

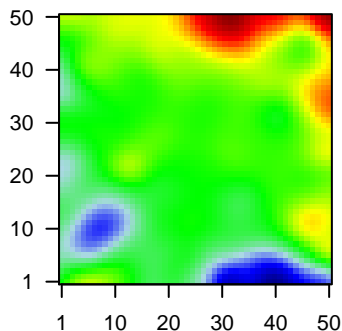
GW_101

Global Summary

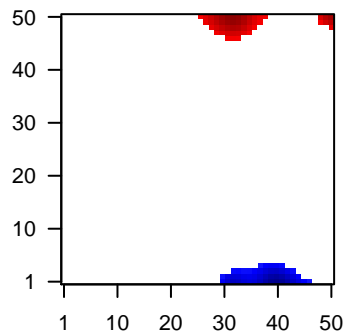
%DE = 0.14
 # genes with $fdr < 0.2$ = 1669 (895 + / 774 -)
 # genes with $fdr < 0.1$ = 1098 (578 + / 520 -)
 # genes with $fdr < 0.05$ = 867 (444 + / 423 -)
 # genes with $fdr < 0.01$ = 537 (275 + / 262 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.15
 <fdr> = 0.86

Profile



Regulated Spots



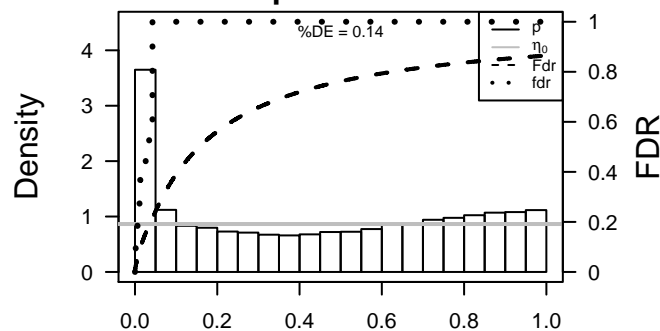
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	131	2.74	2e-16 1e-13	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	1.54	2e-16 1e-13	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
3	1109	2.14	2e-16 1e-13	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
4	216	2.47	2e-16 1e-13	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
5	684	-1.92	2e-16 1e-13	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
6	84290	1.66	2e-16 1e-13	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
7	22802	1.78	2e-16 1e-13	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20'
8	1466	1.5	2e-16 1e-13	5 x 43 cysteine and glycine-rich protein 2 [Source:HGNC Symbol;A
9	1475	1.74	2e-16 1e-13	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
10	92196	2.37	2e-16 1e-13	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
11	2167	1.91	2e-16 1e-13	1 x 44 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
12	51083	1.66	2e-16 1e-13	1 x 15 galanin/GMAP prepropeptide [Source:HGNC Symbol;Acc:41'
13	10457	1.57	2e-16 1e-13	13 x 50 glycoprotein (transmembrane) nmb [Source:HGNC Symbol;A
14	2938	1.77	2e-16 1e-13	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Ac
15	2941	1.56	2e-16 1e-13	3 x 50 glutathione S-transferase alpha 4 [Source:HGNC Symbol;Ac
16	2537	-1.58	2e-16 1e-13	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;f
17	9636	-1.98	2e-16 1e-13	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:40E
18	3848	2.7	2e-16 1e-13	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
19	3851	4	2e-16 1e-13	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
20	84648	-2.03	2e-16 1e-13	1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	11.51	NULL	153	MF structural constituent of ribosome
2	10.73	NULL	8	GSEA C2L10_CDX2_TARGETS_DN
3	9.98	NULL	87	BP translational termination
4	9.96	NULL	81	BP viral transcription
5	9.86	NULL	167	CC ribosome
6	9.45	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
7	9.34	NULL	128	BP translational initiation
8	9.32	NULL	92	BP translational elongation
9	9.15	NULL	92	BP viral life cycle
10	9.15	NULL	253	BP translation
11	9.02	NULL	1318	CC mitochondrion
12	8.16	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
13	8.04	NULL	1033	Chr Chr 2
14	7.73	NULL	51	CC cytosolic large ribosomal subunit
15	7.6	NULL	280	Chr Chr 13
16	7.41	NULL	83	BP respiratory electron transport chain
17	7.12	NULL	37	CC cytosolic small ribosomal subunit
18	6.99	NULL	714	Chr Chr 6
19	6.95	NULL	287	BP viral process
20	6.83	NULL	1233	TF KIM_MYC targets
<i>Underexpressed</i>				
1	-14.78	NULL	1135	Chr Chr 19
2	-13.76	NULL	51	BP type I interferon signaling pathway
3	-11.16	NULL	16	GSEA C2ENAV_INTERFERON_SIGNATURE_IN_CANCER
4	-10.95	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
5	-10.72	NULL	123	BP defense response to virus
6	-9.93	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	-9.8	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
8	-9.58	NULL	31	BP negative regulation of viral genome replication
9	-9.46	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	-9.32	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
11	-9.08	NULL	717	Chr Chr 16
12	-8.72	NULL	417	H.Tiss WIRTH_Immune system
13	-8.12	NULL	274	Lympho SPANG_IL21 DN
14	-7.76	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
15	-7.33	NULL	553	Cancer Lembecke_Colonic Inflammation
16	-7.3	NULL	204	BP cytokine-mediated signaling pathway
17	-7.23	NULL	16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
18	-7.2	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
19	-7.04	NULL	312	BP immune response
20	-6.89	NULL	60	BP interferon-gamma-mediated signaling pathway

p-values



GW_101

Local Summary

%DE = 0.83
 # metagenes = 43
 # genes = 577
 # genes in genesets = 563

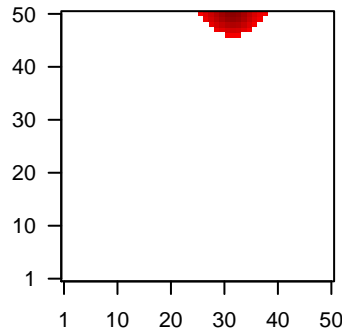
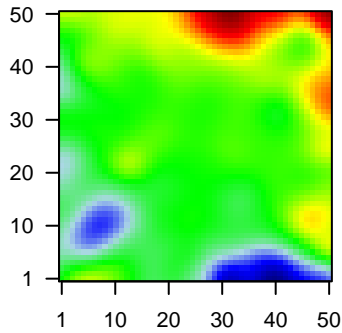
genes with $fdr < 0.1 = 369$ (368 + / 1 -)
 # genes with $fdr < 0.05 = 303$ (303 + / 0 -)
 # genes with $fdr < 0.01 = 139$ (139 + / 0 -)

$\langle r \rangle$ metagenes = 0.87
 $\langle r \rangle$ genes = 0.24

$\langle FC \rangle = 0.38$
 $\langle \text{shrinkage-t} \rangle = 13.35$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.61$

Profile

Spot



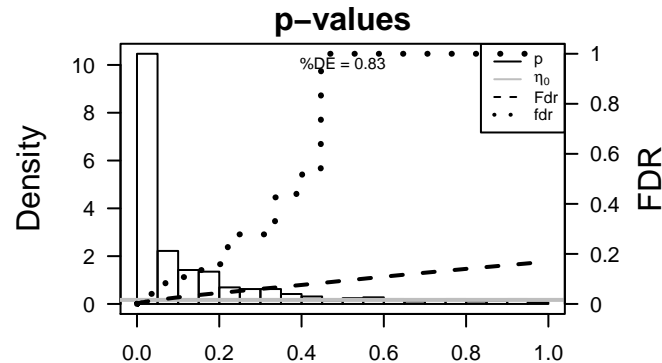
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84833	1.1	2e-09	6e-07	33 x 50 up-regulated during skeletal muscle growth 5 homolog (mous
2	6622	1.06	9e-09	2e-05	27 x 50 synuclein, alpha (non A4 component of amyloid precursor) [S
3	51023	0.96	2e-07	2e-05	32 x 50 mitochondrial ribosomal protein S18C [Source:HGNC Symbo
4	65008	0.91	7e-07	2e-05	32 x 50 mitochondrial ribosomal protein L1 [Source:HGNC Symbol;Ar
5	4259	0.91	8e-07	2e-05	32 x 49 microsomal glutathione S-transferase 3 [Source:HGNC Synt
6	6392	0.91	8e-07	4e-05	31 x 50 succinate dehydrogenase complex, subunit D, integral membr
7	27235	0.89	1e-06	4e-05	31 x 50 coenzyme Q2 4-hydroxybenzoate polyprenyltransferase [Sou
8	6147	0.88	2e-06	6e-05	33 x 49 ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
9	10950	0.87	2e-06	8e-05	28 x 50 BTG family, member 3 [Source:HGNC Symbol;Acc:1132]
10	6154	0.86	3e-06	8e-05	32 x 49 ribosomal protein L26 [Source:HGNC Symbol;Acc:10327]
11	144363	0.85	4e-06	8e-05	31 x 50 LYR motif containing 5 [Source:HGNC Symbol;Acc:27052]
12	1349	0.84	5e-06	8e-05	33 x 50 cytochrome c oxidase subunit VIIb [Source:HGNC Symbol;Ac
13	441951	0.83	5e-06	8e-05	33 x 49 ZNF1 antisense RNA 1 [Source:HGNC Symbol;Acc:33101]
14	84273	0.82	8e-06	8e-05	32 x 49 nitric oxide associated 1 [Source:HGNC Symbol;Acc:28473]
15	6160	0.82	8e-06	8e-05	32 x 49 ribosomal protein L31 [Source:HGNC Symbol;Acc:10334]
16	64776	0.81	1e-05	8e-05	32 x 49 chromosome 11 open reading frame 1 [Source:HGNC Symbc
17	133383	0.81	1e-05	8e-05	32 x 50 SET domain containing 9 [Source:HGNC Symbol;Acc:28508]
18	10799	0.81	1e-05	2e-04	34 x 50 ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;A
19	84693	0.8	1e-05	2e-04	29 x 50 methylmalonyl CoA epimerase [Source:HGNC Symbol;Acc:1f
20	5805	0.8	1e-05	2e-04	30 x 50 6-pyruvoyltetrahydropterin synthase [Source:HGNC Symbol;

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	20	NULL	42 / 153	MF structural constituent of ribosome
2	19.52	NULL	31 / 83	BP respiratory electron transport chain
3	17.39	NULL	52 / 253	BP translation
4	17.08	NULL	39 / 167	CC ribosome
5	16.25	NULL	23 / 81	BP viral transcription
6	16.18	NULL	24 / 87	BP translational termination
7	15.92	NULL	9 / 19	CC mitochondrial proton-transporting ATP synthase complex
8	15.88	NULL	24 / 92	BP translational elongation
9	15.75	NULL	36 / 152	BP cellular metabolic process
10	15.31	NULL	144 / 1318CC	mitochondrion
11	15.07	NULL	15 / 51	CC cytosolic large ribosomal subunit
12	15.05	NULL	23 / 92	BP viral life cycle
13	14.94	NULL	27 / 109	BP SRP-dependent cotranslational protein targeting to membrane
14	14.86	NULL	28 / 128	BP translational initiation
15	14.83	NULL	7 / 10	CC large ribosomal subunit
16	14.78	NULL	51 / 304	CC mitochondrial inner membrane
17	13.1	NULL	25 / 115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
18	12.2	NULL	6 / 13	GSEA C2REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
19	12.06	NULL	7 / 15	BP ATP synthesis coupled proton transport
20	11.7	NULL	6 / 14	BP mitochondrial ATP synthesis coupled proton transport
21	11.68	NULL	33 / 219	BP mRNA metabolic process
22	11.41	NULL	42 / 287	BP viral process
23	11.37	NULL	35 / 242	BP RNA metabolic process
24	10.87	NULL	10 / 23	CC mitochondrial ribosome
25	10.29	NULL	5 / 11	BP ribosomal large subunit biogenesis
26	10.05	NULL	13 / 36	CC mitochondrial respiratory chain complex I
27	9.98	NULL	12 / 34	MF NADH dehydrogenase (ubiquinone) activity
28	9.96	NULL	13 / 35	BP mitochondrial electron transport, NADH to ubiquinone
29	9.68	NULL	6 / 11	Cancer GENTLES_modul5
30	9.66	NULL	4 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
31	9.59	NULL	101 / 1233TF	KIM_MYC targets
32	9.21	NULL	64 / 649	BP gene expression
33	9.04	NULL	5 / 12	BP oxidative phosphorylation
34	9.03	NULL	6 / 16	Cancer GENTLES_modul10
35	9.03	NULL	4 / 9	GSEA C2KEGG_RIBOSOME
36	9.03	NULL	4 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
37	9.03	NULL	4 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
38	9.03	NULL	4 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
39	9.03	NULL	4 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
40	9.03	NULL	4 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT



GW_101

Local Summary

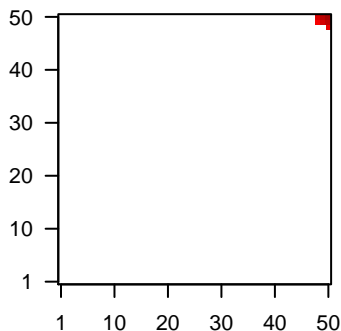
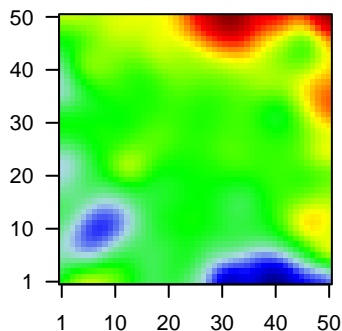
%DE = 0.75
 # metagenes = 7
 # genes = 144
 # genes in genesets = 143
 # genes with $fdr < 0.1$ = 94 (87 + / 7 -)
 # genes with $fdr < 0.05$ = 91 (85 + / 6 -)
 # genes with $fdr < 0.01$ = 63 (59 + / 4 -)

<r> metagenes = 0.98
 <r> genes = 0.3

<FC> = 0.5
 <shrinkage-t> = 17.41
 <p-value> = 0
 <fdr> = 0.43

Profile

Spot



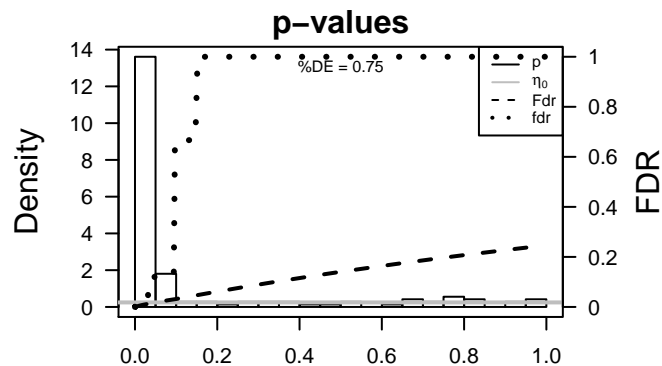
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	216	2.47	2e-16	2e-15	50 x 50 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
2	2938	1.77	2e-16	2e-15	50 x 50 glutathione S-transferase alpha 2 [Source:HGNC Symbol;Acc
3	4922	2.11	2e-16	2e-15	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
4	6657	1.57	2e-16	2e-15	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symb
5	11166	1.44	4e-15	1e-12	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Synt
6	3880	1.39	5e-14	3e-12	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
7	4953	1.36	1e-13	9e-12	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
8	84171	1.33	5e-13	9e-12	50 x 49 lysyl oxidase-like 4 [Source:HGNC Symbol;Acc:17171]
9	28978	1.32	6e-13	6e-11	49 x 50 transmembrane protein 14A [Source:HGNC Symbol;Acc:210
10	1592	1.29	2e-12	1e-10	50 x 50 cytochrome P450, family 26, subfamily A, polypeptide 1 [Sou
11	1780	1.26	8e-12	1e-10	50 x 50 dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC S
12	4915	1.25	9e-12	3e-10	50 x 50 neurotrophic tyrosine kinase, receptor, type 2 [Source:HGNC
13	3866	1.23	2e-11	5e-09	50 x 50 keratin 15 [Source:HGNC Symbol;Acc:6421]
14	56548	1.16	3e-10	5e-09	50 x 50 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
15	57291	1.16	3e-10	7e-09	50 x 50 differentiation antagonizing non-protein coding RNA [Source:
16	928	1.14	5e-10	7e-09	50 x 50 CD9 molecule [Source:HGNC Symbol;Acc:1709]
17	4072	1.13	7e-10	2e-08	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
18	2719	1.12	1e-09	4e-08	50 x 50 glypican 3 [Source:HGNC Symbol;Acc:4451]
19	6446	1	3e-09	4e-08	50 x 50 serum/glucocorticoid regulated kinase 1 [Source:HGNC Syml
20	154664	1.08	4e-09	3e-07	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [So

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	25.28	NULL	3 / 8	GSEA C2JUCDX2_TARGETS_DN
2	24.02	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
3	18.78	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
4	17.6	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
5	17.6	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
6	14.78	NULL	2 / 12	BP cellular aldehyde metabolic process
7	14.29	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
8	13.81	NULL	1 / 9	GSEA C2ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
9	13.81	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
10	13.47	NULL	2 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
11	13.02	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
12	12.98	NULL	1 / 10	GSEA C2MAINA_VHL_TARGETS_UP
13	12.98	NULL	1 / 10	GSEA C2FRIDMAN_SENESCENCE_DN
14	12.88	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
15	12.23	NULL	3 / 13	BP regulation of blood vessel size
16	11.71	NULL	2 / 18	MF acyl-CoA dehydrogenase activity
17	11.67	NULL	1 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
18	11.33	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
19	10.67	NULL	1 / 14	MF Ras GTPase activator activity
20	10.67	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAIN
21	10.67	NULL	1 / 14	GSEA C2MAHADEVAN_IMATINIB_RESISTANCE_UP
22	10.47	NULL	1 / 11	Glio neurons_glio
23	10.25	NULL	1 / 15	GSEA C2DORSAM_HOXA9_TARGETS_UP
24	10.18	NULL	1 / 5	GSEA C2KERLEY_RESPONSE_TO_CISPLATIN_DN
25	10.17	NULL	1 / 4	GSEA C2MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
26	10.14	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
27	10.14	NULL	1 / 7	miRNA target-145
28	10	NULL	2 / 15	GSEA C2YANG_BREAST_CANCER_ESR1_LASER_DN
29	9.84	NULL	2 / 23	BP stem cell differentiation
30	9.71	NULL	2 / 15	GSEA C2DODONELL_TFRC_TARGETS_UP
31	9.35	NULL	1 / 8	GSEA C2REACTOME_E2F_TRANSCRIPTIONAL_TARGETS_AT_G1_S
32	9.35	NULL	1 / 8	miRNA target-450
33	9.22	NULL	1 / 18	BP positive regulation of Ras GTPase activity
34	9.22	NULL	1 / 18	BP retinol metabolic process
35	8.75	NULL	1 / 7	GSEA C2REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
36	8.73	NULL	1 / 15	MF neuropeptide hormone activity
37	8.2	NULL	2 / 20	BP long-term memory
38	8.18	NULL	1 / 10	MF miRNA binding
39	8.18	NULL	3 / 48	BP cerebral cortex development
40	8.16	NULL	2 / 13	GSEA C2COLLER_MYC_TARGETS_UP



GW_101

Local Summary

%DE = 0.96
 # metagenes = 49
 # genes = 580
 # genes in genesets = 548
 # genes with $fdr < 0.1$ = 542 (6 + / 536 -)
 # genes with $fdr < 0.05$ = 501 (5 + / 496 -)
 # genes with $fdr < 0.01$ = 296 (2 + / 294 -)

$\langle r \rangle$ metagenes = 0.77

$\langle r \rangle$ genes = 0.27

$\langle FC \rangle = -0.47$

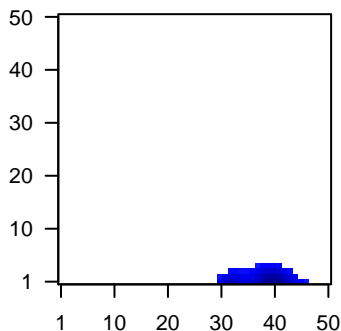
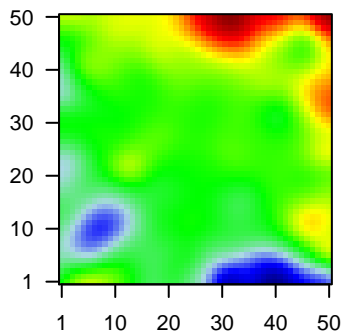
$\langle \text{shrinkage-t} \rangle = -16.6$

$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.51$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	684	-1.92	2e-16	1e-15	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	2537	-1.58	2e-16	1e-15	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;I
3	9636	-1.98	2e-16	1e-15	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405
4	4599	-1.62	2e-16	1e-15	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible
5	10964	-1.45	4e-15	6e-12	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
6	115362	-1.35	2e-13	2e-11	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
7	400818	-1.31	9e-13	9e-11	40 x 1 Neuroblastoma breakpoint family member 1 [Source:UniProt
8	641737	-1.18	6e-12	9e-11	40 x 1
9	4600	-1.26	8e-12	5e-09	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
10	10866	-1.17	2e-10	1e-08	32 x 1 HLA complex P5 (non-protein coding) [Source:HGNC Symbc
11	3123	-1.13	9e-10	1e-08	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:
12	6772	-1.12	1e-09	1e-08	32 x 1 signal transducer and activator of transcription 1, 91kDa [Sou
13	85441	-1.11	1e-09	3e-08	32 x 1 helicase with zinc finger 2, transcriptional coactivator [Source
14	84061	-1.09	3e-09	3e-08	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
15	3136	-1.08	5e-09	3e-08	32 x 1
16	399900	-0.98	7e-09	3e-08	39 x 1
17	51296	-1.06	7e-09	3e-08	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3
18	3105	-0.97	9e-09	3e-08	32 x 1 major histocompatibility complex, class I, A [Source:HGNC S
19	219285	-1.05	1e-08	3e-08	32 x 1 sterile alpha motif domain containing 9-like [Source:HGNC S
20	10581	-0.96	1e-08	3e-08	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC S

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-36.99	NULL	31 / 51	BP type I interferon signaling pathway
2	-33.21	NULL	14 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	-30.62	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	-28.9	NULL	13 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
5	-27.56	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
6	-25.96	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
7	-25.06	NULL	15 / 31	BP negative regulation of viral genome replication
8	-24.63	NULL	11 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
9	-24.44	NULL	40 / 123	BP defense response to virus
10	-21.2	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
11	-21.1	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
12	-20.8	NULL	6 / 6	LymphomaDAVE_MHCII BL DN
13	-20.13	NULL	41 / 204	BP cytokine-mediated signaling pathway
14	-20.1	NULL	13 / 16	GSEA C2MOSELERLE_IFNA_RESPONSE
15	-19.71	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
16	-19.31	NULL	29 / 109	BP response to virus
17	-18.11	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
18	-18.01	NULL	7 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
19	-17.28	NULL	20 / 60	BP interferon-gamma-mediated signaling pathway
20	-17.05	NULL	6 / 12	GSEA C2TSAL_DNAJB4_TARGETS_UP
21	-16.35	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
22	-15.84	NULL	44 / 274	LymphomaSPANG_IL21 DN
23	-15.63	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
24	-15.31	NULL	7 / 10	CC MHC class I protein complex
25	-14.58	NULL	6 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
26	-14.45	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
27	-14.34	NULL	8 / 18	MF peptide antigen binding
28	-14.24	NULL	8 / 23	CC integral to luminal side of endoplasmic reticulum membrane
29	-14	NULL	4 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
30	-13.85	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
31	-13.55	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
32	-13.39	NULL	5 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
33	-13.31	NULL	3 / 13	GSEA C2TSAL_RESPONSE_TO_RADIATION_THERAPY
34	-13.09	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
35	-12.89	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
36	-12.88	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
37	-12.81	NULL	7 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
38	-12.43	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
39	-12.28	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_ON
40	-12.19	NULL	2 / 2	MMML C2SCIEJ_MMML_27

p-values

