

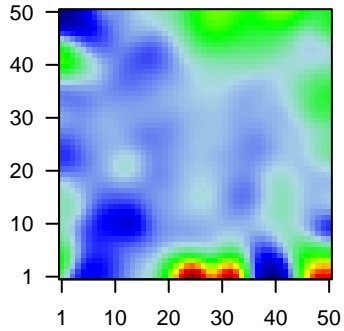
GW_229

Global Summary

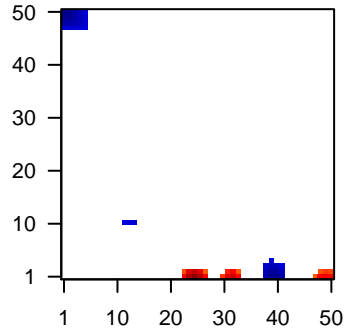
%DE = 0.12
 # genes with fdr < 0.2 = 1532 (878 + / 654 -)
 # genes with fdr < 0.1 = 1170 (690 + / 480 -)
 # genes with fdr < 0.05 = 1061 (630 + / 431 -)
 # genes with fdr < 0.01 = 740 (459 + / 281 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.88

Profile



Regulated Spots



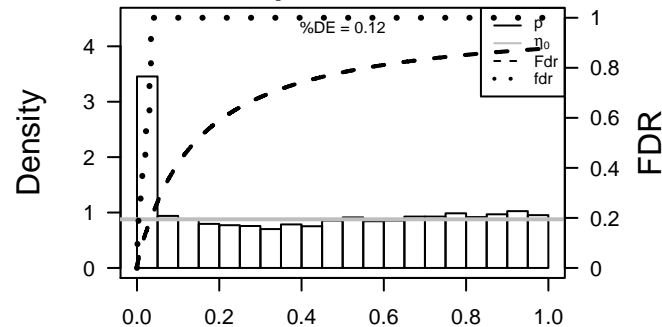
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	79852	-1.19	2e-16	3e-14	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	58	2.47	2e-16	3e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	2.48	2e-16	3e-14	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	131	-1.76	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
5	218	1.19	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
6	445	1.62	2e-16	3e-14	50 x 47 argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
7	330	1.66	2e-16	3e-14	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
8	260436	-1.21	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
9	810	-1.23	2e-16	3e-14	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
10	51806	-1.8	2e-16	3e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
11	131076	1.24	2e-16	3e-14	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
12	4680	1.13	2e-16	3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
13	1056	1.32	2e-16	3e-14	50 x 50 carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
14	1114	2.18	2e-16	3e-14	25 x 1 chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc
15	1158	1.86	2e-16	3e-14	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
16	22802	2.27	2e-16	3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
17	9076	1.77	2e-16	3e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
18	84518	-1.31	2e-16	3e-14	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
19	1359	1.41	2e-16	3e-14	50 x 7 carboxypeptidase A3 (mast cell) [Source:HGNC Symbol;Acc:
20	1382	1.25	2e-16	3e-14	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	15.59	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
2	15.52	NULL	127	H.Tiss WIRTH_Muscle
3	15.18	NULL	51	BP type I interferon signaling pathway
4	14.34	NULL	36	BP muscle filament sliding
5	13.53	NULL	16	H.Tiss WIRTH_Hippocampus
6	12.49	NULL	16	GSEA C2MOSELERLE_IFNA_RESPONSE
7	12.47	NULL	16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
8	11.85	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
9	11.19	NULL	31	BP negative regulation of viral genome replication
10	10.98	NULL	109	BP response to virus
11	10.89	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
12	10.79	NULL	204	BP cytokine-mediated signaling pathway
13	10.37	NULL	44	MF structural constituent of muscle
14	10.3	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
15	10.28	NULL	12	CC myosin filament
16	9.89	NULL	123	BP defense response to virus
17	9.83	NULL	60	BP interferon-gamma-mediated signaling pathway
18	9.49	NULL	10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
19	9.35	NULL	449	Chr Chr 20
20	8.94	NULL	312	BP immune response
<i>Underexpressed</i>				
1	-8.25	NULL	8	GSEA C2RUNNE_GENDER_EFFECT_UP
2	-8.07	NULL	618	Chr Chr 4
3	-7.96	NULL	7	MMML C2SCIEJ_MMML 5
4	-7.44	NULL	33	BP cholesterol biosynthetic process
5	-7.06	NULL	630	Chr Chr X
6	-6.56	NULL	15	GSEA C2REACTOME_CHOLESTEROL_BIOSYNTHESIS
7	-5.79	NULL	34	Chr Chr Y
8	-5.77	NULL	15	GSEA C2PODAR_RESPONSE_TO_ADAPHOSTIN_DN
9	-5.67	NULL	10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
10	-5.32	NULL	14	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B
11	-5.32	NULL	135	H.Tiss WIRTH_Mucosa
12	-5.26	NULL	42	BP keratinization
13	-4.93	NULL	14	BP isoprenoid biosynthetic process
14	-4.69	NULL	21	CC cornified envelope
15	-4.64	NULL	14	GSEA C2KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS
16	-4.53	NULL	39	BP retinoid metabolic process
17	-4.53	NULL	16	GSEA C2MENSE_HYPOXIA_UP
18	-4.51	NULL	2	Cancer GENTLES_modul8
19	-4.47	NULL	15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
20	-4.39	NULL	14	MF glutathione peroxidase activity

p-values



GW_229

Local Summary

%DE = 0.95
 # metagenes = 10
 # genes = 105
 # genes in genesets = 105
 # genes with $fdr < 0.1$ = 91 (90 + / 1 -)
 # genes with $fdr < 0.05$ = 87 (86 + / 1 -)
 # genes with $fdr < 0.01$ = 65 (65 + / 0 -)

<r> metagenes = 0.98

<r> genes = 0.64

<FC> = 0.64

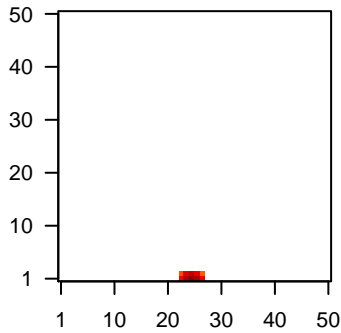
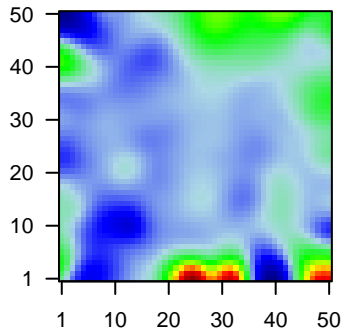
<shrinkage-t> = 22.37

<p-value> = 0

<fdr> = 0.36

Profile

Spot



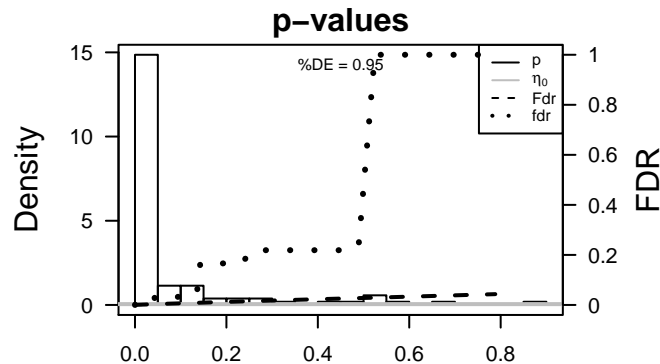
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	58	2.47	2e-16	6e-17	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	2.48	2e-16	6e-17	25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	1114	2.18	2e-16	6e-17	25 x 1 chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc:1
4	1158	1.86	2e-16	6e-17	25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
5	115265	1.79	2e-16	6e-17	25 x 1 DNA-damage-inducible transcript 4-like [Source:HGNC Syrr
6	10324	1.36	2e-16	6e-17	25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:169
7	4151	2.12	2e-16	6e-17	25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]
8	4608	1.91	2e-16	6e-17	25 x 1 myosin binding protein H [Source:HGNC Symbol;Acc:7552]
9	4619	1.31	2e-16	6e-17	25 x 1 myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC
10	4620	1.95	2e-16	6e-17	25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC
11	4632	1.13	2e-16	6e-17	25 x 1 myosin, light chain 1, alkali; skeletal, fast [Source:HGNC Sym
12	4633	1.05	2e-16	6e-17	25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC
13	9499	1.42	2e-16	6e-17	25 x 1 myotilin [Source:HGNC Symbol;Acc:12399]
14	4703	1.29	2e-16	6e-17	25 x 1 nebulin [Source:HGNC Symbol;Acc:7720]
15	6588	1.99	2e-16	6e-17	25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]
16	7134	1.1	2e-16	6e-17	25 x 1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]
17	7136	1.06	2e-16	6e-17	25 x 1 troponin I type 2 (skeletal, fast) [Source:HGNC Symbol;Acc:1
18	7140	1.31	2e-16	6e-17	25 x 1 troponin T type 3 (skeletal, fast) [Source:HGNC Symbol;Acc:1
19	27295	1.02	1e-15	2e-14	25 x 1 PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:20767]
20	1134	1	6e-15	2e-14	25 x 1 cholinergic receptor, nicotinic, alpha 1 (muscle) [Source:HGNC

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	60.04	NULL	11 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F
2	54.53	NULL	23 / 36	BP muscle filament sliding
3	51.47	NULL	57 / 127	H.Tiss WIRTH_Muscle
4	50.87	NULL	11 / 16	H.Tiss WIRTH_Hippocampus
5	43.57	NULL	10 / 12	CC myosin filament
6	38.72	NULL	22 / 44	MF structural constituent of muscle
7	31.39	NULL	8 / 14	CC contractile fiber
8	29.64	NULL	8 / 13	CC muscle myosin complex
9	28.84	NULL	12 / 37	CC sarcomere
10	27.79	NULL	23 / 84	BP muscle contraction
11	24.55	NULL	6 / 12	BP skeletal muscle contraction
12	23.68	NULL	15 / 34	CC myofibril
13	22.37	NULL	5 / 11	BP cardiac muscle tissue morphogenesis
14	22.08	NULL	3 / 15	Cancer BEN-PORATH_UP
15	20.82	NULL	1 / 5	GSEA C2LIU_VAV3_PROSTATE_CARCINOGENESIS_UP
16	20.63	NULL	9 / 37	BP cardiac muscle contraction
17	20.57	NULL	9 / 20	CC I band
18	20.11	NULL	2 / 6	GSEA C2BIOCARTA_HSP27_PATHWAY
19	19.28	NULL	21 / 88	CC Z disc
20	19.1	NULL	2 / 10	BP heart contraction
21	18.79	NULL	8 / 16	CC M band
22	18.06	NULL	4 / 11	CC A band
23	17.83	NULL	2 / 20	MF myosin binding
24	16.33	NULL	7 / 15	BP striated muscle contraction
25	15.52	NULL	3 / 16	GSEA C2DAVICIONI_TARGETS_OF_PAX3_FOXO1_FUSIONS_DN
26	15.17	NULL	7 / 12	MF titin binding
27	15.11	NULL	6 / 18	BP regulation of muscle contraction
28	15.09	NULL	3 / 15	GSEA C2EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION
29	15.04	NULL	3 / 15	BP actin filament-based movement
30	14.99	NULL	7 / 15	GSEA C2REACTOME_STRIATED_MUSCLE_CONTRACTION
31	14.94	NULL	8 / 42	CC myosin complex
32	14.87	NULL	4 / 16	MF microfilament motor activity
33	14.49	NULL	25 / 297	MF actin binding
34	14.24	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_GONADOTROPHINS_DN
35	14.24	NULL	2 / 16	GSEA C2SASSON_RESPONSE_TO_FORSKOLIN_DN
36	14.18	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_UP
37	14.18	NULL	1 / 9	GSEA C2PENG_GLUCOSE_DEPRIVATION_DN
38	13.31	NULL	3 / 37	CC actin filament
39	13.29	NULL	1 / 10	GSEA C2BIOCARTA_EPHA4_PATHWAY
40	13.05	NULL	2 / 15	BP skeletal muscle fiber development



GW_229

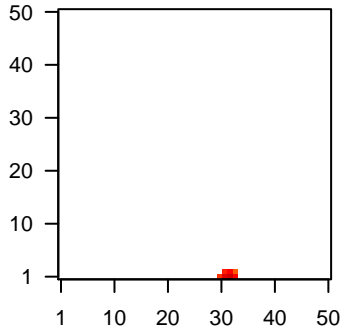
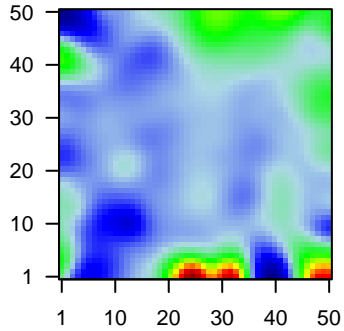
Local Summary

%DE = 0.95
 # metagenes = 7
 # genes = 120
 # genes in genesets = 118
 # genes with $fdr < 0.1 = 105$ (104 + / 1 -)
 # genes with $fdr < 0.05 = 100$ (99 + / 1 -)
 # genes with $fdr < 0.01 = 96$ (95 + / 1 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.45
 $\langle FC \rangle = 0.56$
 $\langle \text{shrinkage-t} \rangle = 19.69$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.22$

Profile

Spot



Local Genelist

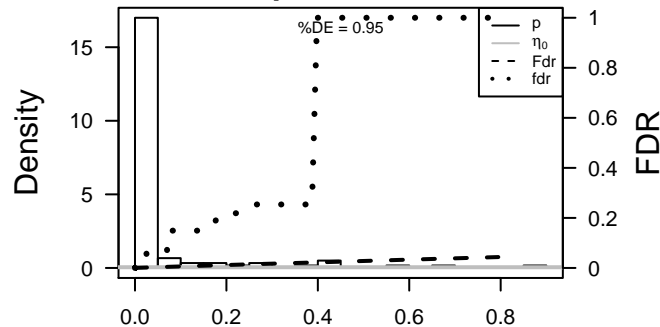
Rank	ID	log(FC)	fdr	p-value	Description
1	6373	1.42	2e-16	1e-16	32 x 1 chemokine (C-X-C motif) ligand 11 [Source:HGNC Symbol;Acc:100000000]
2	94240	1.29	2e-16	1e-16	32 x 1 epithelial stromal interaction 1 (breast) [Source:HGNC Symbol;Acc:100000000]
3	10866	1.11	2e-16	1e-16	32 x 1 HLA complex P5 (non-protein coding) [Source:HGNC Symbol;Acc:100000000]
4	3134	1.2	2e-16	1e-16	32 x 1 major histocompatibility complex, class I, F [Source:HGNC Symbol;Acc:100000000]
5	3136	1.15	2e-16	1e-16	32 x 1
6	10964	1.11	2e-16	1e-16	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Acc:100000000]
7	3433	1.07	2e-16	1e-16	32 x 1 interferon-induced protein with tetratricopeptide repeats 2 [Source:HGNC Symbol;Acc:100000000]
8	10581	1	2e-16	1e-16	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC Symbol;Acc:100000000]
9	10410	1.18	2e-16	1e-16	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC Symbol;Acc:100000000]
10	9636	1.05	2e-16	1e-16	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:100000000]
11	4061	1.09	2e-16	1e-16	32 x 1 lymphocyte antigen 6 complex, locus E [Source:HGNC Symbol;Acc:100000000]
12	54922	-1.13	2e-16	1e-16	30 x 1 Ras interacting protein 1 [Source:HGNC Symbol;Acc:24716]
13	8743	1.17	2e-16	1e-16	32 x 1 tumor necrosis factor (ligand) superfamily, member 10 [Source:HGNC Symbol;Acc:100000000]
14	4599	0.96	4e-16	5e-15	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible [Source:HGNC Symbol;Acc:100000000]
15	8519	1.02	1e-15	2e-14	32 x 1 interferon induced transmembrane protein 1 [Source:HGNC Symbol;Acc:100000000]
16	2633	1	5e-15	8e-14	32 x 1 guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:100000000]
17	55601	0.98	2e-14	1e-13	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC Symbol;Acc:100000000]
18	3628	0.97	4e-14	1e-13	33 x 1 inositol polyphosphate-1-phosphatase [Source:HGNC Symbol;Acc:100000000]
19	10346	0.96	7e-14	1e-13	32 x 1 tripartite motif containing 22 [Source:HGNC Symbol;Acc:1631]
20	115362	0.95	9e-14	1e-13	32 x 1 guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	55.7	NULL	29 / 51	BP type I interferon signaling pathway
2	52.4	NULL	12 / 16	GSEA C2MOSERLE_IFNA_RESPONSE
3	47.84	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	44.26	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
5	43.67	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
6	42.63	NULL	6 / 6	Lymphocyte antigen 6 complex, locus E
7	40.83	NULL	11 / 16	GSEA C2FINAV_INTERFERON_SIGNATURE_IN_CANCER
8	39.49	NULL	10 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQIMOD
9	37.33	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
10	37.16	NULL	13 / 31	BP negative regulation of viral genome replication
11	37.08	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
12	37.03	NULL	31 / 123	BP defense response to virus
13	36.82	NULL	2 / 2	MMML C6SCIEJ_MMML 27
14	35.63	NULL	7 / 10	CC MHC class I protein complex
15	34.22	NULL	27 / 109	BP response to virus
16	34.1	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
17	30.27	NULL	6 / 14	GSEA C2RADEVA_RESPONSE_TO_IFNA1_UP
18	30.14	NULL	34 / 204	BP cytokine-mediated signaling pathway
19	29.54	NULL	6 / 12	GSEA C2TSAL_DNAJB4_TARGETS_UP
20	28.03	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
21	26.97	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
22	26.81	NULL	16 / 60	BP interferon-gamma-mediated signaling pathway
23	26.61	NULL	6 / 14	GSEA C2KU_AKT1_TARGETS_6HR
24	25.77	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
25	24.9	NULL	7 / 18	MF peptide antigen binding
26	24.71	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
27	24.58	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
28	24.58	NULL	3 / 4	MMML C6SCIEJ_MMML 47
29	23.58	NULL	31 / 274	Lymphocyte antigen 6 complex, locus E
30	23.19	NULL	6 / 16	GSEA C2KU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
31	23.12	NULL	5 / 16	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP
32	23.1	NULL	46 / 572	Disease GUDJ_poriasis up
33	20.58	NULL	5 / 18	BP response to interferon-gamma
34	19.88	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
35	19.75	NULL	4 / 12	GSEA C2ZHU_CMV_8_HR_UP
36	19.43	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
37	19.43	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
38	19.3	NULL	3 / 5	GSEA C2BROWNE_INTERFERON_RESPONSIVE_GENES
39	19.24	NULL	28 / 312	BP immune response
40	19	NULL	4 / 10	GSEA C2GRANDVAUX_IRF3_TARGETS_UP

p-values



GW_229

Local Summary

%DE = 0.72
 # metagenes = 7
 # genes = 175
 # genes in genesets = 173

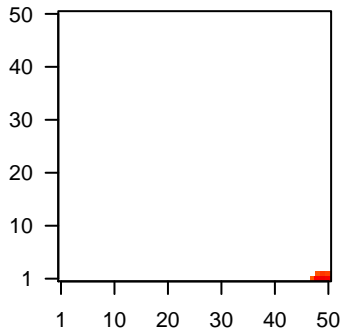
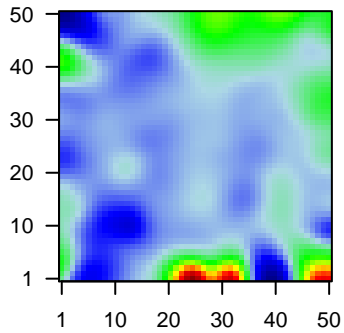
 # genes with $fdr < 0.1$ = 88 (86 + / 2 -)
 # genes with $fdr < 0.05$ = 75 (74 + / 1 -)
 # genes with $fdr < 0.01$ = 53 (52 + / 1 -)

 $\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.65

 $\langle FC \rangle$ = 0.32
 $\langle \text{shrinkage-t} \rangle$ = 11.21
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.57

Profile

Spot



Local Genelist

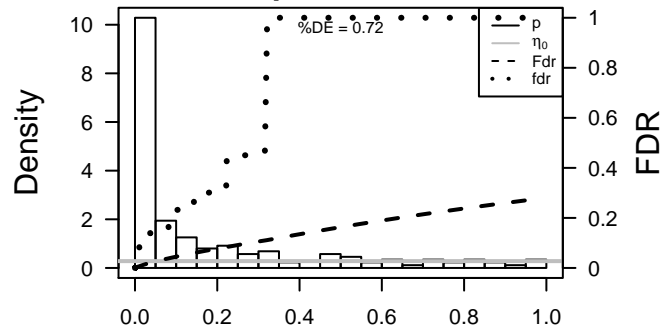
Rank	ID	log(FC)	fdr	p-value	Description
1	330	1.86	2e-16	1e-15	47 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:10342]
2	260436	-1.21	2e-16	1e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:10342]
3	3120	1.05	2e-16	1e-15	47 x 1 major histocompatibility complex, class II, DQ beta 2 [Source:HGNC Symbol;Acc:10342]
4	3126	1.17	2e-16	1e-15	50 x 1 major histocompatibility complex, class II, DR beta 4 [Source:HGNC Symbol;Acc:10342]
5	3620	1.96	2e-16	1e-15	48 x 1 indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:10342]
6	3512	1.33	2e-16	1e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunoglobulin J [Source:HGNC Symbol;Acc:10342]
7	3543	1.03	2e-16	1e-15	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Symbol;Acc:10342]
8	5920	1.15	2e-16	1e-15	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC Symbol;Acc:10342]
9	972	1.04	4e-16	4e-13	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:10342]
10	3113	0.99	8e-15	2e-11	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:10342]
11	3122	0.86	5e-13	5e-10	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:10342]
12	10537	0.87	1e-11	9e-10	50 x 1 ubiquitin D [Source:HGNC Symbol;Acc:18795]
13	6352	0.85	3e-11	1e-08	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:10342]
14	115361	0.8	5e-10	1e-08	48 x 1 guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048]
15	2634	0.8	5e-10	1e-07	47 x 1 guanylate binding protein 2, interferon-inducible [Source:HGNC Symbol;Acc:10342]
16	54855	0.76	3e-09	1e-07	49 x 1 family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:10342]
17	3575	0.75	6e-09	1e-07	50 x 2 interleukin 7 receptor [Source:HGNC Symbol;Acc:6024]
18	5880	0.74	8e-09	1e-06	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP-binding protein RhoC) [Source:HGNC Symbol;Acc:10342]
19	10628	0.7	3e-08	3e-06	48 x 1 thioredoxin interacting protein [Source:HGNC Symbol;Acc:16]
20	3001	0.67	2e-07	3e-06	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated protein 10) [Source:HGNC Symbol;Acc:10342]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	45.94	NULL	12 / 15	CC MHC class II protein complex
2	28.3	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
3	27.9	NULL	3 / 5	GSEA C2WONG_ENDOMETRIAL_CANCER_LATE
4	27.63	NULL	14 / 47	BP antigen processing and presentation
5	26.93	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
6	26.43	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
7	24.23	NULL	2 / 4	MMML C6SCIEJ_MMML_2
8	24.19	NULL	7 / 28	CC transport vesicle membrane
9	24.11	NULL	3 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
10	22.49	NULL	7 / 32	CC ER to Golgi transport vesicle membrane
11	22.29	NULL	41 / 312	BP immune response
12	22.04	NULL	74 / 417	H.Tiss WIRTH_Immune system
13	21.42	NULL	7 / 35	CC trans-Golgi network membrane
14	20.33	NULL	3 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUMOD
15	19.64	NULL	13 / 60	BP T cell costimulation
16	19.14	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
17	18.45	NULL	7 / 46	CC endocytic vesicle membrane
18	17.86	NULL	3 / 7	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
19	17.1	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
20	16.35	NULL	12 / 87	BP antigen processing and presentation of exogenous peptide antigen
21	16.35	NULL	5 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
22	16.29	NULL	9 / 60	BP interferon-gamma-mediated signaling pathway
23	16.08	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
24	15.63	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
25	15.56	NULL	66 / 553	Cancer Lembcke_Colonc Inflammation
26	15.27	NULL	2 / 5	GSEA C2WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
27	15.11	NULL	8 / 52	Chr HSCR6_MHC_QBL
28	14.42	NULL	11 / 84	BP T cell receptor signaling pathway
29	14.34	NULL	5 / 12	BP immunoglobulin mediated immune response
30	14.33	NULL	4 / 22	BP positive regulation of interleukin-12 production
31	14.26	NULL	1 / 7	GSEA C2WONG_IFNA2_RESISTANCE_UP
32	13.72	NULL	1 / 10	BP tryptophan catabolic process
33	13.63	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
34	13.58	NULL	3 / 16	GSEA C2BIOCARTA_CASPASE_PATHWAY
35	13.34	NULL	4 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
36	13.29	NULL	2 / 11	GSEA C2FUJII_YBX1_TARGETS_UP
37	13.2	NULL	1 / 8	GSEA C2GALI_TP53_TARGETS_APOPTOTIC_UP
38	13.08	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
39	13	NULL	1 / 11	GSEA C2NAKAJIMA_EOSINOPHIL
40	12.36	NULL	21 / 162	CC external side of plasma membrane

p-values



GW_229

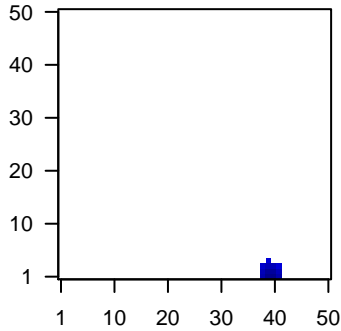
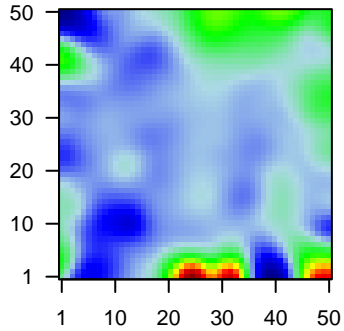
Local Summary

%DE = 0.8
 # metagenes = 13
 # genes = 211
 # genes in genesets = 186
 # genes with $fdr < 0.1 = 107$ (2 + / 105 -)
 # genes with $fdr < 0.05 = 70$ (2 + / 68 -)
 # genes with $fdr < 0.01 = 24$ (0 + / 24 -)

<r> metagenes = 0.99
 <r> genes = 0.52
 <FC> = -0.21
 <shrinkage-t> = -7.55
 <p-value> = 0.04
 <fdr> = 0.73

Profile

Spot



Local Genelist

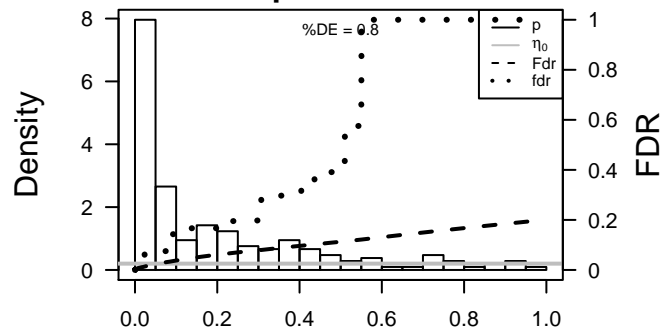
Rank	ID	log(FC)	fdr	p-value	Description
1	440503	-0.69	6e-08	2e-06	39 x 1 perlipin 5 [Source:HGNC Symbol;Acc:33196]
2	440157	-0.68	1e-07	1e-04	39 x 1
3	618	-0.6	2e-06	1e-04	39 x 1 brain cytoplasmic RNA 1 [Source:HGNC Symbol;Acc:1022]
4	22980	-0.59	5e-06	5e-04	41 x 2 transcription factor 25 (basic helix-loop-helix) [Source:HGNC
5	155060	-0.53	3e-05	5e-04	39 x 4
6	8225	-0.53	3e-05	5e-04	41 x 3 GTP binding protein 6 (putative) [Source:HGNC Symbol;Acc:
7	80224	-0.53	4e-05	1e-03	40 x 1 nucleotide binding protein-like [Source:HGNC Symbol;Acc:2t
8	653399	-0.5	1e-04	1e-03	39 x 1 glutathione S-transferase theta pseudogene 2 [Source:HGNC
9	641737	-0.46	1e-04	3e-03	40 x 1
10	440275	-0.47	2e-04	3e-03	40 x 1 eukaryotic translation initiation factor 2 alpha kinase 4 [Source
11	80233	-0.46	3e-04	3e-03	41 x 1 chromosome 17 open reading frame 70 [Source:HGNC Synt
12	250	-0.46	3e-04	3e-03	40 x 1 alkaline phosphatase, placental [Source:HGNC Symbol;Acc:4
13	401494	-0.45	4e-04	3e-03	40 x 1 protein tyrosine phosphatase-like A domain containing 2 [Soi
14	125050	-0.45	5e-04	3e-03	40 x 1 RNA, 7SK small nuclear [Source:HGNC Symbol;Acc:10037]
15	728903	-0.44	5e-04	4e-03	39 x 1
16	146059	-0.4	6e-04	4e-03	40 x 1 codanin 1 [Source:HGNC Symbol;Acc:1713]
17	23132	-0.43	8e-04	4e-03	40 x 3 RAD54-like 2 (S. cerevisiae) [Source:HGNC Symbol;Acc:291
18	256364	-0.43	8e-04	6e-03	41 x 3 echinoderm microtubule associated protein like 3 [Source:HG
19	9647	-0.42	1e-03	6e-03	40 x 3 protein phosphatase, Mg2+/Mn2+ dependent, 1F [Source:HG
20	401261	-0.42	1e-03	6e-03	41 x 1

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.29	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-7.34	NULL	2 / 13	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN
3	-6.89	NULL	2 / 14	BP mitochondrion morphogenesis
4	-6.83	NULL	2 / 14	BP cellular response to estradiol stimulus
5	-5.8	NULL	2 / 15	GSEA C2FIRESTEIN_PROLIFERATION
6	-5.61	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
7	-5.59	NULL	3 / 14	MMML C6SCIEJ_MMML 8
8	-5.49	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
9	-5.44	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
10	-5.36	NULL	1 / 4	GSEA C2KORKOLA_CHORIOCARCINOMA
11	-5.28	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
12	-5.16	NULL	2 / 16	BP cognition
13	-5.07	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
14	-5.07	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
15	-4.99	NULL	1 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
16	-4.93	NULL	2 / 15	GSEA C2CAIRO_HEPATOBLASTOMA_UP
17	-4.9	NULL	1 / 9	GSEA C2ROWELL_AGING_KIDNEY_UP
18	-4.84	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
19	-4.82	NULL	1 / 11	GSEA C2BIOCARTA_EIF2_PATHWAY
20	-4.78	NULL	1 / 4	MMML C6SCIEJ_MMML 44
21	-4.71	NULL	1 / 11	GSEA C2KEGG_FOLATE_BIOSYNTHESIS
22	-4.65	NULL	2 / 23	BP protein N-linked glycosylation
23	-4.52	NULL	1 / 10	BP positive regulation of chemotaxis
24	-4.42	NULL	1 / 16	BP ferrous iron transmembrane transporter activity
25	-4.42	NULL	1 / 16	BP ferrous iron transport
26	-4.4	NULL	3 / 54	BP intrinsic apoptotic signaling pathway
27	-4.39	NULL	1 / 16	BP mitochondrial respiratory chain complex I assembly
28	-4.31	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
29	-4.15	NULL	1 / 12	GSEA C2SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12
30	-4.12	NULL	3 / 24	BP negative regulation of T cell proliferation
31	-4.11	NULL	1 / 14	GSEA C2WANG_PROSTATE_CANCER_ANDROGEN_INDEPENDENT
32	-4.06	NULL	1 / 10	CC oligosaccharyltransferase complex
33	-3.96	NULL	1 / 13	GSEA C2SENGUPTA_EBNA1_ANTICORRELATED
34	-3.95	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
35	-3.95	NULL	1 / 15	GSEA C2REACTOME_FANCONI_ANEMIA_PATHWAY
36	-3.88	NULL	2 / 15	GSEA C2ZHOU_INFLAMMATORY_RESPONSE_LIVE_DN
37	-3.88	NULL	2 / 15	GSEA C2ZHOU_INFLAMMATORY_RESPONSE_LPS_DN
38	-3.81	NULL	1 / 9	GSEA C2TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP
39	-3.81	NULL	1 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
40	-3.79	NULL	1 / 10	BP negative regulation of nitric oxide biosynthetic process

p-values



GW_229

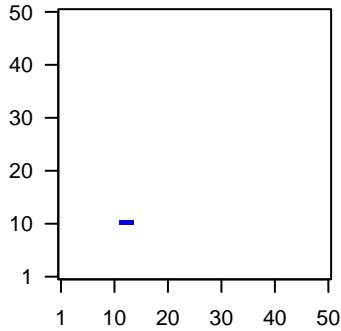
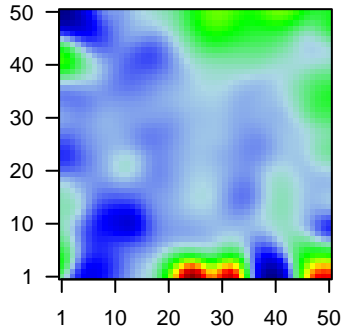
Local Summary

%DE = 0.78
 # metagenes = 3
 # genes = 38
 # genes in genesets = 23
 # genes with fdr < 0.1 = 26 (1 + / 25 -)
 # genes with fdr < 0.05 = 26 (1 + / 25 -)
 # genes with fdr < 0.01 = 19 (1 + / 18 -)

<r> metagenes = 0.98
 <r> genes = 0.52
 <FC> = -0.3
 <shrinkage-t> = -10.49
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



Local Genelist

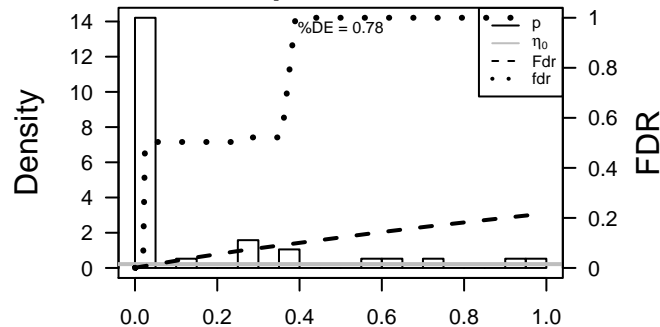
Rank	ID	log(FC)	fdr p-value	Description
1	645037	-0.62	1e-06 2e-05	14 x 11 G antigen 2C [Source:HGNC Symbol;Acc:31958]
2	729442	-0.59	4e-06 9e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
3	4100	-0.54	3e-05 9e-05	14 x 11 melanoma antigen family A, 1 (directs expression of antigen 1)
4	645073	-0.53	3e-05 9e-05	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
5	4109	-0.53	4e-05 2e-04	14 x 11 melanoma antigen family A, 10 [Source:HGNC Symbol;Acc:6]
6	2577	-0.51	8e-05 2e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
7	26748	-0.5	9e-05 2e-04	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
8	729422	-0.49	1e-04 6e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
9	2576	-0.47	3e-04 6e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
10	441520	-0.46	3e-04 6e-04	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC S
11	26749	-0.46	3e-04 6e-04	14 x 11 G antigen 2E [Source:HGNC Symbol;Acc:31960]
12	100008586	-0.45	4e-04 6e-04	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
13	729428	-0.45	5e-04 2e-03	14 x 11 G antigen 12C [Source:HGNC Symbol;Acc:28402]
14	729396	-0.44	7e-04 4e-03	14 x 11 G antigen 12J [Source:HGNC Symbol;Acc:17778]
15	24150	-0.42	1e-03 4e-03	14 x 11 TP53 target 3D [Source:HGNC Symbol;Acc:44657]
16	121355	-0.4	2e-03 4e-03	14 x 11 gametocyte specific factor 1 [Source:HGNC Symbol;Acc:265f
17	50512	-0.39	2e-03 4e-03	12 x 11 podocalyxin-like 2 [Source:HGNC Symbol;Acc:17936]
18	2579	-0.39	2e-03 4e-03	14 x 11 G antigen 12I [Source:HGNC Symbol;Acc:4105]
19	3911	0.37	3e-03 8e-03	12 x 11 laminin, alpha 5 [Source:HGNC Symbol;Acc:6485]
20	729447	-0.37	4e-03 1e-02	14 x 11 G antigen 2A [Source:HGNC Symbol;Acc:4099]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.22	NULL	16 / 630	Chr Chr X
2	-15.66	NULL	1 / 5	GSEA C2CHOI_ATL_ACUTE_STAGE
3	-14.84	NULL	1 / 11	GSEA C2SU_PLACENTA
4	-14.53	NULL	2 / 15	GSEA C2MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
5	-12.78	NULL	1 / 14	GSEA C2NIELSEN_GIST
6	-12.25	NULL	1 / 15	GSEA C2BROWNE_HCMV_INFECTION_8HR_DN
7	-11.78	NULL	1 / 12	GSEA C2RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
8	-11.58	NULL	1 / 10	BP leukocyte tethering or rolling
9	-10.17	NULL	1 / 21	BP negative regulation of Notch signaling pathway
10	-9.75	NULL	1 / 10	GSEA C2SUNODA_CISPLATIN_RESISTANCE_DN
11	-7.56	NULL	1 / 15	GSEA C2LOPEZ_MBD_TARGETS_IMPRINTED_AND_X_LINKED
12	-7.56	NULL	1 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
13	-7.36	NULL	2 / 48	Cancer KUIPER_MM_poor_survival
14	-7.33	NULL	1 / 21	MF glycosaminoglycan binding
15	-7.26	NULL	1 / 16	GSEA C2JAEGER_METASTASIS_UP
16	-6.58	NULL	1 / 16	GSEA C2MID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
17	-6.56	NULL	1 / 21	BP chromatin organization
18	-5.13	NULL	1 / 68	MF histone deacetylase binding
19	-4.19	NULL	1 / 16	GSEA C2ROZANOV_MMP14_TARGETS_DN
20	-3.74	NULL	3 / 419	CC cellular_component
21	-3.41	NULL	3 / 481	BP biological_process
22	-3.1	NULL	3 / 549	MF molecular_function
23	-2.85	NULL	1 / 19	BP oogenesis
24	-2.6	NULL	1 / 120	H.Tiss WIRTH_Testis
25	-2.16	NULL	3 / 579	CC nucleolus
26	-1.98	NULL	2 / 259	BP spermatogenesis
27	-1.86	NULL	1 / 37	BP ovarian follicle development
28	-1.23	NULL	1 / 504	BP negative regulation of transcription from RNA polymerase II promot
29	-1.03	NULL	1 / 318	MF chromatin binding
30	-0.99	NULL	7 / 4640	CC nucleus
31	-0.71	NULL	1 / 188	BP brain development
32	-0.57	NULL	1 / 156	MF protein dimerization activity
33	-0.47	NULL	2 / 717	Chr Chr 16
34	-0.2	NULL	1 / 835	CC integral to plasma membrane
35	-0.19	NULL	1 / 866	Chr Chr 12
36	-0.18	NULL	2 / 1574	BP transcription, DNA-templated
37	-0.12	NULL	1 / 914	Chr Chr 3
38	-0.08	NULL	1 / 16	GSEA C2LANDEMAINE_LUNG_METASTASIS
39	0.06	NULL	0 / 2	Cancer GENTLES_modul8
40	0.06	NULL	0 / 2	Disease BCHETNIA_EBM_down

p-values



GW_229

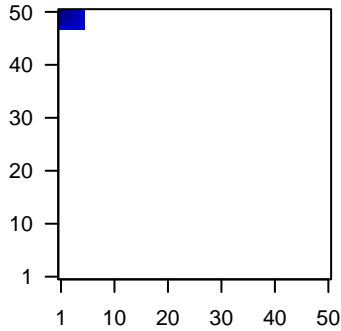
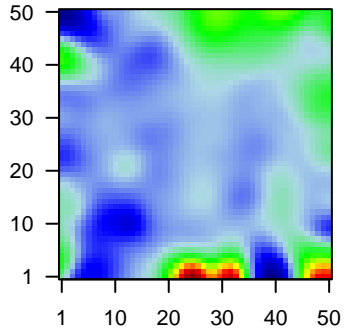
Local Summary

%DE = 0.77
 # metagenes = 20
 # genes = 268
 # genes in genesets = 260
 # genes with $fdr < 0.1$ = 168 (47 + / 121 -)
 # genes with $fdr < 0.05$ = 151 (41 + / 110 -)
 # genes with $fdr < 0.01$ = 127 (34 + / 93 -)

$\langle r \rangle$ metagenes = 0.97
 $\langle r \rangle$ genes = 0.45
 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -6.9$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.41$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	79852	-1.19	2e-16	4e-16	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
2	131	-1.76	2e-16	4e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	218	1.19	2e-16	4e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
4	810	-1.23	2e-16	4e-16	1 x 50 calmodulin-like 3 [Source:HGNC Symbol;Acc:1452]
5	51806	-1.8	2e-16	4e-16	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
6	4680	1.13	2e-16	4e-16	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (
7	22802	2.27	2e-16	4e-16	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
8	84518	-1.31	2e-16	4e-16	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
9	1382	1.25	2e-16	4e-16	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
10	54544	-1.13	2e-16	4e-16	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987
11	1562	-1.29	2e-16	4e-16	1 x 50 cytochrome P450, family 2, subfamily C, polypeptide 18 [Sou
12	126410	-1.1	2e-16	4e-16	1 x 49 cytochrome P450, family 4, subfamily F, polypeptide 22 [Sour
13	55894	-1.22	2e-16	4e-16	1 x 47 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	414325	-1.51	2e-16	4e-16	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
15	9245	1.37	2e-16	4e-16	4 x 50 glucosaminyl (N-acetyl) transferase 3, mucin type [Source:H
16	5653	-1.77	2e-16	4e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
17	3848	1.54	2e-16	4e-16	1 x 47 keratin 1 [Source:HGNC Symbol;Acc:6412]
18	3860	1.24	2e-16	4e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
19	192666	1.5	2e-16	4e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
20	3851	2.28	2e-16	4e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-21.26	NULL	87 / 135	H.Tiss WIRTH_Mucosa
2	-12.58	NULL	17 / 21	CC cornified envelope
3	-12.01	NULL	98 / 572	Disease GUDJ_pсориазis up
4	-10.75	NULL	19 / 42	BP keratinization
5	-10.56	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
6	-9.9	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
7	-9.46	NULL	11 / 19	BP peptide cross-linking
8	-8.67	NULL	2 / 16	BP cobalamin metabolic process
9	-8.49	NULL	6 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
10	-8.47	NULL	7 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
11	-7.84	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
12	-6.8	NULL	7 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
13	-6.4	NULL	5 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
14	-6.18	NULL	4 / 15	GSEA C2AIGNER_ZEB1_TARGETS
15	-6.14	NULL	1 / 14	BP tissue regeneration
16	-6.03	NULL	2 / 6	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_DN
17	-6.02	NULL	2 / 17	Disease BCHETNIA_EBM up
18	-5.91	NULL	1 / 15	BP hormone metabolic process
19	-5.89	NULL	3 / 10	GSEA C2NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN
20	-5.83	NULL	2 / 11	GSEA C2KEGG_ALPHA_LINOLENIC_ACID_METABOLISM
21	-5.52	NULL	4 / 15	MF retinol dehydrogenase activity
22	-5.46	NULL	4 / 39	BP retinoid metabolic process
23	-5.43	NULL	2 / 15	GSEA C2STOSSI_RESPONSE_TO ESTRADIOL
24	-5.26	NULL	3 / 14	BP phosphatidylglycerol acyl-chain remodeling
25	-5.09	NULL	1 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
26	-5.09	NULL	3 / 15	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
27	-5.08	NULL	2 / 14	GSEA C2KEGG_ETHER_LIPID_METABOLISM
28	-5.08	NULL	2 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOL
29	-5.02	NULL	3 / 18	BP retinol metabolic process
30	-5.01	NULL	15 / 122	MF serine-type endopeptidase activity
31	-4.91	NULL	2 / 11	MF gamma-catenin binding
32	-4.91	NULL	1 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_D
33	-4.8	NULL	2 / 8	GSEA C2SCHURINGA_STAT5A_TARGETS_UP
34	-4.8	NULL	3 / 37	BP digestion
35	-4.79	NULL	3 / 32	CC cell-cell adhesion junction
36	-4.78	NULL	57 / 1182	CC extracellular region
37	-4.75	NULL	1 / 8	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIA
38	-4.72	NULL	1 / 11	GSEA C2BENPORATH_ES_2
39	-4.72	NULL	7 / 51	MF protein binding, bridging
40	-4.7	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A

