

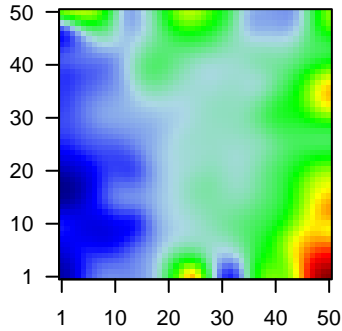
GW_214

Global Summary

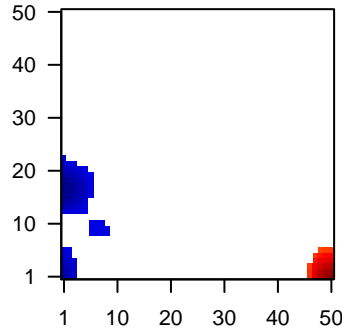
%DE = 0.13
 # genes with fdr < 0.2 = 1570 (937 + / 633 -)
 # genes with fdr < 0.1 = 1210 (761 + / 449 -)
 # genes with fdr < 0.05 = 1029 (668 + / 361 -)
 # genes with fdr < 0.01 = 714 (481 + / 233 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.87

Profile



Regulated Spots



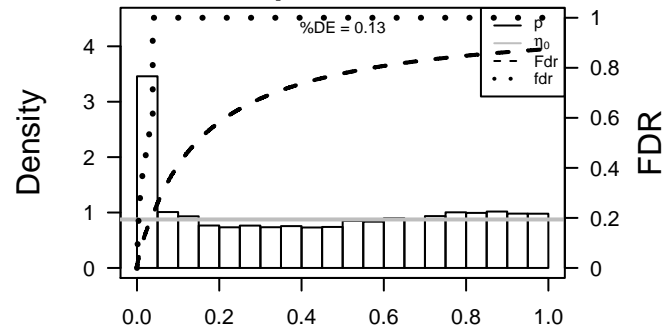
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	58	2.46	2e-16 4e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	1.68	2e-16 4e-14	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	131	1.17	2e-16 4e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	8644	-1.27	2e-16 4e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym
5	445328	-1.71	2e-16 4e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:Hi
6	445	1.28	2e-16 4e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
7	80162	1.19	2e-16 4e-14	43 x 1 ATH1, acid trehalase-like 1 (yeast) [Source:HGNC Symbol;A
8	84419	1.24	2e-16 4e-14	5 x 50 chromosome 15 open reading frame 48 [Source:HGNC Synt
9	730	1.57	2e-16 4e-14	49 x 7 complement component 7 [Source:HGNC Symbol;Acc:1346]
10	760	-1.68	2e-16 4e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
11	51806	-1.38	2e-16 4e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
12	6358	1.19	2e-16 4e-14	50 x 7 chemokine (C-C motif) ligand 14 [Source:HGNC Symbol;Acc
13	6363	1.94	2e-16 4e-14	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
14	6366	1.55	2e-16 4e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
15	595	-1.11	2e-16 4e-14	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
16	930	1.86	2e-16 4e-14	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
17	962	1.33	2e-16 4e-14	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
18	1114	1.91	2e-16 4e-14	25 x 1 chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc
19	1158	1.34	2e-16 4e-14	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
20	22802	2.2	2e-16 4e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.59	NULL	417	H.Tiss WIRTH_Immune system
2	10.94	NULL	553	Cancer Lembecke_Colonic Inflammation
3	10.71	NULL	127	H.Tiss WIRTH_Muscle
4	10.69	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
5	10.66	NULL	16	GSEA C2CRICKMAN_HEAD_AND_NECK_CANCER_F
6	10.3	NULL	4	MMML C6SCIEJ_MMML 23
7	9.74	NULL	36	BP muscle filament sliding
8	9.63	NULL	16	H.Tiss WIRTH_Hippocampus
9	9.05	NULL	135	H.Tiss WIRTH_Mucosa
10	8.81	NULL	9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
11	8.62	NULL	699	Chr Chr 5
12	8.54	NULL	15	GSEA C2CRICKMAN_HEAD_AND_NECK_CANCER_E
13	8	NULL	327	Lymphoma SPANG_CD40 6hrs UP
14	7.95	NULL	28	BP B cell receptor signaling pathway
15	7.78	NULL	11	MF oxygen transporter activity
16	7.39	NULL	44	MF structural constituent of muscle
17	7.23	NULL	15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
18	7.03	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
19	6.99	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
20	6.59	NULL	12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
<i>Underexpressed</i>				
1	-6.42	NULL	743	Chr Chr 7
2	-6.34	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
3	-6.34	NULL	142	Glio wilscher_GBM_Verhaak-PNmmt_expression_C_down
4	-6.26	NULL	74	BP antigen processing and presentation of exogenous peptide antigen
5	-6.12	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	-5.98	NULL	70	BP antigen processing and presentation of exogenous peptide antigen
7	-5.86	NULL	530	Cancer Lembecke_Normal vs Adenoma
8	-5.72	NULL	11	MF platelet-derived growth factor binding
9	-5.64	NULL	12	GSEA C2ZHU_CMV_8_HR_UP
10	-5.53	NULL	91	BP antigen processing and presentation of peptide antigen via MHC cl
11	-5.48	NULL	6	Lymphoma DAVE_MHCCII BL DN
12	-5.43	NULL	10	CC MHC class I protein complex
13	-5.25	NULL	1135	Chr Chr 19
14	-5.17	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	-5.14	NULL	6	GSEA C2NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_UP
16	-5.09	NULL	12	miRNA target-29c
17	-4.99	NULL	18	BP positive regulation of T cell mediated cytotoxicity
18	-4.94	NULL	13	GSEA C2BRUECKNER_TARGETS_OF_MIRLET7A3_DN
19	-4.9	NULL	15	GSEA C2Y_AGING_MIDDLE_DN
20	-4.89	NULL	13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP

p-values



GW_214

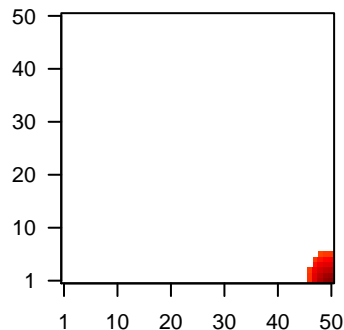
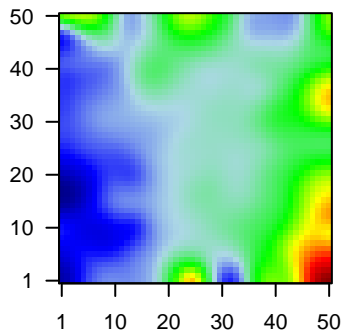
Local Summary

%DE = 0.72
 # metagenes = 26
 # genes = 371
 # genes in genesets = 369
 # genes with $fdr < 0.1$ = 217 (200 + / 17 -)
 # genes with $fdr < 0.05$ = 196 (182 + / 14 -)
 # genes with $fdr < 0.01$ = 157 (145 + / 12 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.52
 $\langle FC \rangle$ = 0.35
 $\langle \text{shrinkage-t} \rangle$ = 12.16
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.46

Profile

Spot



Local Genelist

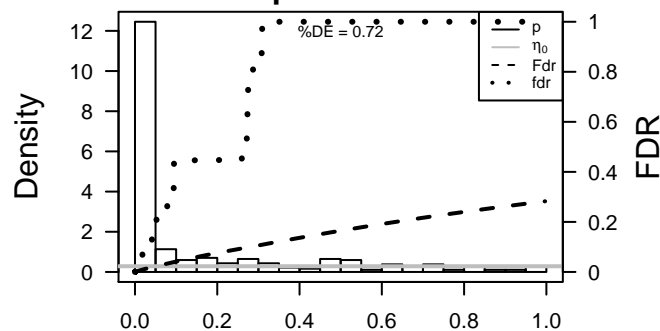
Rank	ID	log(FC)	fdr	p-value	Description
1	6363	1.94	2e-16	3e-15	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc:6363]
2	6366	1.55	2e-16	3e-15	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc:6366]
3	930	1.86	2e-16	3e-15	49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]
4	962	1.33	2e-16	3e-15	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
5	10563	1.46	2e-16	3e-15	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:10563]
6	9214	1.52	2e-16	3e-15	49 x 1 Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;Acc:9214]
7	84824	1.46	2e-16	3e-15	49 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:18504]
8	5730	1.41	2e-16	3e-15	50 x 1 prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:5730]
9	29802	1.27	2e-16	3e-15	47 x 2 pre-B lymphocyte 3 [Source:HGNC Symbol;Acc:12710]
10	23495	1.14	1e-15	4e-13	48 x 1 tumor necrosis factor receptor superfamily, member 13B [Source:HGNC Symbol;Acc:23495]
11	1043	1.11	5e-15	5e-13	50 x 1 CD52 molecule [Source:HGNC Symbol;Acc:1804]
12	3543	1.01	1e-14	5e-13	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:3543]
13	3820	1.09	2e-14	5e-13	50 x 1 killer cell lectin-like receptor subfamily B, member 1 [Source:HGNC Symbol;Acc:3820]
14	1236	1.09	2e-14	6e-13	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:1236]
15	3120	-1.08	3e-14	6e-13	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:HGNC Symbol;Acc:3120]
16	4033	1.08	3e-14	6e-13	49 x 1 lymphoid-restricted membrane protein [Source:HGNC Symbol;Acc:4033]
17	25890	1.08	4e-14	2e-11	50 x 4 ABI family, member 3 (NESH) binding protein [Source:HGNC Symbol;Acc:25890]
18	4283	-1.03	4e-13	2e-11	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:4283]
19	3119	-1.03	4e-13	3e-11	49 x 1 major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:3119]
20	83641	1.02	7e-13	5e-11	50 x 1 family with sequence similarity 107, member B [Source:HGNC Symbol;Acc:83641]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	27.83	NULL	102 / 417	H.Tiss WIRTH_Immune system
2	27.05	NULL	5 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
3	26.71	NULL	119 / 553	Cancer Lembecke_Colonc Inflammation
4	19.05	NULL	12 / 28	BP B cell receptor signaling pathway
5	18.18	NULL	5 / 12	BP dendritic cell chemotaxis
6	16.48	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
7	15.2	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
8	14.87	NULL	4 / 22	BP positive regulation of phosphatidylinositol 3-kinase activity
9	14.78	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
10	14.26	NULL	2 / 10	BP positive regulation of chemotaxis
11	13.94	NULL	8 / 16	GSEA C2SU_THYMUS
12	12.88	NULL	2 / 12	BP positive regulation of receptor-mediated endocytosis
13	12.82	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
14	12.59	NULL	61 / 312	BP immune response
15	12.39	NULL	5 / 14	BP ruffle organization
16	12.18	NULL	3 / 16	GSEA C2GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
17	12.18	NULL	4 / 27	BP release of sequestered calcium ion into cytosol
18	12.17	NULL	6 / 14	GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN
19	12.08	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
20	11.83	NULL	7 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
21	11.73	NULL	4 / 13	BP lymph node development
22	11.6	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
23	11.47	NULL	3 / 14	GSEA C2WINPENNINGCKX_MELANOMA_METASTASIS_DN
24	11.22	NULL	5 / 13	BP negative regulation of B cell proliferation
25	10.87	NULL	31 / 162	CC external side of plasma membrane
26	10.83	NULL	3 / 11	BP activation of Rho GTPase activity
27	10.66	NULL	34 / 327	LymphonSPANG_CD40 6hrs UP
28	10.54	NULL	3 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
29	10.51	NULL	5 / 10	GSEA C2LEE_EARLY_T_LYMPHOCYTE_DN
30	10.44	NULL	5 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_
31	10.39	NULL	10 / 43	MF chemokine activity
32	10.37	NULL	4 / 10	GSEA C2BIOCARTA_MONOCYTE_PATHWAY
33	10.3	NULL	26 / 204	BP cell surface receptor signaling pathway
34	10.1	NULL	2 / 10	GSEA C2SIG_BCR_SIGNALING_PATHWAY
35	10.08	NULL	5 / 10	GSEA C2BIOCARTA_LYM_PATHWAY
36	9.98	NULL	5 / 17	BP B cell homeostasis
37	9.95	NULL	5 / 11	BP positive regulation of B cell differentiation
38	9.95	NULL	3 / 11	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
39	9.94	NULL	4 / 9	GSEA C2SUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
40	9.91	NULL	4 / 22	BP positive regulation of interleukin-12 production

p-values



GW_214

Local Summary

%DE = 0.68
 # metagenes = 16
 # genes = 249
 # genes in genesets = 247

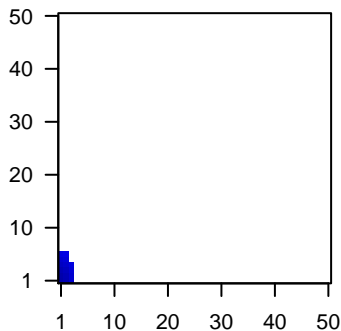
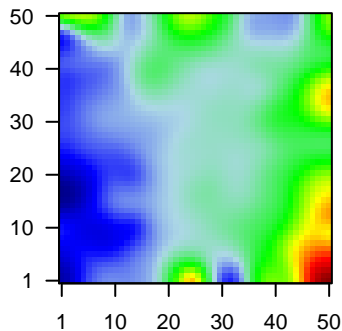
genes with $fdr < 0.1 = 121$ (16 + / 105 -)
 # genes with $fdr < 0.05 = 110$ (14 + / 96 -)
 # genes with $fdr < 0.01 = 98$ (11 + / 87 -)

<r> metagenes = 0.95
 <r> genes = 0.37

<FC> = -0.24
 <shrinkage-t> = -8.4
 <p-value> = 0
 <fdr> = 0.53

Profile

Spot



Local Genelist

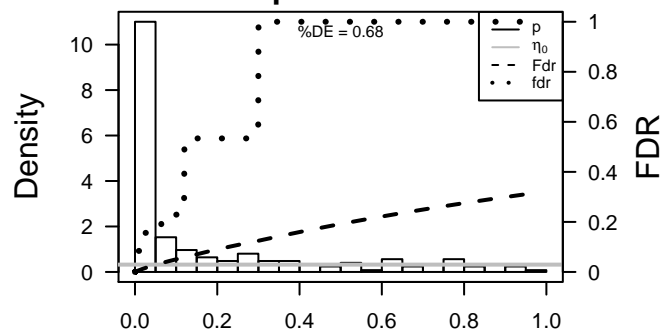
Rank	ID	log(FC)	fdr	p-value	Description
1	595	-1.11	2e-16	4e-15	1 x 6 cyclin D1 [Source:HGNC Symbol;Acc:1582]
2	1277	-1.32	2e-16	4e-15	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	3486	1.44	2e-16	4e-15	1 x 6 insulin-like growth factor binding protein 3 [Source:HGNC Sy
4	4319	2.2	2e-16	4e-15	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Sy
5	12	2.42	2e-16	4e-15	1 x 1
6	55107	-1.12	3e-15	1e-12	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HG
7	1291	-1.09	2e-14	2e-12	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
8	10468	-1.08	4e-14	3e-10	1 x 5 follistatin [Source:HGNC Symbol;Acc:3971]
9	857	-0.99	3e-12	7e-10	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A
10	1290	-0.96	1e-11	7e-10	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
11	27122	-0.95	2e-11	2e-09	1 x 3 dickkopf1 WNT signaling pathway inhibitor 3 [Source:HGNC S
12	8870	-0.94	5e-11	2e-08	1 x 3 immediate early response 3 [Source:HGNC Symbol;Acc:5392
13	768	0.9	3e-10	3e-08	1 x 6 carbonic anhydrase IX [Source:HGNC Symbol;Acc:1383]
14	2195	-0.88	6e-10	5e-08	1 x 5 FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
15	4314	0.86	1e-09	6e-08	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Sou
16	10631	-0.85	2e-09	6e-08	2 x 1 periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
17	2201	-0.85	3e-09	1e-07	1 x 5 fibrillin 2 [Source:HGNC Symbol;Acc:3604]
18	1289	-0.83	5e-09	1e-07	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
19	1948	-0.83	6e-09	2e-07	1 x 5 ephrin-B2 [Source:HGNC Symbol;Acc:3227]
20	51330	-0.82	8e-09	3e-07	1 x 4 tumor necrosis factor receptor superfamily, member 12A [Sou

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-26.4	NULL	7 / 11	MF platelet-derived growth factor binding
2	-24.28	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
3	-23.42	NULL	14 / 16	MMML C2SCIEJ_MMML_1
4	-21.51	NULL	58 / 250	LymphomaL1ENZ_Stromal signature 1
5	-19.51	NULL	13 / 37	BP collagen fibril organization
6	-19.5	NULL	7 / 12	miRNA target-29c
7	-18.31	NULL	4 / 10	BP protein heterotrimerization
8	-16.86	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
9	-16.78	NULL	16 / 57	MF extracellular matrix structural constituent
10	-16.63	NULL	1 / 2	miRNA target-16-1
11	-16.59	NULL	2 / 4	miRNA target-195
12	-16.58	NULL	46 / 190	CC extracellular matrix
13	-15.51	NULL	9 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
14	-15.03	NULL	57 / 242	BP extracellular matrix organization
15	-14.79	NULL	51 / 403	BP cell adhesion
16	-14.67	NULL	10 / 40	BP cellular response to amino acid stimulus
17	-14.17	NULL	6 / 15	GSEA C2VECCI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
18	-14.04	NULL	5 / 13	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
19	-13.98	NULL	24 / 64	BP collagen catabolic process
20	-13.63	NULL	25 / 69	BP extracellular matrix disassembly
21	-13.55	NULL	5 / 16	GSEA C2URS_ADIPOCYTE_DIFFERENTIATION_DN
22	-13.54	NULL	4 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
23	-13.47	NULL	4 / 13	GSEA C2HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENES
24	-13.33	NULL	8 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
25	-13.18	NULL	2 / 5	GSEA C2DASU_IL6_SIGNALING_UP
26	-13.17	NULL	8 / 19	MF extracellular matrix binding
27	-13.13	NULL	2 / 6	miRNA target7b
28	-13	NULL	5 / 16	GSEA C2REACTOME_SIGNALING_BY_PDGF
29	-12.97	NULL	1 / 3	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11
30	-12.82	NULL	22 / 153	CC endoplasmic reticulum lumen
31	-12.82	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
32	-12.77	NULL	4 / 14	GSEA C2LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN
33	-12.48	NULL	4 / 15	GSEA C2REACTOME_NCAM1_INTERACTIONS
34	-12.4	NULL	3 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
35	-12.26	NULL	5 / 16	GSEA C2TURASHVIL_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
36	-12.25	NULL	4 / 13	GSEA C2BRUECKNER_TARGETS_OF_MIRLET7A3_DN
37	-12.2	NULL	14 / 68	CC collagen
38	-12.13	NULL	7 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
39	-12.04	NULL	4 / 16	GSEA C2REACTOME_AXON_GUIDANCE
40	-12.04	NULL	4 / 16	GSEA C2REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWT

p-values



GW_214

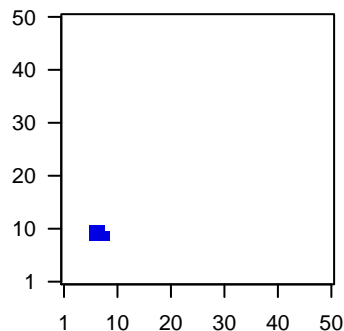
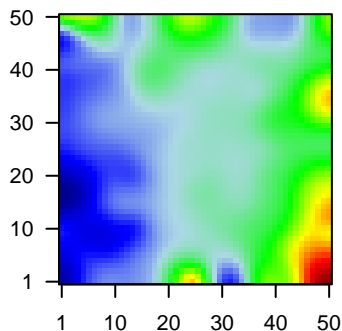
Local Summary

%DE = 0.82
 # metagenes = 11
 # genes = 156
 # genes in genesets = 155
 # genes with fdr < 0.1 = 62 (5 + / 57 -)
 # genes with fdr < 0.05 = 52 (4 + / 48 -)
 # genes with fdr < 0.01 = 7 (1 + / 6 -)

<r> metagenes = 0.97
 <r> genes = 0.33
 <FC> = -0.17
 <shrinkage-t> = -5.8
 <p-value> = 0.1
 <fdr> = 0.85

Profile

Spot



Local Genelist

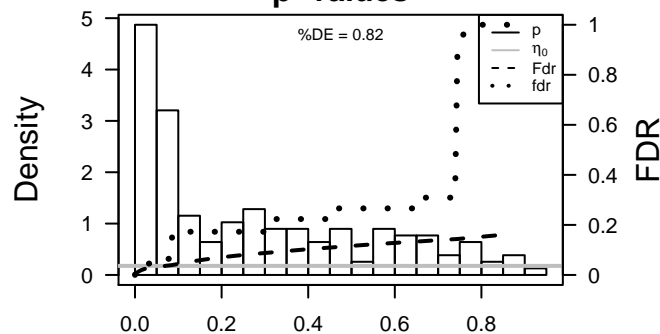
Rank	ID	log(FC)	fdr	p-value	Description
1	57414	-0.71	6e-07	3e-04	9 x 10 rhomboid domain containing 2 [Source:HGNC Symbol;Acc:21
2	10519	0.59	1e-05	4e-03	8 x 11 calcium and integrin binding 1 (calmyrin) [Source:HGNC Sym
3	60673	-0.54	2e-04	5e-03	8 x 9 chromosome 12 open reading frame 44 [Source:HGNC Synt
4	26173	-0.49	5e-04	5e-03	8 x 10 integrator complex subunit 1 [Source:HGNC Symbol;Acc:245
5	2794	-0.48	8e-04	5e-03	9 x 10 guanine nucleotide binding protein-like 1 [Source:HGNC Syr
6	84310	-0.48	8e-04	5e-03	6 x 10 chromosome 7 open reading frame 50 [Source:HGNC Symbc
7	53615	-0.47	9e-04	5e-03	8 x 11 methyl-CpG binding domain protein 3 [Source:HGNC Symbo
8	535	-0.46	1e-03	1e-02	8 x 11 ATPase, H+ transporting, lysosomal V0 subunit a1 [Source:Hi
9	3636	-0.45	2e-03	1e-02	8 x 9 inositol polyphosphate phosphatase-like 1 [Source:HGNC Sy
10	26012	-0.44	2e-03	2e-02	6 x 9 NMDA receptor synaptonuclear signaling and neuronal migra
11	162073	0.42	3e-03	2e-02	6 x 11 inositol 1,4,5-trisphosphate receptor interacting protein-like 2
12	83985	-0.42	3e-03	2e-02	7 x 10 spinster homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:
13	29886	-0.41	4e-03	2e-02	6 x 10 sorting nexin 8 [Source:HGNC Symbol;Acc:14972]
14	83590	-0.4	5e-03	3e-02	8 x 11 transmembrane and ubiquitin-like domain containing 1 [Sour
15	9040	-0.38	7e-03	3e-02	8 x 11 ubiquitin-conjugating enzyme E2M [Source:HGNC Symbol;A
16	7226	-0.38	8e-03	3e-02	9 x 10 transient receptor potential cation channel, subfamily M, mem
17	90678	-0.38	8e-03	3e-02	6 x 10 leucine rich repeat and sterile alpha motif containing 1 [Sourc
18	9277	-0.37	1e-02	3e-02	7 x 10 WD repeat domain 46 [Source:HGNC Symbol;Acc:13923]
19	29924	-0.36	1e-02	5e-02	6 x 9 epsin 1 [Source:HGNC Symbol;Acc:21604]
20	126119	-0.35	1e-02	5e-02	6 x 9 Josephin domain containing 2 [Source:HGNC Symbol;Acc:28

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.46	NULL	2 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON
2	-8.1	NULL	2 / 12	GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
3	-8.03	NULL	1 / 5	miRNA target-205
4	-7.48	NULL	2 / 16	CC NuRD complex
5	-6.8	NULL	3 / 19	MF hydrolase activity, acting on acid anhydrides, in phosphorus-contain
6	-6.77	NULL	37 / 1135	Chr Chr 19
7	-6.76	NULL	1 / 7	GSEA C2SANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2
8	-6.59	NULL	2 / 11	GSEA C2BIOCARTA_AHSP_PATHWAY
9	-6.5	NULL	2 / 14	Cancer LIU_COMMON_CANCER_GENES
10	-6.49	NULL	2 / 11	CC holo TFIIF complex
11	-6.36	NULL	2 / 11	BP positive regulation of protein dephosphorylation
12	-6.3	NULL	2 / 12	BP porphyrin-containing compound biosynthetic process
13	-6.21	NULL	1 / 8	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
14	-5.92	NULL	2 / 29	BP ATP hydrolysis coupled proton transport
15	-5.89	NULL	2 / 24	BP tissue development
16	-5.67	NULL	1 / 12	CC integrator complex
17	-5.67	NULL	1 / 12	BP snRNA processing
18	-5.52	NULL	1 / 10	BP cellular response to gonadotropin stimulus
19	-5.44	NULL	2 / 27	BP negative regulation of neuron projection development
20	-5.44	NULL	1 / 13	BP inner cell mass cell proliferation
21	-5.36	NULL	1 / 8	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_UP
22	-5.27	NULL	2 / 10	BP mitotic nuclear envelope reassembly
23	-5.06	NULL	2 / 18	BP porphyrin-containing compound metabolic process
24	-5.04	NULL	1 / 9	GSEA C2XU_GH1_AUTOCRINE_TARGETS_UP
25	-4.9	NULL	2 / 25	MF phosphatidylinositol-3,4,5-trisphosphate binding
26	-4.8	NULL	2 / 21	BP nucleotide-excision repair, DNA damage removal
27	-4.8	NULL	1 / 13	CC nuclear euchromatin
28	-4.79	NULL	1 / 10	GSEA C2HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_DN
29	-4.79	NULL	1 / 15	GSEA C2BIOCARTA_MTA3_PATHWAY
30	-4.78	NULL	2 / 20	BP heme biosynthetic process
31	-4.76	NULL	2 / 24	MF exonuclease activity
32	-4.7	NULL	1 / 5	GSEA C2CHEN_HOXA5_TARGETS_6HR_DN
33	-4.62	NULL	2 / 15	GSEA C2REACTOME_ERK_MAPK_TARGETS
34	-4.62	NULL	2 / 15	GSEA C2REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTI
35	-4.61	NULL	1 / 14	BP regulation of dendrite morphogenesis
36	-4.52	NULL	1 / 15	BP phosphatidylinositol dephosphorylation
37	-4.51	NULL	2 / 14	GSEA C2RIZKI_TUMOR_INVASIVENESS_2D_DN
38	-4.46	NULL	2 / 16	GSEA C2REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED
39	-4.44	NULL	1 / 15	BP regulation of neuronal synaptic plasticity
40	-4.4	NULL	1 / 10	MF omega peptidase activity

p-values



GW_214

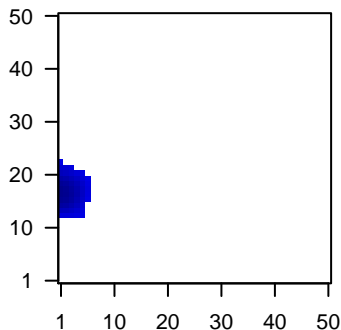
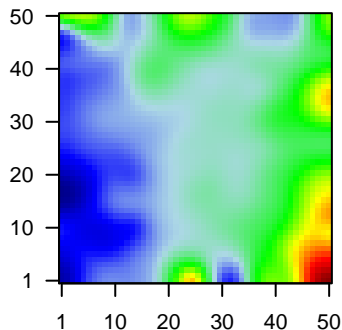
Local Summary

%DE = 0.72
 # metagenes = 54
 # genes = 500
 # genes in genesets = 494
 # genes with $fdr < 0.1$ = 228 (21 + / 207 -)
 # genes with $fdr < 0.05$ = 144 (14 + / 130 -)
 # genes with $fdr < 0.01$ = 57 (9 + / 48 -)

<r> metagenes = 0.92
 <r> genes = 0.25
 <FC> = -0.21
 <shrinkage-t> = -7.18
 <p-value> = 0.04
 <fdr> = 0.73

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	80154	1.22	2e-16	1e-14	1 x 23
2	4495	1.47	2e-16	1e-14	1 x 16 metallothionein 1G [Source:HGNC Symbol;Acc:7399]
3	51702	1.68	2e-16	1e-14	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;A
4	64978	0.8	2e-08	4e-06	3 x 19 mitochondrial ribosomal protein L38 [Source:HGNC Symbol;f
5	3237	-0.77	6e-08	4e-06	1 x 16 homeobox D11 [Source:HGNC Symbol;Acc:5134]
6	10428	-0.77	7e-08	2e-05	1 x 15 craniofacial development protein 1 [Source:HGNC Symbol;Ac
7	3217	-0.74	2e-07	7e-05	1 x 15 homeobox B7 [Source:HGNC Symbol;Acc:5118]
8	441089	-0.7	7e-07	7e-05	1 x 19
9	728489	-0.69	1e-06	8e-05	1 x 19 DNL-type zinc finger [Source:HGNC Symbol;Acc:33879]
10	6227	-0.68	2e-06	8e-05	1 x 17 ribosomal protein S21 [Source:HGNC Symbol;Acc:10409]
11	220064	-0.67	2e-06	2e-04	1 x 14 oral cancer overexpressed 1 [Source:HGNC Symbol;Acc:175
12	283869	0.65	4e-06	2e-04	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
13	430	0.64	6e-06	2e-04	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HG
14	375757	-0.64	7e-06	3e-04	1 x 21 SWI5 recombination repair homolog (yeast) [Source:HGNC S
15	51337	0.63	9e-06	7e-04	3 x 21 thioesterase superfamily member 6 [Source:HGNC Symbol;A
16	23246	-0.62	1e-05	1e-03	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
17	51657	-0.6	3e-05	1e-03	1 x 21 serine/threonine/tyrosine interacting-like 1 [Source:HGNC Sy
18	27294	-0.59	4e-05	1e-03	1 x 16 dihydrodiol dehydrogenase (dimeric) [Source:HGNC Symbol;
19	8772	-0.58	4e-05	3e-03	1 x 14 Fas (TNFRSF6)-associated via death domain [Source:HGNC
20	2017	-0.57	6e-05	3e-03	1 x 14 cortactin [Source:HGNC Symbol;Acc:3338]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-9.22	NULL	4 / 13	BP ribosomal small subunit biogenesis
2	-8.64	NULL	20 / 96	BP rRNA processing
3	-8.35	NULL	13 / 66	BP positive regulation of ubiquitin-protein ligase activity involved in m
4	-8.16	NULL	4 / 10	MF NADH dehydrogenase activity
5	-8.14	NULL	5 / 10	GSEA C2REACTOME_HIV_LIFE_CYCLE
6	-8.05	NULL	13 / 70	BP regulation of ubiquitin-protein ligase activity involved in mitotic cell
7	-7.81	NULL	12 / 62	BP negative regulation of ubiquitin-protein ligase activity involved in c
8	-7.78	NULL	13 / 74	BP anaphase-promoting complex-dependent proteasomal ubiquitin-c
9	-7.46	NULL	4 / 11	GSEA C2REACTOME_HIV_INFECTION
10	-7.39	NULL	9 / 37	CC mitochondrial nucleoid
11	-7.33	NULL	11 / 55	CC proteasome complex
12	-7.32	NULL	109 / 1318	CC mitochondrion
13	-7.21	NULL	10 / 48	BP regulation of cellular amino acid metabolic process
14	-7.1	NULL	26 / 153	MF structural constituent of ribosome
15	-6.77	NULL	5 / 16	GSEA C2MOOHTA_HUMAN_MITODB_6_2002
16	-6.75	NULL	52 / 579	CC nucleolus
17	-6.63	NULL	5 / 16	GSEA C2WONG_MITOCHONDRIA_GENE_MODULE
18	-6.49	NULL	5 / 17	CC proteasome accessory complex
19	-6.44	NULL	48 / 530	Cancer Lembcke_Normal vs Adenoma
20	-6.23	NULL	3 / 11	GSEA C2REACTOME_CHAPERONIN_MEDIATED_PROTEIN_FOLDING
21	-6.16	NULL	26 / 287	BP viral process
22	-6.11	NULL	31 / 253	BP translation
23	-6.1	NULL	3 / 15	GSEA C2REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PP
24	-6.09	NULL	5 / 17	CC proteasome core complex
25	-6.06	NULL	10 / 63	BP DNA damage response, signal transduction by p53 class mediator
26	-6.02	NULL	3 / 10	GSEA C2REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS
27	-5.99	NULL	4 / 16	GSEA C2MOOHTA_MITOCHONDRIA
28	-5.91	NULL	3 / 10	GSEA C2TOMIDA_METASTASIS_UP
29	-5.89	NULL	5 / 18	MF threonine-type endopeptidase activity
30	-5.86	NULL	4 / 16	GSEA C2OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP
31	-5.82	NULL	6 / 16	GSEA C2KORKOLA_EMBRYONAL_CARCINOMA_UP
32	-5.82	NULL	7 / 34	MF NADH dehydrogenase (ubiquinone) activity
33	-5.71	NULL	2 / 6	MMML C2SCIEJ_MMML 29
34	-5.66	NULL	3 / 15	GSEA C2Y_AGING_MIDDLE_DN
35	-5.65	NULL	10 / 70	BP antigen processing and presentation of exogenous peptide antigen
36	-5.63	NULL	3 / 8	GSEA C2MUELLER_PLURINET
37	-5.63	NULL	3 / 14	GSEA C2NIKOLSKY_BREAST_CANCER_7P22_AMPLICON
38	-5.61	NULL	7 / 36	CC mitochondrial respiratory chain complex I
39	-5.57	NULL	4 / 15	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
40	-5.56	NULL	2 / 4	TF MYC_Cell growth and proliferation UP

p-values

