14	1e-08	4e-06	39 x 1 CDKN2A interacting protein N-terminal like [Source:HGNC S
4	641737	-1.03	3e-07	4e-06	40 x 1
5	84061	-1.09	5e-07	4e-06	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
6	28996	-1.08	7e-07	4e-06	40 x 1 homeodomain interacting protein kinase 2 [Source:HGNC Sy
7	142679	-1.07	9e-07	4e-06	38 x 1 dual specificity phosphatase 19 [Source:HGNC Symbol;Acc:1
8	399761	-1.06	1e-06	4e-06	39 x 1 BMS1 pseudogene 5 [Source:HGNC Symbol;Acc:23653]
9	100128288	-1.05	1e-06	4e-06	39 x 1
10	319085	-1.04	1e-06	4e-06	39 x 1 ITPK1 antisense RNA 1 [Source:HGNC Symbol;Acc:20132]
11	399900	-0.95	2e-06	2e-05	39 x 1
12	25862	-1	4e-06	2e-05	40 x 1 ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20
13	728903	-0.98	7e-06	2e-05	39 x 1
14	440353	-0.98	7e-06	2e-05	40 x 1
15	23162	-0.97	7e-06	2e-05	39 x 1 mitogen-activated protein kinase 8 interacting protein 3 [Sou
16	5900	-0.97	8e-06	2e-05	39 x 2 ral guanine nucleotide dissociation stimulator [Source:HGNC
17	441087	-0.96	1e-05	2e-05	39 x 1
18	85452	-0.95	1e-05	2e-05	39 x 1 chromosome 1 open reading frame 222 [Source:HGNC Synt
19	9723	-0.95	1e-05	2e-05	38 x 1 sema domain, immunoglobulin domain (Ig), short basic doma
20	90586	-0.95	1e-05	2e-05	39 x 1 amine oxidase, copper containing 4, pseudogene [Source:HC

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.91	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-8.59	NULL	3 / 14	MMML C6ACIEJ_MMML 8
3	-7.79	NULL	3 / 16	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_UP
4	-7.73	NULL	2 / 19	MF mitogen-activated protein kinase kinase binding
5	-7.72	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
6	-6.64	NULL	2 / 16	BP cognition
7	-6.12	NULL	1 / 9	GSEA C2BROWNE_HCMV_INFECTION_1HR_DN
8	-6.02	NULL	2 / 29	BP positive regulation of JUN kinase activity
9	-6.01	NULL	1 / 6	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
10	-6	NULL	1 / 4	GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_UP
11	-5.98	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
12	-5.92	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
13	-5.85	NULL	1 / 10	CC oligosaccharyltransferase complex
14	-5.69	NULL	1 / 10	BP negative regulation of JUN kinase activity
15	-5.47	NULL	2 / 14	BP cellular response to estradiol stimulus
16	-5.35	NULL	2 / 19	BP sprouting angiogenesis
17	-5.31	NULL	1 / 6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
18	-5.17	NULL	1 / 10	BP lung morphogenesis
19	-5.16	NULL	1 / 12	BP retina layer formation
20	-5.14	NULL	1 / 10	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_L
21	-5.12	NULL	1 / 4	MMML C6ACIEJ_MMML 44
22	-5.04	NULL	1 / 10	BP negative regulation of cell-matrix adhesion
23	-5.01	NULL	2 / 15	Glo Donson-chemokines/cytokines-associated with LTS in HGA
24	-5	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
25	-4.97	NULL	4 / 44	BP meiosis
26	-4.91	NULL	1 / 13	BP DNA damage response, signal transduction by p53 class mediator
27	-4.91	NULL	1 / 13	BP SMAD protein signal transduction
28	-4.88	NULL	1 / 11	CC axolemma
29	-4.88	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
30	-4.85	NULL	1 / 11	GSEA C2FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP
31	-4.78	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
32	-4.78	NULL	1 / 14	BP magnesium ion transport
33	-4.7	NULL	1 / 14	GSEA C2WILCOX_PRESPONSE_TO_ROGESTERONE_DN
34	-4.68	NULL	2 / 20	BP negative regulation of JNK cascade
35	-4.5	NULL	1 / 15	GSEA C2WANG_LMO4_TARGETS_UP
36	-4.5	NULL	1 / 15	GSEA C2ODONNELL_TFRC_TARGETS_UP
37	-4.5	NULL	1 / 15	GSEA C2RODRIGUES_THYROID_CARCINOMA_DN
38	-4.5	NULL	1 / 15	GSEA C2SUNG_METASTASIS_STROMA_DN
39	-4.5	NULL	1 / 15	GSEA C2LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_UP
40	-4.5	NULL	1 / 15	GSEA C2DE_Y1_TARGETS_DN

p-values



# GW\_248

## Local Summary

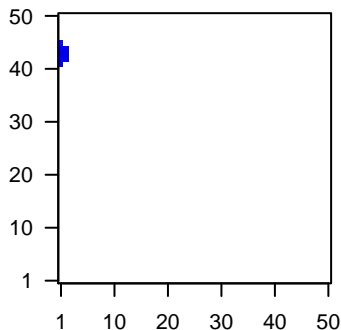
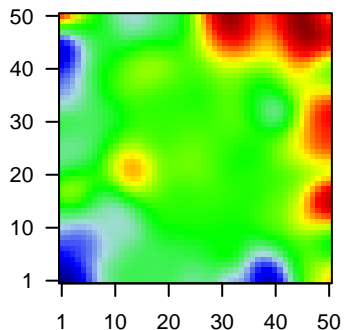
%DE = 0.77  
 # metagenes = 8  
 # genes = 135  
 # genes in genesets = 134  
 # genes with  $fdr < 0.1$  = 88 ( 5 + / 83 - )  
 # genes with  $fdr < 0.05$  = 81 ( 4 + / 77 - )  
 # genes with  $fdr < 0.01$  = 63 ( 2 + / 61 - )

<r> metagenes = 0.98  
 <r> genes = 0.4

<FC> = -0.55  
 <shrinkage-t> = -19.27  
 <p-value> = 0  
 <fdr> = 0.42

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5744	-1.67	1e-14	8e-12	1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;A
2	3306	1.58	3e-13	2e-11	1 x 42 heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:5235
3	1001	-1.55	8e-13	7e-11	1 x 43 cadherin 3, type 1, P-cadherin (placental) [Source:HGNC Sy
4	3489	-1.51	3e-12	2e-09	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
5	10509	-1.41	7e-11	5e-09	1 x 42 sema domain, immunoglobulin domain (lg), transmembrane c
6	6665	-1.38	2e-10	2e-08	1 x 45 SRY (sex determining region Y)-box 15 [Source:HGNC Synt
7	771	-1.33	7e-10	2e-08	1 x 44 carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
8	2167	-1.31	1e-09	1e-07	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
9	2697	-1.27	5e-09	2e-07	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
10	2810	-1.14	1e-08	7e-07	1 x 45 stratifin [Source:HGNC Symbol;Acc:10773]
11	55214	-1.17	6e-08	7e-07	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
12	9935	-1.17	6e-08	7e-07	1 x 45 v-maf avian musculoaponeurotic fibrosarcoma oncogene hor
13	51200	-1.15	1e-07	7e-07	1 x 44 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
14	760	-1.14	1e-07	7e-07	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	50805	-1.14	1e-07	7e-07	1 x 43 iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
16	8140	-1.14	1e-07	3e-06	1 x 43 solute carrier family 7 (amino acid transporter light chain, L s
17	3038	-1.1	4e-07	3e-06	1 x 43 hyaluronan synthase 3 [Source:HGNC Symbol;Acc:4820]
18	1288	-1.1	4e-07	6e-06	1 x 43 collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
19	2150	-1.07	7e-07	6e-06	1 x 44 coagulation factor II (thrombin) receptor-like 1 [Source:HGNC
20	147495	-1.07	9e-07	6e-06	2 x 44 adenomatosis polyposis coli down-regulated 1 [Source:HGNC

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-15.25	NULL	2 / 2	miRNA target-199a*
2	-14.2	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
3	-13.86	NULL	2 / 10	BP skeletal muscle tissue regeneration
4	-11.89	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
5	-11.59	NULL	2 / 15	GSEA C2AIGNER_ZEB1_TARGETS
6	-11.32	NULL	7 / 85	Glio laffaire_hypermeth_LGG_vs_control
7	-11.24	NULL	4 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	-11.09	NULL	4 / 12	BP hemidesmosome assembly
9	-11.06	NULL	2 / 15	GSEA C2NGUYEN_NOTCH1_TARGETS_UP
10	-10.87	NULL	8 / 112	Glio Christensen_hypermethylated_in_grade2_oligoastrocytoma
11	-10.79	NULL	9 / 82	CC intermediate filament
12	-10.79	NULL	2 / 15	GSEA C2STOSSI_RESPONSE_TO ESTRADIOL
13	-10.74	NULL	1 / 7	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
14	-10.49	NULL	9 / 132	Glio Christensen_hypermethylated_in_grade3_oligoastrocytoma
15	-10.33	NULL	2 / 15	GSEA C2KANG_CISPLATIN_RESISTANCE_UP
16	-10.2	NULL	2 / 9	GSEA C2KORKOLA_CORRELATED_WITH_POU5F1
17	-9.71	NULL	2 / 12	CC fascia adherens
18	-9.69	NULL	1 / 7	GSEA C2YE_METASTATIC_LIVER_CANCER
19	-9.23	NULL	2 / 15	GSEA C2AMIT_EGF_RESPONSE_240_MCF10A
20	-9.18	NULL	1 / 8	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP
21	-9.16	NULL	5 / 83	Glio Christensen_hypermethylated_in_secondary_glioblastoma
22	-8.98	NULL	2 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
23	-8.96	NULL	8 / 142	Glio Christensen_hypermethylated_in_grade2_oligodendroglioma
24	-8.88	NULL	1 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
25	-8.78	NULL	4 / 32	CC cell-cell adherens junction
26	-8.76	NULL	2 / 16	Glio VERHAAK_MES subtype
27	-8.71	NULL	29 / 572	Disease GUDJ_poriasis up
28	-8.69	NULL	1 / 10	BP surfactant homeostasis
29	-8.6	NULL	3 / 12	BP keratinocyte proliferation
30	-8.4	NULL	2 / 15	Pathw AcGUSTAFSON_PI3K_DN
31	-8.33	NULL	1 / 4	GSEA C2NIELSEN_LEIOMYOSARCOMA_DN
32	-8.25	NULL	6 / 70	BP cell junction assembly
33	-8.23	NULL	3 / 26	BP positive regulation of vasodilation
34	-8.22	NULL	2 / 22	BP bicarbonate transport
35	-8.04	NULL	6 / 110	Glio Christensen_hypermethylated_in_grade3_astrocytoma
36	-7.97	NULL	1 / 6	miRNA target-miR-126
37	-7.97	NULL	1 / 4	MMML C2SCIEJ_MMML_47
38	-7.92	NULL	2 / 11	GSEA C2MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
39	-7.81	NULL	1 / 4	miRNA target-miR-206
40	-7.63	NULL	2 / 25	BP one-carbon metabolic process

p-values

