

GW_058

Global Summary

%DE = 0.15
 # genes with $fdr < 0.2$ = 1889 (1044 + / 845 -)
 # genes with $fdr < 0.1$ = 1630 (918 + / 712 -)
 # genes with $fdr < 0.05$ = 1299 (751 + / 548 -)
 # genes with $fdr < 0.01$ = 874 (530 + / 344 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.1
 <fdr> = 0.85

Global Genelist

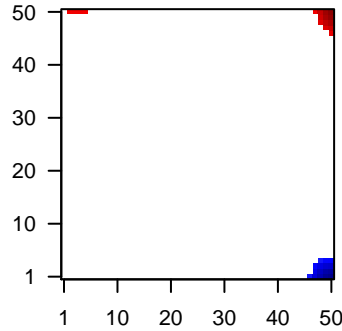
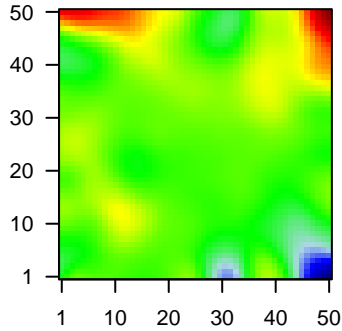
Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.46	2e-16	5e-14	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:16371]
2	131	1.52	2e-16	5e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:HGNC Symbol;Acc:16371]
3	8644	-1.51	2e-16	5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:16371]
4	1109	-1.69	2e-16	5e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Symbol;Acc:16371]
5	214	1.52	2e-16	5e-14	50 x 50 activated leukocyte cell adhesion molecule [Source:HGNC Symbol;Acc:16371]
6	445328	-1.49	2e-16	5e-14	4 x 46 Rho guanine nucleotide exchange factor (GEF) 35 [Source:HGNC Symbol;Acc:16371]
7	479	1.63	2e-16	5e-14	7 x 50 ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Source:HGNC Symbol;Acc:16371]
8	10409	-1.51	2e-16	5e-14	1 x 2 brain abundant, membrane attached signal protein 1 [Source:HGNC Symbol;Acc:16371]
9	339512	2.28	2e-16	5e-14	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:16371]
10	84290	1.81	2e-16	5e-14	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
11	131076	1.48	2e-16	5e-14	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:16371]
12	60437	1.46	2e-16	5e-14	8 x 50 cadherin 26 [Source:HGNC Symbol;Acc:15902]
13	1048	2.8	2e-16	5e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [Source:HGNC Symbol;Acc:16371]
14	4680	1.75	2e-16	5e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 [Source:HGNC Symbol;Acc:16371]
15	629	-1.64	2e-16	5e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
16	91612	1.49	2e-16	5e-14	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:2032]
17	9076	2.27	2e-16	5e-14	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:2032]
18	1308	-1.69	2e-16	5e-14	1 x 43 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2197]
19	1277	1.96	2e-16	5e-14	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
20	1278	1.73	2e-16	5e-14	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]

Global Geneset Analysis

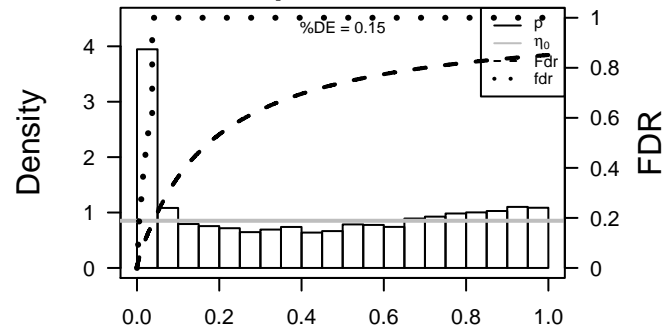
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.58	NULL	135	H.Tiss WIRTH_Mucosa
2	10.99	NULL	743	Chr Chr 7
3	8.17	NULL	449	Chr Chr 20
4	8.1	NULL	504	Chr Chr 15
5	7.59	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	7.29	NULL	7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
7	7.13	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
8	6.62	NULL	15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
9	6.36	NULL	24	TF Tissue/AQUERIZAS_Trachea
10	6.33	NULL	37	BP collagen fibril organization
11	6.3	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
12	6.02	NULL	1749	MF DNA binding
13	5.93	NULL	717	Chr Chr 16
14	5.88	NULL	11	MF platelet-derived growth factor binding
15	5.87	NULL	1581	BP regulation of transcription, DNA-dependent
16	5.82	NULL	19	BP peptide cross-linking
17	5.68	NULL	15	GSEA C2AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP
18	5.49	NULL	19	BP anatomical structure formation involved in morphogenesis
19	5.47	NULL	13	H.Tiss WIRTH_Tonsil
20	5.43	NULL	823	MF sequence-specific DNA binding transcription factor activity
<i>Underexpressed</i>				
1	-14.1	NULL	417	H.Tiss WIRTH_Immune system
2	-13.78	NULL	553	Cancer Lembecke_Colonic Inflammation
3	-12.88	NULL	312	BP immune response
4	-9.53	NULL	81	BP viral transcription
5	-9.34	NULL	92	BP translational elongation
6	-9.31	NULL	87	BP translational termination
7	-9.24	NULL	109	BP SRP-dependent cotranslational protein targeting to membrane
8	-9.09	NULL	60	BP interferon-gamma-mediated signaling pathway
9	-8.97	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
10	-8.97	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
11	-8.97	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
12	-8.97	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
13	-8.88	NULL	92	BP viral life cycle
14	-8.65	NULL	51	BP type I interferon signaling pathway
15	-8.61	NULL	204	BP cytokine-mediated signaling pathway
16	-8.58	NULL	153	MF structural constituent of ribosome
17	-8.49	NULL	128	BP translational initiation
18	-7.89	NULL	74	BP regulation of immune response
19	-7.81	NULL	253	BP translation
20	-7.79	NULL	167	CC ribosome

Profile

Regulated Spots



p-values



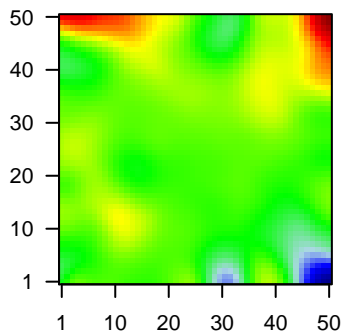
GW_058

Local Summary

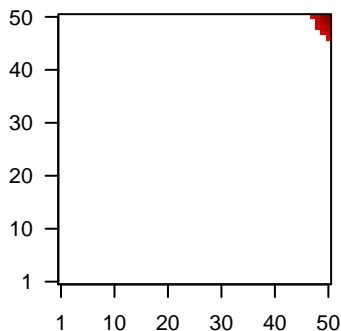
%DE = 0.76
 # metagenes = 13
 # genes = 208
 # genes in genesets = 206
 # genes with $fdr < 0.1$ = 132 (117 + / 15 -)
 # genes with $fdr < 0.05$ = 116 (104 + / 12 -)
 # genes with $fdr < 0.01$ = 97 (89 + / 8 -)

<r> metagenes = 0.97
 <r> genes = 0.28
 <FC> = 0.51
 <shrinkage-t> = 17.95
 <p-value> = 0
 <fdr> = 0.42

Profile



Spot



Local Genelist

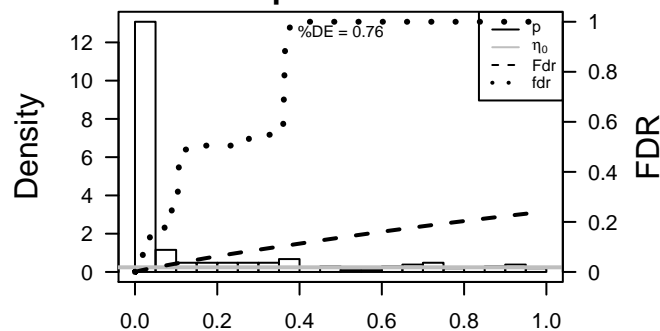
Rank	ID	log(FC)	fdr	p-value	Description
1	154664	1.46	2e-16	7e-16	50 x 50 ATP-binding cassette, sub-family A (ABC1), member 13 [Source:HGNC Symbol;Acc:20322]
2	214	1.52	2e-16	7e-16	50 x 50 activated leukocyte cell adhesion molecule [Source:HGNC Symbol;Acc:20322]
3	339512	2.28	2e-16	7e-16	50 x 50 chromosome 1 open reading frame 110 [Source:HGNC Symbol;Acc:20322]
4	9076	2.27	2e-16	7e-16	49 x 50 claudin 1 [Source:HGNC Symbol;Acc:20322]
5	29785	1.47	2e-16	7e-16	50 x 50 cytochrome P450, family 2, subfamily S, polypeptide 1 [Source:HGNC Symbol;Acc:20322]
6	10655	1.94	2e-16	7e-16	50 x 50 doublesex and mab-3 related transcription factor 2 [Source:HGNC Symbol;Acc:20322]
7	1780	1.65	2e-16	7e-16	50 x 50 dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC Symbol;Acc:20322]
8	10643	2.03	2e-16	7e-16	48 x 50 insulin-like growth factor 2 mRNA binding protein 3 [Source:HGNC Symbol;Acc:20322]
9	3880	3.42	2e-16	7e-16	50 x 49 keratin 19 [Source:HGNC Symbol;Acc:6436]
10	4922	3.99	2e-16	7e-16	50 x 50 neurotensin [Source:HGNC Symbol;Acc:8038]
11	4953	2.05	2e-16	7e-16	50 x 50 ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109]
12	9182	1.56	2e-16	7e-16	50 x 50 Ras association (RalGDS/AF-6) domain family (N-terminal) member 1 [Source:HGNC Symbol;Acc:20322]
13	56963	2.02	2e-16	7e-16	50 x 50 repulsive guidance molecule family member a [Source:HGNC Symbol;Acc:20322]
14	83959	1.61	2e-16	7e-16	50 x 50 solute carrier family 4, sodium borate transporter, member 11 [Source:HGNC Symbol;Acc:20322]
15	6657	1.84	2e-16	7e-16	50 x 50 SRY (sex determining region Y)-box 2 [Source:HGNC Symbol;Acc:20322]
16	11166	1.59	2e-16	7e-16	50 x 50 SRY (sex determining region Y)-box 21 [Source:HGNC Symbol;Acc:20322]
17	256764	1.67	2e-16	7e-16	50 x 50 WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
18	8702	1.43	9e-16	1e-13	50 x 50 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 [Source:HGNC Symbol;Acc:20322]
19	4072	1.43	9e-16	1e-13	50 x 50 epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:20322]
20	3856	1.43	9e-16	1e-13	50 x 48 keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	24.92	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
2	24.06	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
3	14.76	NULL	3 / 9	GSEA C2REACTOME_METABOLISM_OF_AMINO_ACIDS
4	13.09	NULL	1 / 11	Glio neurons_glio
5	12.15	NULL	2 / 11	GSEA C2SMID_BREAST_CANCER_BASAL_UP
6	11.92	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
7	11.21	NULL	1 / 11	GSEA C2WHITESIDE_CISPLATIN_RESISTANCE_DN
8	10.97	NULL	1 / 15	MF neuropeptide hormone activity
9	10.84	NULL	4 / 13	BP regulation of blood vessel size
10	10.6	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
11	10.35	NULL	2 / 10	GSEA C2CONRAD_STEM_CELL
12	10.29	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
13	10.19	NULL	1 / 13	GSEA C2CHEN_LUNG_CANCER_SURVIVAL
14	9.76	NULL	1 / 14	GSEA C2JIANG_SILENCED_BY_METHYLATION_UP
15	9.38	NULL	1 / 15	GSEA C2E_SKI_TARGETS_UP
16	9.38	NULL	1 / 15	GSEA C2LEE_LIVER_CANCER_HEPATOBLAST
17	9.29	NULL	2 / 18	CC costamere
18	9.13	NULL	2 / 11	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
19	9.06	NULL	2 / 15	GSEA C2YANG_BREAST_CANCER_ESR1_LASER_DN
20	9.04	NULL	1 / 16	CC dystrophin-associated glycoprotein complex
21	9.04	NULL	1 / 16	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_UP
22	8.83	NULL	1 / 2	miRNA target-127
23	8.68	NULL	2 / 13	BP epithelial tube branching involved in lung morphogenesis
24	8.65	NULL	2 / 13	GSEA C2COLLER_MYC_TARGETS_UP
25	8.64	NULL	1 / 7	GSEA C2REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ACTIVITY
26	8.23	NULL	2 / 14	GSEA C2VEL_MYCN_TARGETS_WITH_E_BOX
27	7.98	NULL	1 / 8	GSEA C2PUJANA_CHEK2_PCC_NETWORK
28	7.92	NULL	4 / 14	GSEA C2VANTVEER_BREAST_CANCER_METASTASIS_DN
29	7.83	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_ESR1_UP
30	7.73	NULL	1 / 21	BP sarcomere organization
31	7.73	NULL	3 / 9	GSEA C2BROWNE_HCMV_INFECTION_8HR_UP
32	7.72	NULL	1 / 7	GSEA C2REACTOME_G1_S_TRANSITION
33	7.72	NULL	1 / 7	miRNA target-145
34	7.57	NULL	1 / 8	GSEA C2NIELSEN_LIPOSARCOMA_UP
35	7.55	NULL	3 / 11	GSEA C2TO_PTTG1_TARGETS_UP
36	7.46	NULL	2 / 14	GSEA C2AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
37	7.33	NULL	2 / 23	BP stem cell differentiation
38	7.27	NULL	2 / 13	GSEA C2JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
39	7.19	NULL	2 / 16	GSEA C2VANTVEER_BREAST_CANCER_ESR1_DN
40	7.19	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C7

p-values



GW_058

Local Summary

%DE = 0.94
 # metagenes = 4
 # genes = 74
 # genes in genesets = 72
 # genes with $fdr < 0.1$ = 61 (49 + / 12 -)
 # genes with $fdr < 0.05$ = 44 (42 + / 2 -)
 # genes with $fdr < 0.01$ = 43 (41 + / 2 -)

$\langle r \rangle$ metagenes = 0.99

$\langle r \rangle$ genes = 0.46

$\langle FC \rangle = 0.51$

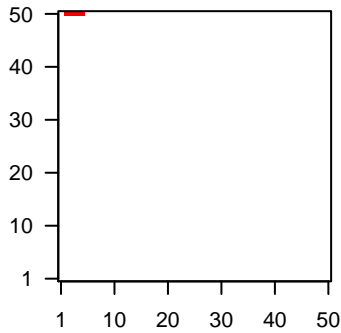
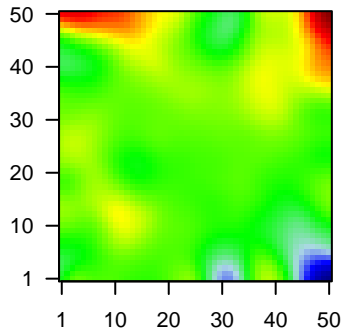
$\langle \text{shrinkage-t} \rangle = 17.98$

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

$\langle fdr \rangle = 0.41$

Profile

Spot



Local Genelist

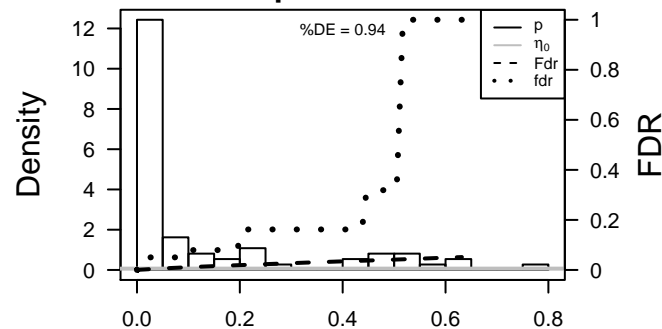
Rank	ID	log(FC)	fdr	p-value	Description
1	1048	2.8	2e-16	4e-16	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
2	5083	2.06	2e-16	4e-16	5 x 50 paired box 9 [Source:HGNC Symbol;Acc:8623]
3	6337	1.84	2e-16	4e-16	3 x 50 sodium channel, non-voltage-gated 1 alpha subunit [Source:
4	57447	1.38	7e-15	3e-13	5 x 50 NDRG family member 2 [Source:HGNC Symbol;Acc:14460]
5	1999	1.33	6e-14	3e-13	5 x 50 E74-like factor 3 (ets domain transcription factor, epithelial-s
6	1577	1.31	2e-13	3e-13	4 x 50 cytochrome P450, family 3, subfamily A, polypeptide 5 [Sourc
7	131177	1.31	2e-13	2e-11	3 x 50 family with sequence similarity 3, member D [Source:HGNC s
8	7108	1.23	4e-12	5e-10	4 x 50 transmembrane 7 superfamily member 2 [Source:HGNC Sym
9	51195	1.15	1e-10	6e-10	5 x 50 Rap guanine nucleotide exchange factor (GEF)-like 1 [Sourc
10	7113	1.13	2e-10	2e-08	5 x 50 transmembrane protease, serine 2 [Source:HGNC Symbol;Ac
11	9314	1.04	5e-09	2e-08	4 x 50 Kruppel-like factor 4 (gut) [Source:HGNC Symbol;Acc:6348]
12	79852	1.02	1e-08	2e-08	3 x 50 epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
13	220963	1.01	1e-08	3e-07	4 x 50 solute carrier family 16, member 9 [Source:HGNC Symbol;Ac
14	8681	0.95	1e-07	3e-07	5 x 50 phospholipase A2, group IVB (cytosolic) [Source:HGNC Symi
15	7263	0.94	1e-07	3e-07	5 x 50 thiosulfate sulfurtransferase (rhodanese) [Source:HGNC Sym
16	1571	0.92	2e-07	3e-07	5 x 50 cytochrome P450, family 2, subfamily E, polypeptide 1 [Sourc
17	26298	0.92	3e-07	8e-07	4 x 50 ets homologous factor [Source:HGNC Symbol;Acc:3246]
18	89778	0.9	4e-07	1e-06	5 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 11 (c
19	118932	0.89	6e-07	1e-06	4 x 50 ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:28321]
20	51228	0.8	1e-06	1e-06	2 x 50 glycolipid transfer protein [Source:HGNC Symbol;Acc:24867]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	22.25	NULL	3 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
2	21.48	NULL	2 / 13	H.Tiss WIRTH_Tonsil
3	17.31	NULL	3 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
4	16.85	NULL	2 / 12	MF sodium channel activity
5	16.63	NULL	2 / 9	GSEA C2REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE
6	16.63	NULL	2 / 9	GSEA C2REACTOME_PHASE_1_FUNCTIONALIZATION_OF_COMPOUND
7	15.87	NULL	13 / 135	H.Tiss WIRTH_Mucosa
8	14.73	NULL	2 / 15	BP sodium ion transmembrane transport
9	14.73	NULL	2 / 15	GSEA C2KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION
10	14.68	NULL	2 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
11	14.68	NULL	2 / 11	GSEA C2REACTOME_BIOLOGICAL_OXIDATIONS
12	14.68	NULL	2 / 11	GSEA C2REACTOME_XENOBIOTICS
13	14.48	NULL	2 / 14	GSEA C2XIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
14	13.68	NULL	3 / 24	TF Tissu@AQUERIZAS_Trachea
15	13.49	NULL	2 / 16	GSEA C2FRASOR_TAMOXIFEN_RESPONSE_UP
16	13.25	NULL	2 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
17	13.22	NULL	2 / 18	BP sensory perception of taste
18	12.43	NULL	2 / 20	MF WW domain binding
19	11.41	NULL	1 / 7	GSEA C2KEGG_STEROID_HORMONE_BIOSYNTHESIS
20	10.87	NULL	1 / 13	GSEA C2KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP
21	10.64	NULL	1 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
22	10.4	NULL	1 / 14	GSEA C2NELSON_RESPONSE_TO_ANDROGEN_DN
23	10.22	NULL	2 / 13	GSEA C2YANG_BREAST_CANCER_ESR1_UP
24	9.97	NULL	1 / 15	GSEA C2LUI_THYROID_CANCER_CLUSTER_2
25	9.87	NULL	1 / 9	GSEA C2DORN_ADENOVIRUS_INFECTION_32HR_UP
26	9.7	NULL	1 / 9	GSEA C2KEGG_RETINOL_METABOLISM
27	9.36	NULL	2 / 27	BP negative regulation of smooth muscle cell proliferation
28	9.28	NULL	3 / 83	CC anchored to membrane
29	9.23	NULL	1 / 10	GSEA C2DORN_ADENOVIRUS_INFECTION_12HR_DN
30	9.13	NULL	1 / 9	GSEA C2JAIN_NFKB_SIGNALING
31	9.07	NULL	1 / 10	GSEA C2BORCZUK_MALIGNANT_MESOTHELIOMA_DN
32	8.83	NULL	3 / 28	BP negative regulation of ERK1 and ERK2 cascade
33	8.79	NULL	2 / 26	MF oxygen binding
34	8.66	NULL	1 / 19	CC cortical actin cytoskeleton
35	8.64	NULL	3 / 30	BP excretion
36	8.56	NULL	1 / 12	Glio Phillips PN up vs MES & Prolif
37	8.55	NULL	1 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
38	8.54	NULL	1 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
39	8.54	NULL	1 / 10	GSEA C2REACTOME_TRANSFORMATION_OF_LANOSTEROL_TO_CHOLE
40	8.47	NULL	1 / 24	BP endoderm development

p-values



GW_058

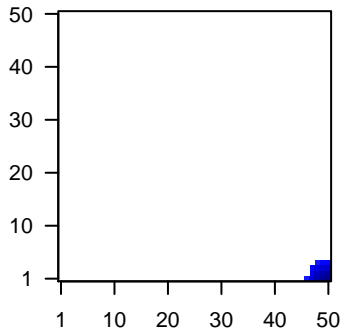
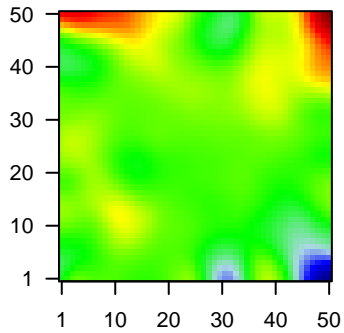
Local Summary

%DE = 0.95
 # metagenes = 16
 # genes = 272
 # genes in genesets = 270
 # genes with $fdr < 0.1$ = 249 (6 + / 243 -)
 # genes with $fdr < 0.05$ = 241 (6 + / 235 -)
 # genes with $fdr < 0.01$ = 220 (4 + / 216 -)

<r> metagenes = 0.99
 <r> genes = 0.59
 <FC> = -0.6
 <shrinkage-t> = -20.98
 <p-value> = 0
 <fdr> = 0.23

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3113	-1.42	2e-15	2e-14	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source:HGNC Symbol;Acc:6740]
2	3001	-1.41	2e-15	4e-14	48 x 1 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated protein 10) [Source:HGNC Symbol;Acc:9361]
3	3122	-1.29	8e-15	4e-14	50 x 1 major histocompatibility complex, class II, DR alpha [Source:HGNC Symbol;Acc:9070]
4	3128	-1.38	8e-15	5e-14	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudogene) [Source:HGNC Symbol;Acc:26632]
5	3936	-1.37	1e-14	5e-14	50 x 1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:9361]
6	3002	-1.37	1e-14	4e-13	49 x 1 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated protein 10.2) [Source:HGNC Symbol;Acc:9361]
7	5920	-1.33	6e-14	4e-13	48 x 1 retinoic acid receptor responder (tazarotene induced) 3 [Source:HGNC Symbol;Acc:26632]
8	10563	-1.33	7e-14	2e-12	50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;Acc:9070]
9	5880	-1.31	2e-13	7e-12	50 x 1 ras-related C3 botulinum toxin substrate 2 (rho family, small GTP-binding protein RhoC) [Source:HGNC Symbol;Acc:9361]
10	972	-1.28	7e-13	2e-11	50 x 1 CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:9361]
11	3059	-1.24	3e-12	2e-11	50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC Symbol;Acc:26632]
12	4069	-1.24	3e-12	9e-11	50 x 2 lysozyme [Source:HGNC Symbol;Acc:6740]
13	5341	-1.2	1e-11	9e-11	50 x 1 pleckstrin [Source:HGNC Symbol;Acc:9070]
14	713	-1.19	2e-11	9e-11	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:9361]
15	54504	1.19	2e-11	3e-10	50 x 4 carboxypeptidase, vitellogenic-like [Source:HGNC Symbol;Acc:26632]
16	5552	-1.15	9e-11	3e-10	50 x 1 serglycin [Source:HGNC Symbol;Acc:9361]
17	6347	-1.15	1e-10	3e-10	50 x 4 chemokine (C-C motif) ligand 2 [Source:HGNC Symbol;Acc:9361]
18	260436	-1.15	1e-10	3e-10	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc:26632]
19	5730	-1.15	1e-10	3e-09	50 x 1 prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:26632]
20	91607	-1.11	4e-10	3e-09	48 x 4 schlafen family member 11 [Source:HGNC Symbol;Acc:26632]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-31.59	NULL	91 / 417	H.Tiss WIRTH_Immune system
2	-29.36	NULL	12 / 15	CC MHC class II protein complex
3	-25.51	NULL	96 / 553	Cancer Lembcke_Colonc Inflammation
4	-20.02	NULL	52 / 312	BP immune response
5	-19.68	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
6	-18.91	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
7	-18.27	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
8	-18.19	NULL	44 / 265	Glio willscher_GBM_Verhaak-CL_expression_B_up
9	-18.19	NULL	44 / 265	Glio willscher_GBM_Verhaak-MES_expression_B_up
10	-18.19	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
11	-18.19	NULL	44 / 265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
12	-17.94	NULL	15 / 47	BP antigen processing and presentation
13	-17.16	NULL	7 / 15	GSEA C2FINAK_BREAST_CANCER_SDPP_SIGNATURE
14	-16.94	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HGA
15	-16.19	NULL	6 / 11	GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY
16	-14.92	NULL	5 / 12	GSEA C2BIOCARTA_CTL_PATHWAY
17	-14.91	NULL	17 / 74	BP regulation of immune response
18	-14.9	NULL	5 / 13	GSEA C2HAHTOLA_CTL_PATHOGENESIS
19	-14.53	NULL	15 / 60	BP T cell costimulation
20	-14.18	NULL	5 / 12	BP immunoglobulin mediated immune response
21	-13.82	NULL	2 / 3	GSEA C2KEGG_VIRAL_MYOCARDITIS
22	-13.7	NULL	4 / 16	BP cytolysis
23	-13.63	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
24	-13.56	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMENT_ACTIVATION
25	-13.54	NULL	5 / 11	GSEA C2BIOCARTA_THELPER_PATHWAY
26	-13.48	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
27	-13.46	NULL	2 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
28	-13.17	NULL	4 / 8	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_DN
29	-13.14	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
30	-13.03	NULL	5 / 10	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
31	-12.92	NULL	8 / 16	GSEA C2SU_THYMUS
32	-12.83	NULL	2 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
33	-12.81	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
34	-12.8	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
35	-12.76	NULL	2 / 5	GSEA C2WEST_ADRENOCORICAL_GARCINOMA_VS_ADENOMA_DN
36	-12.45	NULL	25 / 162	CC external side of plasma membrane
37	-12.35	NULL	2 / 3	MMML C2SCIEJ_MMML_7
38	-12.3	NULL	4 / 8	GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
39	-12.16	NULL	13 / 87	BP antigen processing and presentation of exogenous peptide antigens
40	-12.01	NULL	31 / 316	Cancer SPANG_BCL6-index2

p-values

