

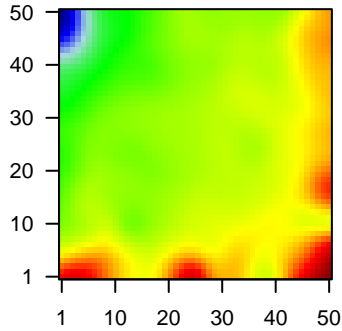
# GW\_175

## Global Summary

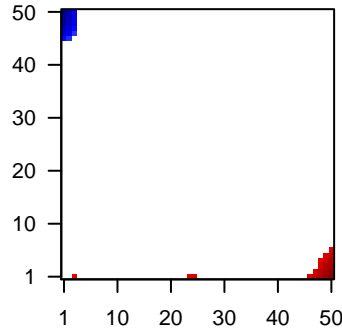
%DE = 0.15  
 # genes with fdr < 0.2 = 2029 ( 1169 + / 860 - )  
 # genes with fdr < 0.1 = 1693 ( 991 + / 702 - )  
 # genes with fdr < 0.05 = 1319 ( 775 + / 544 - )  
 # genes with fdr < 0.01 = 1020 ( 599 + / 421 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.07  
 <fdr> = 0.85

Profile



Regulated Spots



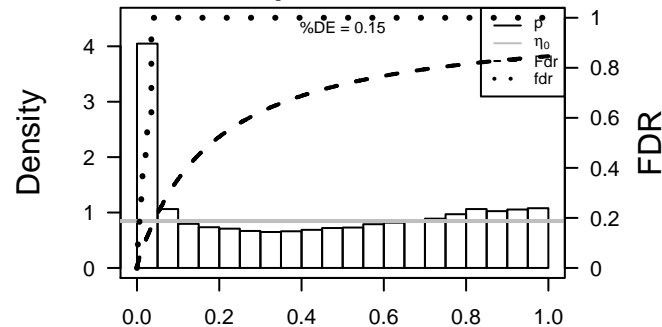
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	58	3.82	2e-16	2e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.47	2e-16	2e-14	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	100	1.53	2e-16	2e-14	30 x 1 adenosine deaminase [Source:HGNC Symbol;Acc:186]
4	8745	1.82	2e-16	2e-14	50 x 50 ADAM metallopeptidase domain 23 [Source:HGNC Symbol;A
5	131	-2.43	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
6	165	1.43	2e-16	2e-14	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
7	113146	-1.45	2e-16	2e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
8	57016	-2.82	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
9	441282	-2.26	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S]
10	216	2.28	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
11	218	-1.82	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
12	501	-1.46	2e-16	2e-14	6 x 46 aldehyde dehydrogenase 7 family, member A1 [Source:HGNC
13	55107	1.74	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC
14	341	1.78	2e-16	2e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
15	348	1.58	2e-16	2e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
16	22809	1.32	2e-16	2e-14	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:7]
17	25805	1.59	2e-16	2e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC S]
18	8424	1.55	2e-16	2e-14	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
19	618	1.49	2e-16	2e-14	39 x 1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
20	664	-1.7	2e-16	2e-14	2 x 43 BCL2/adenovirus E1B 19kDa interacting protein 3 [Source:H

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.64	NULL	127	H.Tiss WIRTH_Muscle
2	14.64	NULL	36	BP muscle filament sliding
3	13.97	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
4	13.48	NULL	16	H.Tiss WIRTH_Hippocampus
5	13.28	NULL	190	CC extracellular matrix
6	11.89	NULL	43	MF chemokine activity
7	11.85	NULL	312	BP immune response
8	11.43	NULL	44	MF structural constituent of muscle
9	10.59	NULL	250	LymphoortENZ_Stromal signature 1
10	10.38	NULL	553	Cancer Lembcke_Colonc Inflammation
11	10.13	NULL	683	CC extracellular space
12	9.04	NULL	37	CC sarcomere
13	8.94	NULL	242	BP extracellular matrix organization
14	8.68	NULL	162	CC external side of plasma membrane
15	8.38	NULL	417	H.Tiss WIRTH_Immune system
16	8.26	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
17	8.21	NULL	15	CC MHC class II protein complex
18	8.12	NULL	57	MF extracellular matrix structural constituent
19	8.1	NULL	69	BP extracellular matrix disassembly
20	8.1	NULL	957	Chr Chr 11
<i>Underexpressed</i>				
1	-30.44	NULL	135	H.Tiss WIRTH_Mucosa
2	-16.48	NULL	572	Disease GUDJ_psooriasis up
3	-16.02	NULL	21	CC cornified envelope
4	-14.88	NULL	42	BP keratinization
5	-13.29	NULL	53	BP keratinocyte differentiation
6	-12.99	NULL	76	BP epidermis development
7	-8.99	NULL	519	Chr Chr 14
8	-8.59	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
9	-8.31	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
10	-8.14	NULL	7	MMML C2SCIEJ_MMML 5
11	-8.05	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
12	-7.93	NULL	15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	-7.76	NULL	19	BP peptide cross-linking
14	-7.6	NULL	44	CC keratin filament
15	-7.54	NULL	504	Chr Chr 15
16	-7.32	NULL	1720	Chr Chr 1
17	-6.44	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
18	-6.43	NULL	82	CC intermediate filament
19	-6.27	NULL	38	BP epithelial cell differentiation
20	-6.16	NULL	34	Chr Chr Y

p-values



# GW\_175

## Local Summary

%DE = 0.87  
 # metagenes = 1  
 # genes = 34  
 # genes in genesets = 34  
 # genes with  $fdr < 0.1 = 25$  ( 25 + / 0 - )  
 # genes with  $fdr < 0.05 = 25$  ( 25 + / 0 - )  
 # genes with  $fdr < 0.01 = 21$  ( 21 + / 0 - )

<r> metagenes = NA

<r> genes = 0.63

<FC> = 0.64

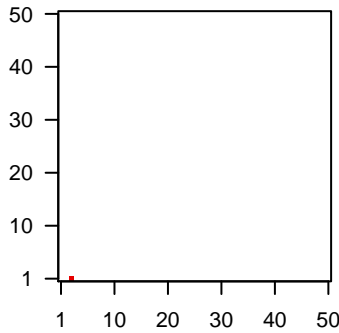
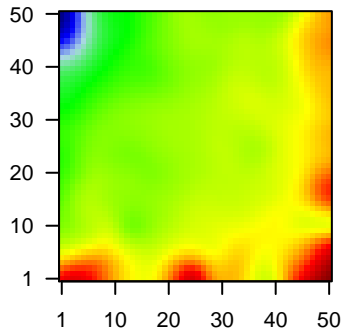
<shrinkage-t> = 22.35

<p-value> = 0

<fdr> = 0.27

Profile

Spot



## Local Genelist

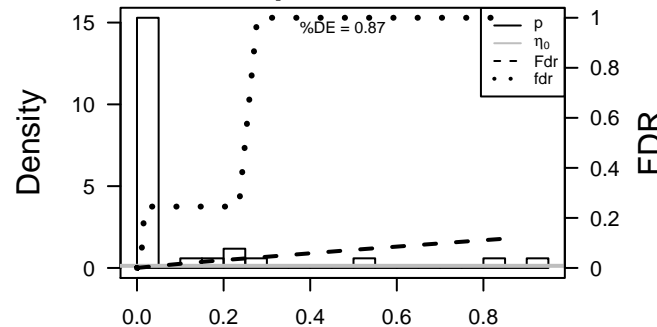
Rank	ID	log(FC)	fdr	p-value	Description
1	165	1.43	2e-16	5e-16	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
2	4320	2.57	2e-16	5e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Sy
3	9315	1.1	1e-11	2e-10	3 x 1 neuronal regeneration related protein [Source:HGNC Symbol
4	633	0.98	6e-11	6e-10	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
5	1490	1.03	2e-10	9e-10	3 x 1 connective tissue growth factor [Source:HGNC Symbol;Acc:2
6	1462	1.01	4e-10	4e-08	3 x 1 versican [Source:HGNC Symbol;Acc:2464]
7	25878	0.93	1e-08	9e-07	3 x 1 matrix-remodelling associated 5 [Source:HGNC Symbol;Acc:
8	11167	0.84	2e-07	4e-06	3 x 1 follistatin-like 1 [Source:HGNC Symbol;Acc:3972]
9	23452	0.77	2e-06	4e-06	3 x 1 angiotensin-like 2 [Source:HGNC Symbol;Acc:490]
10	5999	0.77	2e-06	7e-06	3 x 1 regulator of G-protein signaling 4 [Source:HGNC Symbol;Acc:
11	7168	0.74	5e-06	7e-06	3 x 1 tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:12010]
12	6678	0.74	5e-06	2e-05	3 x 1 secreted protein, acidic, cysteine-rich (osteonectin) [Source:J
13	6423	0.72	9e-06	4e-05	3 x 1 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:
14	115908	0.68	2e-05	4e-05	3 x 1 collagen triple helix repeat containing 1 [Source:HGNC Symb
15	5159	0.68	3e-05	5e-05	3 x 1 platelet-derived growth factor receptor, beta polypeptide [Sou
16	57124	0.65	5e-05	5e-05	3 x 1 CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
17	3490	0.64	7e-05	5e-05	3 x 1 insulin-like growth factor binding protein 7 [Source:HGNC Sy
18	7169	0.64	7e-05	5e-05	3 x 1 tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
19	80781	0.64	8e-05	5e-04	3 x 1 collagen, type XVIII, alpha 1 [Source:HGNC Symbol;Acc:219]
20	1009	0.58	3e-04	5e-04	3 x 1 cadherin 11, type 2, OB-cadherin (osteoblast) [Source:HGNC

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	56.9	NULL	3 / 5	GSEA C2COLLER_MYC_TARGETS_DN
2	45.77	NULL	1 / 2	miRNA target-18
3	36.56	NULL	1 / 3	GSEA C2KONDO_HYPOXIA
4	28.44	NULL	2 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
5	27.63	NULL	1 / 11	GSEA C2ERRECCHIA_RESPONSE_TO_TGFB1_C5
6	22.95	NULL	4 / 16	MMML C2SCIEJ_MMML_1
7	22.6	NULL	3 / 15	GSEA C2EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
8	22.25	NULL	2 / 11	BP dermatan sulfate biosynthetic process
9	22.24	NULL	3 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
10	20.7	NULL	19 / 250	LymphocyteStromal signature 1
11	20.37	NULL	1 / 5	GSEA C2VERNELL_RETINOBLASTOMA_PATHWAY_DN
12	20.12	NULL	11 / 190	CC extracellular matrix
13	20.11	NULL	3 / 15	GSEA C2INDGREN_BLADEER_CANCER_HIGH_RECURRENCE
14	20.02	NULL	2 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
15	18.93	NULL	2 / 14	BP chondroitin sulfate catabolic process
16	18.53	NULL	1 / 6	GSEA C2MAINA_HYPOXIA_VHL_TARGETS_UP
17	18.44	NULL	3 / 19	MF extracellular matrix binding
18	18.42	NULL	2 / 16	GSEA C2NEWMAN_ERCC6_TARGETS_DN
19	18.16	NULL	2 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
20	17.64	NULL	1 / 9	GSEA C2ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_UP
21	17.36	NULL	1 / 6	GSEA C2BENPORATH_OCT4_TARGETS
22	17.36	NULL	1 / 6	GSEA C2BENPORATH_NOS_TARGETS
23	17.35	NULL	2 / 10	GSEA C2MAINA_VHL_TARGETS_UP
24	17.31	NULL	3 / 63	CC Golgi lumen
25	16.69	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27
26	16.57	NULL	2 / 37	BP collagen fibril organization
27	16.12	NULL	2 / 14	GSEA C2MAINA_VHL_TARGETS_DN
28	16.12	NULL	2 / 15	Cancer LIU_PROSTATE_CANCER_DN
29	16	NULL	2 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
30	16	NULL	2 / 13	GSEA C2INDGREN_BLADEER_CANCER_CLUSTER_2B
31	15.83	NULL	3 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
32	15.41	NULL	2 / 15	GSEA C2BROWNE_HCMV_INFECTION_20HR_DN
33	15.41	NULL	2 / 15	GSEA C2DASU_IL6_SIGNALING_SCAR_DN
34	15.32	NULL	1 / 7	GSEA C2TUNODA_CISPLATIN_RESISTANCE_UP
35	15.21	NULL	8 / 183	CC proteinaceous extracellular matrix
36	14.81	NULL	2 / 10	BP positive regulation of endothelial cell apoptotic process
37	14.78	NULL	2 / 16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
38	14.78	NULL	2 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
39	14.69	NULL	2 / 15	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
40	14.61	NULL	2 / 21	MF glycosaminoglycan binding

p-values



# GW\_175

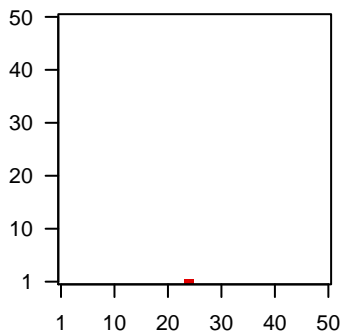
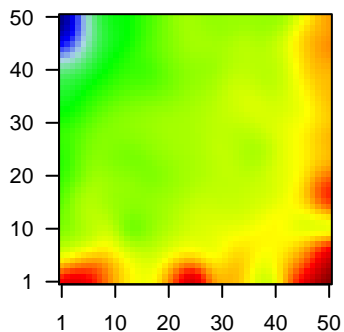
## Local Summary

%DE = 0.97  
 # metagenes = 2  
 # genes = 79  
 # genes in genesets = 79  
 # genes with  $fdr < 0.1 = 76$  ( 74 + / 2 - )  
 # genes with  $fdr < 0.05 = 76$  ( 74 + / 2 - )  
 # genes with  $fdr < 0.01 = 63$  ( 63 + / 0 - )

<r> metagenes = 1  
 <r> genes = 0.69  
 <FC> = 0.94  
 <shrinkage-t> = 32.94  
 <p-value> = 0  
 <fdr> = 0.21

Profile

Spot



## Local Genelist

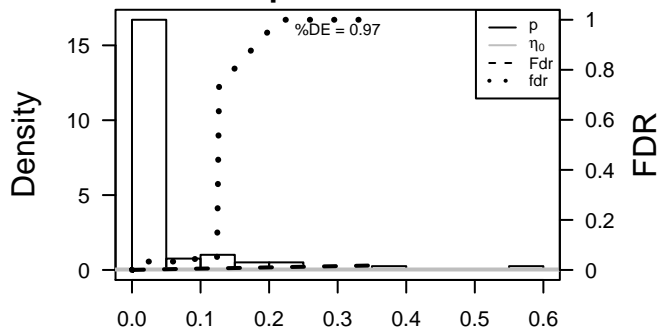
Rank	ID	log(FC)	fdr	p-value	Description
1	58	3.82	2e-16	3e-17	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.47	2e-16	3e-17	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1158	2.39	2e-16	3e-17	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
4	1917	1.56	2e-16	3e-17	25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HG
5	2027	1.34	2e-16	3e-17	25 x 1 enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:3354]
6	2318	1.82	2e-16	3e-17	25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]
7	10324	1.8	2e-16	3e-17	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
8	4151	2.26	2e-16	3e-17	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
9	4620	2.46	2e-16	3e-17	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
10	4625	1.47	2e-16	3e-17	25 x 1 myosin, heavy chain 7, cardiac muscle, beta [Source:HGNC
11	4632	1.39	2e-16	3e-17	25 x 1 myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
12	4633	1.85	2e-16	3e-17	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
13	9499	1.51	2e-16	3e-17	25 x 1 myotilin [Source:HGNC Symbol;Acc:12399]
14	4703	1.77	2e-16	3e-17	25 x 1 nebulin [Source:HGNC Symbol;Acc:7720]
15	6588	3.16	2e-16	3e-17	25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]
16	8557	1.85	2e-16	3e-17	25 x 1 titin-cap [Source:HGNC Symbol;Acc:11610]
17	7060	1.85	2e-16	3e-17	25 x 1 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]
18	7125	1.6	2e-16	3e-17	25 x 1 troponin C type 2 (fast) [Source:HGNC Symbol;Acc:11944]
19	29895	1.29	2e-15	2e-15	25 x 1 myosin light chain, phosphorylatable, fast skeletal muscle [So
20	202333	1.28	2e-15	1e-14	25 x 1 cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:14

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	64.17	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
2	60.7	NULL	21 / 36	BP muscle filament sliding
3	57.23	NULL	46 / 127	H.Tiss WIRTH_Muscle
4	57.11	NULL	9 / 16	H.Tiss WIRTH_Hippocampus
5	42.69	NULL	19 / 44	MF structural constituent of muscle
6	37.51	NULL	8 / 12	CC myosin filament
7	35.34	NULL	11 / 37	CC sarcomere
8	29.76	NULL	6 / 13	CC muscle myosin complex
9	27.73	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
10	27.33	NULL	19 / 84	BP muscle contraction
11	26.32	NULL	7 / 14	CC contractile fiber
12	26.19	NULL	6 / 12	BP skeletal muscle contraction
13	24.88	NULL	11 / 34	CC myofibril
14	24.55	NULL	1 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
15	24.41	NULL	9 / 20	CC I band
16	23.59	NULL	3 / 15	Cancer BEN-PORATH_UP
17	22.46	NULL	9 / 37	BP cardiac muscle contraction
18	22.42	NULL	7 / 16	CC M band
19	21.41	NULL	17 / 88	CC Z disc
20	19.88	NULL	2 / 10	BP heart contraction
21	19.81	NULL	5 / 12	MF titin binding
22	19.07	NULL	2 / 20	MF myosin binding
23	18.77	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
24	18.77	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
25	18.66	NULL	6 / 18	BP regulation of muscle contraction
26	17.96	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
27	17.55	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
28	16.37	NULL	2 / 14	GSEA C2BIOCARTA_UCALPAIN_PATHWAY
29	16.25	NULL	4 / 11	CC A band
30	15.84	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
31	15.84	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
32	15.71	NULL	5 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
33	15.69	NULL	2 / 15	GSEA C2BIOCARTA_INTEGRIN_PATHWAY
34	15.66	NULL	1 / 12	GSEA C2BIOCARTA_NO1_PATHWAY
35	15.66	NULL	1 / 12	GSEA C2BIOCARTA_RAB_PATHWAY
36	15.33	NULL	3 / 16	MF microfilament motor activity
37	15.05	NULL	2 / 12	BP muscle fiber development
38	14.9	NULL	1 / 13	GSEA C2NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP
39	14.9	NULL	1 / 13	GSEA C2BIOCARTA_SALMONELLA_PATHWAY
40	14.9	NULL	1 / 13	GSEA C2BIOCARTA_NFAT_PATHWAY

p-values



# GW\_175

## Local Summary

%DE = 0.81  
 # metagenes = 18  
 # genes = 312  
 # genes in genesets = 310

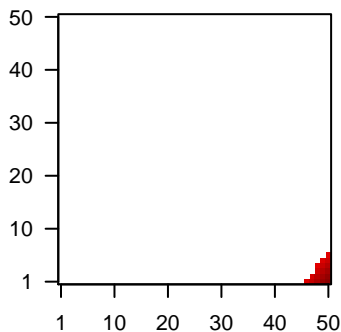
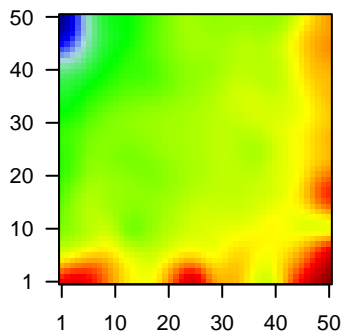
# genes with  $fdr < 0.1 = 210$  ( 208 + / 2 - )  
 # genes with  $fdr < 0.05 = 204$  ( 202 + / 2 - )  
 # genes with  $fdr < 0.01 = 162$  ( 161 + / 1 - )

<r> metagenes = 0.97  
 <r> genes = 0.53

<FC> = 0.57  
 <shrinkage-t> = 19.86  
 <p-value> = 0  
 <fdr> = 0.38

Profile

Spot



## Local Genelist

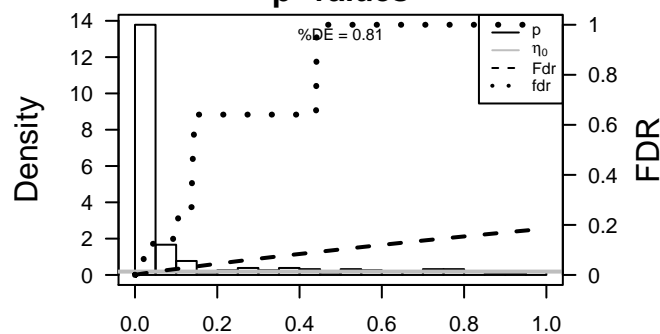
Rank	ID	log(FC)	fdr	p-value	Description
1	341	1.78	2e-16	5e-16	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
2	348	1.58	2e-16	5e-16	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
3	713	1.85	2e-16	5e-16	50 x 1 complement component 1, q subcomponent, B chain [Source
4	714	1.54	2e-16	5e-16	50 x 1 complement component 1, q subcomponent, C chain [Source
5	6364	1.99	2e-16	5e-16	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
6	6352	1.65	2e-16	5e-16	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
7	914	1.44	2e-16	5e-16	49 x 1 CD2 molecule [Source:HGNC Symbol;Acc:1639]
8	10563	1.48	2e-16	5e-16	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
9	4283	2.16	2e-16	5e-16	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
10	1593	1.44	2e-16	5e-16	50 x 3 cytochrome P450, family 27, subfamily A, polypeptide 1 [Sou
11	1805	1.53	2e-16	5e-16	50 x 5 dermatopontin [Source:HGNC Symbol;Acc:3011]
12	5168	1.79	2e-16	5e-16	50 x 2 ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc
13	3002	1.79	2e-16	5e-16	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
14	2999	1.38	2e-16	5e-16	47 x 1 granzyme H (cathepsin G-like 2, protein h-CCPX) [Source:H
15	3003	1.39	2e-16	5e-16	49 x 1 granzyme K (granzyme 3; tryptase II) [Source:HGNC Symbol
16	3109	1.32	2e-16	5e-16	50 x 1 major histocompatibility complex, class II, DM beta [Source:H
17	3113	1.4	2e-16	5e-16	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source
18	3122	1.38	2e-16	5e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:t
19	4069	1.82	2e-16	5e-16	50 x 2 lysozyme [Source:HGNC Symbol;Acc:6740]
20	4256	1.53	2e-16	5e-16	50 x 6 matrix Gla protein [Source:HGNC Symbol;Acc:7060]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.94	NULL	12 / 15	CC MHC class II protein complex
2	22.55	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
3	22.4	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
4	22	NULL	54 / 312	BP immune response
5	21.17	NULL	89 / 417	H.Tiss WIRTH_Immune system
6	19.12	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
7	18.34	NULL	7 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
8	18.34	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
9	17.66	NULL	15 / 47	BP antigen processing and presentation
10	17.37	NULL	2 / 4	MMML C6SCIEJ_MMMML_2
11	16.37	NULL	9 / 43	MF chemokine activity
12	15.86	NULL	99 / 553	Cancer Lembcke_Colonc Inflammation
13	15.62	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
14	15.32	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
15	15.21	NULL	5 / 14	GSEA C2WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER
16	15.19	NULL	4 / 16	BP cytolysis
17	15.16	NULL	15 / 60	BP T cell costimulation
18	15.12	NULL	5 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
19	15.12	NULL	43 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
20	15.12	NULL	43 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
21	15.12	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
22	15.12	NULL	43 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
23	15.1	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
24	14.74	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
25	14.58	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
26	14.17	NULL	5 / 13	Cancer GENTLES_modul18
27	14.15	NULL	4 / 11	GSEA C2APPEL_IMATINIB_RESPONSE
28	14	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
29	13.55	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
30	13.27	NULL	2 / 7	GSEA C2BIOCARTA_COMP_PATHWAY
31	13.25	NULL	28 / 162	CC external side of plasma membrane
32	12.75	NULL	3 / 15	GSEA C2HAHTOLA_SEZARY_SYNDROM_DN
33	12.53	NULL	7 / 28	CC transport vesicle membrane
34	12.44	NULL	8 / 16	GSEA C2SU_THYMUS
35	12.35	NULL	5 / 12	BP dendritic cell chemotaxis
36	12.32	NULL	9 / 35	CC trans-Golgi network membrane
37	12.32	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
38	12.29	NULL	2 / 8	GSEA C2BIOCARTA_CLASSIC_PATHWAY
39	12.29	NULL	2 / 8	GSEA C2REACTOME_COMPLEMENT_CASCADE
40	12.29	NULL	2 / 8	GSEA C2REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT

p-values



# GW\_175

## Local Summary

%DE = 0.97  
 # metagenes = 17  
 # genes = 233  
 # genes in genesets = 227

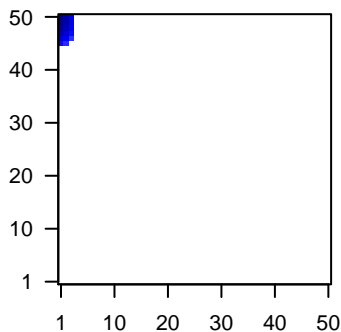
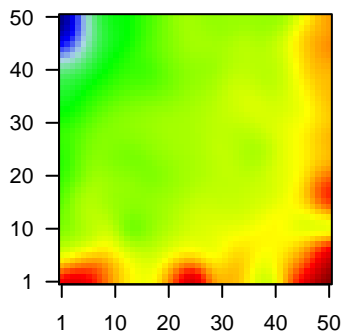
# genes with  $fdr < 0.1$  = 221 ( 6 + / 215 - )  
 # genes with  $fdr < 0.05$  = 221 ( 6 + / 215 - )  
 # genes with  $fdr < 0.01$  = 215 ( 6 + / 209 - )

<r> metagenes = 0.95  
 <r> genes = 0.44

<FC> = -1.09  
 <shrinkage-t> = -38.55  
 <p-value> = 0  
 <fdr> = 0.06

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.43	2e-16	2e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.82	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-2.26	2e-16	2e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	218	-1.82	2e-16	2e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	8424	1.55	2e-16	2e-17	3 x 48 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma
6	387695	-1.87	2e-16	2e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
7	64073	-1.81	2e-16	2e-17	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt
8	375791	-1.86	2e-16	2e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
9	84290	-1.55	2e-16	2e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
10	4680	-1.77	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
11	84518	-2.22	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
12	54544	-1.43	2e-16	2e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
13	49860	-1.82	2e-16	2e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
14	1672	-1.68	2e-16	2e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
15	55894	-1.57	2e-16	2e-17	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
16	414325	-2.26	2e-16	2e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
17	1673	-1.78	2e-16	2e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
18	93099	-1.43	2e-16	2e-17	1 x 47 dermokine [Source:HGNC Symbol;Acc:25063]
19	1824	-1.46	2e-16	2e-17	1 x 48 desmocollin 2 [Source:HGNC Symbol;Acc:3036]
20	1828	-1.55	2e-16	2e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-61.52	NULL	83 / 135	H.Tiss WIRTH_Mucosa
2	-36.98	NULL	18 / 21	CC cornified envelope
3	-32.45	NULL	97 / 572	Disease GUDJ_pсориазис up
4	-31.09	NULL	19 / 42	BP keratinization
5	-29.68	NULL	24 / 53	BP keratinocyte differentiation
6	-26.31	NULL	23 / 76	BP epidermis development
7	-19.96	NULL	10 / 19	BP peptide cross-linking
8	-19.04	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
9	-17.39	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
10	-16.98	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
11	-15.11	NULL	12 / 21	CC desmosome
12	-14.76	NULL	6 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
13	-14.06	NULL	10 / 44	CC keratin filament
14	-13.68	NULL	16 / 82	CC intermediate filament
15	-13	NULL	23 / 186	MF structural molecule activity
16	-12.86	NULL	5 / 10	MF RAGE receptor binding
17	-12.55	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
18	-12.49	NULL	10 / 52	BP negative regulation of endopeptidase activity
19	-12.33	NULL	7 / 29	BP regulation of proteolysis
20	-11.97	NULL	13 / 79	MF serine-type endopeptidase inhibitor activity
21	-11.69	NULL	4 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
22	-11.33	NULL	4 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN
23	-11.12	NULL	57 / 1182	CC extracellular region
24	-11.1	NULL	7 / 38	BP epithelial cell differentiation
25	-11.08	NULL	6 / 13	BP negative regulation of peptidase activity
26	-11.02	NULL	3 / 13	BP intermediate filament cytoskeleton organization
27	-10.98	NULL	5 / 15	GSEA C2AIGNER_ZEB1_TARGETS
28	-10.73	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
29	-10.54	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
30	-10.32	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
31	-10.15	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
32	-10.1	NULL	5 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
33	-9.91	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
34	-9.9	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
35	-9.89	NULL	3 / 12	BP cellular aldehyde metabolic process
36	-9.89	NULL	4 / 27	BP response to bacterium
37	-9.85	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
38	-9.75	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
39	-9.67	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
40	-9.24	NULL	5 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN

p-values

