

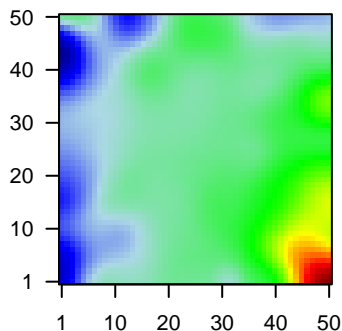
GW_281

Global Summary

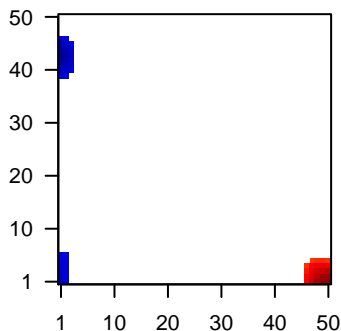
%DE = 0.16
 # genes with $fdr < 0.2$ = 2230 (1215 + / 1015 -)
 # genes with $fdr < 0.1$ = 1868 (1042 + / 826 -)
 # genes with $fdr < 0.05$ = 1422 (806 + / 616 -)
 # genes with $fdr < 0.01$ = 1023 (599 + / 424 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.08
 <fdr> = 0.84

Profile



Regulated Spots



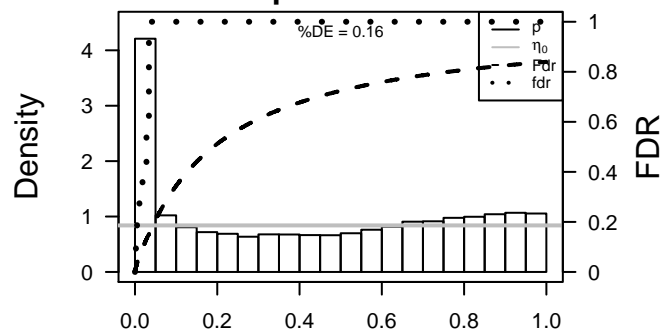
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	25890	1.98	2e-16	2e-14	50 x 4 ABI family, member 3 (NESH) binding protein [Source:HGNC
2	133	-1.87	2e-16	2e-14	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
3	57016	-2.32	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
4	441282	-1.92	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
5	8644	-1.81	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
6	1109	-1.92	2e-16	2e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
7	55107	-1.96	2e-16	2e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
8	54518	1.76	2e-16	2e-14	50 x 1 amyloid beta (A4) precursor protein-binding, family B, membe
9	9459	1.66	2e-16	2e-14	50 x 1 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
10	260436	3.58	2e-16	2e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
11	730	1.95	2e-16	2e-14	49 x 7 complement component 7 [Source:HGNC Symbol;Acc:1346]
12	760	-2.21	2e-16	2e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	57172	1.74	2e-16	2e-14	49 x 1 calcium/calmodulin-dependent protein kinase I [Source:HG
14	6363	2.68	2e-16	2e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
15	6366	3	2e-16	2e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
16	1236	2.13	2e-16	2e-14	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
17	930	2.8	2e-16	2e-14	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
18	919	1.63	2e-16	2e-14	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
19	939	1.85	2e-16	2e-14	49 x 1 CD27 molecule [Source:HGNC Symbol;Acc:11922]
20	915	1.68	2e-16	2e-14	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC S

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	26.19	NULL	417	H.Tiss WIRTH_Immune system
2	14.98	NULL	15	CC MHC class II protein complex
3	12.78	NULL	553	Cancer Lembcke_Colonc Inflammation
4	11.79	NULL	327	Lymphoma SPANG_CD40 6hrs UP
5	11.11	NULL	60	BP T cell costimulation
6	10.81	NULL	28	BP B cell receptor signaling pathway
7	10.65	NULL	84	BP T cell receptor signaling pathway
8	9.19	NULL	16	GSEA CZSU_THYMUS
9	8.97	NULL	47	BP antigen processing and presentation
10	8.93	NULL	316	Cancer SPANG_BCL6-index2
11	8.88	NULL	312	BP immune response
12	8.51	NULL	9	GSEA CZMILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
13	8.2	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
14	7.99	NULL	14	Lymphoma WRIGHT_GCB UP
15	7.95	NULL	28	BP B cell activation
16	7.67	NULL	162	CC external side of plasma membrane
17	7.65	NULL	10	GSEA CZLEE_DIFFERENTIATING_T_LYMPHOCYTE
18	7.55	NULL	8	Glio Donson-migration tethering and rolling-associated with LTS in HG
19	7.44	NULL	14	GSEA CZFINETTI_BREAST_CANCER_KINOME_GREEN
20	7.29	NULL	32	CC ER to Golgi transport vesicle membrane
<i>Underexpressed</i>				
1	-13.34	NULL	242	BP extracellular matrix organization
2	-12.08	NULL	69	BP extracellular matrix disassembly
3	-11.72	NULL	64	BP collagen catabolic process
4	-11.5	NULL	572	Disease GUDJ_psooriasis up
5	-10.35	NULL	530	Cancer Lembcke_Normal vs Adenoma
6	-10.3	NULL	12	BP hemidesmosome assembly
7	-9.99	NULL	83	CC basement membrane
8	-9.57	NULL	76	BP epidermis development
9	-8.97	NULL	190	CC extracellular matrix
10	-8.95	NULL	117	Glio GIEZELT_GBM_WT_up_VS_mut
11	-8.16	NULL	15	GSEA CZCROMER_TUMORIGENESIS_UP
12	-8.14	NULL	16	GSEA CZHUPER_BREAST_BASAL_VS_LUMINAL_UP
13	-7.58	NULL	11	GSEA CZBIOCARTA_PLATELETAPP_PATHWAY
14	-7.58	NULL	153	CC endoplasmic reticulum lumen
15	-7.58	NULL	35	Glio Colman_survival_associated
16	-7.42	NULL	1182	CC extracellular region
17	-7.03	NULL	11	MF platelet-derived growth factor binding
18	-7.01	NULL	68	Glio cultured astroglia vs. in vivo astrocytes
19	-7	NULL	12	miRNA target-29c
20	-6.89	NULL	16	MMML CSICJ_MMML 1

p-values



GW_281

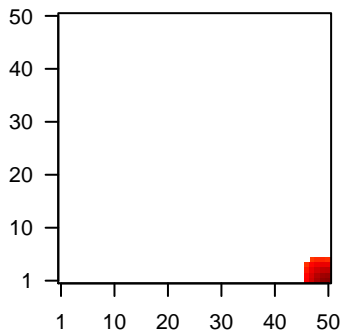
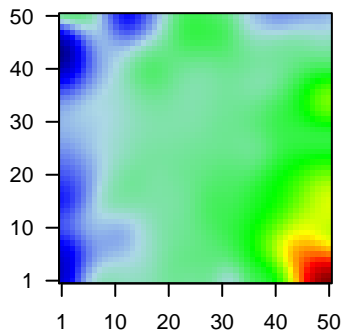
Local Summary

%DE = 0.91
 # metagenes = 24
 # genes = 354
 # genes in genesets = 352
 # genes with $fdr < 0.1$ = 312 (310 + / 2 -)
 # genes with $fdr < 0.05$ = 294 (293 + / 1 -)
 # genes with $fdr < 0.01$ = 276 (276 + / 0 -)

<r> metagenes = 0.98
 <r> genes = 0.55
 <FC> = 1.09
 <shrinkage-t> = 38.26
 <p-value> = 0
 <fdr> = 0.16

Profile

Spot



Local Genelist

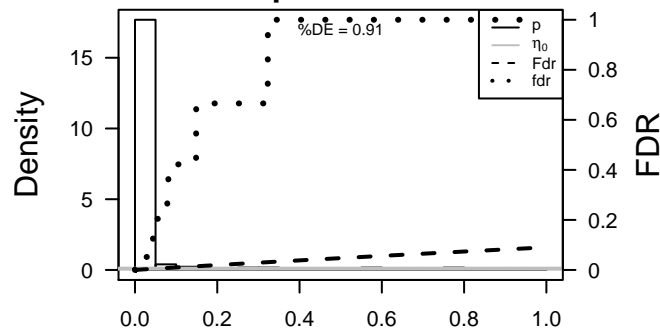
Rank	ID	log(FC)	fdr	p-value	Description
1	25890	1.98	2e-16	1e-16	50 x 4 ABI family, member 3 (NESH) binding protein [Source:HGNC
2	54518	1.76	2e-16	1e-16	50 x 1 amyloid beta (A4) precursor protein-binding, family B, mem
3	9459	1.66	2e-16	1e-16	50 x 1 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou
4	260436	3.58	2e-16	1e-16	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symb
5	57172	1.74	2e-16	1e-16	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG
6	6363	2.68	2e-16	1e-16	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
7	6366	3	2e-16	1e-16	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
8	1236	2.13	2e-16	1e-16	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
9	930	2.8	2e-16	1e-16	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
10	919	1.63	2e-16	1e-16	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
11	939	1.85	2e-16	1e-16	49 x 1 CD27 molecule [Source:HGNC Symbol;Acc:11922]
12	915	1.68	2e-16	1e-16	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC S
13	962	2.19	2e-16	1e-16	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
14	1043	2.13	2e-16	1e-16	50 x 1 CD52 molecule [Source:HGNC Symbol;Acc:1804]
15	963	1.8	2e-16	1e-16	50 x 1 CD53 molecule [Source:HGNC Symbol;Acc:1686]
16	969	1.91	2e-16	1e-16	50 x 1 CD69 molecule [Source:HGNC Symbol;Acc:1694]
17	974	1.8	2e-16	1e-16	48 x 1 CD79b molecule, immunoglobulin-associated beta [Source:+
18	9308	1.71	2e-16	1e-16	50 x 3 CD83 molecule [Source:HGNC Symbol;Acc:1703]
19	11151	1.83	2e-16	1e-16	50 x 1 coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc
20	26999	1.76	2e-16	1e-16	49 x 1 cytoplasmic FMR1 interacting protein 2 [Source:HGNC Symb

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	33.89	NULL	105 / 417	H.Tiss WIRTH_Immune system
2	31.96	NULL	117 / 553	Cancer Lembocke_Colonc Inflammation
3	26.51	NULL	12 / 15	CC MHC class II protein complex
4	19.86	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	19.34	NULL	64 / 312	BP immune response
6	19.12	NULL	12 / 28	BP B cell receptor signaling pathway
7	17.59	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
8	17.15	NULL	4 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
9	17.05	NULL	6 / 8	Glio Donsor-migration tethering and rolling-associated with LTS in HG
10	17.05	NULL	19 / 60	BP T cell costimulation
11	15.72	NULL	8 / 16	GSEA C2SU_THYMUS
12	15.62	NULL	15 / 47	BP antigen processing and presentation
13	15.35	NULL	54 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
14	15.35	NULL	54 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
15	15.35	NULL	54 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
16	15.35	NULL	54 / 265	Glio wilscher_GBM_Verhaak-PNmt_expression_B_down
17	15.14	NULL	5 / 12	BP dendritic cell chemotaxis
18	14.66	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
19	14.54	NULL	7 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
20	14.33	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
21	13.62	NULL	28 / 162	CC external side of plasma membrane
22	13.08	NULL	19 / 84	BP T cell receptor signaling pathway
23	13.03	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
24	13.02	NULL	8 / 13	Cancer GENTLES_modul18
25	12.45	NULL	5 / 11	BP positive regulation of B cell differentiation
26	12.38	NULL	18 / 74	BP regulation of immune response
27	12.37	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
28	12.16	NULL	35 / 327	Lymphoma SPANG_CD40 6hrs UP
29	11.79	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
30	11.71	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
31	11.56	NULL	6 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
32	11.32	NULL	4 / 14	BP ruffle organization
33	11.11	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
34	11	NULL	35 / 316	Cancer SPANG_BCL6-index2
35	10.86	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
36	10.85	NULL	6 / 14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
37	10.73	NULL	5 / 12	BP immunoglobulin mediated immune response
38	10.61	NULL	5 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
39	10.48	NULL	4 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
40	10.47	NULL	4 / 10	GSEA C2LEE_EARLY_T_LYMPHOCYTE_DN

p-values



GW_281

Local Summary

%DE = 0.89
 # metagenes = 12
 # genes = 205
 # genes in genesets = 203

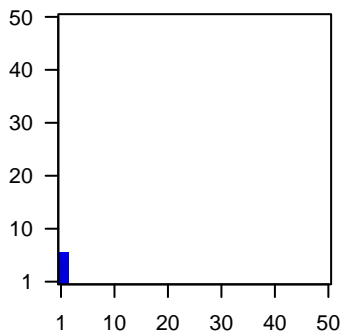
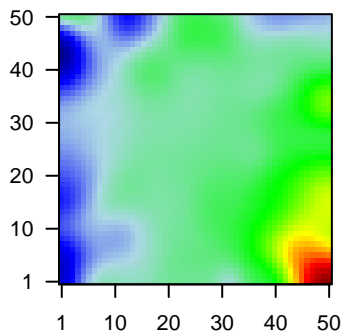
genes with $fdr < 0.1 = 164$ (8 + / 156 -)
 # genes with $fdr < 0.05 = 164$ (8 + / 156 -)
 # genes with $fdr < 0.01 = 148$ (6 + / 142 -)

$\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.37

$\langle FC \rangle = -0.75$
 $\langle \text{shrinkage-t} \rangle = -26.35$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.25$

Profile

Spot



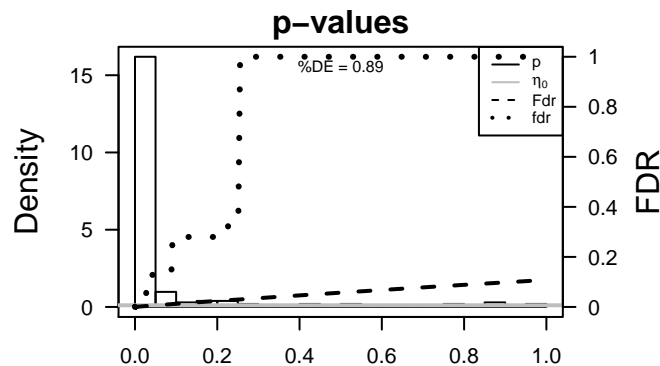
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	55107	-1.96	2e-16	3e-16	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC Symbol;Acc:2197]
2	1277	-2.5	2e-16	3e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1282	-1.68	2e-16	3e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
4	1289	-1.78	2e-16	3e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	1290	-1.67	2e-16	3e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
6	1294	-1.86	2e-16	3e-16	1 x 5 collagen, type VII, alpha 1 [Source:HGNC Symbol;Acc:2214]
7	285761	-1.71	2e-16	3e-16	1 x 4 discoidin, CUB and LCCL domain containing 1 [Source:HGNC Symbol;Acc:285761]
8	2195	-2.02	2e-16	3e-16	1 x 5 FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
9	6624	-1.53	2e-16	3e-16	1 x 6 fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)
10	3576	-2.41	2e-16	3e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	3918	-1.8	2e-16	3e-16	1 x 4 laminin, gamma 2 [Source:HGNC Symbol;Acc:6493]
12	4312	-2.76	2e-16	3e-16	1 x 1 matrix metallopeptidase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:4312]
13	4319	-1.99	2e-16	3e-16	1 x 3 matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:4319]
14	4314	-2.73	2e-16	3e-16	1 x 1 matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:4314]
15	4502	-1.72	2e-16	3e-16	1 x 3 metallothionein 2A [Source:HGNC Symbol;Acc:7406]
16	5328	-1.95	2e-16	3e-16	1 x 3 plasminogen activator, urokinase [Source:HGNC Symbol;Acc:5328]
17	5054	-1.7	2e-16	3e-16	1 x 2 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1)
18	51330	-1.62	4e-16	1e-14	1 x 4 tumor necrosis factor receptor superfamily, member 12A [Source:HGNC Symbol;Acc:51330]
19	27122	-1.59	1e-15	2e-12	1 x 3 dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Symbol;Acc:27122]
20	4489	-1.35	2e-13	2e-12	1 x 4 metallothionein 1A [Source:HGNC Symbol;Acc:7393]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-29.96	NULL	47 / 242	BP extracellular matrix organization
2	-29.75	NULL	19 / 64	BP collagen catabolic process
3	-29.36	NULL	20 / 69	BP extracellular matrix disassembly
4	-28.48	NULL	6 / 11	MF platelet-derived growth factor binding
5	-26.15	NULL	10 / 16	CC MMLL1
6	-25.92	NULL	10 / 15	GSEA C2:GROMER_TUMORIGENESIS_UP
7	-24.36	NULL	6 / 12	miRNA target-29c
8	-24.3	NULL	33 / 190	CC extracellular matrix
9	-23.26	NULL	6 / 10	GSEA C2:VERRECCHIA_RESPONSE_TO_TGFB1_C4
10	-23.03	NULL	7 / 16	GSEA C2:FARMER_BREAST_CANCER_CLUSTER_5
11	-21.08	NULL	5 / 11	GSEA C2:BIOCARTA_PLATELETAPP_PATHWAY
12	-20.95	NULL	10 / 40	BP cellular response to amino acid stimulus
13	-20.07	NULL	6 / 15	GSEA C2:LEE_LIVER_CANCER_HEPATOBLAST
14	-19.3	NULL	4 / 12	GSEA C2:Y_AGING_MIDDLE_UP
15	-18.84	NULL	10 / 37	BP collagen fibril organization
16	-18.34	NULL	31 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
17	-18.34	NULL	31 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
18	-18.34	NULL	31 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
19	-18.34	NULL	31 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
20	-18.29	NULL	5 / 11	Glio Phillips MES up vs Prolif & PN
21	-18.25	NULL	35 / 250	Lymphoma L1210 Stromal signature 1
22	-17.97	NULL	5 / 13	GSEA C2:MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
23	-17.86	NULL	12 / 57	MF extracellular matrix structural constituent
24	-16.71	NULL	13 / 68	CC cultured astroglia vs. in vivo astrocytes
25	-16.39	NULL	77 / 1182	Glio extracellular region
26	-16.37	NULL	56 / 683	CC extracellular space
27	-16.27	NULL	14 / 83	CC basement membrane
28	-15.97	NULL	10 / 35	Glio Colman_survival_associated
29	-15.76	NULL	42 / 403	BP cell adhesion
30	-15.62	NULL	1 / 3	GSEA C2:REN_MIF_TARGETS_DN
31	-15.29	NULL	7 / 15	GSEA C2:ONDER_CDH1_SIGNALING_VIA_CTNNB1
32	-15.25	NULL	4 / 9	GSEA C2:ZERBINI_RESPONSE_TO_SULINDAC_UP
33	-14.81	NULL	43 / 553	Cancer Lembecke_Colonc Inflammation
34	-14.68	NULL	4 / 13	GSEA C2:BRUECKNER_TARGETS_OF_MIRLET7A3_DN
35	-14.47	NULL	3 / 10	BP protein heterotrimerization
36	-14.47	NULL	9 / 68	CC collagen
37	-14.32	NULL	2 / 6	GSEA C2:SEIKE_LUNG_CANCER_POOR_SURVIVAL
38	-14.29	NULL	5 / 16	GSEA C2:BEJUM_TARGETS_OF_PAX3_FOXP1_FUSION_DN
39	-14.26	NULL	6 / 14	GSEA C2:VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
40	-14.18	NULL	16 / 153	CC endoplasmic reticulum lumen



GW_281

Local Summary

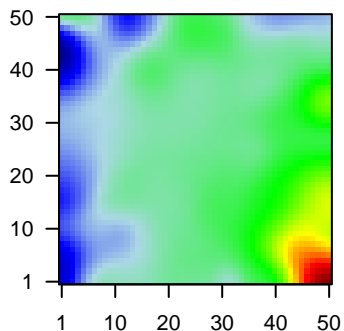
%DE = 0.93
 # metagenes = 22
 # genes = 272
 # genes in genesets = 267

genes with $fdr < 0.1$ = 246 (4 + / 242 -)
 # genes with $fdr < 0.05$ = 226 (4 + / 222 -)
 # genes with $fdr < 0.01$ = 201 (3 + / 198 -)

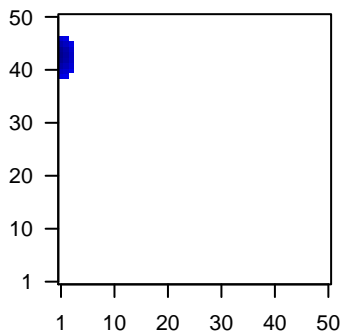
<r> metagenes = 0.95
 <r> genes = 0.35

<FC> = -0.8
 <shrinkage-t> = -28.2
 <p-value> = 0
 <fdr> = 0.23

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	133	-1.87	2e-16	2e-16	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
2	760	-2.21	2e-16	2e-16	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
3	1001	-1.8	2e-16	2e-16	1 x 43 cadherin 3, type 1, P-cadherin (placental) [Source:HGNC Sy
4	1308	-2.32	2e-16	2e-16	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
5	2171	-1.74	2e-16	2e-16	1 x 46 fatty acid binding protein 5 (psoriasis-associated) [Source:HC
6	2697	-1.99	2e-16	2e-16	1 x 44 gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;A
7	3429	-1.83	2e-16	2e-16	1 x 42 interferon, alpha-inducible protein 27 [Source:HGNC Symbol
8	3861	-2.01	2e-16	2e-16	1 x 45 keratin 14 [Source:HGNC Symbol;Acc:6416]
9	3868	-2.91	2e-16	2e-16	1 x 46 keratin 16 [Source:HGNC Symbol;Acc:6423]
10	3872	-2.59	2e-16	2e-16	1 x 43 keratin 17 [Source:HGNC Symbol;Acc:6427]
11	3852	-1.6	2e-16	2e-16	1 x 44 keratin 5 [Source:HGNC Symbol;Acc:6442]
12	55214	-1.96	2e-16	2e-16	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
13	81706	-1.74	2e-16	2e-16	1 x 43 protein phosphatase 1, regulatory (inhibitor) subunit 14C [Sou
14	5744	-2.13	2e-16	2e-16	1 x 43 parathyroid hormone-like hormone [Source:HGNC Symbol;A
15	5947	-1.96	2e-16	2e-16	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:1
16	6273	-1.86	2e-16	2e-16	1 x 44 S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:
17	6513	-1.76	2e-16	2e-16	1 x 43 solute carrier family 2 (facilitated glucose transporter), membr
18	144406	-2.03	2e-16	2e-16	1 x 42 WD repeat domain 66 [Source:HGNC Symbol;Acc:28506]
19	8140	-1.62	4e-16	9e-14	1 x 43 solute carrier family 7 (amino acid transporter light chain, L sy
20	244	-1.55	5e-15	1e-13	1 x 43 annexin A8-like 2 [Source:HGNC Symbol;Acc:23335]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.57	NULL	5 / 12	BP hemidesmosome assembly
2	-18.46	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	-17.52	NULL	12 / 76	BP epidermis development
4	-16.77	NULL	22 / 135	H.Tiss WIRTH_Mucosa
5	-16.71	NULL	2 / 2	miRNA target-199a*
6	-15.93	NULL	14 / 82	CC intermediate filament
7	-15.88	NULL	59 / 572	Disease GUUDJ_psoriasis up
8	-14.69	NULL	4 / 13	BP intermediate filament cytoskeleton organization
9	-12.6	NULL	2 / 6	GSEA C2WALLACE_PROSTATE_CANCER_DN
10	-12.46	NULL	3 / 17	BP morphogenesis of an epithelium
11	-12.32	NULL	3 / 25	BP response to zinc ion
12	-11.89	NULL	10 / 82	MF structural constituent of cytoskeleton
13	-11.03	NULL	3 / 35	CC cell periphery
14	-10.58	NULL	5 / 44	CC keratin filament
15	-10.44	NULL	3 / 16	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_DN
16	-10.17	NULL	2 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
17	-10.06	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
18	-10.06	NULL	3 / 12	GSEA C2MIZUKAMI_HYPOXIA_UP
19	-10.06	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_TARGETS_DN
20	-9.86	NULL	3 / 12	BP keratinocyte proliferation
21	-9.83	NULL	4 / 16	GSEA C2ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
22	-9.69	NULL	2 / 8	GSEA C2SIBULAN_UV_RESPONSE_NORMAL_UP
23	-9.55	NULL	3 / 38	BP epithelial cell differentiation
24	-9.25	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
25	-9.24	NULL	7 / 21	CC desmosome
26	-9.18	NULL	1 / 4	MMML C2SCIEJ_MMML 47
27	-8.92	NULL	6 / 70	BP cell junction assembly
28	-8.81	NULL	2 / 15	GSEA C2NGUYEN_NOTCH1_TARGETS_UP
29	-8.78	NULL	2 / 10	BP skeletal muscle tissue regeneration
30	-8.64	NULL	5 / 32	CC cell-cell adherens junction
31	-8.55	NULL	4 / 20	MF scaffold protein binding
32	-8.55	NULL	2 / 9	GSEA C2RODWELL_AGING_KIDNEY_UP
33	-8.54	NULL	3 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
34	-8.53	NULL	3 / 26	BP positive regulation of vasodilation
35	-8.53	NULL	3 / 10	MF gap junction channel activity
36	-8.46	NULL	13 / 186	MF structural molecule activity
37	-8.45	NULL	3 / 16	GSEA C2YANG_BREAST_CANCER_ESR1_DN
38	-8.22	NULL	3 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
39	-8.2	NULL	2 / 8	GSEA C2LIU_CDX2_TARGETS_DN
40	-8.15	NULL	3 / 10	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G3

p-values

