

# GW\_109

## Global Summary

%DE = 0.14  
 # genes with  $fdr < 0.2$  = 1753 ( 1008 + / 745 - )  
 # genes with  $fdr < 0.1$  = 1565 ( 924 + / 641 - )  
 # genes with  $fdr < 0.05$  = 1291 ( 801 + / 490 - )  
 # genes with  $fdr < 0.01$  = 922 ( 596 + / 326 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.09  
 <fdr> = 0.86

## Global Genelist

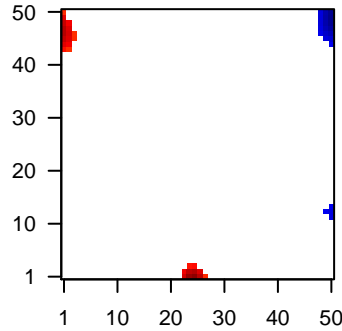
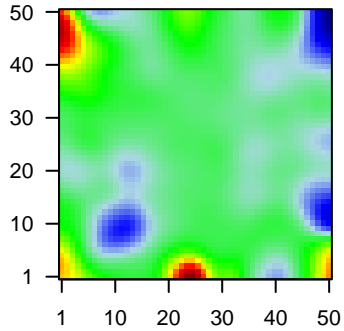
Rank	ID	log(FC)	fdr	p-value	Description
1	154664	-1.1	2e-16	2e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:11390]
2	58	3.73	2e-16	2e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:11390]
3	8644	-1.17	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:11390]
4	1109	-1.16	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:11390]
5	218	-1.16	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC Symbol;Acc:11390]
6	242	1.54	2e-16	2e-14	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Symbol;Acc:11390]
7	347	1.32	2e-16	2e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
8	151516	1.15	2e-16	2e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;Acc:11390]
9	445	-1.5	2e-16	2e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:758]
10	9212	1.2	2e-16	2e-14	45 x 48 aurora kinase B [Source:HGNC Symbol;Acc:11390]
11	655	-1.39	2e-16	2e-14	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:11390]
12	115749	-1.12	2e-16	2e-14	50 x 50 chromosome 12 open reading frame 56 [Source:HGNC Symbol;Acc:11390]
13	388115	1.24	2e-16	2e-14	26 x 2 chromosome 15 open reading frame 52 [Source:HGNC Symbol;Acc:11390]
14	284254	1.1	2e-16	2e-14	6 x 50 dynactin associated protein [Source:HGNC Symbol;Acc:2680]
15	339512	1.6	2e-16	2e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:11390]
16	260436	-1.51	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:11390]
17	760	1.67	2e-16	2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
18	857	1.12	2e-16	2e-14	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;Acc:11390]
19	875	-1.61	2e-16	2e-14	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:151]
20	6363	1.59	2e-16	2e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:11390]

## Global Geneset Analysis

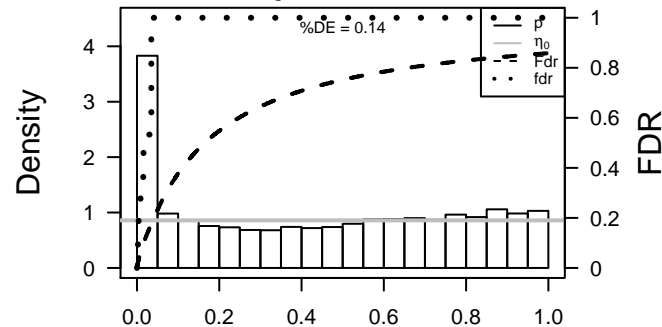
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	22.77	NULL	127	H.Tiss WIRTH_Muscle
2	19.25	NULL	36	BP muscle filament sliding
3	17.85	NULL	16	H.Tiss WIRTH_Hippocampus
4	17.73	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
5	16.79	NULL	135	H.Tiss WIRTH_Mucosa
6	13.14	NULL	15	CC MHC class II protein complex
7	12.9	NULL	44	MF structural constituent of muscle
8	12.52	NULL	76	BP epidermis development
9	12.36	NULL	21	CC cornified envelope
10	11.58	NULL	572	Disease GUDJ_psooriasis up
11	11.43	NULL	42	BP keratinization
12	10.96	NULL	37	CC sarcomere
13	10.89	NULL	21	CC clathrin-coated endocytic vesicle membrane
14	10.43	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
15	10.1	NULL	3	MMML C6S CIEJ_MMML 7
16	10.08	NULL	84	BP muscle contraction
17	9.96	NULL	312	BP immune response
18	9.78	NULL	12	CC myosin filament
19	9.71	NULL	53	BP keratinocyte differentiation
20	9.66	NULL	34	CC myofibril
<i>Underexpressed</i>				
1	-9.61	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
2	-9.38	NULL	7	MMML C6S CIEJ_MMML 5
3	-8.34	NULL	386	Chr Chr 22
4	-6.95	NULL	1033	Chr Chr 2
5	-6.7	NULL	20	Lymphoma OSOLOWSKI_red UP
6	-6.52	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
7	-6.33	NULL	34	Chr Chr Y
8	-6.17	NULL	296	MF oxidoreductase activity
9	-5.57	NULL	434	BP oxidation-reduction process
10	-5.31	NULL	390	BP metabolic process
11	-5.16	NULL	9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
12	-5.06	NULL	9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
13	-5.02	NULL	1318	CC mitochondrion
14	-4.97	NULL	8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
15	-4.9	NULL	10	GSEA C2REACTOME_TRANSLATION
16	-4.67	NULL	15	GSEA C2RIGIE_AMINO_ACID_DEPRIVATION
17	-4.65	NULL	3274	CC integral to membrane
18	-4.65	NULL	9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
19	-4.63	NULL	9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
20	-4.63	NULL	9	GSEA C2REACTOME_VIRAL_MRNA_TRANSLATION

Profile

Regulated Spots



p-values



# GW\_109

## Local Summary

%DE = 0.85  
 # metagenes = 11  
 # genes = 104  
 # genes in genesets = 104  
 # genes with  $fdr < 0.1$  = 85 ( 84 + / 1 - )  
 # genes with  $fdr < 0.05$  = 83 ( 82 + / 1 - )  
 # genes with  $fdr < 0.01$  = 72 ( 72 + / 0 - )

<r> metagenes = 0.99

<r> genes = 0.64

<FC> = 0.88

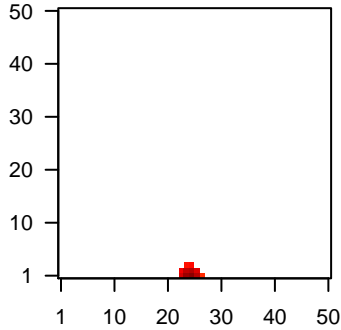
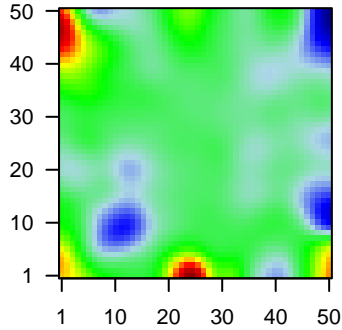
<shrinkage-t> = 30.8

<p-value> = 0

<fdr> = 0.22

Profile

Spot



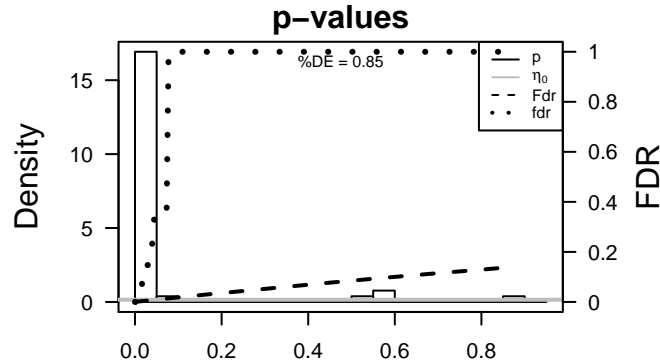
## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	58	3.73	2e-16	1e-16	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	388115	1.24	2e-16	1e-16	26 x 2 chromosome 15 open reading frame 52 [Source:HGNC Synt
3	1158	3.05	2e-16	1e-16	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	202333	1.56	2e-16	1e-16	25 x 1 cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14:
5	1917	1.45	2e-16	1e-16	25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
6	2027	1.8	2e-16	1e-16	25 x 1 enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
7	2273	1.68	2e-16	1e-16	25 x 1 four and a half LIM domains 1 [Source:HGNC Symbol;Acc:37
8	2318	1.48	2e-16	1e-16	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
9	283120	2.1	2e-16	1e-16	25 x 1 H19, imprinted maternally expressed transcript (non-protein i
10	126393	1.5	2e-16	1e-16	25 x 1 heat shock protein, alpha-crystallin-related, B6 [Source:HGNC
11	10324	2.23	2e-16	1e-16	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
12	4151	2.23	2e-16	1e-16	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
13	4604	1.51	2e-16	1e-16	25 x 1 myosin binding protein C, slow type [Source:HGNC Symbol;A
14	4606	1.29	2e-16	1e-16	25 x 1 myosin binding protein C, fast type [Source:HGNC Symbol;Ac
15	4620	2.94	2e-16	1e-16	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
16	4625	2.25	2e-16	1e-16	25 x 1 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
17	4632	1.6	2e-16	1e-16	25 x 1 myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
18	4633	1.59	2e-16	1e-16	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
19	29895	1.54	2e-16	1e-16	25 x 1 myosin light chain, phosphorylatable, fast skeletal muscle [So
20	8736	1.57	2e-16	1e-16	25 x 1 myomesin 1 [Source:HGNC Symbol;Acc:7613]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	63.45	NULL	57 / 127	H.Tiss WIRTH_Muscle
2	58.9	NULL	23 / 36	BP muscle filament sliding
3	57.92	NULL	11 / 16	H.Tiss WIRTH_Hippocampus
4	55.26	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
5	44.41	NULL	22 / 44	MF structural constituent of muscle
6	34.78	NULL	10 / 12	CC myosin filament
7	32.89	NULL	12 / 37	CC sarcomere
8	32.61	NULL	8 / 13	CC muscle myosin complex
9	30.29	NULL	23 / 84	BP muscle contraction
10	26.09	NULL	15 / 34	CC myofibril
11	25.79	NULL	8 / 14	CC contractile fiber
12	25.57	NULL	6 / 12	BP skeletal muscle contraction
13	24.67	NULL	8 / 16	CC M band
14	22.36	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
15	22.08	NULL	21 / 88	CC Z disc
16	20.1	NULL	6 / 18	BP regulation of muscle contraction
17	18.73	NULL	7 / 12	MF titin binding
18	18.46	NULL	9 / 37	BP cardiac muscle contraction
19	17.66	NULL	9 / 20	CC I band
20	17.39	NULL	3 / 15	Cancer BEN-PORATH_UP
21	17.29	NULL	7 / 15	BP striated muscle contraction
22	17.29	NULL	4 / 16	MF microfilament motor activity
23	16.86	NULL	4 / 14	BP adult heart development
24	16.27	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
25	16.18	NULL	2 / 10	BP creatine metabolic process
26	16.16	NULL	4 / 11	CC A band
27	15.96	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
28	15.96	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
29	15.61	NULL	7 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
30	15.52	NULL	3 / 13	CC pseudopodium
31	14.96	NULL	25 / 297	MF actin binding
32	14.95	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
33	14.79	NULL	2 / 14	GSEA C2BIOCARTA_UCALPAIN_PATHWAY
34	14.26	NULL	8 / 42	CC myosin complex
35	14.19	NULL	2 / 15	GSEA C2BIOCARTA_INTEGRIN_PATHWAY
36	13.37	NULL	1 / 12	GSEA C2BIOCARTA_NO1_PATHWAY
37	13.37	NULL	1 / 12	GSEA C2BIOCARTA_RAB_PATHWAY
38	13.33	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
39	13.33	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
40	13.17	NULL	5 / 26	BP ventricular cardiac muscle tissue morphogenesis



# GW\_109

## Local Summary

%DE = 0.78  
 # metagenes = 16  
 # genes = 267  
 # genes in genesets = 260

# genes with  $fdr < 0.1$  = 186 ( 163 + / 23 - )  
 # genes with  $fdr < 0.05$  = 168 ( 150 + / 18 - )  
 # genes with  $fdr < 0.01$  = 161 ( 145 + / 16 - )

<r> metagenes = 0.92  
 <r> genes = 0.39

<FC> = 0.51  
 <shrinkage-t> = 17.94  
 <p-value> = 0  
 <fdr> = 0.33

## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	8644	-1.17	2e-16	3e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
2	218	-1.16	2e-16	3e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
3	242	1.54	2e-16	3e-16	1 x 48 arachidonate 12-lipoxygenase, 12R type [Source:HGNC Syr
4	151516	1.15	2e-16	3e-16	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
5	760	1.67	2e-16	3e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
6	9022	1.36	2e-16	3e-16	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2
7	84518	1.73	2e-16	3e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
8	49860	1.96	2e-16	3e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
9	55894	1.34	2e-16	3e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
10	414325	1.51	2e-16	3e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
11	1823	1.17	2e-16	3e-16	1 x 45 desmocollin 1 [Source:HGNC Symbol;Acc:3035]
12	1828	2.03	2e-16	3e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
13	6785	1.14	2e-16	3e-16	2 x 46 ELOVL fatty acid elongase 4 [Source:HGNC Symbol;Acc:144
14	2171	1.29	2e-16	3e-16	1 x 46 fatty acid binding protein 5 (psoriasis-associated) [Source:HC
15	220832	1.25	2e-16	3e-16	1 x 45 fatty acid binding protein 5 pseudogene 3 [Source:HGNC Syr
16	128876	2.24	2e-16	3e-16	1 x 48 family with sequence similarity 83, member C [Source:HGNC
17	9982	1.31	2e-16	3e-16	1 x 47 fibroblast growth factor binding protein 1 [Source:HGNC Sym
18	2706	1.52	2e-16	3e-16	1 x 47 gap junction protein, beta 2, 26kDa [Source:HGNC Symbol;A
19	10804	1.8	2e-16	3e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
20	2877	-1.49	2e-16	3e-16	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Syr

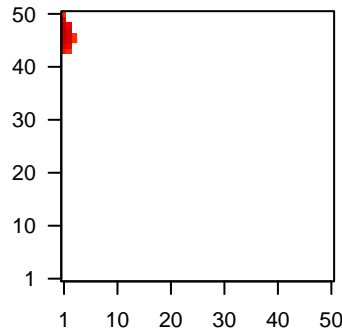
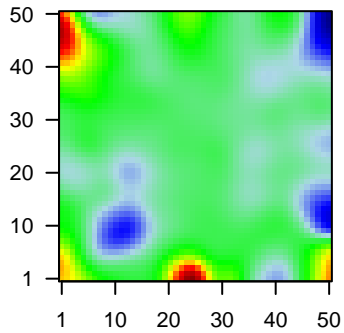
## Local Geneset Analysis

Overexpression

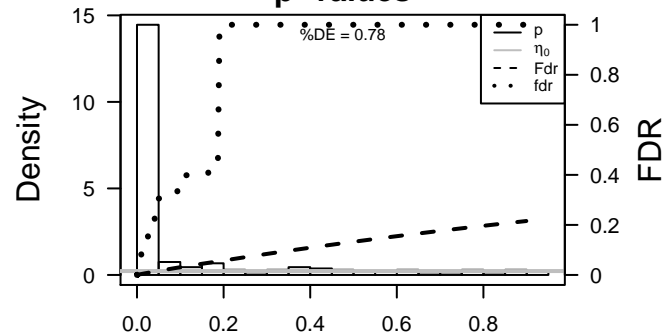
Rank	GSZ	p-value	#in/all	Geneset
1	39.3	NULL	76 / 135	H.Tiss WIRTH_Mucosa
2	33.67	NULL	18 / 21	CC cornified envelope
3	30.74	NULL	20 / 42	BP keratinization
4	28.14	NULL	26 / 76	BP epidermis development
5	23.79	NULL	24 / 53	BP keratinocyte differentiation
6	22.16	NULL	12 / 21	CC desmosome
7	18.2	NULL	101 / 572	Disease GUUDJ_psooriasis up
8	17.05	NULL	10 / 19	BP peptide cross-linking
9	16.18	NULL	13 / 44	CC keratin filament
10	14.95	NULL	21 / 82	CC intermediate filament
11	14.81	NULL	4 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
12	12.74	NULL	6 / 15	GSEA C2AIGNER_ZEB1_TARGETS
13	12.6	NULL	30 / 186	MF structural molecule activity
14	12.17	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
15	11.36	NULL	4 / 13	GSEA C2REACTOME_GAP_JUNCTION_TRAFFICKING
16	11.32	NULL	3 / 12	GSEA C2REACTOME_GAP_JUNCTION_ASSEMBLY
17	10.81	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
18	10.72	NULL	4 / 21	CC gap junction
19	10.5	NULL	3 / 13	BP intermediate filament cytoskeleton organization
20	9.96	NULL	3 / 15	CC connexon complex
21	9.73	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
22	9.6	NULL	3 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
23	9.05	NULL	2 / 11	MF gamma-catenin binding
24	8.98	NULL	7 / 38	BP epithelial cell differentiation
25	8.97	NULL	3 / 12	BP hemidesmosome assembly
26	8.72	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_24HR
27	8.7	NULL	4 / 25	BP response to zinc ion
28	8.23	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
29	8.09	NULL	11 / 82	MF structural constituent of cytoskeleton
30	7.92	NULL	3 / 10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING
31	7.51	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
32	7.37	NULL	4 / 37	CC lateral plasma membrane
33	7.36	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
34	7.33	NULL	3 / 17	BP morphogenesis of an epithelium
35	7.28	NULL	2 / 10	BP lipoxygenase pathway
36	7.16	NULL	3 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
37	7.05	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
38	6.92	NULL	4 / 10	MF RAGE receptor binding
39	6.81	NULL	1 / 7	GSEA C2KONDO_PROSTATE_CANCER_WITH_H3K27ME3
40	6.8	NULL	2 / 10	MF gap junction channel activity

Profile

Spot



p-values



# GW\_109

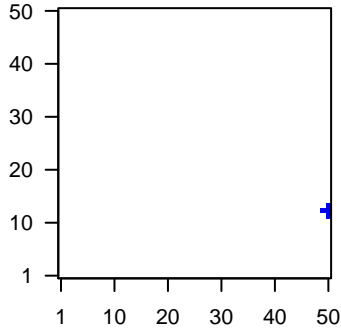
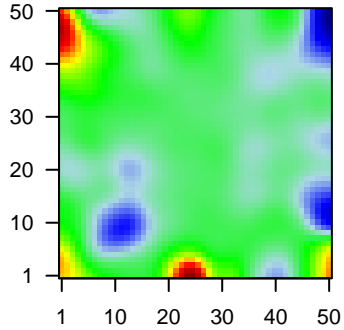
## Local Summary

%DE = 0.95  
 # metagenes = 4  
 # genes = 63  
 # genes in genesets = 63  
 # genes with  $fdr < 0.1 = 50$  ( 2 + / 48 - )  
 # genes with  $fdr < 0.05 = 50$  ( 2 + / 48 - )  
 # genes with  $fdr < 0.01 = 45$  ( 2 + / 43 - )

$\langle r \rangle$  metagenes = 0.98  
 $\langle r \rangle$  genes = 0.37  
 $\langle FC \rangle = -0.4$   
 $\langle \text{shrinkage-t} \rangle = -14.01$   
 $\langle p\text{-value} \rangle = 0$   
 $\langle fdr \rangle = 0.37$

Profile

Spot



## Local Genelist

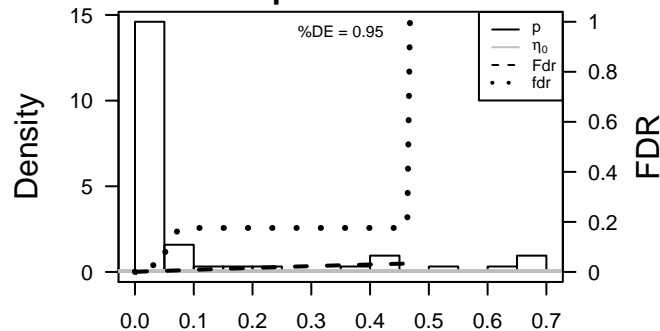
Rank	ID	log(FC)	fdr	p-value	Description
1	9249	-1.18	2e-16	2e-16	50 x 13 dehydrogenase/reductase (SDR family) member 3 [Source:HGNC Symbol;Acc:5021]
2	3169	-1.12	2e-16	2e-16	50 x 12 forkhead box A1 [Source:HGNC Symbol;Acc:5021]
3	2568	-1.28	2e-16	2e-16	50 x 13 gamma-aminobutyric acid (GABA) A receptor, pi [Source:HGNC Symbol;Acc:5021]
4	6920	-1.24	2e-16	2e-16	50 x 13 transcription elongation factor A (SII), 3 [Source:HGNC Symbol;Acc:5021]
5	634	-1.07	2e-15	7e-09	50 x 12 carcinoembryonic antigen-related cell adhesion molecule 1 (I) [Source:HGNC Symbol;Acc:5021]
6	51316	-0.8	2e-09	1e-08	50 x 13 placenta-specific 8 [Source:HGNC Symbol;Acc:19254]
7	9071	-0.78	6e-09	6e-08	50 x 12 claudin 10 [Source:HGNC Symbol;Acc:2033]
8	27134	-0.74	4e-08	6e-08	50 x 12 tight junction protein 3 [Source:HGNC Symbol;Acc:11829]
9	79085	-0.74	4e-08	6e-08	50 x 13 solute carrier family 25 (mitochondrial carrier; phosphate carrier) member 1 [Source:HGNC Symbol;Acc:19254]
10	260293	-0.73	6e-08	2e-07	50 x 14 cytochrome P450, family 4, subfamily X, polypeptide 1 [Source:HGNC Symbol;Acc:11829]
11	2139	-0.71	1e-07	1e-06	50 x 13 eyes absent homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11829]
12	55268	-0.67	5e-07	3e-06	50 x 14 enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:11829]
13	2205	0.65	1e-06	1e-05	50 x 13 Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide chain [Source:HGNC Symbol;Acc:11829]
14	55930	-0.61	6e-06	1e-05	50 x 13 myosin VC [Source:HGNC Symbol;Acc:7604]
15	7100	-0.6	8e-06	1e-05	50 x 14 toll-like receptor 5 [Source:HGNC Symbol;Acc:11851]
16	169166	-0.59	1e-05	4e-05	50 x 13 sorting nexin 31 [Source:HGNC Symbol;Acc:28605]
17	79695	-0.57	3e-05	4e-05	50 x 12 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase (UDP-GlcNAc 4-epimerase) [Source:HGNC Symbol;Acc:11829]
18	123036	-0.55	4e-05	4e-05	49 x 13 tandem C2 domains, nuclear [Source:HGNC Symbol;Acc:19254]
19	9423	0.55	5e-05	2e-04	50 x 13 netrin 1 [Source:HGNC Symbol;Acc:8029]
20	26751	-0.52	1e-04	3e-04	49 x 13 SH3 and SYLF domain containing 1 [Source:HGNC Symbol;Acc:11829]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-26.52	NULL	2 / 7	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_DN
2	-22.34	NULL	1 / 5	GSEA C2SMID_BREAST_CANCER_ERBB2_DN
3	-16.48	NULL	1 / 8	GSEA C2HEIDENBLAD_AMPLICON_12P11_12_UP
4	-15.64	NULL	1 / 7	GSEA C2NEBEN_AML_WITH_FLT3_OR_NRAS_UP
5	-14.68	NULL	2 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_BULK_UP
6	-14.36	NULL	1 / 10	MF GABA-A receptor activity
7	-13.65	NULL	1 / 8	GSEA C2HASLINGER_B CLL_WITH_6Q21_DELETION
8	-13.61	NULL	1 / 4	GSEA C2NICK_RESPONSE_TO_PROC_TREATMENT_UP
9	-13.55	NULL	1 / 11	GSEA C2IAZARI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
10	-13.26	NULL	2 / 15	BP hormone metabolic process
11	-13.24	NULL	2 / 20	Lymphocyte immune response 2
12	-13.01	NULL	2 / 10	GSEA C2YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
13	-12.52	NULL	1 / 10	BP prostate gland epithelium morphogenesis
14	-12.4	NULL	1 / 11	CC photoreceptor outer segment membrane
15	-12.36	NULL	1 / 12	BP regulation of DNA-dependent transcription, elongation
16	-12.28	NULL	2 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
17	-12.04	NULL	2 / 7	GSEA C2NAKAMURA_BRONCHIAL_AND_BRONCHIOLAR_EPITHELIA
18	-11.72	NULL	1 / 14	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_UP
19	-11.72	NULL	1 / 14	GSEA C2TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
20	-11.72	NULL	1 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
21	-11.25	NULL	1 / 15	GSEA C2SABATES_COLORECTAL_ADENOMA_UP
22	-11.25	NULL	1 / 15	GSEA C2LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
23	-11.21	NULL	1 / 11	GSEA C2FUJII_YBX1_TARGETS_UP
24	-11.21	NULL	1 / 13	GSEA C2ZIRN_TRETINOIN_RESPONSE_UP
25	-11.21	NULL	1 / 12	BP neuron fate specification
26	-11.06	NULL	2 / 8	GSEA C2NAKAMURA_LUNG_CANCER_DIFFERENTIATION_MARKERS
27	-10.83	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_UP
28	-10.83	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_UP
29	-10.83	NULL	1 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_UP
30	-10.83	NULL	1 / 16	GSEA C2DOANE_BREAST_CANCER_ESR1_DN
31	-10.83	NULL	1 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
32	-10.83	NULL	1 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
33	-10.83	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
34	-10.68	NULL	1 / 13	BP epithelial tube branching involved in lung morphogenesis
35	-10.68	NULL	1 / 13	GSEA C2WONG_ENDOMETRIUM_CANCER_UP
36	-10.39	NULL	1 / 5	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_DN
37	-10.29	NULL	1 / 15	GSEA C2ZIRN_TRETINOIN_RESPONSE_WT1_UP
38	-10.22	NULL	1 / 14	BP negative regulation of epithelial to mesenchymal transition
39	-10.21	NULL	2 / 16	GSEA C2BOYALT_LIVER_CANCER_SUBCLASS_G1_UP
40	-10.19	NULL	2 / 15	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN

p-values



# GW\_109

## Local Summary

%DE = 0.87  
 # metagenes = 18  
 # genes = 239  
 # genes in genesets = 238

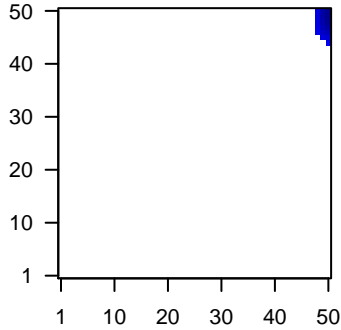
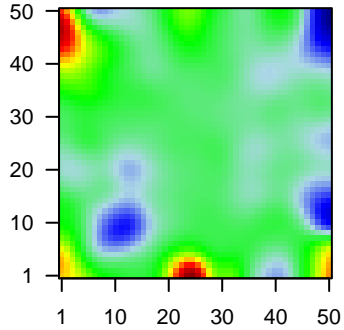
# genes with  $fdr < 0.1 = 166$  ( 5 + / 161 - )  
 # genes with  $fdr < 0.05 = 144$  ( 4 + / 140 - )  
 # genes with  $fdr < 0.01 = 98$  ( 2 + / 96 - )

<r> metagenes = 0.96  
 <r> genes = 0.26

<FC> = -0.38  
 <shrinkage-t> = -13.3  
 <p-value> = 0  
 <fdr> = 0.5

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	154664	-1.1	2e-16	5e-16	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:15747]
2	445	-1.5	2e-16	5e-16	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:7512]
3	655	-1.39	2e-16	5e-16	50 x 50 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1034]
4	115749	-1.12	2e-16	5e-16	50 x 50 chromosome 12 open reading frame 56 [Source:HGNC Symt]
5	339512	1.6	2e-16	5e-16	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symt]
6	875	-1.61	2e-16	5e-16	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:1512]
7	3880	-2.66	2e-16	5e-16	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
8	3856	-1.28	2e-16	5e-16	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
9	4922	-1.16	2e-16	5e-16	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
10	139728	-1.42	2e-16	5e-16	49 x 49 pregnancy up-regulated nonubiquitous CaM kinase [Source:HGNC Symbol;Acc:15974]
11	23321	-1.12	2e-16	5e-16	50 x 50 tripartite motif containing 2 [Source:HGNC Symbol;Acc:15974]
12	256764	-1.75	2e-16	5e-16	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
13	7546	-1.18	2e-16	5e-16	48 x 50 Zic family member 2 [Source:HGNC Symbol;Acc:12873]
14	3790	-1.07	2e-15	7e-14	50 x 50 potassium voltage-gated channel, delayed-rectifier, subfamily A member 1 [Source:HGNC Symbol;Acc:12873]
15	4953	-1.06	4e-15	4e-12	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
16	286676	-1	1e-13	5e-12	50 x 49 immunoglobulin-like domain containing receptor 1 [Source:HGNC Symbol;Acc:12873]
17	200634	-0.98	3e-13	1e-11	50 x 49 keratinocyte associated protein 3 [Source:HGNC Symbol;Acc:12873]
18	1056	-0.97	7e-13	2e-11	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
19	7345	-0.95	1e-12	2e-11	50 x 46 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) 1 [Source:HGNC Symbol;Acc:12873]
20	5625	-0.95	2e-12	1e-10	50 x 48 proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Acc:12873]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-17.92	NULL	3 / 8	GSEA C2JUCDX2_TARGETS_DN
2	-13.07	NULL	4 / 13	BP regulation of blood vessel size
3	-12.83	NULL	1 / 11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN
4	-12.46	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
5	-11.68	NULL	1 / 13	GSEA C2CHEN_LUNG_CANCER_SURVIVAL
6	-11.45	NULL	2 / 12	GSEA C2KAYO_AGING_MUSCLE_UP
7	-11.23	NULL	1 / 5	GSEA C2NIELSEN_SCHWANNOMA_DN
8	-11.2	NULL	1 / 14	GSEA C2JIANG_SILENCED_BY_METHYLATION_UP
9	-11.12	NULL	3 / 15	GSEA C2JDAYAKUMAR_MED1_TARGETS_UP
10	-11.04	NULL	3 / 12	GSEA C2HELLER_SILENCED_BY_METHYLATION_DN
11	-11.02	NULL	5 / 15	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
12	-10.94	NULL	2 / 13	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_UP
13	-10.86	NULL	1 / 6	GSEA C2SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
14	-10.77	NULL	1 / 15	GSEA C2E_SKI_TARGETS_UP
15	-10.77	NULL	1 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
16	-10.62	NULL	4 / 19	BP cellular amino acid biosynthetic process
17	-10.48	NULL	2 / 14	GSEA C2KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
18	-10.38	NULL	1 / 16	CC dystrophin-associated glycoprotein complex
19	-10.38	NULL	1 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_UP
20	-10.09	NULL	2 / 15	GSEA C2KRIGE_AMINO_ACID_DEPRIVATION
21	-9.94	NULL	12 / 167	BP cellular nitrogen compound metabolic process
22	-9.73	NULL	2 / 16	GSEA C2GARASHI_ATF4_TARGETS_DN
23	-9.73	NULL	2 / 16	GSEA C2GAJATE_RESPONSE_TO TRABECTEDIN_UP
24	-9.71	NULL	1 / 18	CC costamere
25	-9.58	NULL	3 / 16	GSEA C2KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
26	-9.2	NULL	1 / 8	GSEA C2BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP
27	-8.89	NULL	1 / 21	BP sarcomere organization
28	-8.4	NULL	2 / 16	GSEA C2GOUYER_TATI_TARGETS_DN
29	-8.3	NULL	9 / 34	BP glutathione metabolic process
30	-8.23	NULL	2 / 15	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
31	-8.18	NULL	3 / 31	BP response to nutrient levels
32	-8.09	NULL	2 / 13	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT
33	-7.92	NULL	3 / 15	GSEA C2KEGG_ARGININE_AND_PROLINE_METABOLISM
34	-7.9	NULL	1 / 8	GSEA C2MCCABE_HOXC6_TARGETS_UP
35	-7.9	NULL	2 / 14	GSEA C2KEGG_CYSSTEINE_AND_METHIONINE_METABOLISM
36	-7.79	NULL	2 / 18	BP superoxide metabolic process
37	-7.65	NULL	1 / 11	GSEA C2BENPORATH_MYC_TARGETS_WITH_EBOX
38	-7.65	NULL	1 / 11	GSEA C2TARTE_PLASMA_CELL_VS_PLASMABLAST_UP
39	-7.65	NULL	1 / 11	GSEA C2HELLER_HDAC_TARGETS_DN
40	-7.65	NULL	1 / 11	GSEA C2HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN

p-values

