

GW_297

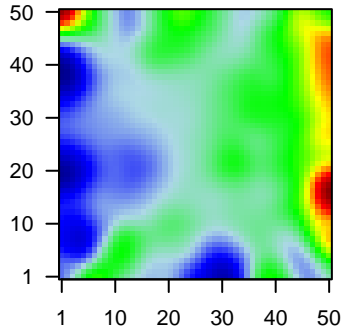
Global Summary

%DE = 0.14
 # genes with fdr < 0.2 = 1686 (1018 + / 668 -)
 # genes with fdr < 0.1 = 1271 (807 + / 464 -)
 # genes with fdr < 0.05 = 1117 (727 + / 390 -)
 # genes with fdr < 0.01 = 768 (536 + / 232 -)

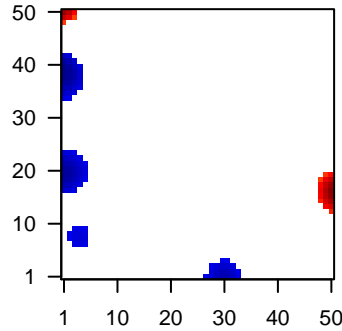
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.11
 <fdr> = 0.86

Profile



Regulated Spots



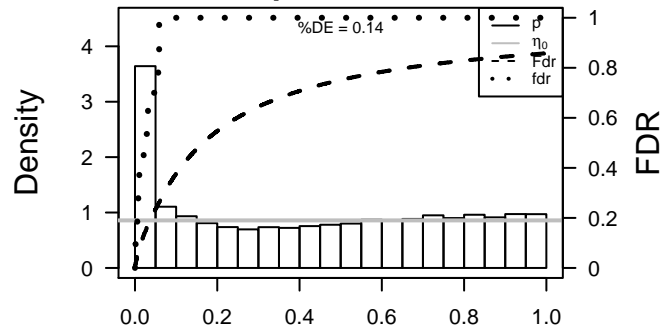
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	1.79	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	1.23	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
3	55107	1.65	2e-16	3e-14	1 x 5 anoctamin 1, calcium activated chloride channel [Source:HGNC]
4	51326	1.73	2e-16	3e-14	42 x 1 ADP-ribosylation factor-like 17B [Source:HGNC Symbol;Acc]
5	9915	1.47	2e-16	3e-14	50 x 1 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HGNC]
6	25805	1.67	2e-16	3e-14	8 x 1 BMP and activin membrane-bound inhibitor [Source:HGNC Symbol;Acc]
7	8424	1.41	2e-16	3e-14	3 x 48 butyrobaine (gamma), 2-oxoglutarate dioxygenase (gamma)
8	260436	2.08	2e-16	3e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbol;Acc]
9	23705	1.62	2e-16	3e-14	50 x 7 cell adhesion molecule 1 [Source:HGNC Symbol;Acc:5951]
10	827	1.23	2e-16	3e-14	44 x 13 calpain 6 [Source:HGNC Symbol;Acc:1483]
11	22794	1.26	2e-16	3e-14	48 x 41 cancer susceptibility candidate 3 [Source:HGNC Symbol;Acc]
12	6364	-1.24	2e-16	3e-14	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc]
13	970	1.34	2e-16	3e-14	33 x 2 CD70 molecule [Source:HGNC Symbol;Acc:11937]
14	91612	1.48	2e-16	3e-14	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:200]
15	1298	1.38	2e-16	3e-14	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:2218]
16	49860	2.32	2e-16	3e-14	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
17	441520	1.26	2e-16	3e-14	14 x 11 cancer/testis antigen family 45, member A2 [Source:HGNC Symbol;Acc:441520]
18	1545	2.48	2e-16	3e-14	50 x 4 cytochrome P450, family 1, subfamily B, polypeptide 1 [Source:HGNC Symbol;Acc:1545]
19	1593	1.39	2e-16	3e-14	50 x 3 cytochrome P450, family 27, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:1593]
20	1828	1.6	2e-16	3e-14	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	14.8	NULL	135	H.Tiss WIRTH_Mucosa
2	9.82	NULL	618	Chr Chr 4
3	9.75	NULL	1033	Chr Chr 2
4	8.57	NULL	16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
5	8.08	NULL	6	GSEA C2FARMER_BREAST_CANCER_CLUSTER_8
6	7.81	NULL	21	MF glycosaminoglycan binding
7	7.56	NULL	5	GSEA C2OHM_EMBRYONIC_CARCINOMA_UP
8	7.33	NULL	11	BP planar cell polarity pathway involved in neural tube closure
9	7.29	NULL	19	MF Wnt-activated receptor activity
10	7.08	NULL	7	GSEA C2NIELSEN_SYNOVIAL_SARCOMA_UP
11	6.73	NULL	15	BP digestive tract morphogenesis
12	6.6	NULL	375	Disease GUDJ_poriasis down
13	6.46	NULL	122	miRNA target-miR-330
14	6.43	NULL	37	BP synapse assembly
15	6.4	NULL	58	Glio OPC
16	6.33	NULL	142	Glio wilscher_GBM_Verhaak-CL_expression_C_up
17	6.33	NULL	142	Glio wilscher_GBM_Verhaak-PNmut_expression_C_down
18	6.17	NULL	24	TF Tissue/AQUERIZAS_Trachea
19	6.05	NULL	26	MF Wnt-protein binding
20	6.03	NULL	225	miRNA target-miR-374
<i>Underexpressed</i>				
1	-7.35	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
2	-7.35	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
3	-7.35	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
4	-7.35	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
5	-7.29	NULL	957	Chr Chr 11
6	-7.12	NULL	553	Cancer Lembecke_Colonc Inflammation
7	-6.09	NULL	6	Glio Martinez_Glio_hypometh
8	-6.02	NULL	127	H.Tiss WIRTH_Muscle
9	-5.9	NULL	1135	Chr Chr 19
10	-5.07	NULL	51	BP type I interferon signaling pathway
11	-5.05	NULL	269	BP inflammatory response
12	-4.97	NULL	74	BP antigen processing and presentation of exogenous peptide antigen
13	-4.92	NULL	37	Glio Christensen_hypomethylated_in_ependymoma
14	-4.73	NULL	7	MMML C6CIEJ_MMML 9
15	-4.73	NULL	16	GSEA C2HAHTOLA_MYCOSIS_FUNGOIDES_UP
16	-4.67	NULL	16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
17	-4.54	NULL	18	MF peptide antigen binding
18	-4.53	NULL	11	GSEA C2YAMANAKA_GLIOMASTOMA_SURVIVAL_UP
19	-4.51	NULL	10	BP surfactant homeostasis
20	-4.43	NULL	73	BP defense response to bacterium

p-values



GW_297

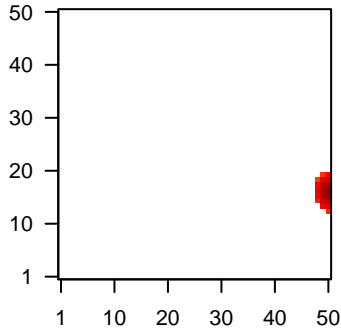
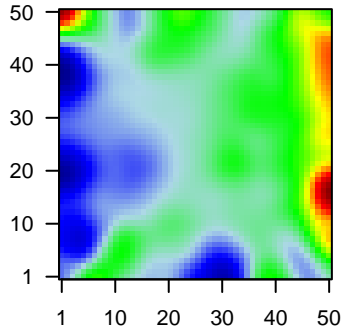
Local Summary

%DE = 0.82
 # metagenes = 20
 # genes = 253
 # genes in genesets = 251
 # genes with fdr < 0.1 = 151 (142 + / 9 -)
 # genes with fdr < 0.05 = 124 (121 + / 3 -)
 # genes with fdr < 0.01 = 91 (90 + / 1 -)

<r> metagenes = 0.95
 <r> genes = 0.3
 <FC> = 0.4
 <shrinkage-t> = 14.15
 <p-value> = 0
 <fdr> = 0.51

Profile

Spot



Local Genelist

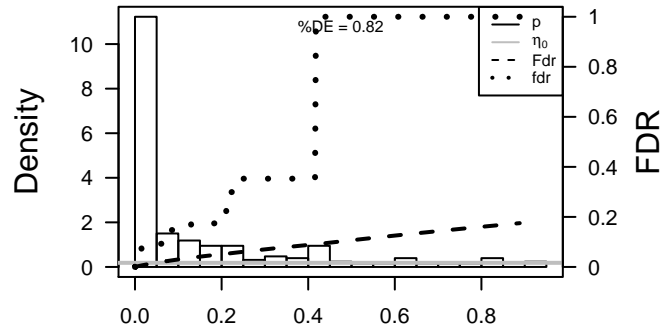
Rank	ID	log(FC)	fdr	p-value	Description
1	9915	1.47	2e-16	6e-16	50 x 17 aryl-hydrocarbon receptor nuclear translocator 2 [Source:HGNC Symbol;Acc:22181]
2	1298	1.38	2e-16	6e-16	50 x 17 collagen, type IX, alpha 2 [Source:HGNC Symbol;Acc:22181]
3	1959	1.58	2e-16	6e-16	50 x 19 early growth response 2 [Source:HGNC Symbol;Acc:3239]
4	221061	1.25	2e-16	6e-16	50 x 16 family with sequence similarity 171, member A1 [Source:HGNC Symbol;Acc:221061]
5	8857	1.25	2e-16	6e-16	50 x 13 Fc fragment of IgG binding protein [Source:HGNC Symbol;Acc:8857]
6	2248	2.21	2e-16	6e-16	50 x 19 fibroblast growth factor 3 [Source:HGNC Symbol;Acc:3681]
7	728715	2.04	2e-16	6e-16	50 x 18
8	26018	1.46	2e-16	6e-16	50 x 16 leucine-rich repeats and immunoglobulin-like domains 1 [Source:HGNC Symbol;Acc:26018]
9	4602	1.93	2e-16	6e-16	50 x 16 v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:4602]
10	4613	1.43	2e-16	6e-16	50 x 17 v-myc avian myelocytomatosis viral oncogene neuroblastoma associated protein 1 [Source:HGNC Symbol;Acc:4613]
11	83988	1.68	2e-16	6e-16	50 x 17 neurocalcin delta [Source:HGNC Symbol;Acc:7655]
12	9603	1.43	2e-16	6e-16	50 x 18 nuclear factor, erythroid 2-like 3 [Source:HGNC Symbol;Acc:9603]
13	54959	1.77	2e-16	6e-16	50 x 17 odontogenic, ameloblast associated [Source:HGNC Symbol;Acc:54959]
14	494470	1.7	2e-16	6e-16	50 x 17 ring finger protein 165 [Source:HGNC Symbol;Acc:31696]
15	6228	1.55	2e-16	6e-16	50 x 14 ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
16	57556	1.5	2e-16	6e-16	50 x 17 sema domain, transmembrane domain (TM), and cytoplasmic tail domain [Source:HGNC Symbol;Acc:57556]
17	30812	1.23	2e-16	6e-16	50 x 18 SRY (sex determining region Y)-box 8 [Source:HGNC Symbol;Acc:30812]
18	79805	1.69	2e-16	6e-16	50 x 18 vasohibin 2 [Source:HGNC Symbol;Acc:25723]
19	56994	1.19	2e-15	4e-13	50 x 16 choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17594]
20	2205	1.15	2e-14	4e-13	50 x 13 Fc fragment of IgE, high affinity I, receptor for; alpha polypept [Source:HGNC Symbol;Acc:2205]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	19.51	NULL	6 / 16	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_A
2	13.15	NULL	3 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_UP
3	12.7	NULL	4 / 34	BP thymus development
4	12.29	NULL	2 / 14	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_DN
5	10.44	NULL	3 / 15	GSEA C2NAKAJIMA_MAST_CELL
6	10.24	NULL	1 / 5	GSEA C2STAEGE_EWING_FAMILY_TUMOR
7	10.1	NULL	1 / 3	miRNA target-223
8	9.94	NULL	4 / 40	TF Tissue/AQUERIZAS_Fetal brain
9	9.7	NULL	2 / 16	GSEA C2SASAKI_ADULT_T_CELL_LEUKEMIA
10	9.6	NULL	2 / 15	BP embryonic digestive tract development
11	9.57	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
12	9.39	NULL	2 / 12	GSEA C2KIM_WT1_TARGETS_12HR_UP
13	9.38	NULL	2 / 16	GSEA C2RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATE
14	9.28	NULL	1 / 5	TF MYC_TFs
15	9.28	NULL	1 / 5	miRNA target-101
16	9.03	NULL	3 / 15	GSEA C2DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
17	8.94	NULL	3 / 15	GSEA C2MASSARWEH_RESPONSE_TO ESTRADIOL
18	8.94	NULL	1 / 9	GSEA C2BASSO_CD40_SIGNALING_UP
19	8.94	NULL	1 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2
20	8.79	NULL	2 / 12	GSEA C2PROVENZANI_METASTASIS_UP
21	8.72	NULL	1 / 12	MF fibroblast growth factor receptor binding
22	8.72	NULL	1 / 12	BP organ induction
23	8.68	NULL	2 / 10	BP positive regulation of histone H3-K4 methylation
24	8.29	NULL	2 / 14	GSEA C2SMID_BREAST_CANCER_LUMINAL_A_UP
25	8.27	NULL	1 / 8	GSEA C2REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTO
26	7.96	NULL	2 / 15	GSEA C2POOLA_INVASIVE_BREAST_CANCER_DN
27	7.96	NULL	1 / 11	BP homeostasis of number of cells
28	7.96	NULL	1 / 11	Pathway AcBENTINK_e2f3.2
29	7.96	NULL	1 / 11	GSEA C2DOANE_BREAST_CANCER_ESR1_UP
30	7.96	NULL	1 / 11	GSEA C2TURJANSKI_MAPK1_AND_MAPK2_TARGETS
31	7.9	NULL	2 / 16	GSEA C2WU_HBX_TARGETS_3_UP
32	7.77	NULL	2 / 12	GSEA C2CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP
33	7.72	NULL	2 / 13	miRNA target-34a
34	7.61	NULL	4 / 41	TF Tissue/AQUERIZAS_Thymus
35	7.59	NULL	4 / 42	BP B cell differentiation
36	7.57	NULL	1 / 12	GSEA C2DING_LUNG_CANCER_BY_MUTATION_RATE
37	7.48	NULL	2 / 4	miRNA target-204
38	7.38	NULL	1 / 16	BP post-anal tail morphogenesis
39	7.36	NULL	2 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
40	7.34	NULL	1 / 7	GSEA C2KANG_CISPLATIN_RESISTANCE_DN

p-values



GW_297

Local Summary

%DE = 0.87
 # metagenes = 7
 # genes = 132
 # genes in genesets = 129

genes with $fdr < 0.1 = 97$ (82 + / 15 -)
 # genes with $fdr < 0.05 = 97$ (82 + / 15 -)
 # genes with $fdr < 0.01 = 82$ (72 + / 10 -)

<r> metagenes = 0.99
 <r> genes = 0.52

<FC> = 0.48
 <shrinkage-t> = 16.93
 <p-value> = 0
 <fdr> = 0.31

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	1.79	2e-16	3e-16	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	218	1.23	2e-16	3e-16	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
3	49860	2.32	2e-16	3e-16	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
4	1828	1.6	2e-16	3e-16	1 x 48 desmoglein 1 [Source:HGNC Symbol;Acc:3048]
5	163351	1.97	2e-16	3e-16	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S]
6	43849	1.28	2e-16	3e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6]
7	3860	1.57	2e-16	3e-16	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
8	3851	2.77	2e-16	3e-16	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
9	4118	2.09	2e-16	3e-16	1 x 50 mal, T-cell differentiation protein [Source:HGNC Symbol;Acc
10	374897	1.6	2e-16	3e-16	1 x 49 suprabasin [Source:HGNC Symbol;Acc:24950]
11	6707	1.59	2e-16	3e-16	1 x 50 small proline-rich protein 3 [Source:HGNC Symbol;Acc:1126
12	7053	1.71	2e-16	3e-16	1 x 50 transglutaminase 3 [Source:HGNC Symbol;Acc:11779]
13	57016	1.19	3e-15	3e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
14	29094	1.18	3e-15	3e-13	1 x 48 lectin, galactoside-binding-like [Source:HGNC Symbol;Acc:2
15	26085	1.15	2e-14	2e-12	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6]
16	92196	1.1	2e-13	2e-12	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
17	1475	1.09	3e-13	3e-11	1 x 50 cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
18	57152	1.04	4e-12	3e-11	1 x 50 secreted LY6/PLAUR domain containing 1 [Source:HGNC Sy
19	11005	1.04	4e-12	3e-10	1 x 50 serine peptidase inhibitor, Kazal type 5 [Source:HGNC Symb
20	7051	0.99	4e-11	3e-10	1 x 50 transglutaminase 1 [Source:HGNC Symbol;Acc:11777]

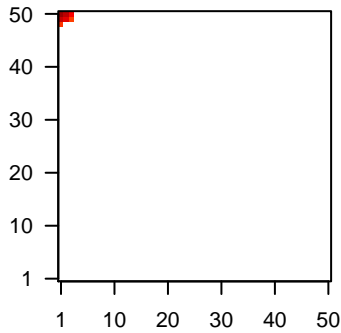
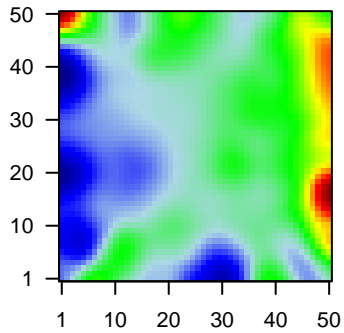
Local Geneset Analysis

Overexpression

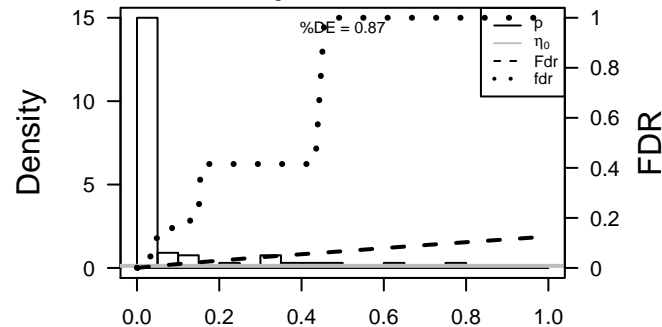
Rank	GSZ	p-value	#in/all	Geneset
1	50.68	NULL	62 / 135	H.Tiss WIRTH_Mucosa
2	26.28	NULL	7 / 19	BP peptide cross-linking
3	22.81	NULL	13 / 21	CC cornified envelope
4	19.72	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
5	19.65	NULL	15 / 42	BP keratinization
6	18.72	NULL	17 / 53	BP keratinocyte differentiation
7	16.47	NULL	6 / 13	BP negative regulation of peptidase activity
8	16.37	NULL	2 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
9	15.61	NULL	16 / 76	BP epidermis development
10	13.59	NULL	64 / 572	Disease GUDJ_psooriasis up
11	13.35	NULL	5 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	12.29	NULL	3 / 12	BP cellular aldehyde metabolic process
13	12.2	NULL	5 / 21	CC desmosome
14	12.05	NULL	2 / 12	MF retinol binding
15	11.97	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
16	11.51	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS KERATINOCYTE_DN
17	11.5	NULL	2 / 13	BP retinoic acid metabolic process
18	11.44	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
19	11.41	NULL	2 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
20	11.12	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
21	10.88	NULL	8 / 52	BP negative regulation of endopeptidase activity
22	10.27	NULL	4 / 38	BP epithelial cell differentiation
23	10.24	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
24	10.16	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
25	9.89	NULL	3 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
26	9.71	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
27	9.7	NULL	2 / 15	GSEA C2ALONSO_METASTASIS_NEURAL_UP
28	9.7	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
29	9.66	NULL	1 / 11	Glio VERHAAK_Brain
30	9.46	NULL	2 / 10	GSEA C2REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
31	9.4	NULL	3 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
32	9.33	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
33	9.18	NULL	1 / 12	MF channel activity
34	9	NULL	2 / 10	GSEA C2KEGG_LINOLEIC_ACID_METABOLISM
35	8.95	NULL	5 / 29	BP regulation of proteolysis
36	8.84	NULL	4 / 16	GSEA C2LEE_LIVER_CANCER_MYC_TGFA_UP
37	8.75	NULL	1 / 13	GSEA C2HASLINGER_B CLL_WITH_MUTATED_VH_GENES
38	8.42	NULL	10 / 79	MF serine-type endopeptidase inhibitor activity
39	8.42	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
40	8.37	NULL	4 / 44	CC keratin filament

Profile

Spot



p-values



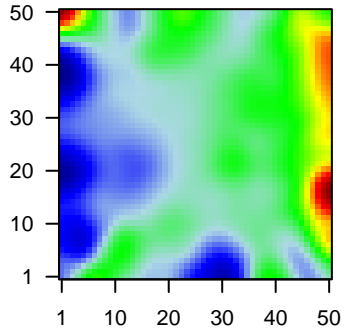
GW_297

Local Summary

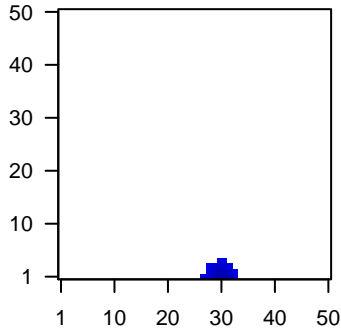
%DE = 0.72
 # metagenes = 20
 # genes = 183
 # genes in genesets = 180
 # genes with $fdr < 0.1 = 115$ (15 + / 100 -)
 # genes with $fdr < 0.05 = 62$ (6 + / 56 -)
 # genes with $fdr < 0.01 = 41$ (5 + / 36 -)

<r> metagenes = 0.89
 <r> genes = 0.33
 <FC> = -0.24
 <shrinkage-t> = -8.29
 <p-value> = 0.01
 <fdr> = 0.61

Profile



Spot



Local Genelist

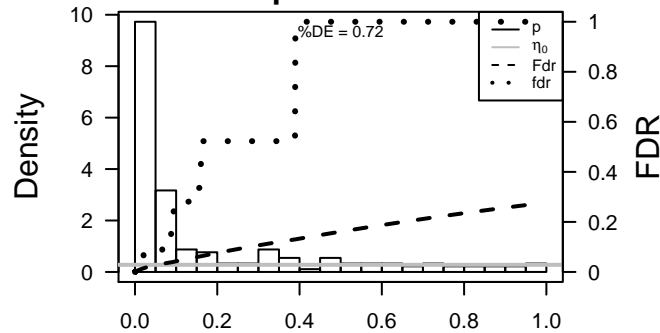
Rank	ID	log(FC)	fdr	p-value	Description
1	970	1.34	2e-16	1e-14	33 x 2 CD70 molecule [Source:HGNC Symbol;Acc:11937]
2	10581	-1	5e-13	1e-10	32 x 1 interferon induced transmembrane protein 2 [Source:HGNC S
3	4321	-1.05	3e-12	9e-10	32 x 1 matrix metalloproteinase 12 (macrophage elastase) [Source:H
4	7453	-1.01	2e-11	2e-09	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1:
5	10410	-0.9	6e-11	2e-07	32 x 1 interferon induced transmembrane protein 3 [Source:HGNC S
6	1591	0.87	8e-09	2e-07	33 x 2 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
7	3135	-0.87	8e-09	2e-07	32 x 1 major histocompatibility complex, class I, G [Source:HGNC S
8	629	-0.85	1e-08	3e-07	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
9	9560	-0.85	2e-08	3e-07	32 x 1 chemokine (C-C motif) ligand 4-like 1 [Source:HGNC Symbc
10	5610	0.84	2e-08	3e-07	32 x 1 eukaryotic translation initiation factor 2-alpha kinase 2 [Sour
11	3627	0.83	3e-08	6e-07	32 x 1 chemokine (C-X-C motif) ligand 10 [Source:HGNC Symbol;A
12	9536	-0.82	4e-08	3e-06	31 x 2 prostaglandin E synthase [Source:HGNC Symbol;Acc:9599]
13	1200	-0.79	1e-07	3e-06	29 x 1 tripeptidyl peptidase I [Source:HGNC Symbol;Acc:2073]
14	51296	-0.79	2e-07	4e-06	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3
15	5699	-0.78	2e-07	2e-05	32 x 1 proteasome (prosome, macropain) subunit, beta type, 10 [So
16	10211	-0.75	5e-07	7e-05	28 x 2 flotillin 1 [Source:HGNC Symbol;Acc:3757]
17	3134	-0.71	2e-06	2e-04	32 x 1 major histocompatibility complex, class I, F [Source:HGNC S)
18	53	-0.67	8e-06	2e-04	30 x 2 acid phosphatase 2, lysosomal [Source:HGNC Symbol;Acc:1
19	254102	-0.66	1e-05	2e-04	29 x 2 EH domain binding protein 1-like 1 [Source:HGNC Symbol;A
20	100	-0.66	1e-05	2e-04	30 x 1 adenosine deaminase [Source:HGNC Symbol;Acc:186]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-27.58	NULL	29 / 51	BP type I interferon signaling pathway
2	-26.12	NULL	6 / 6	Lymphom GSEA C2A0AVE_MHCCII BL DN
3	-23.68	NULL	8 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
4	-23.4	NULL	7 / 10	CC MHC class I protein complex
5	-20.63	NULL	8 / 18	BP positive regulation of T cell mediated cytotoxicity
6	-18.45	NULL	5 / 18	BP response to interferon-gamma
7	-18.27	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
8	-18.07	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
9	-17.94	NULL	7 / 18	MF peptide antigen binding
10	-16.89	NULL	2 / 2	MMML C2SCICJ_MMMML 27
11	-16.4	NULL	1 / 2	miRNA target-152
12	-15.46	NULL	10 / 52	Chr Chr HSCHR6_MHC_QBL
13	-14.56	NULL	36 / 204	BP cytokine-mediated signaling pathway
14	-14.18	NULL	12 / 70	BP antigen processing and presentation of exogenous peptide antigen
15	-13.9	NULL	3 / 9	GSEA C2FURUKAWA_DUSP6_TARGETS_PC135_UP
16	-13.75	NULL	12 / 74	BP antigen processing and presentation of exogenous peptide antigen
17	-13.34	NULL	17 / 60	BP interferon-gamma-mediated signaling pathway
18	-13.34	NULL	3 / 8	GSEA C2KEGG_PRIMARY_IMMUNODEFICIENCY
19	-13.32	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
20	-13.22	NULL	11 / 16	GSEA C2JROSEVIC_RESPONSE_TO_IMIQUIMOD
21	-13	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
22	-12.91	NULL	1 / 3	miRNA target-148a
23	-12.45	NULL	13 / 74	BP regulation of immune response
24	-12.41	NULL	3 / 9	GSEA C2DER_IFN_ALPHA_RESPONSE_UP
25	-12.41	NULL	3 / 9	GSEA C2DER_IFN_GAMMA_RESPONSE_UP
26	-12.39	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
27	-12.3	NULL	14 / 31	BP negative regulation of viral genome replication
28	-12.27	NULL	12 / 91	BP antigen processing and presentation of peptide antigen via MHC cl
29	-12.24	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
30	-12.22	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
31	-11.72	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
32	-11.64	NULL	3 / 14	GSEA C2REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION
33	-11.39	NULL	6 / 32	CC ER to Golgi transport vesicle membrane
34	-11.27	NULL	5 / 23	CC integral to luminal side of endoplasmic reticulum membrane
35	-11.09	NULL	29 / 316	Cancer SPANG_BCL6-index2
36	-11.07	NULL	3 / 16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
37	-11.01	NULL	35 / 274	Lymphom SPANG_IL21 DN
38	-10.31	NULL	34 / 312	BP immune response
39	-10.29	NULL	2 / 11	GSEA C2FUJII_YBX1_TARGETS_UP
40	-9.86	NULL	3 / 14	GSEA C2JINDESTD_DENDRITIC_CELL_MATURATION_A

p-values



GW_297

Local Summary

%DE = 0.76
 # metagenes = 14
 # genes = 104
 # genes in genesets = 104

genes with $fdr < 0.1 = 55$ (1 + / 54 -)
 # genes with $fdr < 0.05 = 33$ (1 + / 32 -)
 # genes with $fdr < 0.01 = 13$ (1 + / 12 -)

<r> metagenes = 0.94
 <r> genes = 0.31

<FC> = -0.22
 <shrinkage-t> = -7.58
 <p-value> = 0.06
 <fdr> = 0.74

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	124583	0.65	1e-05	0.001	3 x 9 calcium activated nucleotidase 1 [Source:HGNC Symbol;Acc:
2	57522	-0.6	6e-05	0.001	3 x 7 SLIT-ROBO Rho GTPase activating protein 1 [Source:HGNC
3	91300	-0.58	1e-04	0.002	5 x 9 R3H domain containing 4 [Source:HGNC Symbol;Acc:28270]
4	29950	-0.56	2e-04	0.002	4 x 8 SERTA domain containing 1 [Source:HGNC Symbol;Acc:179:
5	92799	-0.55	3e-04	0.002	5 x 10 SH3KBP1 binding protein 1 [Source:HGNC Symbol;Acc:1921
6	56926	-0.53	4e-04	0.002	5 x 10 nicalin [Source:HGNC Symbol;Acc:26923]
7	5360	-0.53	5e-04	0.002	4 x 7 phospholipid transfer protein [Source:HGNC Symbol;Acc:909
8	2907	-0.52	5e-04	0.007	5 x 8 glutamate receptor, ionotropic, N-methyl D-aspartate-associ
9	7165	-0.49	1e-03	0.007	3 x 8 tumor protein D52-like 2 [Source:HGNC Symbol;Acc:12007]
10	6723	-0.49	1e-03	0.007	5 x 9 spermidine synthase [Source:HGNC Symbol;Acc:11296]
11	221955	-0.48	1e-03	0.007	5 x 10 diacylglycerol lipase, beta [Source:HGNC Symbol;Acc:28923
12	57801	-0.47	2e-03	0.007	4 x 8 hes family bHLH transcription factor 4 [Source:HGNC Symbol
13	80152	-0.46	2e-03	0.008	3 x 9 centromere protein T [Source:HGNC Symbol;Acc:25787]
14	1025	-0.46	2e-03	0.034	4 x 10 cyclin-dependent kinase 9 [Source:HGNC Symbol;Acc:1780]
15	2683	-0.41	6e-03	0.034	4 x 8 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polyp
16	1072	-0.37	7e-03	0.034	4 x 8 cofilin 1 (non-muscle) [Source:HGNC Symbol;Acc:1874]
17	81	-0.41	7e-03	0.034	5 x 10 actinin, alpha 4 [Source:HGNC Symbol;Acc:166]
18	79797	-0.39	1e-02	0.034	4 x 10 zinc finger protein 408 [Source:HGNC Symbol;Acc:20041]
19	7408	-0.38	1e-02	0.034	4 x 8 vasodilator-stimulated phosphoprotein [Source:HGNC Symb
20	10897	-0.38	1e-02	0.034	3 x 8 Yip1 interacting factor homolog A (S. cerevisiae) [Source:HGI

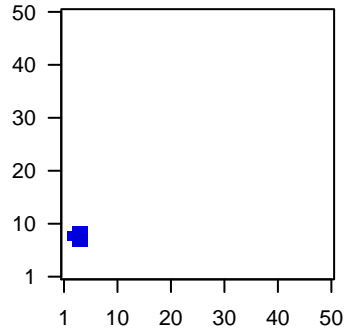
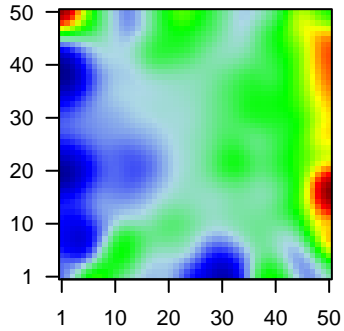
Local Geneset Analysis

Underexpression

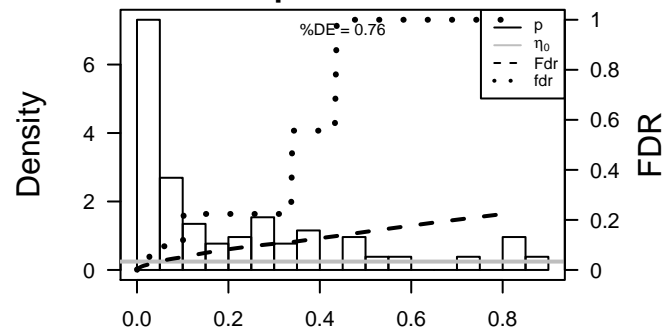
Rank	GSZ	p-value	#in/all	Geneset
1	-11.99	NULL	3 / 16	GSEA C2REACTOME_SIGNALING_BY_ROBO_RECEPTOR
2	-11.05	NULL	3 / 13	GSEA C2SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO
3	-10.21	NULL	2 / 10	GSEA C2HONMA_DOCETAXEL_RESISTANCE
4	-9.07	NULL	1 / 6	GSEA C2LUI_THYROID_CANCER_CLUSTER_4
5	-8.4	NULL	3 / 45	Glio wilscher_GBM_Verhaak-PNwt_expression_J_up
6	-8.36	NULL	1 / 7	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
7	-8.24	NULL	2 / 16	CC lamellipodium membrane
8	-7.85	NULL	3 / 44	BP Rho protein signal transduction
9	-7.8	NULL	1 / 8	GSEA C2NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
10	-7.72	NULL	1 / 7	miRNA target miR-399-3p
11	-7.72	NULL	2 / 13	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT
12	-7.72	NULL	2 / 13	GSEA C2RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN
13	-7.7	NULL	2 / 16	BP polyamine metabolic process
14	-7.56	NULL	2 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
15	-7.55	NULL	2 / 16	GSEA C2WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_H2O2
16	-7.39	NULL	2 / 11	GSEA C2KEGG_REGULATION_OF_ACTIN_CYTOSKELETON
17	-7.33	NULL	1 / 9	GSEA C2ACOSTA_UV_RESPONSE_VIA_ERCC3_UP
18	-7.33	NULL	1 / 9	GSEA C2KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP
19	-7.27	NULL	1 / 7	GSEA C2NEBEN_AML_WITH_FLT3_OR_NRAS_UP
20	-7.19	NULL	4 / 63	miRNA target miR-392
21	-7.18	NULL	3 / 33	MF Rho GTPase binding
22	-7.15	NULL	2 / 15	GSEA C2RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
23	-7.15	NULL	4 / 53	CC endoplasmic reticulum-Golgi intermediate compartment
24	-7.11	NULL	1 / 5	GSEA C2SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_D
25	-7.02	NULL	1 / 6	GSEA C2WIELAND_UP_BY_HBV_INFECTION
26	-7.02	NULL	1 / 6	GSEA C2SA_FAS_SIGNALING
27	-6.93	NULL	1 / 10	GSEA C2AMUNDSON_RESPONSE_TO_ARSENITE
28	-6.89	NULL	2 / 25	MF Rho GTPase activator activity
29	-6.76	NULL	2 / 13	GSEA C2REACTOME_FORMATION_OF_PLATELET_PLUG
30	-6.76	NULL	2 / 13	GSEA C2REACTOME_HEMOSTASIS
31	-6.76	NULL	2 / 13	GSEA C2REACTOME_PLATELET_ACTIVATION
32	-6.53	NULL	2 / 15	GSEA C2GHO_ATF5_TARGETS_DN
33	-6.36	NULL	1 / 9	GSEA C2REACTOME_HIV1_TRANSCRIPTION_ELONGATION
34	-6.28	NULL	1 / 12	GSEA C2HAMAL_APOPTOSIS_VIA_TRAIL_DN
35	-6.28	NULL	1 / 12	GSEA C2HELLER_SILENCED_BY_METHYLATION_DN
36	-6.28	NULL	1 / 12	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_DN
37	-6.28	NULL	1 / 12	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
38	-6.28	NULL	1 / 12	GSEA C2KEGG_PPAR_SIGNALING_PATHWAY
39	-6.26	NULL	2 / 15	GSEA C2KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS
40	-6.24	NULL	2 / 14	GSEA C2REACTOME_FURTHER_PLATELET_RELEASE

Profile

Spot



p-values



GW_297

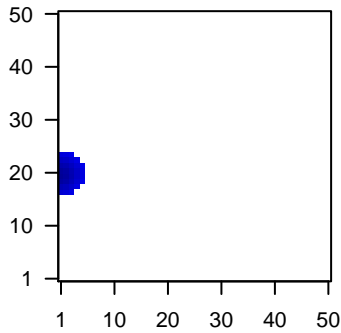
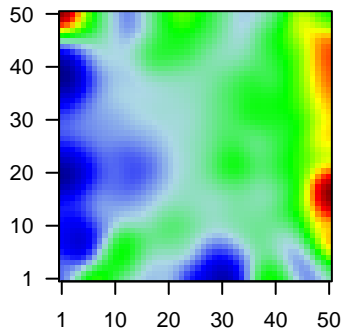
Local Summary

%DE = 0.58
 # metagenes = 34
 # genes = 350
 # genes in genesets = 345
 # genes with $fdr < 0.1$ = 61 (0 + / 61 -)
 # genes with $fdr < 0.05$ = 55 (0 + / 55 -)
 # genes with $fdr < 0.01$ = 23 (0 + / 23 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.27
 $\langle FC \rangle = -0.2$
 $\langle \text{shrinkage-t} \rangle = -7.02$
 $\langle p\text{-value} \rangle = 0.07$
 $\langle fdr \rangle = 0.78$

Profile

Spot



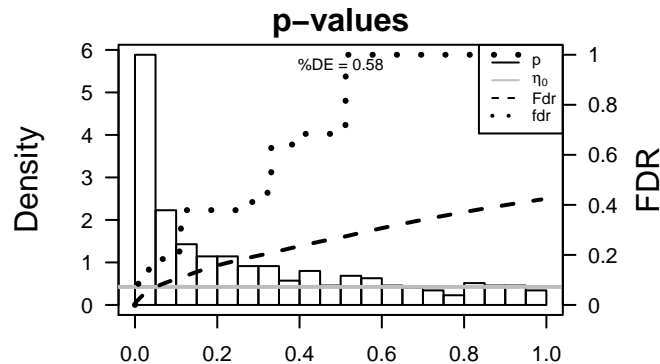
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	3006	-1.07	1e-12	2e-08	5 x 20 histone cluster 1, H1c [Source:HGNC Symbol;Acc:4716]
2	1152	-0.96	2e-10	1e-06	1 x 17 creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
3	430	-0.86	9e-09	5e-06	2 x 20 achaete-scute family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:1991]
4	8045	-0.82	4e-08	1e-04	2 x 22 Ras association (RalGDS/AF-6) domain family (N-terminal) member 1 [Source:HGNC Symbol;Acc:1991]
5	1173	-0.74	8e-07	2e-04	1 x 20 adaptor-related protein complex 2, mu 1 subunit [Source:HGNC Symbol;Acc:1991]
6	51702	-0.71	2e-06	3e-04	1 x 21 peptidyl arginine deiminase, type III [Source:HGNC Symbol;Acc:1991]
7	9409	-0.69	4e-06	2e-03	2 x 21 peroxisomal biogenesis factor 16 [Source:HGNC Symbol;Acc:1991]
8	5702	-0.64	2e-05	2e-03	1 x 19 proteasome (prosome, macropain) 26S subunit, ATPase, 3 [Source:HGNC Symbol;Acc:1991]
9	230	-0.63	3e-05	3e-03	2 x 17 aldolase C, fructose-bisphosphate [Source:HGNC Symbol;Acc:1991]
10	79763	-0.61	5e-05	4e-03	3 x 19 isochorismatase domain containing 2 [Source:HGNC Symbol;Acc:1991]
11	51204	-0.58	1e-04	4e-03	2 x 18 translational activator of mitochondrially encoded cytochrome c oxidase subunit 1 [Source:HGNC Symbol;Acc:1991]
12	118881	-0.56	2e-04	4e-03	1 x 22 catechol-O-methyltransferase domain containing 1 [Source:HGNC Symbol;Acc:1991]
13	10572	-0.56	2e-04	4e-03	3 x 18 SIVA1, apoptosis-inducing factor [Source:HGNC Symbol;Acc:1991]
14	123355	-0.55	2e-04	4e-03	1 x 23 leucine rich repeat containing 28 [Source:HGNC Symbol;Acc:1991]
15	90990	-0.55	2e-04	4e-03	1 x 23 kinesin family member C2 [Source:HGNC Symbol;Acc:29530]
16	10682	-0.55	2e-04	4e-03	3 x 20 emopamil binding protein (sterol isomerase) [Source:HGNC Symbol;Acc:1991]
17	6510	-0.55	2e-04	4e-03	2 x 19 solute carrier family 1 (neutral amino acid transporter), member 1 [Source:HGNC Symbol;Acc:1991]
18	51400	-0.55	2e-04	8e-03	1 x 18 protein phosphatase methylesterase 1 [Source:HGNC Symbol;Acc:1991]
19	4715	-0.54	4e-04	8e-03	1 x 17 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22 [Source:HGNC Symbol;Acc:1991]
20	284085	-0.53	4e-04	8e-03	3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-10.8	NULL	3 / 5	GSEA C2NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON
2	-10.13	NULL	2 / 7	GSEA C2REACTOME_SIGNALING_BY_WNT
3	-9.53	NULL	5 / 16	GSEA C2BIOCARTA_PTDINS_PATHWAY
4	-9.41	NULL	1 / 7	MMML C2SCIEJ_MMML_9
5	-8.74	NULL	2 / 7	GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE
6	-8.74	NULL	2 / 7	GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_P27
7	-8.74	NULL	2 / 7	GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27
8	-8.74	NULL	2 / 7	GSEA C2REACTOME_STABILIZATION_OF_P53
9	-7.78	NULL	1 / 10	GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP
10	-7.54	NULL	3 / 14	GSEA C2CHANG_CORE_SERUM_RESPONSE_UP
11	-7.39	NULL	1 / 9	GSEA C2GOUYER_TUMOR_INVASIVENESS
12	-7.39	NULL	1 / 11	GSEA C2REACTOME_APOPTOSIS_INDUCED_DNA_FRAGMENTATION
13	-7.26	NULL	2 / 13	GSEA C2REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSE
14	-7.09	NULL	2 / 10	BP drug transmembrane transport
15	-6.98	NULL	1 / 10	BP creatine metabolic process
16	-6.97	NULL	2 / 14	GSEA C2REACTOME_NEURORANSMITTER_RECEPTOR_BINDING_AND_TRANSMISSION
17	-6.94	NULL	86 / 1318	CC mitochondrion
18	-6.85	NULL	2 / 11	GSEA C2WONG_PROTEASOME_GENE_MODULE
19	-6.78	NULL	3 / 9	GSEA C2BIOCARTA_GLYCOLYSIS_PATHWAY
20	-6.26	NULL	3 / 15	GSEA C2REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_CYCLE
21	-6.22	NULL	1 / 15	GSEA C2GEORGANTAS_HSC_MARKERS
22	-6.21	NULL	3 / 14	GSEA C2LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
23	-6.15	NULL	2 / 11	GSEA C2REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING
24	-6.02	NULL	1 / 6	GSEA C2REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1
25	-5.86	NULL	3 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
26	-5.86	NULL	2 / 12	GSEA C2REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS
27	-5.76	NULL	2 / 12	GSEA C2WANG_SMARCE1_TARGETS_DN
28	-5.66	NULL	21 / 153	MF structural constituent of ribosome
29	-5.56	NULL	3 / 17	CC proteasome accessory complex
30	-5.54	NULL	1 / 7	GSEA C2KEGG_PROTEASOME
31	-5.54	NULL	1 / 7	GSEA C2REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_OF_G1
32	-5.54	NULL	1 / 7	GSEA C2REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE
33	-5.54	NULL	1 / 7	GSEA C2REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G
34	-5.53	NULL	3 / 13	GSEA C2REACTOME_GLYCOLYSIS
35	-5.5	NULL	3 / 12	BP apoptotic nuclear changes
36	-5.48	NULL	3 / 16	GSEA C2GRATIAS_RETINOBLASTOMA_16Q24
37	-5.44	NULL	2 / 9	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_UP
38	-5.42	NULL	3 / 10	MF monosaccharide binding
39	-5.37	NULL	2 / 14	GSEA C2REACTOME_EGFR_DOWNREGULATION
40	-5.36	NULL	1 / 16	GSEA C2DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN



GW_297

Local Summary

%DE = 0.66
 # metagenes = 30
 # genes = 310
 # genes in genesets = 303

 # genes with $fdr < 0.1 = 120$ (9 + / 111 -)
 # genes with $fdr < 0.05 = 90$ (4 + / 86 -)
 # genes with $fdr < 0.01 = 48$ (2 + / 46 -)

 $\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.25

 $\langle FC \rangle = -0.24$
 $\langle \text{shrinkage-t} \rangle = -8.36$
 $\langle p\text{-value} \rangle = 0.02$
 $\langle fdr \rangle = 0.67$

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	723790	-1.11	1e-13	8e-11	2 x 38 histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
2	133	-0.99	9e-13	1e-08	1 x 42 adrenomedullin [Source:HGNC Symbol;Acc:259]
3	8337	-0.97	1e-10	1e-07	2 x 38 histone cluster 2, H2aa3 [Source:HGNC Symbol;Acc:4736]
4	8942	-0.91	1e-09	4e-07	1 x 40 kynureninase [Source:HGNC Symbol;Acc:6469]
5	4015	-0.88	5e-09	6e-06	1 x 41 lysyl oxidase [Source:HGNC Symbol;Acc:6664]
6	29775	-0.82	6e-08	9e-06	1 x 42 caspase recruitment domain family, member 10 [Source:HGN
7	1942	-0.79	1e-07	3e-05	1 x 40 ephrin-A1 [Source:HGNC Symbol;Acc:3221]
8	90102	-0.76	4e-07	3e-05	1 x 42 pleckstrin homology-like domain, family B, member 2 [Source
9	55214	-0.75	7e-07	3e-05	1 x 42 leprecan-like 1 [Source:HGNC Symbol;Acc:19317]
10	10397	-0.67	1e-06	3e-05	1 x 42 N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:
11	8339	-0.72	1e-06	3e-05	4 x 38 histone cluster 1, H2bc [Source:HGNC Symbol;Acc:4757]
12	8986	-0.72	2e-06	3e-05	1 x 40 ribosomal protein S6 kinase, 90kDa, polypeptide 4 [Source:H
13	4233	-0.72	2e-06	5e-05	1 x 41 met proto-oncogene [Source:HGNC Symbol;Acc:7029]
14	8338	-0.71	2e-06	5e-05	2 x 37 histone cluster 2, H2ac [Source:HGNC Symbol;Acc:4738]
15	3229	-0.71	3e-06	1e-04	1 x 42 homeobox C13 [Source:HGNC Symbol;Acc:5125]
16	54704	-0.7	4e-06	3e-04	3 x 40 pyruvate dehydrogenase phosphatase catalytic subunit 1 [Sou
17	54795	-0.66	1e-05	3e-04	1 x 36 transient receptor potential cation channel, subfamily M, merr
18	51734	-0.66	1e-05	5e-04	1 x 39 methionine sulfoxide reductase B1 [Source:HGNC Symbol;Ac
19	112399	-0.65	1e-05	8e-04	1 x 40 egl-9 family hypoxia-inducible factor 3 [Source:HGNC Symb
20	154	0.63	3e-05	8e-04	1 x 40 adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286

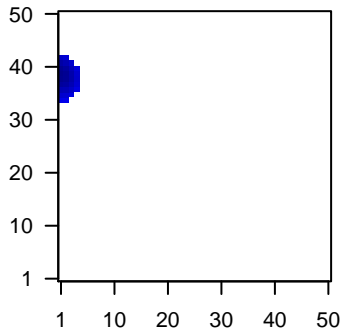
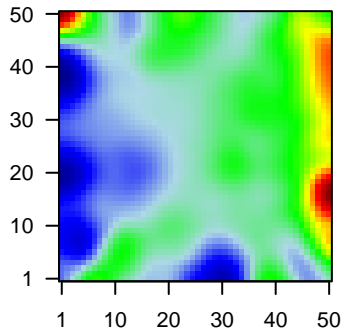
Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-19.2	NULL	2 / 2	miRNA target-199a*
2	-16.27	NULL	3 / 7	MMML C6ACIEJ_MMML_9
3	-14.96	NULL	3 / 15	GSEA C2FARMER_BREAST_CANCER_CLUSTER_3
4	-14.45	NULL	3 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_4
5	-13.05	NULL	2 / 12	GSEA C2ZHAN_V1_LATE_DIFFERENTIATION_GENES_DN
6	-12.06	NULL	2 / 8	GSEA C2WILLIAMS_ESR2_TARGETS_DN
7	-11.47	NULL	2 / 12	GSEA C2MIZUKAMI_HYPOXIA_UP
8	-10.93	NULL	3 / 8	GSEA C2SIBULAN_UV_RESPONSE_NORMAL_UP
9	-10.28	NULL	2 / 13	GSEA C2REACTOME_PACKAGING_OF_TELOMERE_ENDS
10	-9.98	NULL	7 / 47	CC nucleosome
11	-9.51	NULL	2 / 10	GSEA C2DAZARD_UV_RESPONSE_CLUSTER_G3
12	-9.4	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_120_MCF10A
13	-8.72	NULL	1 / 7	GSEA C2REACTOME_CALCITONIN_LIKE_LIGAND_RECEPTORS
14	-8.52	NULL	1 / 5	GSEA C2ELVIDGE_HIF2A_TARGETS_UP
15	-8.5	NULL	2 / 10	GSEA C2NIELSEN_MALIGNANT_FIBROUS_HISTIOCYTOMA_UP
16	-8.09	NULL	2 / 15	GSEA C2KARAKAS_TGFB1_SIGNALING
17	-8.02	NULL	1 / 6	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
18	-7.98	NULL	2 / 11	GSEA C2MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER
19	-7.83	NULL	1 / 4	miRNA target-206
20	-7.59	NULL	1 / 4	GSEA C2GARASHI_ATF4_TARGETS_UP
21	-7.16	NULL	1 / 10	BP negative regulation of vascular permeability
22	-7.04	NULL	1 / 5	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NC
23	-6.97	NULL	7 / 86	BP nucleosome assembly
24	-6.93	NULL	1 / 10	GSEA C2REACTOME_RNA_POLYMERASE_I_PROMOTER_OPENING
25	-6.93	NULL	3 / 15	GSEA C2SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B
26	-6.92	NULL	1 / 5	GSEA C2CHOI_ATL_ACUTE_STAGE
27	-6.8	NULL	2 / 17	BP cAMP-mediated signaling
28	-6.65	NULL	3 / 30	miRNA target-206
29	-6.57	NULL	2 / 19	MF L-ascorbic acid binding
30	-6.51	NULL	4 / 16	GSEA C2AMUNDSON_DNA_DAMAGE_RESPONSE_TP53
31	-6.47	NULL	1 / 12	BP androgen metabolic process
32	-6.47	NULL	1 / 12	BP cAMP biosynthetic process
33	-6.37	NULL	2 / 16	GSEA C2SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP
34	-6.36	NULL	1 / 6	GSEA C2KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV
35	-6.26	NULL	1 / 6	GSEA C2TAKAYAMA_BOUND_BY_AR
36	-6.25	NULL	1 / 12	GSEA C2ZHU_CMV_8_HR_UP
37	-6.21	NULL	3 / 15	GSEA C2KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOL
38	-6.18	NULL	1 / 13	BP positive regulation of heart rate
39	-6.18	NULL	1 / 13	GSEA C2HASINA_NOL7_TARGETS_UP
40	-6.18	NULL	1 / 13	GSEA C2SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN

Profile

Spot



p-values

