

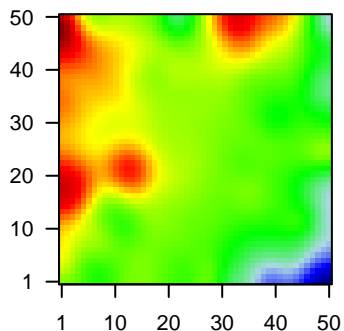
GW_265

Global Summary

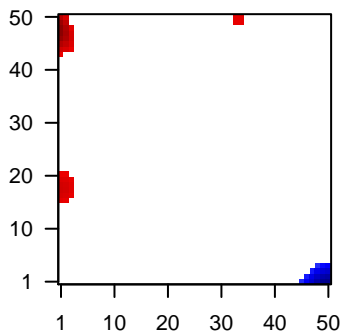
%DE = 0.12
 # genes with fdr < 0.2 = 1449 (730 + / 719 -)
 # genes with fdr < 0.1 = 1101 (535 + / 566 -)
 # genes with fdr < 0.05 = 797 (373 + / 424 -)
 # genes with fdr < 0.01 = 526 (234 + / 292 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.14
 <fdr> = 0.88

Profile



Regulated Spots



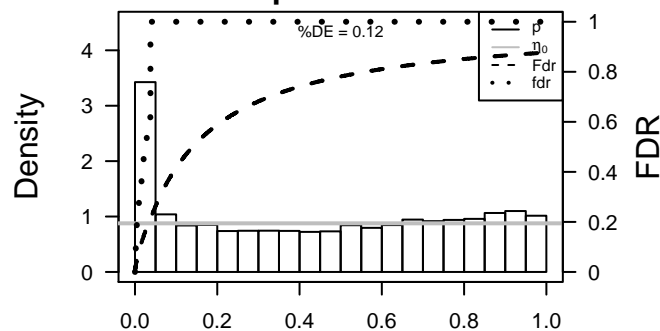
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	387695	2.06	2e-16	7e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
2	54544	1.59	2e-16	7e-14	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
3	1958	-1.73	2e-16	7e-14	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
4	2353	-2.07	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:t
5	2354	-1.99	2e-16	7e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source
6	2634	-1.56	2e-16	7e-14	47 x 1 guanylate binding protein 2, interferon-inducible [Source:HG
7	10804	1.55	2e-16	7e-14	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
8	2946	-1.56	2e-16	7e-14	50 x 50 glutathione S-transferase mu 2 (muscle) [Source:HGNC Syrr
9	121355	1.92	2e-16	7e-14	14 x 11 gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265
10	3001	-1.67	2e-16	7e-14	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associat
11	3122	-1.72	2e-16	7e-14	50 x 1 major histocompatibility complex, class II, DR alpha [Source:t
12	3489	1.66	2e-16	7e-14	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
13	3512	-1.81	2e-16	7e-14	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglob
14	3543	-1.85	2e-16	7e-14	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
15	53833	1.62	2e-16	7e-14	1 x 46 interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
16	3848	1.97	2e-16	7e-14	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
17	3860	-1.61	2e-16	7e-14	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
18	3880	-2.47	2e-16	7e-14	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
19	9119	1.55	2e-16	7e-14	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]
20	3856	-1.66	2e-16	7e-14	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.88	NULL	42	BP keratinization
2	15.5	NULL	21	CC cornified envelope
3	13.41	NULL	135	H.Tiss WIRTH_Mucosa
4	13.09	NULL	153	MF structural constituent of ribosome
5	12.89	NULL	1318	CC mitochondrion
6	12.73	NULL	253	BP translation
7	11.11	NULL	167	CC ribosome
8	10.18	NULL	128	BP translational initiation
9	9.94	NULL	53	BP keratinocyte differentiation
10	9.51	NULL	1233	TF KIM_MYC targets
11	9.38	NULL	92	BP translational elongation
12	9.31	NULL	87	BP translational termination
13	9.29	NULL	81	BP viral transcription
14	9.03	NULL	304	CC mitochondrial inner membrane
15	8.91	NULL	19	BP peptide cross-linking
16	8.56	NULL	152	BP cellular metabolic process
17	8.56	NULL	83	BP respiratory electron transport chain
18	8.42	NULL	92	BP viral life cycle
19	8.4	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
20	8.06	NULL	115	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated
<i>Underexpressed</i>				
1	-15.08	NULL	417	H.Tiss WIRTH_Immune system
2	-14.29	NULL	312	BP immune response
3	-13.98	NULL	553	Cancer Lembecke_Colonc Inflammation
4	-10.9	NULL	15	CC MHC class II protein complex
5	-10.85	NULL	10	GSEA C2PCHASSOT_SKIN_WOUND
6	-10.09	NULL	316	Cancer SPANG_BCL6-index2
7	-9.59	NULL	24	TF Tissue/AQUERIZAS_Trachea
8	-9.02	NULL	327	Lymphoma SPANG_CD40 6hrs UP
9	-8.99	NULL	274	Lymphoma SPANG_IL21 DN
10	-8.97	NULL	162	CC external side of plasma membrane
11	-8.77	NULL	47	BP antigen processing and presentation
12	-8.63	NULL	23	CC integral to luminal side of endoplasmic reticulum membrane
13	-8.29	NULL	60	BP T cell costimulation
14	-8.29	NULL	60	BP interferon-gamma-mediated signaling pathway
15	-8.24	NULL	11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
16	-8.12	NULL	32	CC ER to Golgi transport vesicle membrane
17	-8.12	NULL	1581	BP regulation of transcription, DNA-dependent
18	-8.09	NULL	823	MF sequence-specific DNA binding transcription factor activity
19	-7.97	NULL	126	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
20	-7.74	NULL	22	Lymphoma SPANG_NFKB BL DN

p-values



GW_265

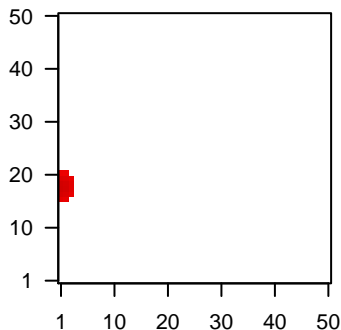
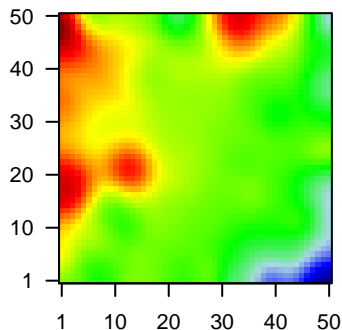
Local Summary

%DE = 0.87
 # metagenes = 16
 # genes = 211
 # genes in genesets = 209
 # genes with $fdr < 0.1 = 139$ (137 + / 2 -)
 # genes with $fdr < 0.05 = 119$ (117 + / 2 -)
 # genes with $fdr < 0.01 = 59$ (57 + / 2 -)

<r> metagenes = 0.97
 <r> genes = 0.32
 <FC> = 0.39
 <shrinkage-t> = 13.51
 <p-value> = 0.02
 <fdr> = 0.59

Profile

Spot



Local Genelist

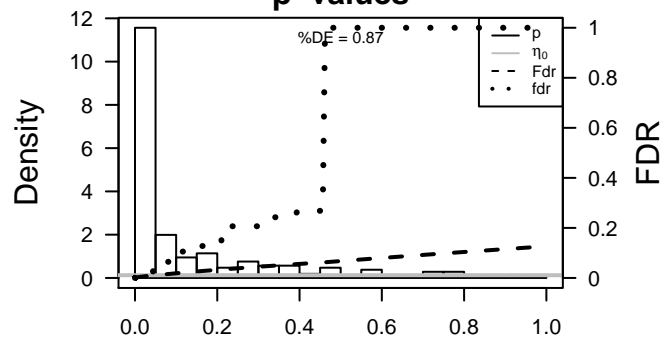
Rank	ID	log(FC)	fdr	p-value	Description
1	283869	-1.13	3e-09	7e-06	1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	51042	0.97	3e-07	7e-06	1 x 19 zinc finger protein 593 [Source:HGNC Symbol;Acc:30943]
3	1537	0.95	5e-07	1e-05	2 x 18 cytochrome c-1 [Source:HGNC Symbol;Acc:2579]
4	57761	0.93	9e-07	1e-05	1 x 17 tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]
5	4715	0.92	1e-06	2e-05	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22
6	10360	0.9	2e-06	1e-04	1 x 17 nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:
7	84948	0.83	1e-05	1e-04	1 x 16 tigger transposable element derived 5 [Source:HGNC Symbo
8	23246	0.82	1e-05	1e-04	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
9	430	0.82	2e-05	2e-04	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HG
10	54512	0.8	2e-05	2e-04	1 x 16 exosome component 4 [Source:HGNC Symbol;Acc:18189]
11	84300	0.78	4e-05	2e-04	2 x 18 ubiquinol-cytochrome c reductase complex assembly factor 2
12	2184	0.78	4e-05	2e-04	1 x 18 fumarylacetoacetate hydrolase (fumarylacetoacetase) [Sourc
13	728489	0.78	4e-05	2e-04	1 x 19 DNL-type zinc finger [Source:HGNC Symbol;Acc:33879]
14	6227	0.77	4e-05	3e-04	1 x 17 ribosomal protein S21 [Source:HGNC Symbol;Acc:10409]
15	51253	0.77	5e-05	5e-04	1 x 19 mitochondrial ribosomal protein L37 [Source:HGNC Symbol;A
16	29914	0.75	8e-05	5e-04	1 x 19 UbiA prenyltransferase domain containing 1 [Source:HGNC S
17	51025	0.74	1e-04	5e-04	3 x 18 presequence translocase-associated motor 16 homolog (S. c
18	26519	0.73	1e-04	5e-04	1 x 19 translocase of inner mitochondrial membrane 10 homolog (ye
19	55630	0.72	1e-04	5e-04	1 x 16 solute carrier family 39 (zinc transporter), member 4 [Source:
20	131076	-0.72	2e-04	5e-04	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	13.4	NULL	18 / 153	MF structural constituent of ribosome
2	12.98	NULL	5 / 19	CC mitochondrial small ribosomal subunit
3	11.3	NULL	20 / 253	BP translation
4	11.11	NULL	16 / 167	CC ribosome
5	9.46	NULL	3 / 13	BP ribosomal small subunit biogenesis
6	9.41	NULL	2 / 4	TF MYC_Cell growth and proliferation UP
7	9.41	NULL	3 / 14	GSEA C2PENG_RAPAMYCIN_RESPONSE_DN
8	8.74	NULL	11 / 96	BP rRNA processing
9	8.71	NULL	55 / 1318	CC mitochondrion
10	8.13	NULL	3 / 15	CC mitochondrial large ribosomal subunit
11	7.43	NULL	17 / 304	CC mitochondrial inner membrane
12	7.3	NULL	3 / 16	GSEA C2WONG_EMBRYONIC_STEM_CELL_CORE
13	7.29	NULL	2 / 14	GSEA C2REACTOME_CD28_CO_STIMULATION
14	7.29	NULL	2 / 14	GSEA C2REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING
15	6.99	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
16	6.99	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF
17	6.99	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
18	6.99	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
19	6.94	NULL	5 / 47	BP protein targeting to mitochondrion
20	6.81	NULL	4 / 23	CC mitochondrial ribosome
21	6.7	NULL	2 / 11	GSEA C2REACTOME_MTORC1_MEDIATED_SIGNALLING
22	6.69	NULL	7 / 83	BP respiratory electron transport chain
23	6.65	NULL	3 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
24	6.55	NULL	2 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN
25	6.55	NULL	5 / 34	MF NADH dehydrogenase (ubiquinone) activity
26	6.54	NULL	3 / 25	CC small ribosomal subunit
27	6.46	NULL	4 / 15	GSEA C2VANTVEER_BREAST_CANCER_BRCA1_UP
28	6.43	NULL	1 / 3	TF MYC_Tumor supressor genes UP
29	6.33	NULL	5 / 36	CC mitochondrial respiratory chain complex I
30	6.27	NULL	2 / 18	MF ribonucleoprotein complex binding
31	6.13	NULL	3 / 12	BP apoptotic nuclear changes
32	6.08	NULL	3 / 14	Pathw AcBENTINK_myc.1
33	6.04	NULL	1 / 9	GSEA C2MARZEC_IL2_SIGNALING_UP
34	5.97	NULL	3 / 16	GSEA C2NIKOLSKY_BREAST_CANCER_20Q11_AMPLICON
35	5.85	NULL	24 / 579	CC nucleolus
36	5.84	NULL	3 / 15	GSEA C2REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_P
37	5.76	NULL	2 / 14	GSEA C2REACTOME_PI3K_AKT_SIGNALLING
38	5.68	NULL	1 / 10	GSEA C2NOJIMA_SFRP2_TARGETS_UP
39	5.68	NULL	1 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
40	5.66	NULL	4 / 15	GSEA C2WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP

p-values



GW_265

Local Summary

%DE = 0.79
 # metagenes = 20
 # genes = 290
 # genes in genesets = 283

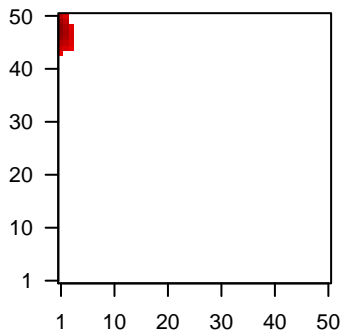
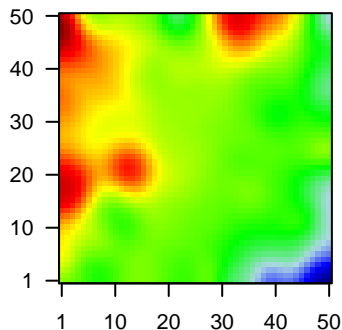
genes with $fdr < 0.1 = 192$ (170 + / 22 -)
 # genes with $fdr < 0.05 = 180$ (159 + / 21 -)
 # genes with $fdr < 0.01 = 138$ (122 + / 16 -)

$\langle r \rangle$ metagenes = 0.91
 $\langle r \rangle$ genes = 0.39

$\langle FC \rangle = 0.53$
 $\langle \text{shrinkage-t} \rangle = 18.7$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.39$

Profile

Spot



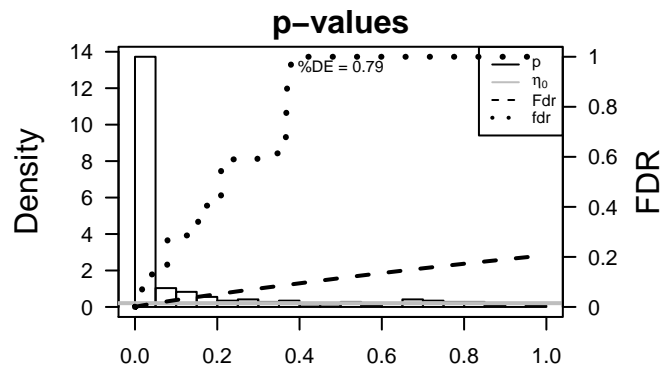
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	387695	2.06	2e-16	5e-16	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
2	54544	1.59	2e-16	5e-16	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
3	10804	1.55	2e-16	5e-16	1 x 47 gap junction protein, beta 6, 30kDa [Source:HGNC Symbol;A
4	3489	1.66	2e-16	5e-16	1 x 44 insulin-like growth factor binding protein 6 [Source:HGNC Sy
5	53833	1.62	2e-16	5e-16	1 x 46 interleukin 20 receptor beta [Source:HGNC Symbol;Acc:6004
6	3848	1.97	2e-16	5e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
7	3860	-1.61	2e-16	5e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
8	9119	1.55	2e-16	5e-16	1 x 44 keratin 75 [Source:HGNC Symbol;Acc:24431]
9	388533	2.74	2e-16	5e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
10	84648	2.36	2e-16	5e-16	1 x 48 late cornified envelope 3D [Source:HGNC Symbol;Acc:16615
11	3963	1.68	2e-16	5e-16	1 x 47 lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol
12	653499	1.84	2e-16	5e-16	1 x 47 lectin, galactoside-binding, soluble, 7 [Source:HGNC Symbol
13	643479	1.55	2e-16	5e-16	1 x 49
14	4014	1.94	2e-16	5e-16	2 x 48 loricrin [Source:HGNC Symbol;Acc:6663]
15	66004	1.78	2e-16	5e-16	1 x 50 Ly6/neurotoxin 1 [Source:HGNC Symbol;Acc:29604]
16	4118	-1.68	2e-16	5e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
17	5947	-2.21	2e-16	5e-16	1 x 43 retinol binding protein 1, cellular [Source:HGNC Symbol;Acc:!
18	6283	1.6	2e-16	5e-16	1 x 49 S100 calcium binding protein A12 [Source:HGNC Symbol;Acc
19	374897	2	2e-16	5e-16	1 x 49 suprabasin [Source:HGNC Symbol;Acc:24950]
20	57152	2.83	2e-16	5e-16	1 x 50 secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	42.72	NULL	18 / 21	CC cornified envelope
2	35.19	NULL	20 / 42	BP keratinization
3	33.32	NULL	82 / 135	H.Tiss WIRTH_Mucosa
4	30.34	NULL	24 / 53	BP keratinocyte differentiation
5	23.56	NULL	26 / 76	BP epidermis development
6	21.75	NULL	10 / 19	BP peptide cross-linking
7	20.35	NULL	106 / 572	Disease GUDJ_poriasis up
8	14.81	NULL	5 / 10	MF RAGE receptor binding
9	14.15	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
10	13.64	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
11	13.3	NULL	9 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
12	11.07	NULL	30 / 186	MF structural molecule activity
13	10.51	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
14	10.4	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
15	9.76	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
16	9.61	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
17	9.36	NULL	13 / 44	CC keratin filament
18	8.99	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
19	8.85	NULL	8 / 51	MF protein binding, bridging
20	8.37	NULL	6 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
21	8.32	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
22	8.23	NULL	3 / 10	GSEA C2AJULA_IL22_AND_IL17A_SIGNALING
23	7.9	NULL	12 / 21	CC desmosome
24	7.58	NULL	4 / 12	H.Tiss WIRTH_Prim_lymphoid_organ
25	7.48	NULL	5 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
26	7.37	NULL	5 / 23	MF peptidase inhibitor activity
27	7.37	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
28	7.35	NULL	3 / 10	GSEA C2NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
29	7.29	NULL	21 / 82	CC intermediate filament
30	7.24	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
31	7.03	NULL	64 / 1182	CC extracellular region
32	6.98	NULL	1 / 5	GSEA C2BUSA_SAM68_TARGETS_UP
33	6.91	NULL	14 / 79	MF serine-type endopeptidase inhibitor activity
34	6.89	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
35	6.84	NULL	11 / 82	MF structural constituent of cytoskeleton
36	6.75	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
37	6.71	NULL	5 / 16	GSEA C2JAEGER_METASTASIS_DN
38	6.55	NULL	2 / 7	GSEA C2YE_METASTATIC_LIVER_CANCER
39	6.41	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
40	6.39	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN



GW_265

Local Summary

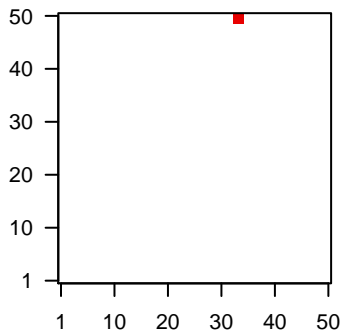
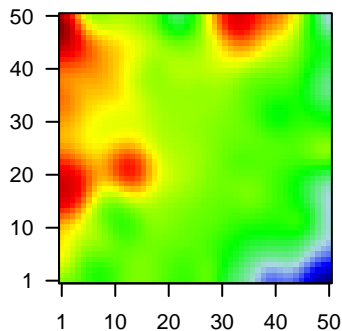
%DE = 0.92
 # metagenes = 4
 # genes = 60
 # genes in genesets = 58
 # genes with $fdr < 0.1 = 54$ (54 + / 0 -)
 # genes with $fdr < 0.05 = 48$ (48 + / 0 -)
 # genes with $fdr < 0.01 = 29$ (29 + / 0 -)

<r> metagenes = 0.99
 <r> genes = 0.32

<FC> = 0.44
 <shrinkage-t> = 15.39
 <p-value> = 0.01
 <fdr> = 0.54

Profile

Spot



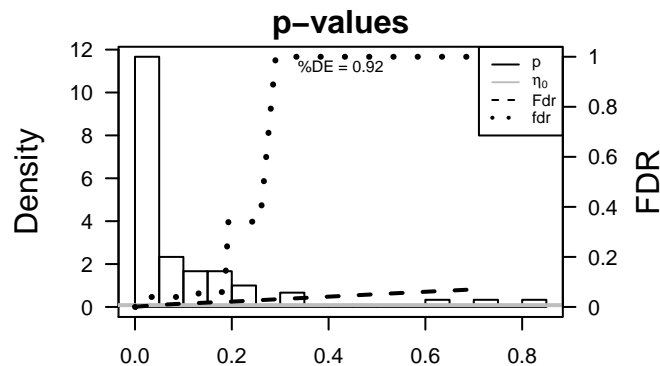
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	84833	1.03	5e-08	5e-05	33 x 50 up-regulated during skeletal muscle growth 5 homolog (mous
2	7388	0.84	1e-05	1e-04	33 x 50 ubiquinol-cytochrome c reductase hinge protein [Source:HG
3	441951	0.76	6e-05	1e-04	33 x 49 ZNF1 antisense RNA 1 [Source:HGNC Symbol;Acc:33101]
4	55505	0.75	7e-05	5e-04	34 x 50 NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:14378]
5	64976	0.71	2e-04	5e-04	34 x 50 mitochondrial ribosomal protein L40 [Source:HGNC Symbol;f
6	6147	0.68	3e-04	5e-04	33 x 49 ribosomal protein L23a [Source:HGNC Symbol;Acc:10317]
7	4701	0.67	4e-04	5e-04	34 x 49 NDUFA7 protein [Source:UniProtKB/TrEMBL;Acc:Q6FG42]
8	6390	0.65	6e-04	5e-04	34 x 49 succinate dehydrogenase complex, subunit B, iron sulfur (lp)
9	10799	0.64	8e-04	5e-04	34 x 50 ribonuclease P/MRP 40kDa subunit [Source:HGNC Symbol;f
10	51642	0.63	9e-04	5e-04	34 x 49 mitochondrial ribosomal protein L48 [Source:HGNC Symbol;f
11	10987	0.63	9e-04	5e-04	33 x 50 COP9 signalosome subunit 5 [Source:HGNC Symbol;Acc:22
12	6165	0.62	1e-03	5e-04	33 x 49 ribosomal protein L35a [Source:HGNC Symbol;Acc:10345]
13	29093	0.62	1e-03	2e-03	33 x 50 mitochondrial ribosomal protein L22 [Source:HGNC Symbol;f
14	4724	0.6	2e-03	2e-03	33 x 50 NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (f
15	28985	0.59	2e-03	2e-03	33 x 49 malignant T cell amplified sequence 1 [Source:HGNC Symbo
16	51020	0.56	3e-03	2e-03	34 x 50 HD domain containing 2 [Source:HGNC Symbol;Acc:21078]
17	4694	0.56	3e-03	2e-03	33 x 49 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7
18	26589	0.56	3e-03	2e-03	34 x 50 mitochondrial ribosomal protein L46 [Source:HGNC Symbol;f
19	51121	0.54	4e-03	2e-03	34 x 50 ribosomal protein L26-like 1 [Source:HGNC Symbol;Acc:170
20	653147	0.54	4e-03	4e-03	34 x 50

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	29.21	NULL	16 / 83	BP respiratory electron transport chain
2	21.07	NULL	16 / 152	BP cellular metabolic process
3	19.38	NULL	7 / 34	MF NADH dehydrogenase (ubiquinone) activity
4	19.08	NULL	7 / 35	BP mitochondrial electron transport, NADH to ubiquinone
5	18.78	NULL	7 / 36	CC mitochondrial respiratory chain complex I
6	17.47	NULL	19 / 304	CC mitochondrial inner membrane
7	16.64	NULL	2 / 8	GSEA C2REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
8	15.51	NULL	2 / 9	GSEA C2KEGG_RIBOSOME
9	15.51	NULL	2 / 9	GSEA C2REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBU
10	15.51	NULL	2 / 9	GSEA C2REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S
11	15.51	NULL	2 / 9	GSEA C2REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND
12	15.51	NULL	2 / 9	GSEA C2REACTOME_PEPTIDE_CHAIN_ELONGATION
13	15.51	NULL	2 / 9	GSEA C2REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
14	15.51	NULL	2 / 9	GSEA C2REACTOME_VIRAL_MRNA_TRANSLATION
15	14.57	NULL	2 / 10	GSEA C2REACTOME_TRANSLATION
16	14.56	NULL	2 / 10	CC large ribosomal subunit
17	14.33	NULL	3 / 23	CC mitochondrial ribosome
18	14.24	NULL	2 / 11	GSEA C2BIOCARTA_ETC_PATHWAY
19	13.37	NULL	2 / 11	Cancer GENTLES_modul5
20	13.32	NULL	4 / 26	MF cytochrome-c oxidase activity
21	13.25	NULL	2 / 13	CC mitochondrial respiratory chain
22	12.48	NULL	3 / 16	BP mitochondrial respiratory chain complex I assembly
23	12.29	NULL	2 / 19	CC mitochondrial proton-transporting ATP synthase complex
24	11.35	NULL	2 / 20	BP aerobic respiration
25	10.81	NULL	27 / 1318	CC mitochondrion
26	10.74	NULL	7 / 153	MF structural constituent of ribosome
27	10.57	NULL	2 / 10	GSEA C2CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_1
28	10.25	NULL	7 / 167	CC ribosome
29	10.24	NULL	1 / 7	MMML C6SCIEJ_MMML_48
30	10.06	NULL	1 / 2	miRNA target-375
31	10.04	NULL	3 / 18	MF 2 iron, 2 sulfur cluster binding
32	10	NULL	2 / 16	GSEA C2LAHO_COLORECTAL_CANCER_SERRATED_UP
33	9.42	NULL	2 / 16	GSEA C2BARIS_THYROID_CANCER_UP
34	9.39	NULL	8 / 253	BP translation
35	8.92	NULL	2 / 12	BP oxidative phosphorylation
36	8.86	NULL	4 / 81	BP viral transcription
37	8.77	NULL	5 / 128	BP translational initiation
38	8.5	NULL	4 / 87	BP translational termination
39	8.44	NULL	1 / 12	GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP
40	8.31	NULL	2 / 27	MF rRNA binding



GW_265

Local Summary

%DE = 0.91
 # metagenes = 18
 # genes = 289
 # genes in genesets = 286

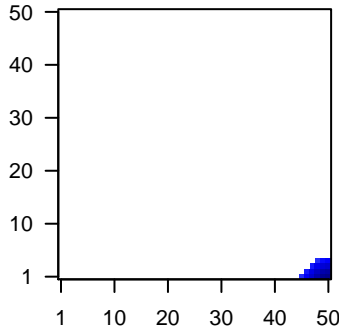
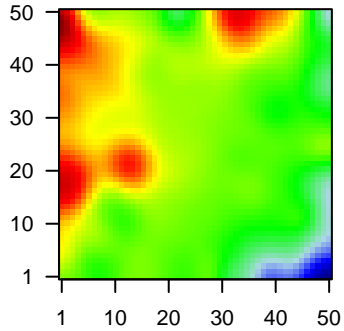
genes with $fdr < 0.1 = 256$ (2 + / 254 -)
 # genes with $fdr < 0.05 = 245$ (2 + / 243 -)
 # genes with $fdr < 0.01 = 159$ (2 + / 157 -)

<r> metagenes = 0.99
 <r> genes = 0.57

<FC> = -0.62
 <shrinkage-t> = -21.63
 <p-value> = 0
 <fdr> = 0.39

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	2634	-1.56	2e-16	7e-16	47 x 1 guanylate binding protein 2, interferon-inducible [Source:HGNC]
2	3001	-1.67	2e-16	7e-16	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated
3	3122	-1.72	2e-16	7e-16	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC]
4	3512	-1.81	2e-16	7e-16	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin
5	3543	-1.85	2e-16	7e-16	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:1677]
6	3936	-1.63	2e-16	7e-16	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:1677]
7	10628	-1.89	2e-16	7e-16	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:1677]
8	10537	-1.58	2e-16	7e-16	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
9	5920	-1.52	1e-15	3e-14	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC Symbol;Acc:1677]
10	4283	-1.5	2e-15	5e-14	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Acc:1677]
11	5996	-1.49	4e-15	1e-13	50 x 1 regulator of G-protein signaling 1 [Source:HGNC Symbol;Acc:1677]
12	3002	-1.47	8e-15	7e-13	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
13	3123	-1.44	4e-14	7e-13	45 x 1 major histocompatibility complex, class II, DR beta 1 [Source:HGNC]
14	54855	-1.42	6e-14	7e-13	49 x 1 family with sequence similarity 46, member C [Source:HGNC]
15	25849	-1.41	9e-14	1e-12	50 x 2 prostate androgen-regulated mucin-like protein 1 [Source:HGNC]
16	915	-1.4	1e-13	1e-12	49 x 1 CD3d molecule, delta (CD3-TCR complex) [Source:HGNC Symbol;Acc:1677]
17	3113	-1.39	2e-13	1e-12	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC]
18	115361	-1.39	2e-13	2e-11	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048]
19	919	-1.34	2e-12	2e-11	50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]
20	5552	-1.33	2e-12	2e-10	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-34.45	NULL	13 / 15	CC MHC class II protein complex
2	-30.05	NULL	93 / 417	H.Tiss WIRTH_Immune system
3	-25.46	NULL	54 / 312	BP immune response
4	-24.45	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
5	-22.44	NULL	18 / 60	BP T cell costimulation
6	-22.39	NULL	97 / 553	Cancer Lembcke_Colonc Inflammation
7	-22.01	NULL	16 / 47	BP antigen processing and presentation
8	-21.86	NULL	7 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
9	-20.83	NULL	8 / 21	CC clathrin-coated endocytic vesicle membrane
10	-20.08	NULL	3 / 3	MMML C6SCIEJ_MMML 7
11	-19.84	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
12	-19.8	NULL	8 / 23	CC integral to luminal side of endoplasmic reticulum membrane
13	-19.61	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
14	-19.56	NULL	6 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
15	-19.14	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDDP_SIGNATURE
16	-19.08	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
17	-19.04	NULL	6 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
18	-18.36	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
19	-18.19	NULL	2 / 4	MMML C6SCIEJ_MMML 2
20	-17.74	NULL	8 / 28	CC transport vesicle membrane
21	-17.29	NULL	18 / 84	BP T cell receptor signaling pathway
22	-17.25	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
23	-16.46	NULL	8 / 32	CC ER to Golgi transport vesicle membrane
24	-15.79	NULL	9 / 35	CC trans-Golgi network membrane
25	-15.25	NULL	7 / 13	Cancer GENTLES_modul18
26	-15.24	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
27	-15.22	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
28	-14.92	NULL	5 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
29	-14.77	NULL	12 / 60	BP interferon-gamma-mediated signaling pathway
30	-14.12	NULL	18 / 74	BP regulation of immune response
31	-14	NULL	44 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
32	-14	NULL	44 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
33	-14	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
34	-14	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
35	-13.8	NULL	4 / 8	GSEA C2BIOCARTA_TCRA_PATHWAY
36	-13.79	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
37	-13.7	NULL	4 / 8	GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN
38	-13.68	NULL	5 / 14	GSEA C2BIOCARTA_NO2I12_PATHWAY
39	-13.59	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
40	-13.56	NULL	9 / 46	CC endocytic vesicle membrane

p-values

