

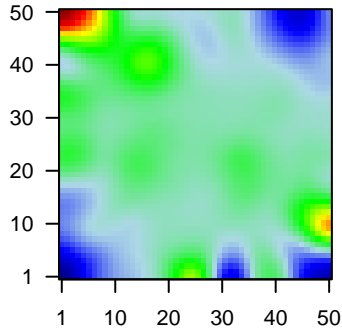
GW_032

Global Summary

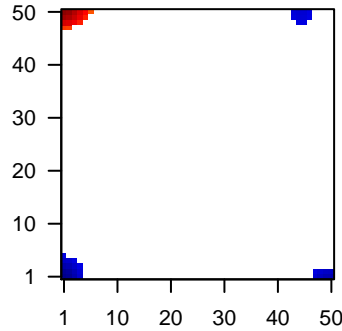
%DE = 0.14
 # genes with fdr < 0.2 = 1908 (999 + / 909 -)
 # genes with fdr < 0.1 = 1578 (840 + / 738 -)
 # genes with fdr < 0.05 = 1348 (730 + / 618 -)
 # genes with fdr < 0.01 = 970 (546 + / 424 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.08
 <fdr> = 0.86

Profile



Regulated Spots

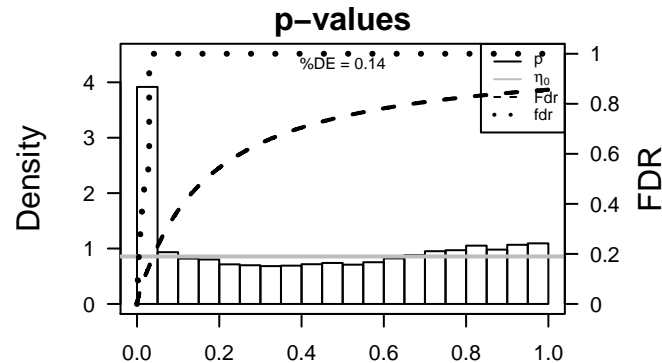


Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.28	2e-16	2e-14	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.76	2e-16	2e-14	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	58	3.91	2e-16	2e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
4	216	2.41	2e-16	2e-14	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	218	1.84	2e-16	2e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	347	2.23	2e-16	2e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
7	374569	1.73	2e-16	2e-14	4 x 50 asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
8	563	1.94	2e-16	2e-14	50 x 10 alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol
9	80341	2.88	2e-16	2e-14	50 x 10 BPI fold containing family B, member 2 [Source:HGNC Symbo
10	684	-2.44	2e-16	2e-14	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
11	92747	4.95	2e-16	2e-14	50 x 10 BPI fold containing family B, member 1 [Source:HGNC Symbo
12	140683	1.96	2e-16	2e-14	18 x 37 BPI fold containing family A, member 2 [Source:HGNC Symbo
13	29113	2.08	2e-16	2e-14	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
14	394263	2.07	2e-16	2e-14	3 x 50
15	352999	2.95	2e-16	2e-14	50 x 10 chromosome 6 open reading frame 58 [Source:HGNC Symbc
16	375791	2.2	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
17	6364	-2.16	2e-16	2e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc
18	1001	-1.8	2e-16	2e-14	1 x 43 cadherin 3, type 1, P-cadherin (placental) [Source:HGNC Sy
19	1041	1.8	2e-16	2e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
20	1048	1.95	2e-16	2e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	27.39	NULL	135	H.Tiss WIRTH_Mucosa
2	16.08	NULL	21	CC cornified envelope
3	14.84	NULL	127	H.Tiss WIRTH_Muscle
4	14.49	NULL	42	BP keratinization
5	13.97	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
6	13.45	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
7	12.13	NULL	36	BP muscle filament sliding
8	11.56	NULL	16	H.Tiss WIRTH_Hippocampus
9	11.38	NULL	53	BP keratinocyte differentiation
10	10.74	NULL	44	MF structural constituent of muscle
11	10.37	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
12	8.17	NULL	76	BP epidermis development
13	8.1	NULL	84	BP muscle contraction
14	8.07	NULL	13	CC muscle myosin complex
15	7.93	NULL	12	CC myosin filament
16	7.47	NULL	375	Disease GUDJ_psooriasis down
17	7.33	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
18	7.26	NULL	12	BP cellular aldehyde metabolic process
19	7.09	NULL	37	CC sarcomere
20	6.89	NULL	21	CC desmosome
<i>Underexpressed</i>				
1	-18.9	NULL	553	Cancer Lembcke_Colonc Inflammation
2	-14.05	NULL	417	H.Tiss WIRTH_Immune system
3	-13.62	NULL	51	BP type I interferon signaling pathway
4	-12.98	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
5	-12.98	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
6	-12.98	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
7	-12.98	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
8	-12.73	NULL	312	BP immune response
9	-12.64	NULL	242	BP extracellular matrix organization
10	-12.62	NULL	142	Glio willscher_GBM_Verhaak-CL_expression_C_up
11	-12.62	NULL	142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
12	-12.55	NULL	204	BP cytokine-mediated signaling pathway
13	-12.49	NULL	250	LymphomaL1ENZ_Stromal signature 1
14	-12.39	NULL	69	BP extracellular matrix disassembly
15	-12.16	NULL	15	GSEA C2CROMER_TUMORIGENESIS_UP
16	-12.05	NULL	190	CC extracellular matrix
17	-12.01	NULL	64	BP collagen catabolic process
18	-11.19	NULL	11	MF platelet-derived growth factor binding
19	-11	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
20	-10.99	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5



GW_032

Local Summary

%DE = 0.98
 # metagenes = 17
 # genes = 264
 # genes in genesets = 258

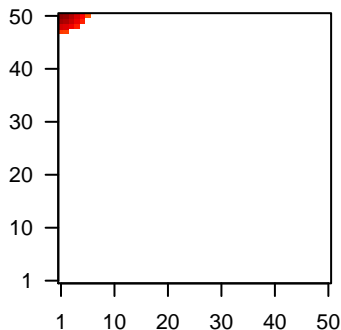
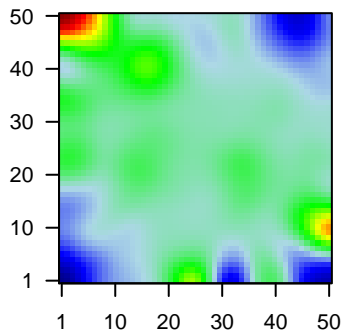
genes with $fdr < 0.1 = 253$ (249 + / 4 -)
 # genes with $fdr < 0.05 = 253$ (249 + / 4 -)
 # genes with $fdr < 0.01 = 244$ (240 + / 4 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.43

$\langle FC \rangle = 1.27$
 $\langle \text{shrinkage-t} \rangle = 44.63$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.08$

Profile

Spot



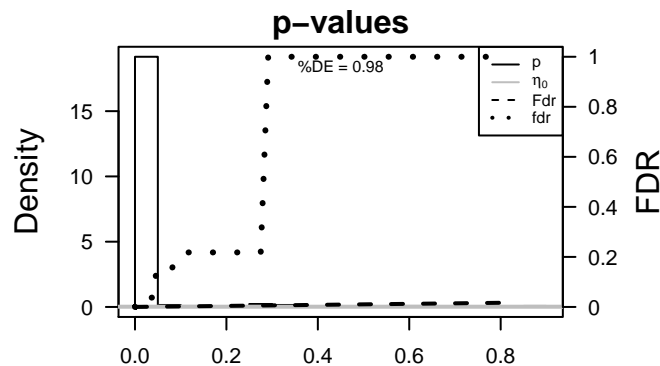
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	144568	2.28	2e-16	2e-17	1 x 50 alpha-2-macroglobulin-like 1 [Source:HGNC Symbol;Acc:23
2	55	1.76	2e-16	2e-17	4 x 50 acid phosphatase, prostate [Source:HGNC Symbol;Acc:125]
3	218	1.84	2e-16	2e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	374569	1.73	2e-16	2e-17	4 x 50 asparaginase homolog (S. cerevisiae) [Source:HGNC Symbo
5	29113	2.08	2e-16	2e-17	2 x 47 chromosome 6 open reading frame 15 [Source:HGNC Symbc
6	394263	2.07	2e-16	2e-17	3 x 50
7	375791	2.2	2e-16	2e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
8	1048	1.95	2e-16	2e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
9	4680	2.07	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	22802	2.15	2e-16	2e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
11	9022	2.09	2e-16	2e-17	1 x 50 chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2f
12	84518	2.45	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
13	54544	2.23	2e-16	2e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
14	49860	3.09	2e-16	2e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	1577	2.26	2e-16	2e-17	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
16	1828	2.83	2e-16	2e-17	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
17	131177	2.39	2e-16	2e-17	3 x 50 family with sequence similarity 3, member D [Source:HGNC f
18	115572	1.75	2e-16	2e-17	1 x 48 family with sequence similarity 46, member B [Source:HGNC
19	163351	2	2e-16	2e-17	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S
20	9245	2.18	2e-16	2e-17	4 x 50 glucosaminyl (N-acetyl) transferase 3, mucin type [Source:H

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	57.76	NULL	84 / 135	H.Tiss WIRTH_Mucosa
2	35.98	NULL	17 / 21	CC cornified envelope
3	30.68	NULL	19 / 42	BP keratinization
4	25.31	NULL	22 / 53	BP keratinocyte differentiation
5	24.32	NULL	91 / 572	Disease GUDJ_psooriasis up
6	18.09	NULL	21 / 76	BP epidermis development
7	18.05	NULL	10 / 19	BP peptide cross-linking
8	17.23	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
9	15.27	NULL	9 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	14.22	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
11	12.41	NULL	5 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
12	12.16	NULL	8 / 38	BP epithelial cell differentiation
13	11.67	NULL	5 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
14	11.36	NULL	6 / 15	GSEA C2LN_SILENCED_BY_TUMOR_MICROENVIRONMENT
15	10.96	NULL	5 / 10	MF RAGE receptor binding
16	10.83	NULL	6 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
17	10.75	NULL	6 / 13	BP negative regulation of peptidase activity
18	10.68	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
19	10.22	NULL	5 / 21	CC desmosome
20	10.17	NULL	4 / 14	GSEA C2KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
21	10.07	NULL	4 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
22	9.91	NULL	61 / 1182	CC extracellular region
23	9.42	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	9.39	NULL	21 / 186	MF structural molecule activity
25	8.94	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
26	8.92	NULL	8 / 44	CC keratin filament
27	8.69	NULL	9 / 83	CC anchored to membrane
28	8.69	NULL	5 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
29	8.37	NULL	3 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
30	8.36	NULL	15 / 122	MF serine-type endopeptidase activity
31	8.34	NULL	4 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
32	8.3	NULL	3 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
33	8.14	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
34	8.1	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
35	8.04	NULL	11 / 79	MF serine-type endopeptidase inhibitor activity
36	7.97	NULL	4 / 23	MF peptidase inhibitor activity
37	7.74	NULL	3 / 11	GSEA C2REACTOME_XENOBIOTICS
38	7.64	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
39	7.57	NULL	3 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
40	7.54	NULL	15 / 201	CC apical plasma membrane



GW_032

Local Summary

%DE = 0.91
 # metagenes = 16
 # genes = 257
 # genes in genesets = 255

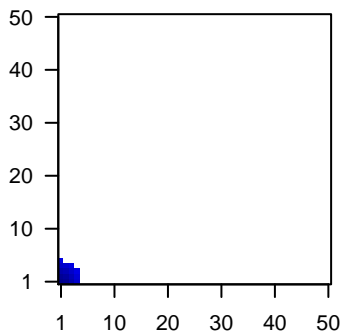
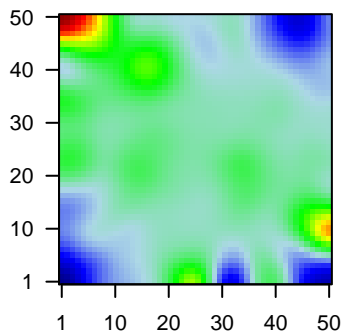
 # genes with $fdr < 0.1$ = 203 (11 + / 192 -)
 # genes with $fdr < 0.05$ = 200 (10 + / 190 -)
 # genes with $fdr < 0.01$ = 174 (9 + / 165 -)

 $\langle r \rangle$ metagenes = 0.96
 $\langle r \rangle$ genes = 0.38

 $\langle FC \rangle = -0.75$
 $\langle \text{shrinkage-t} \rangle = -26.46$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.29$

Profile

Spot



Local Genelist

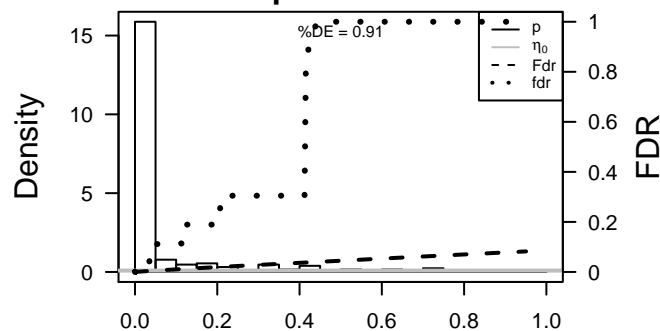
Rank	ID	log(FC)	fdr	p-value	Description
1	1277	-2.73	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
2	1278	-2.6	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
3	1281	-2.59	2e-16	2e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
4	1282	-2.11	2e-16	2e-16	2 x 1 collagen, type IV, alpha 1 [Source:HGNC Symbol;Acc:2202]
5	1289	-1.94	2e-16	2e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1290	-2.01	2e-16	2e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
7	1293	-2.2	2e-16	2e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
8	1687	-1.88	2e-16	2e-16	1 x 4 deafness, autosomal dominant 5 [Source:HGNC Symbol;Acc:6724]
9	3490	-1.76	2e-16	2e-16	3 x 1 insulin-like growth factor binding protein 7 [Source:HGNC Symbol;Acc:6025]
10	3576	-2.59	2e-16	2e-16	1 x 1 interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	3956	-1.76	2e-16	2e-16	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:6724]
12	4060	-1.88	2e-16	2e-16	2 x 1 lumican [Source:HGNC Symbol;Acc:6724]
13	4312	-2.24	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:HGNC Symbol;Acc:6724]
14	4319	-1.85	2e-16	2e-16	1 x 3 matrix metalloproteinase 10 (stromelysin 2) [Source:HGNC Symbol;Acc:6724]
15	4320	-1.89	2e-16	2e-16	3 x 1 matrix metalloproteinase 11 (stromelysin 3) [Source:HGNC Symbol;Acc:6724]
16	4314	-1.93	2e-16	2e-16	1 x 1 matrix metalloproteinase 3 (stromelysin 1, progelatinase) [Source:HGNC Symbol;Acc:6724]
17	4318	-2.23	2e-16	2e-16	1 x 1 matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa stromelysin) [Source:HGNC Symbol;Acc:6724]
18	10630	-1.74	2e-16	2e-16	1 x 2 podoplanin [Source:HGNC Symbol;Acc:29602]
19	5328	-2.16	2e-16	2e-16	1 x 3 plasminogen activator, urokinase [Source:HGNC Symbol;Acc:29602]
20	5270	-1.84	2e-16	2e-16	1 x 3 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1) [Source:HGNC Symbol;Acc:29602]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-39.62	NULL	12 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
2	-39.45	NULL	15 / 16	MMML C6ACIEJ_MMML 1
3	-39.43	NULL	59 / 190	CC extracellular matrix
4	-39.03	NULL	7 / 11	MF platelet-derived growth factor binding
5	-38.26	NULL	29 / 64	BP collagen catabolic process
6	-37.97	NULL	32 / 69	BP extracellular matrix disassembly
7	-37.08	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
8	-37.07	NULL	68 / 242	BP extracellular matrix organization
9	-35.74	NULL	8 / 12	miRNA target-29c
10	-32.09	NULL	69 / 250	Lymphocyte ENZ_Stromal signature 1
11	-28.51	NULL	15 / 37	BP collagen fibril organization
12	-27.6	NULL	20 / 57	MF extracellular matrix structural constituent
13	-23.4	NULL	11 / 40	BP cellular response to amino acid stimulus
14	-23.02	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
15	-23.01	NULL	8 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
16	-22.68	NULL	12 / 19	MF extracellular matrix binding
17	-22.65	NULL	37 / 183	CC proteinaceous extracellular matrix
18	-22.27	NULL	40 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
19	-22.27	NULL	40 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
20	-22.27	NULL	40 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
21	-22.27	NULL	40 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
22	-21.46	NULL	73 / 683	CC extracellular space
23	-21.07	NULL	12 / 35	Glio Colman_survival_associated
24	-20.82	NULL	8 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
25	-20.69	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
26	-20.65	NULL	99 / 1182	CC extracellular region
27	-20.29	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
28	-20.1	NULL	16 / 68	CC collagen
29	-19.84	NULL	4 / 10	BP protein heterotrimerization
30	-19.5	NULL	61 / 553	Cancer Lembecke_Colonc Inflammation
31	-19.25	NULL	23 / 119	Lymphocyte BOSOLOWSKI_green total
32	-19.19	NULL	4 / 6	GSEA C2AGARWAL_AKT_PATHWAY_TARGETS
33	-18.93	NULL	8 / 15	GSEA C2ONDER_CDH1_SIGNALING_VIA_CTNNB1
34	-18.88	NULL	6 / 13	GSEA C2FRIDMAN_SENESCENCE_UP
35	-18.72	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
36	-18.55	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_L
37	-18.31	NULL	5 / 12	GSEA C2Y_AGING_MIDDLE_UP
38	-18.3	NULL	4 / 5	GSEA C2COLLER_MYC_TARGETS_DN
39	-18.21	NULL	6 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
40	-17.94	NULL	52 / 403	BP cell adhesion

p-values



GW_032

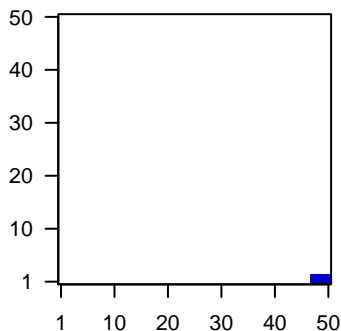
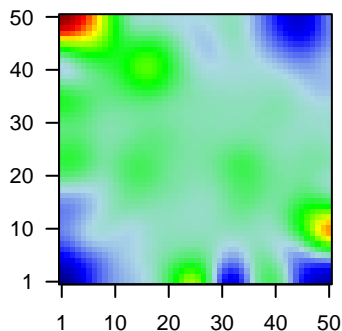
Local Summary

%DE = 0.89
 # metagenes = 8
 # genes = 186
 # genes in genesets = 184
 # genes with $fdr < 0.1$ = 152 (3 + / 149 -)
 # genes with $fdr < 0.05$ = 151 (3 + / 148 -)
 # genes with $fdr < 0.01$ = 129 (2 + / 127 -)

<r> metagenes = 1
 <r> genes = 0.65
 <FC> = -0.66
 <shrinkage-t> = -23.08
 <p-value> = 0
 <fdr> = 0.31

Profile

Spot



Local Genelist

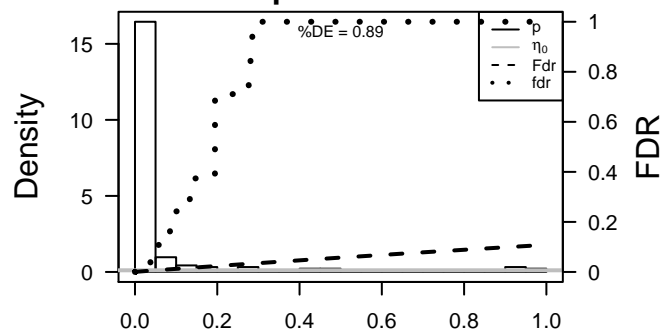
Rank	ID	log(FC)	fdr	p-value	Description
1	4069	3.05	2e-16	1e-15	50 x 2 lysozyme [Source:HGNC Symbol;Acc:6740]
2	5880	-1.79	2e-16	1e-15	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small C)
3	10537	-1.71	2e-16	1e-15	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
4	5552	-1.67	7e-16	1e-12	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
5	3002	-1.55	7e-14	1e-12	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
6	4283	-1.53	1e-13	1e-12	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:18795]
7	3059	-1.52	2e-13	4e-12	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:18795]
8	713	-1.5	4e-13	5e-11	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:18795]
9	5996	-1.44	3e-12	8e-11	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:18795]
10	7351	-1.42	6e-12	4e-10	50 x 1 uncoupling protein 2 (mitochondrial, proton carrier) [Source:HGNC Symbol;Acc:18795]
11	3512	1.38	2e-11	8e-10	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
12	3620	-1.34	8e-11	8e-10	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:18795]
13	23180	-1.33	1e-10	8e-10	50 x 1 raftlin, lipid raft linker 1 [Source:HGNC Symbol;Acc:30278]
14	1236	-1.33	1e-10	1e-08	50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Acc:18795]
15	3936	-1.27	7e-10	2e-08	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:18795]
16	10563	-1.25	1e-09	2e-08	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:18795]
17	5341	-1.22	3e-09	2e-08	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
18	962	-1.22	4e-09	2e-08	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
19	55303	-1.21	4e-09	3e-08	50 x 1 GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:18795]
20	924	-1.2	6e-09	5e-08	49 x 1 CD7 molecule [Source:HGNC Symbol;Acc:1695]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-33.45	NULL	79 / 417	H.Tiss WIRTH_Immune system
2	-25.02	NULL	70 / 553	Cancer Lemboke_Colonc Inflammation
3	-23.59	NULL	12 / 15	CC MHC class II protein complex
4	-22.71	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
5	-19.36	NULL	6 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
6	-18.63	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
7	-18.6	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
8	-18.4	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
9	-17.87	NULL	42 / 312	BP immune response
10	-17.7	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
11	-17.66	NULL	2 / 4	MMML C2SCIEJ_MMML_2
12	-16.63	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
13	-16.53	NULL	4 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
14	-15.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
15	-15.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
16	-15.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
17	-15.6	NULL	29 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	-15.22	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENTATION
19	-14.84	NULL	14 / 47	BP antigen processing and presentation
20	-14.74	NULL	5 / 13	Cancer GENTLES_modul18
21	-14.39	NULL	4 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
22	-14.36	NULL	16 / 74	BP regulation of immune response
23	-14.32	NULL	21 / 162	CC external side of plasma membrane
24	-13.96	NULL	7 / 16	GSEA C2SU_THYMUS
25	-13.89	NULL	4 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
26	-13.85	NULL	4 / 10	GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_SURVIVORS
27	-13.59	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
28	-13.01	NULL	4 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
29	-12.93	NULL	4 / 12	BP dendritic cell chemotaxis
30	-12.83	NULL	13 / 60	BP T cell costimulation
31	-12.82	NULL	5 / 16	GSEA C2FERRANDO_TAL1_NEIGHBORS
32	-12.82	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
33	-12.81	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
34	-12.74	NULL	6 / 24	CC immunological synapse
35	-12.43	NULL	5 / 12	BP immunoglobulin mediated immune response
36	-12.36	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
37	-12.27	NULL	4 / 13	BP lymph node development
38	-12.03	NULL	8 / 45	BP T cell activation
39	-12.03	NULL	4 / 14	BP ruffle organization
40	-12	NULL	6 / 28	Lymphoma GAVE_Immune response 1

p-values



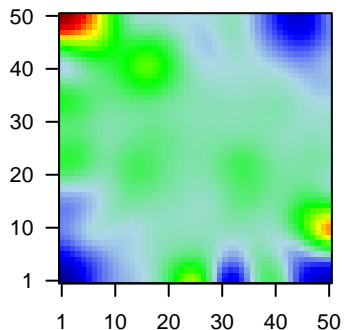
GW_032

Local Summary

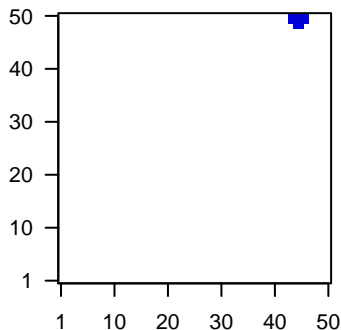
%DE = 0.99
 # metagenes = 10
 # genes = 148
 # genes in genesets = 146
 # genes with $fdr < 0.1$ = 142 (0 + / 142 -)
 # genes with $fdr < 0.05$ = 142 (0 + / 142 -)
 # genes with $fdr < 0.01$ = 136 (0 + / 136 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.48
 $\langle FC \rangle = -0.64$
 $\langle \text{shrinkage-t} \rangle = -22.28$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.31$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3428	-1.4	1e-11	8e-10	45 x 50 interferon, gamma-inducible protein 16 [Source:HGNC Symb
2	3992	-1.29	4e-10	2e-08	45 x 50 fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574]
3	5984	-1.16	2e-08	2e-08	46 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syr
4	116832	-1.14	3e-08	2e-08	46 x 50 ribosomal protein L39-like [Source:HGNC Symbol;Acc:17094
5	7153	-1.14	4e-08	2e-08	45 x 49 topoisomerase (DNA) II alpha 170kDa [Source:HGNC Symbc
6	55689	-1.13	4e-08	2e-08	46 x 50 YEATS domain containing 2 [Source:HGNC Symbol;Acc:2541
7	1894	-1.13	4e-08	6e-08	45 x 50 epithelial cell transforming sequence 2 oncogene [Source:HG
8	55165	-1.1	1e-07	6e-08	44 x 50 centrosomal protein 55kDa [Source:HGNC Symbol;Acc:1161;
9	8318	-1.09	1e-07	6e-08	45 x 49 cell division cycle 45 [Source:HGNC Symbol;Acc:1739]
10	6790	-1.09	1e-07	1e-07	44 x 50 aurora kinase A [Source:HGNC Symbol;Acc:11393]
11	10635	-1.07	2e-07	7e-07	45 x 50 RAD51 associated protein 1 [Source:HGNC Symbol;Acc:169;
12	9833	-1.03	7e-07	7e-07	44 x 50 maternal embryonic leucine zipper kinase [Source:HGNC Syr
13	1033	-1.01	1e-06	2e-06	43 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
14	54443	-0.97	3e-06	2e-06	43 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:1408
15	9133	-0.97	3e-06	2e-06	45 x 49 cyclin B2 [Source:HGNC Symbol;Acc:1580]
16	9787	-0.95	4e-06	2e-06	43 x 50 discs, large (Drosophila) homolog-associated protein 5 [Sour
17	22974	-0.94	5e-06	2e-06	44 x 50 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:1;
18	113130	-0.94	6e-06	2e-06	44 x 49 cell division cycle associated 5 [Source:HGNC Symbol;Acc:1;
19	1163	-0.93	7e-06	2e-06	44 x 50 CDC28 protein kinase regulatory subunit 1B [Source:HGNC S
20	1164	-0.93	7e-06	5e-06	44 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC S)

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-62.11	NULL	68 / 142	Glio willscher_GBM_Verhaak-CL_expression_C_up
2	-62.11	NULL	68 / 142	Glio willscher_GBM_Verhaak-PNmut_expression_C_down
3	-34.56	NULL	12 / 16	GSEA C2FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
4	-33.64	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_2
5	-32.84	NULL	20 / 57	Glio developing astrocytes
6	-32.31	NULL	8 / 10	GSEA C2MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
7	-32.17	NULL	11 / 15	GSEA C2FINETTI_BREAST_CANCER_KINOME_RED
8	-31.98	NULL	10 / 14	MMLL C2SCIEJ_MMLL_4
9	-31.96	NULL	10 / 14	GSEA C2ZHAN_MULTIPLE_MYELOMA_PR_UP
10	-30.27	NULL	10 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	-28.85	NULL	10 / 16	GSEA C2EGUCHI_CELL_CYCLE_RB1_TARGETS
12	-28.39	NULL	9 / 13	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
13	-24.69	NULL	51 / 370	BP mitotic cell cycle
14	-24.61	NULL	7 / 15	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_DN
15	-24.56	NULL	8 / 15	GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_DN
16	-24.13	NULL	9 / 16	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
17	-24.1	NULL	8 / 15	GSEA C2LEE_EARLY_T_LYMPHOCYTE_UP
18	-23.99	NULL	9 / 18	BP spindle organization
19	-23.64	NULL	52 / 572	Disease GUDJ_psooriasis_up
20	-22.99	NULL	55 / 530	Cancer Lembecke_Normal vs Adenoma
21	-21.21	NULL	7 / 14	GSEA C2AMUNDSON_GAMMA_RADIATION_RESPONSE
22	-20.43	NULL	7 / 16	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP
23	-20.03	NULL	8 / 16	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
24	-19.59	NULL	6 / 15	GSEA C2CHANG_CYCLING_GENES
25	-19.3	NULL	32 / 232	BP mitosis
26	-18.97	NULL	6 / 16	GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_DN
27	-18.87	NULL	7 / 16	Cancer WOLFER_overlap genes
28	-18.85	NULL	15 / 56	CC chromosome, centromeric region
29	-18.75	NULL	6 / 16	Cancer RHODES_UNDIFFERENTIATED_CANCER
30	-18.65	NULL	7 / 15	GSEA C2Y_AGING_MIDDLE_DN
31	-17.77	NULL	6 / 16	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
32	-17.65	NULL	4 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
33	-17.48	NULL	5 / 16	GSEA C2CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN
34	-17.43	NULL	11 / 68	Cancer SHAUGHNESSY_MM high risk
35	-17.32	NULL	6 / 15	GSEA C2TANG_SENESCENCE_TP53_TARGETS_DN
36	-17.22	NULL	6 / 14	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
37	-17.2	NULL	10 / 15	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
38	-17	NULL	6 / 13	GSEA C2WINPENNINGKX_MELANOMA_METASTASIS_UP
39	-16.79	NULL	10 / 68	Glio cultured astroglia vs. in vivo astrocytes
40	-16.64	NULL	5 / 14	GSEA C2LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP

p-values

