

# GW\_147

## Global Summary

%DE = 0.16  
 # genes with  $fdr < 0.2$  = 2185 ( 1157 + / 1028 - )  
 # genes with  $fdr < 0.1$  = 1924 ( 1039 + / 885 - )  
 # genes with  $fdr < 0.05$  = 1601 ( 883 + / 718 - )  
 # genes with  $fdr < 0.01$  = 1192 ( 674 + / 518 - )

# genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.06  
 <fdr> = 0.84

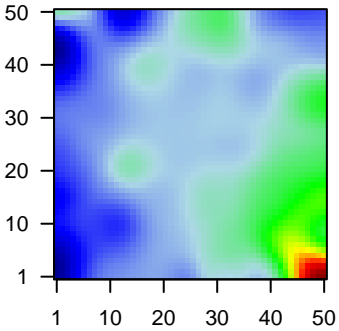
## Global Genelist

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	9744	1.46	2e-16	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [S
2	27299	1.6	2e-16	ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]
3	131	1.53	2e-16	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	133	-1.65	2e-16	adrenomedullin [Source:HGNC Symbol;Acc:259]
5	1646	-1.49	2e-16	aldo-keto reductase family 1, member C2 [Source:HGNC Sy
6	8644	-2.44	2e-16	aldo-keto reductase family 1, member C3 [Source:HGNC Sy
7	1109	-2.59	2e-16	aldo-keto reductase family 1, member C4 [Source:HGNC Sy
8	216	1.5	2e-16	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	115701	1.63	2e-16	alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
10	55107	-2.2	2e-16	anoctamin 1, calcium activated chloride channel [Source:HG
11	54518	1.52	2e-16	amyloid beta (A4) precursor protein-binding, family B, mem
12	341	1.76	2e-16	apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
13	348	1.52	2e-16	apolipoprotein E [Source:HGNC Symbol;Acc:613]
14	55843	1.66	2e-16	Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
15	9459	1.62	2e-16	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
16	92591	1.8	2e-16	ankyrin repeat and SOCS box containing 16 [Source:HGNC S
17	640	1.44	2e-16	B lymphoid tyrosine kinase [Source:HGNC Symbol;Acc:1057]
18	26228	1.55	2e-16	signal transducing adaptor family member 1 [Source:HGNC S
19	695	1.51	2e-16	Bruton agammaglobulinemia tyrosine kinase [Source:HGNC :
20	399948	1.92	2e-16	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3:

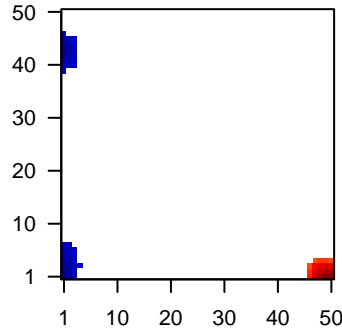
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	28.94	NULL	417	H.Tiss WIRTH_Immune system
2	17.26	NULL	553	Cancer Lembcke_Colonc Inflammation
3	13.39	NULL	15	CC MHC class II protein complex
4	13.3	NULL	312	BP immune response
5	12.08	NULL	316	Cancer SPANG_BCL6-index2
6	11.74	NULL	28	BP B cell receptor signaling pathway
7	11.45	NULL	60	BP T cell costimulation
8	10.77	NULL	327	Lymphom SPANG_CD40 6hrs UP
9	10.32	NULL	84	BP T cell receptor signaling pathway
10	10.29	NULL	16	GSEA C2SU_THYMUS
11	10.18	NULL	11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
12	10.06	NULL	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
13	10.03	NULL	11	GSEA C2BIOCARTA_THELPER_PATHWAY
14	9.98	NULL	74	BP regulation of immune response
15	9.67	NULL	162	CC external side of plasma membrane
16	9.5	NULL	13	Cancer GENTLES_modul18
17	9.4	NULL	12	BP dendritic cell chemotaxis
18	9.25	NULL	47	BP antigen processing and presentation
19	9	NULL	28	BP B cell activation
20	8.33	NULL	14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
<i>Underexpressed</i>				
1	-13.97	NULL	242	BP extracellular matrix organization
2	-11.86	NULL	190	CC extracellular matrix
3	-11.48	NULL	69	BP extracellular matrix disassembly
4	-10.86	NULL	83	CC basement membrane
5	-10.78	NULL	530	Cancer Lembcke_Normal vs Adenoma
6	-10.36	NULL	64	BP collagen catabolic process
7	-8.9	NULL	16	MMML C2SCIEJ_MMML_1
8	-8.9	NULL	11	MF platelet-derived growth factor binding
9	-8.76	NULL	12	miRNA target-29c
10	-8.52	NULL	57	MF extracellular matrix structural constituent
11	-8.21	NULL	68	Glio cultured astroglia vs. in vivo astrocytes
12	-8.2	NULL	117	Glio GIEZELT_GBM_WT_up_VS_mut
13	-7.77	NULL	183	CC proteinaceous extracellular matrix
14	-7.68	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
15	-7.63	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
16	-7.63	NULL	37	BP collagen fibril organization
17	-7.27	NULL	12	BP hemidesmosome assembly
18	-7.09	NULL	16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
19	-7.05	NULL	10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
20	-7.01	NULL	403	BP cell adhesion

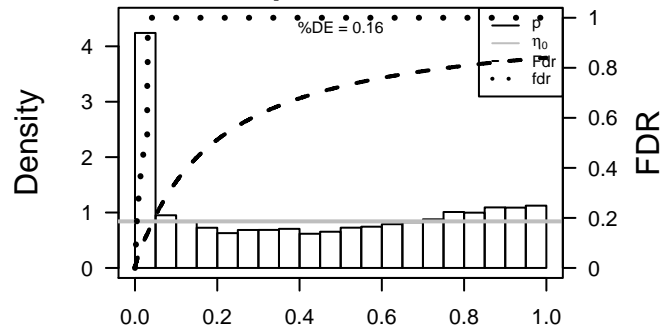
Profile



Regulated Spots



p-values



# GW\_147

## Local Summary

%DE = 0.98  
 # metagenes = 19  
 # genes = 295  
 # genes in genesets = 293

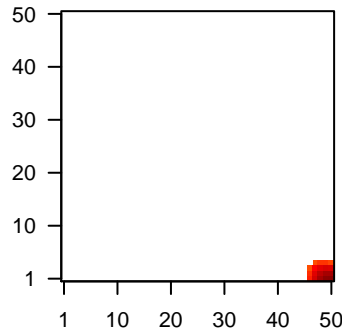
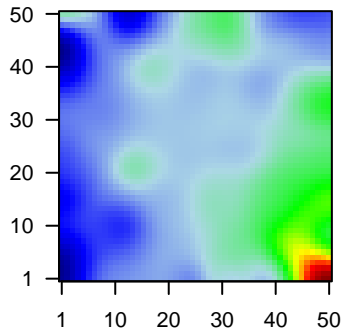
# genes with  $fdr < 0.1$  = 288 ( 287 + / 1 - )  
 # genes with  $fdr < 0.05$  = 284 ( 283 + / 1 - )  
 # genes with  $fdr < 0.01$  = 281 ( 280 + / 1 - )

<r> metagenes = 0.99  
 <r> genes = 0.59

<FC> = 1.3  
 <shrinkage-t> = 45.14  
 <p-value> = 0  
 <fdr> = 0.04

Profile

Spot



## Local Genelist

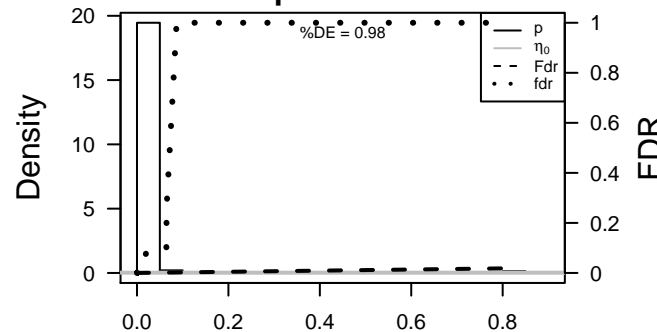
Rank	ID	log(FC)	fdr	p-value	Description
1	9744	1.46	2e-16	1e-17	49 x 1 ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [S
2	27299	1.6	2e-16	1e-17	49 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]
3	115701	1.63	2e-16	1e-17	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
4	54518	1.52	2e-16	1e-17	50 x 1 amyloid beta (A4) precursor protein-binding, family B, mem
5	341	1.76	2e-16	1e-17	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
6	348	1.52	2e-16	1e-17	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
7	55843	1.66	2e-16	1e-17	50 x 1 Rho GTPase activating protein 15 [Source:HGNC Symbol;Ac
8	9459	1.62	2e-16	1e-17	50 x 1 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
9	92591	1.8	2e-16	1e-17	48 x 2 ankyrin repeat and SOCS box containing 16 [Source:HGNC S
10	695	1.51	2e-16	1e-17	49 x 1 Bruton agammaglobulinemia tyrosine kinase [Source:HGNC :
11	260436	3.9	2e-16	1e-17	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
12	57172	2.63	2e-16	1e-17	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
13	6363	3.47	2e-16	1e-17	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
14	6364	2.25	2e-16	1e-17	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
15	6366	3.15	2e-16	1e-17	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
16	1236	2.29	2e-16	1e-17	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
17	930	2.98	2e-16	1e-17	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
18	914	1.75	2e-16	1e-17	49 x 1 CD2 molecule [Source:HGNC Symbol;Acc:1639]
19	919	1.92	2e-16	1e-17	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
20	939	2.04	2e-16	1e-17	49 x 1 CD27 molecule [Source:HGNC Symbol;Acc:11922]

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	34.47	NULL	99 / 417	H.Tiss WIRTH_Immune system
2	31.44	NULL	105 / 553	Cancer Lembocke_Colonc Inflammation
3	30.08	NULL	12 / 15	CC MHC class II protein complex
4	22.15	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	21.53	NULL	55 / 312	BP immune response
6	18.89	NULL	18 / 60	BP T cell costimulation
7	18.2	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
8	18.09	NULL	5 / 12	BP dendritic cell chemotaxis
9	17.87	NULL	7 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
10	17.77	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDP_SIGNATURE
11	17.71	NULL	15 / 47	BP antigen processing and presentation
12	17.06	NULL	8 / 13	Cancer GENTLES_modul18
13	17.02	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
14	16.89	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
15	16.79	NULL	8 / 16	GSEA C2SU_THYMUS
16	16.75	NULL	11 / 28	BP B cell receptor signaling pathway
17	16.24	NULL	49 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
18	16.24	NULL	49 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
19	16.24	NULL	49 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
20	16.24	NULL	49 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
21	15.96	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
22	15	NULL	27 / 162	CC external side of plasma membrane
23	14.85	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
24	14.81	NULL	18 / 74	BP regulation of immune response
25	14.2	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
26	14.07	NULL	18 / 84	BP T cell receptor signaling pathway
27	13.98	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
28	13.55	NULL	6 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
29	13.43	NULL	5 / 8	GSEA C2BIOCARTA_TCR_PATHWAY
30	13.29	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
31	13.27	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
32	12.6	NULL	6 / 14	GSEA C2BIOCARTA_NO2IL12_PATHWAY
33	11.93	NULL	7 / 16	Lymphoma/RIGHT_ABC_UP
34	11.93	NULL	5 / 11	BP positive regulation of B cell differentiation
35	11.89	NULL	4 / 8	GSEA C2BIOCARTA_TCAPOPTOSIS_PATHWAY
36	11.88	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
37	11.83	NULL	7 / 28	CC transport vesicle membrane
38	11.72	NULL	2 / 10	BP positive regulation of chemotaxis
39	11.69	NULL	4 / 14	BP ruffle organization
40	11.66	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_

p-values



# GW\_147

## Local Summary

%DE = 0.87  
 # metagenes = 21  
 # genes = 316  
 # genes in genesets = 313

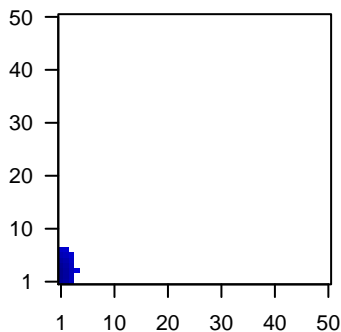
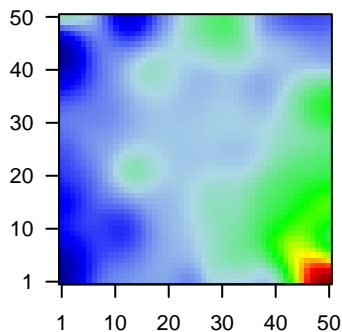
# genes with  $fdr < 0.1$  = 242 ( 7 + / 235 - )  
 # genes with  $fdr < 0.05$  = 231 ( 7 + / 224 - )  
 # genes with  $fdr < 0.01$  = 196 ( 6 + / 190 - )

<r> metagenes = 0.94  
 <r> genes = 0.34

<FC> = -0.65  
 <shrinkage-t> = -22.88  
 <p-value> = 0  
 <fdr> = 0.31

Profile

Spot



## Local Genelist

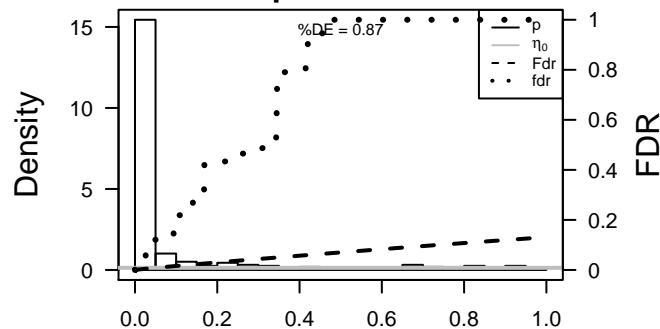
Rank	ID	log(FC)	fdr	p-value	Description
1	55107	-2.2	2e-16	4e-16	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:2197]
2	1277	-2.46	2e-16	4e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	-1.53	2e-16	4e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	-1.66	2e-16	4e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1282	-1.93	2e-16	4e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
6	1289	-2.09	2e-16	4e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
7	1290	-2.07	2e-16	4e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
8	1294	-2.15	2e-16	4e-16	1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
9	10644	-1.63	2e-16	4e-16	1 x 6 insulin-like growth factor 2 mRNA binding protein 2 [Source:HGNC Symbol;Acc:2214]
10	3576	-1.74	2e-16	4e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	3918	-1.61	2e-16	4e-16	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
12	4312	-2.27	2e-16	4e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:2214]
13	4319	-1.54	2e-16	4e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:2214]
14	4320	-1.45	2e-16	4e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Symbol;Acc:2214]
15	4314	-2.17	2e-16	4e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:2214]
16	4502	-1.81	2e-16	4e-16	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
17	5328	-1.87	2e-16	4e-16	1 x 3 plasminogen activator, urokinase [Source:HGNC Symbol;Acc:2214]
18	7045	-1.34	2e-16	4e-16	1 x 2 transforming growth factor, beta-induced, 68kDa [Source:HGNC Symbol;Acc:2214]
19	7058	-1.54	2e-16	4e-16	2 x 1 thrombospondin 2 [Source:HGNC Symbol;Acc:11786]
20	3371	-1.46	2e-16	4e-16	1 x 3 tenascin C [Source:HGNC Symbol;Acc:5318]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-32.65	NULL	63 / 242	BP extracellular matrix organization
2	-31.5	NULL	14 / 16	MMML C6ACIEJ_MMML 1
3	-29.64	NULL	7 / 11	MF platelet-derived growth factor binding
4	-29.12	NULL	48 / 190	CC extracellular matrix
5	-28.6	NULL	24 / 64	BP collagen catabolic process
6	-28.59	NULL	25 / 69	BP extracellular matrix disassembly
7	-28.17	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
8	-27.69	NULL	7 / 12	miRNA target-29c
9	-25.21	NULL	62 / 250	Lymphocyte_TNStromal signature 1
10	-23.49	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
11	-22.89	NULL	15 / 37	BP collagen fibril organization
12	-21.09	NULL	20 / 83	CC basement membrane
13	-21.06	NULL	17 / 57	MF extracellular matrix structural constituent
14	-20.87	NULL	10 / 40	BP cellular response to amino acid stimulus
15	-19.77	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
16	-18.57	NULL	40 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
17	-18.57	NULL	40 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
18	-18.57	NULL	40 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
19	-18.57	NULL	40 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
20	-18.48	NULL	5 / 11	GSEA C2BIOCARTA_PLATELETAPP_PATHWAY
21	-18.27	NULL	7 / 16	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
22	-18.24	NULL	56 / 403	BP cell adhesion
23	-17.45	NULL	105 / 1182	CC extracellular region
24	-17.35	NULL	14 / 68	CC collagen
25	-17.17	NULL	14 / 68	Glio cultured astroglia vs. in vivo astrocytes
26	-17.08	NULL	6 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
27	-16.96	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
28	-16.87	NULL	7 / 14	GSEA C2VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
29	-16.65	NULL	33 / 183	CC proteinaceous extracellular matrix
30	-16.32	NULL	73 / 683	CC extracellular space
31	-16.13	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
32	-15.99	NULL	24 / 153	CC endoplasmic reticulum lumen
33	-15.9	NULL	8 / 19	MF extracellular matrix binding
34	-15.69	NULL	8 / 13	GSEA C2MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
35	-15.61	NULL	59 / 553	Cancer Lembecke_Colonc Inflammation
36	-15.35	NULL	12 / 35	Glio Colman_survival_associated
37	-15.23	NULL	4 / 12	GSEA C2Y_AGING_MIDDLE_UP
38	-14.81	NULL	5 / 11	Glio Phillips MES up vs Prolif & PN
39	-14.8	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
40	-14.58	NULL	6 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION

p-values



# GW\_147

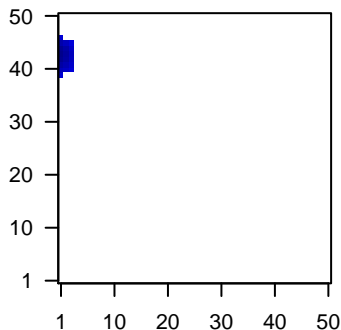
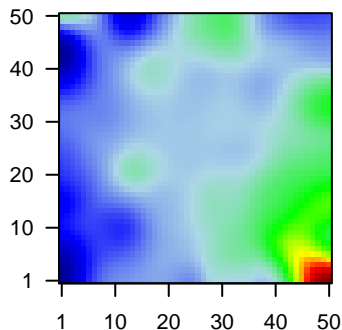
## Local Summary

%DE = 0.95  
 # metagenes = 20  
 # genes = 262  
 # genes in genesets = 258  
 # genes with  $fdr < 0.1$  = 236 ( 7 + / 229 - )  
 # genes with  $fdr < 0.05$  = 227 ( 6 + / 221 - )  
 # genes with  $fdr < 0.01$  = 191 ( 5 + / 186 - )

<r> metagenes = 0.96  
 <r> genes = 0.36  
 <FC> = -0.66  
 <shrinkage-t> = -23.35  
 <p-value> = 0  
 <fdr> = 0.26

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	133	-1.65	2e-16	2e-16	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
2	760	-1.7	2e-16	2e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	2167	-1.44	2e-16	2e-16	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
4	3489	-1.55	2e-16	2e-16	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
5	3613	-1.55	2e-16	2e-16	1 x 46 inositol(myo)-1(or 4)-monophosphatase 2 [Source:HGNC Sy
6	3868	-1.76	2e-16	2e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
7	3872	-2.13	2e-16	2e-16	1 x 43 keratin 17 [Source:HGNC Symbol;Acc:6427]
8	55214	-2.07	2e-16	2e-16	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
9	5744	-1.94	2e-16	2e-16	1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;A
10	5836	-1.52	2e-16	2e-16	1 x 44 phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:9
11	5947	-1.53	2e-16	2e-16	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:
12	8710	1.49	2e-16	2e-16	1 x 46 serpin peptidase inhibitor, clade B (ovalbumin), member 7 [Sc
13	8140	-1.54	2e-16	2e-16	1 x 43 solute carrier family 7 (amino acid transporter light chain, L s
14	50805	-1.4	2e-15	9e-15	1 x 43 iroquois homeobox 4 [Source:HGNC Symbol;Acc:6129]
15	113146	-1.38	2e-15	9e-15	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
16	7280	-1.39	2e-15	9e-15	1 x 45 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412]
17	2697	-1.38	3e-15	9e-14	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
18	51200	-1.35	1e-14	9e-14	1 x 44 carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
19	10397	-1.23	2e-14	9e-14	1 x 42 N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:
20	6513	-1.34	2e-14	1e-12	1 x 43 solute carrier family 2 (facilitated glucose transporter), memb

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-17.1	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
2	-15.52	NULL	2 / 2	miRNA target-199a*
3	-13.34	NULL	12 / 76	BP epidermis development
4	-12.81	NULL	59 / 572	Disease GUDJ_poriasis up
5	-12.7	NULL	21 / 135	H.Tiss WIRTH_Mucosa
6	-12.66	NULL	14 / 82	CC intermediate filament
7	-12.31	NULL	5 / 12	BP hemidesmosome assembly
8	-11.94	NULL	3 / 17	BP morphogenesis of an epithelium
9	-11.57	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
10	-10.74	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
11	-10.46	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
12	-10.16	NULL	3 / 12	GSEA C2MIZUKAMI_HYPOXIA_UP
13	-10.08	NULL	4 / 13	BP intermediate filament cytoskeleton organization
14	-9.83	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
15	-9.51	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
16	-9.47	NULL	2 / 7	GSEA C2YE_METASTATIC_LIVER_CANCER
17	-9.25	NULL	10 / 82	MF structural constituent of cytoskeleton
18	-9.11	NULL	2 / 12	H.Tiss WIRTH_Prim. lymphoid organs
19	-9.11	NULL	2 / 15	GSEA C2NGUYEN_NOTCH1_TARGETS_UP
20	-9.06	NULL	2 / 5	GSEA C2FERRARI_RESPONSE_TO_FENRETINIDE_DN
21	-8.99	NULL	3 / 25	BP response to zinc ion
22	-8.91	NULL	6 / 21	CC desmosome
23	-8.91	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
24	-8.9	NULL	3 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
25	-8.47	NULL	3 / 26	BP positive regulation of vasodilation
26	-8.45	NULL	2 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
27	-8.45	NULL	3 / 35	CC cell periphery
28	-8.41	NULL	3 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
29	-8.24	NULL	2 / 9	GSEA C2KYNG_DNA_DAMAGE_UP
30	-8.24	NULL	2 / 9	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP
31	-8.23	NULL	2 / 10	BP skeletal muscle tissue regeneration
32	-8.21	NULL	3 / 15	GSEA C2PRAMONJAGO_SOX4_TARGETS_UP
33	-7.98	NULL	3 / 10	GSEA C2AZARD_UV_RESPONSE_CLUSTER_G3
34	-7.86	NULL	5 / 32	CC cell-cell adherens junction
35	-7.83	NULL	3 / 16	GSEA C2ELVIDGE_HYPOXIA_BY_DMOG_UP
36	-7.77	NULL	1 / 7	GSEA C2BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3
37	-7.76	NULL	3 / 16	GSEA C2HARRIS_HYPOXIA
38	-7.76	NULL	2 / 14	GSEA C2VANHARANTA_UTERINE_FIBROID_DN
39	-7.74	NULL	2 / 10	GSEA C2RUGO_ENVIRONMENTAL_STRESS_RESPONSE_UP
40	-7.74	NULL	2 / 10	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAM

p-values

