

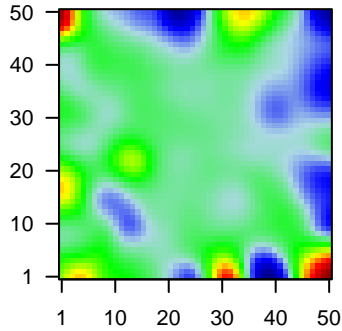
GW_075

Global Summary

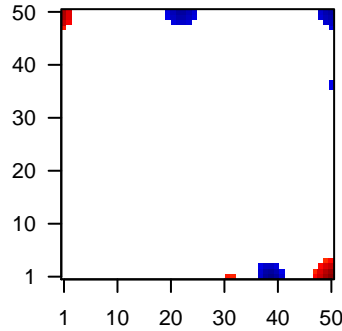
%DE = 0.14
 # genes with $fdr < 0.2$ = 1666 (988 + / 678 -)
 # genes with $fdr < 0.1$ = 1258 (769 + / 489 -)
 # genes with $fdr < 0.05$ = 1059 (648 + / 411 -)
 # genes with $fdr < 0.01$ = 733 (474 + / 259 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.12
 <fdr> = 0.86

Profile



Regulated Spots



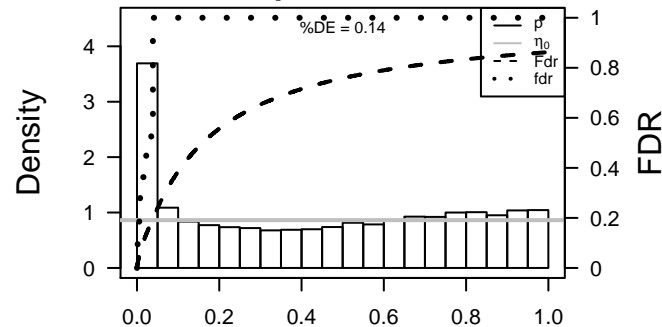
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	58	-1.36	2e-16 5e-14	25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	8644	1.62	2e-16 5e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Syr
3	1109	1.98	2e-16 5e-14	13 x 50 aldo-keto reductase family 1, member C4 [Source:HGNC Syr
4	222	2.13	2e-16 5e-14	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
5	151516	1.77	2e-16 5e-14	1 x 46 aspartic peptidase, retroviral-like 1 [Source:HGNC Symbol;A
6	713	1.6	2e-16 5e-14	50 x 1 complement component 1, q subcomponent, B chain [Source
7	260436	2.14	2e-16 5e-14	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
8	51806	2	2e-16 5e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
9	875	1.37	2e-16 5e-14	49 x 47 cystathionine-beta-synthase [Source:HGNC Symbol;Acc:15
10	131076	1.58	2e-16 5e-14	1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc
11	6366	1.6	2e-16 5e-14	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
12	6352	1.65	2e-16 5e-14	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:
13	57124	1.7	2e-16 5e-14	3 x 1 CD248 molecule, endosialin [Source:HGNC Symbol;Acc:182
14	1041	2.04	2e-16 5e-14	1 x 46 corneodesmosin [Source:HGNC Symbol;Acc:1802]
15	629	1.35	2e-16 5e-14	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
16	1823	1.36	2e-16 5e-14	1 x 45 desmocollin 1 [Source:HGNC Symbol;Acc:3035]
17	25975	1.36	2e-16 5e-14	48 x 50 EGF-like-domain, multiple 6 [Source:HGNC Symbol;Acc:323
18	2353	-1.51	2e-16 5e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:+
19	2354	-2.19	2e-16 5e-14	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source
20	2745	1.79	2e-16 5e-14	50 x 3 glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	12.67	NULL	714	Chr Chr 6
2	12.56	NULL	572	Disease GUDJ_psooriasis up
3	11.39	NULL	21	CC cornified envelope
4	10.7	NULL	449	Chr Chr 20
5	9.98	NULL	743	Chr Chr 7
6	9.78	NULL	13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
7	9.17	NULL	553	Cancer Lembecke_Colonc Inflammation
8	8.84	NULL	42	BP keratinization
9	8.83	NULL	31	BP negative regulation of viral genome replication
10	8.23	NULL	51	BP type I interferon signaling pathway
11	8.14	NULL	10	MF RAGE receptor binding
12	7.71	NULL	10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
13	7.61	NULL	16	GSEA C2ZHANG_INTERFERON_RESPONSE
14	7.5	NULL	16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
15	7.34	NULL	265	Glio willscher_GBM_Verhaak-CL_expression_B_up
16	7.34	NULL	265	Glio willscher_GBM_Verhaak-MES_expression_B_up
17	7.34	NULL	265	Glio willscher_GBM_Verhaak-PNwt_expression_B_down
18	7.34	NULL	265	Glio willscher_GBM_Verhaak-PNmut_expression_B_down
19	7.28	NULL	16	GSEA C2MOSERLE_IFNA_RESPONSE
20	7.18	NULL	8	GSEA C2ROETH_TERT_TARGETS_UP
<i>Underexpressed</i>				
1	-10.12	NULL	630	Chr Chr X
2	-8.88	NULL	10	GSEA C2CHASSOT_SKIN_WOUND
3	-8.2	NULL	24	TF Tissue/AQUERIZAS_Trachea
4	-7.82	NULL	232	Chr Chr 18
5	-7.74	NULL	16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
6	-7.43	NULL	15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
7	-7.23	NULL	368	miRNA target-mir-344
8	-7.11	NULL	4640	CC nucleus
9	-7.08	NULL	310	miRNA target-mir-330
10	-7.08	NULL	16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
11	-6.62	NULL	463	miRNA target-mir-301a
12	-6.5	NULL	16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
13	-6.44	NULL	823	MF sequence-specific DNA binding transcription factor activity
14	-6.43	NULL	16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
15	-6.39	NULL	16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
16	-6.37	NULL	1720	Chr Chr 1
17	-6.34	NULL	335	miRNA target-mir-342-5p
18	-6.29	NULL	545	miRNA target-mir-330
19	-6.23	NULL	504	BP negative regulation of transcription from RNA polymerase II promot
20	-6.23	NULL	603	miRNA target-mir-32a

p-values



GW_075

Local Summary

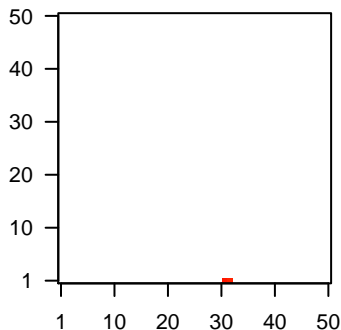
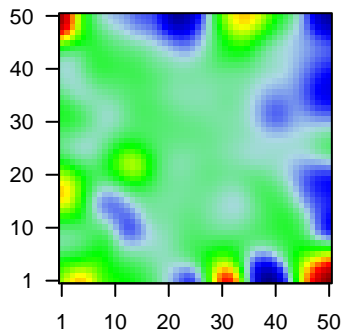
%DE = 0.81
 # metagenes = 2
 # genes = 100
 # genes in genesets = 98
 # genes with fdr < 0.1 = 65 (62 + / 3 -)
 # genes with fdr < 0.05 = 60 (58 + / 2 -)
 # genes with fdr < 0.01 = 57 (55 + / 2 -)

<r> metagenes = 1
 <r> genes = 0.51

<FC> = 0.49
 <shrinkage-t> = 17.19
 <p-value> = 0
 <fdr> = 0.38

Profile

Spot



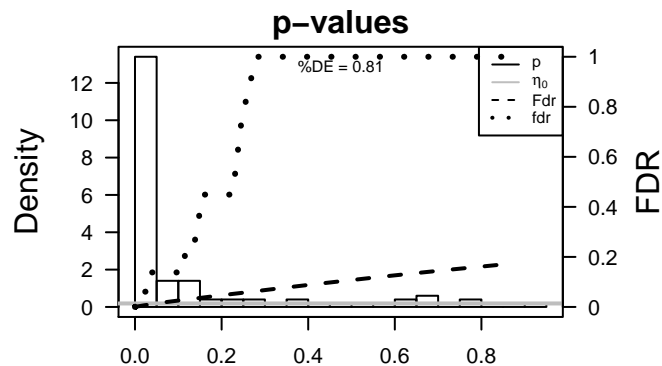
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	629	1.35	2e-16	1e-15	32 x 1 complement factor B [Source:HGNC Symbol;Acc:1037]
2	51191	1.48	2e-16	1e-15	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
3	3433	1.59	2e-16	1e-15	32 x 1 interferon-induced protein with tetratricopeptide repeats 2 [Sc
4	9636	1.78	2e-16	1e-15	32 x 1 ISG15 ubiquitin-like modifier [Source:HGNC Symbol;Acc:405
5	4600	1.16	1e-12	1e-11	32 x 1 myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
6	8638	1.15	1e-12	4e-11	32 x 1 2'-5'-oligoadenylate synthetase-like [Source:HGNC Symbol;
7	2537	1.13	3e-12	2e-09	32 x 1 interferon, alpha-inducible protein 6 [Source:HGNC Symbol;/
8	55008	1.02	3e-10	2e-09	32 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
9	6355	1.02	3e-10	2e-09	32 x 1 chemokine (C-C motif) ligand 8 [Source:HGNC Symbol;Acc:
10	55601	1.02	3e-10	4e-09	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 [Source:HGNC
11	3434	1.01	6e-10	9e-09	32 x 1 interferon-induced protein with tetratricopeptide repeats 1 [Sc
12	684	0.98	1e-09	9e-09	32 x 1 bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
13	10964	0.98	1e-09	3e-07	32 x 1 interferon-induced protein 44-like [Source:HGNC Symbol;Ac
14	85441	0.91	2e-08	3e-07	32 x 1 helicase with zinc finger 2, transcriptional coactivator [Source
15	51296	0.88	5e-08	3e-07	32 x 1 solute carrier family 15 (oligopeptide transporter), member 3 [
16	4599	0.81	6e-08	1e-06	32 x 1 myxovirus (influenza virus) resistance 1, interferon-inducible
17	10561	0.85	2e-07	1e-06	32 x 1 interferon-induced protein 44 [Source:HGNC Symbol;Acc:16
18	91351	0.84	2e-07	1e-06	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like [Source;t
19	23586	0.84	2e-07	1e-06	32 x 1 DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 [Source:HGNC
20	7453	0.83	3e-07	3e-06	32 x 1 tryptophanyl-tRNA synthetase [Source:HGNC Symbol;Acc:1:

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	52.57	NULL	9 / 10	GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
2	51.38	NULL	28 / 51	BP type I interferon signaling pathway
3	48.7	NULL	10 / 16	GSEA C2EINAV_INTERFERON_SIGNATURE_IN_CANCER
4	48.19	NULL	10 / 13	GSEA C2BOWIE_RESPONSE_TO_TAMOXIFEN
5	47.71	NULL	6 / 8	GSEA C2ROETH_TERT_TARGETS_UP
6	45.4	NULL	11 / 16	GSEA C2ZHANG_INTERFERON_RESPONSE
7	44.68	NULL	10 / 16	GSEA C2UROSEVIC_RESPONSE_TO_IMIQUIMOD
8	38.83	NULL	13 / 31	BP negative regulation of viral genome replication
9	37.97	NULL	12 / 16	GSEA C2MOERLE_IFNA_RESPONSE
10	35.93	NULL	26 / 109	BP response to virus
11	33.78	NULL	7 / 10	GSEA C2GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	32.38	NULL	30 / 123	BP defense response to virus
13	31.65	NULL	6 / 16	GSEA C2XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
14	31.26	NULL	3 / 4	MMML C6SCIEJ_MMML_47
15	30.24	NULL	3 / 5	GSEA C2KIM_LRRC3B_TARGETS
16	29.56	NULL	6 / 14	GSEA C2XU_AKT1_TARGETS_6HR
17	28.8	NULL	6 / 12	GSEA C2TSAL_DNAJB4_TARGETS_UP
18	27.42	NULL	3 / 4	GSEA C2KRASNOSELSKAYA_ILF3_TARGETS_UP
19	26.9	NULL	4 / 10	GSEA C2DAUER_STAT3_TARGETS_DN
20	26.23	NULL	4 / 15	GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP
21	25.97	NULL	33 / 204	BP cytokine-mediated signaling pathway
22	25.71	NULL	8 / 11	GSEA C2BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
23	25.62	NULL	7 / 16	GSEA C2MAHADEVAN_RESPONSE_TO_MP470_UP
24	25.46	NULL	5 / 6	LymphomBAVE_MHCII BL DN
25	25.28	NULL	5 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
26	22.53	NULL	2 / 2	MMML C6SCIEJ_MMML_27
27	22.24	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
28	21.72	NULL	6 / 14	Glio Donson-immune cell intra signaling-associated with LTS in HGA
29	21.61	NULL	6 / 32	BP negative regulation of type I interferon production
30	20.98	NULL	30 / 274	LymphomBPANG_IL21 DN
31	20.69	NULL	4 / 14	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
32	19.74	NULL	46 / 572	Disease GUDJ_poriasis up
33	19.52	NULL	6 / 14	GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_UP
34	19.51	NULL	9 / 51	MF double-stranded RNA binding
35	19	NULL	6 / 10	CC MHC class I protein complex
36	17.69	NULL	4 / 16	GSEA C2SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION
37	17.06	NULL	3 / 10	BP positive regulation of interferon-alpha production
38	16.86	NULL	3 / 16	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP
39	16.29	NULL	2 / 12	GSEA C2BROWNE_HCMV_INFECTION_4HR_UP
40	16.07	NULL	3 / 16	GSEA C2TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP



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Local Summary

%DE = 0.6
 # metagenes = 13
 # genes = 245
 # genes in genesets = 243

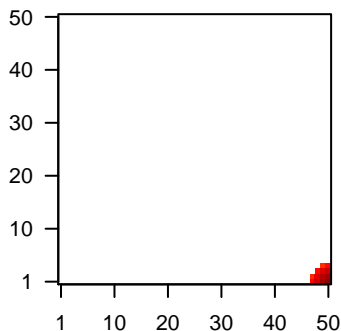
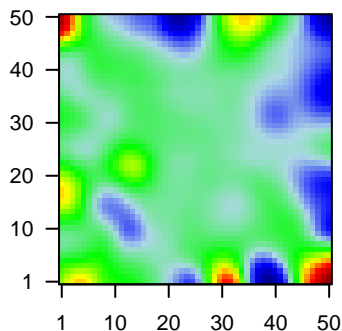
genes with $fdr < 0.1 = 119$ (109 + / 10 -)
 # genes with $fdr < 0.05 = 87$ (83 + / 4 -)
 # genes with $fdr < 0.01 = 67$ (63 + / 4 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.6

$\langle FC \rangle = 0.31$
 $\langle \text{shrinkage-t} \rangle = 10.7$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.59$

Profile

Spot



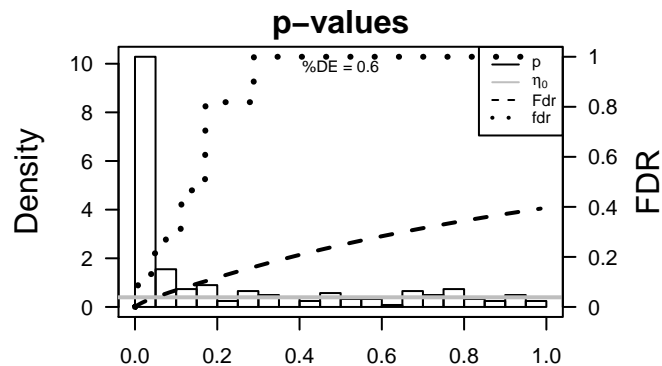
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	713	1.6	2e-16	2e-15	50 x 1 complement component 1, q subcomponent, B chain [Source
2	260436	2.14	2e-16	2e-15	50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
3	6366	1.6	2e-16	2e-15	50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
4	6352	1.65	2e-16	2e-15	48 x 1 chemokine (C-C motif) ligand 5 [Source:HGNC Symbol;Acc:1
5	2745	1.79	2e-16	2e-15	50 x 3 glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:43
6	3113	1.46	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source
7	3128	1.57	2e-16	2e-15	50 x 1 major histocompatibility complex, class II, DR beta 6 (pseudo
8	3512	-1.42	2e-16	2e-15	50 x 1 immunoglobulin J polypeptide, linker protein for immunogloblu
9	23643	1.53	2e-16	2e-15	50 x 3 lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
10	714	1.21	8e-14	2e-11	50 x 1 complement component 1, q subcomponent, C chain [Source
11	1436	1.18	4e-13	2e-11	50 x 1 colony stimulating factor 1 receptor [Source:HGNC Symbol;A
12	3109	1.18	4e-13	1e-09	50 x 1 major histocompatibility complex, class II, DM beta [Source:H
13	5336	1.09	2e-11	1e-09	48 x 3 phospholipase C, gamma 2 (phosphatidylinositol-specific) [S
14	4283	-1.07	3e-11	1e-09	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac
15	3122	1	4e-11	3e-09	50 x 1 major histocompatibility complex, class II, DR alpha [Source:t
16	64231	1.06	7e-11	6e-08	50 x 1 membrane-spanning 4-domains, subfamily A, member 6A [E
17	3543	0.92	7e-10	2e-07	49 x 1 immunoglobulin lambda-like polypeptide 1 [Source:HGNC Sy
18	55303	0.96	4e-09	2e-07	50 x 1 GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
19	27299	0.95	4e-09	6e-07	49 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]
20	2359	0.93	1e-08	6e-07	50 x 3 formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	24.05	NULL	12 / 15	CC MHC class II protein complex
2	23.79	NULL	2 / 4	GSEA C2REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
3	18.45	NULL	5 / 12	BP dendritic cell chemotaxis
4	17.93	NULL	39 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
5	17.93	NULL	39 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
6	17.93	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
7	17.93	NULL	39 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
8	17.27	NULL	2 / 7	GSEA C2BIOCARTA_COMP_PATHWAY
9	16.02	NULL	2 / 8	GSEA C2BIOCARTA_CLASSIC_PATHWAY
10	16.02	NULL	2 / 8	GSEA C2REACTOME_COMPLEMENT_CASCADE
11	16.02	NULL	2 / 8	GSEA C2REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
12	15.1	NULL	3 / 6	GSEA C2SANA_RESPONSE_TO_IFNG_UP
13	15.02	NULL	15 / 47	BP antigen processing and presentation
14	14.99	NULL	4 / 21	BP cellular response to interferon-gamma
15	14.35	NULL	9 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
16	13.97	NULL	13 / 60	BP T cell costimulation
17	13.76	NULL	3 / 9	GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
18	13.71	NULL	5 / 17	BP positive regulation of neutrophil chemotaxis
19	13.32	NULL	2 / 5	GSEA C2WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
20	13.18	NULL	47 / 312	BP immune response
21	13.08	NULL	86 / 417	H.Tiss WIRTH_Immune system
22	12.97	NULL	4 / 7	Glio Donson-cytotoxic effectors-associated with LTS in HGA
23	12.86	NULL	86 / 553	Cancer Lembcke_Colonc Inflammation
24	12.55	NULL	5 / 12	BP immunoglobulin mediated immune response
25	12.42	NULL	2 / 6	GSEA C2UL_THYROID_CANCER_CLUSTER_4
26	12.32	NULL	7 / 21	CC clathrin-coated endocytic vesicle membrane
27	12.01	NULL	2 / 3	MMML C2SCIEJ_MMML 7
28	11.75	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
29	11.72	NULL	7 / 23	CC integral to luminal side of endoplasmic reticulum membrane
30	11.44	NULL	9 / 43	BP positive regulation of T cell proliferation
31	11.43	NULL	3 / 15	GSEA C2CROONQUIST_NRAS_SIGNALING_UP
32	11.43	NULL	4 / 14	BP ruffle organization
33	11.26	NULL	2 / 10	BP positive regulation of chemotaxis
34	11.13	NULL	3 / 27	BP lipopolysaccharide-mediated signaling pathway
35	11.04	NULL	3 / 16	GSEA C2KAAB_FAILED_HEART_VENTRICLE_DN
36	10.94	NULL	1 / 6	GSEA C2RAY_ALZHEIMERS_DISEASE
37	10.76	NULL	17 / 74	BP regulation of immune response
38	10.74	NULL	4 / 27	BP release of sequestered calcium ion into cytosol
39	10.5	NULL	7 / 28	CC transport vesicle membrane
40	10.47	NULL	3 / 15	GSEA C2HAHTOLA_SEZARY_SYNDROM_DN



GW_075

Local Summary

%DE = 0.83
 # metagenes = 7
 # genes = 140
 # genes in genesets = 136

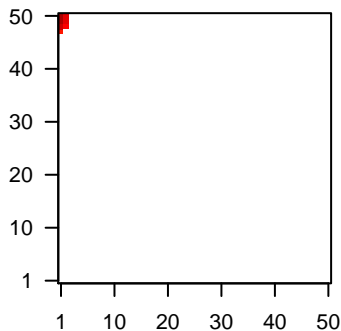
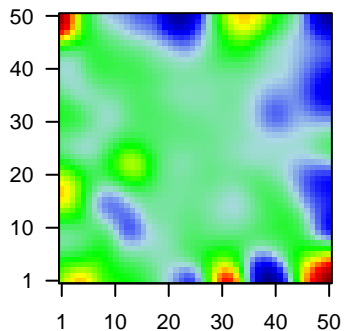
genes with $fdr < 0.1 = 97$ (73 + / 24 -)
 # genes with $fdr < 0.05 = 97$ (73 + / 24 -)
 # genes with $fdr < 0.01 = 82$ (63 + / 19 -)

$\langle r \rangle$ metagenes = 0.98
 $\langle r \rangle$ genes = 0.51

$\langle FC \rangle = 0.45$
 $\langle \text{shrinkage-t} \rangle = 15.98$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.32$

Profile

Spot



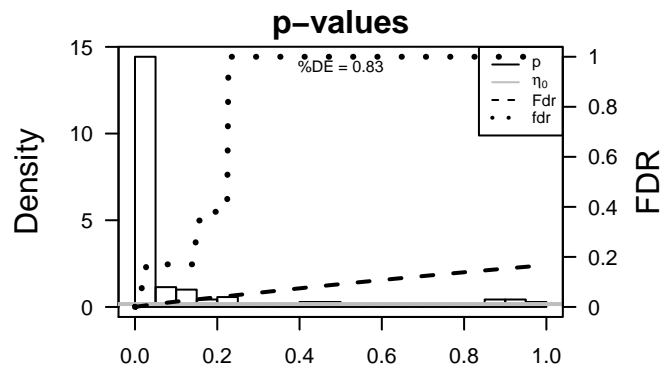
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	8644	1.62	2e-16	2e-16	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symb
2	222	2.13	2e-16	2e-16	1 x 49 aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
3	26525	1.48	2e-16	2e-16	1 x 49 interleukin 36 receptor antagonist [Source:HGNC Symbol;Acc
4	43849	1.36	2e-16	2e-16	1 x 50 kallikrein-related peptidase 12 [Source:HGNC Symbol;Acc:6
5	25818	1.48	2e-16	2e-16	1 x 47 kallikrein-related peptidase 5 [Source:HGNC Symbol;Acc:63
6	5653	2.13	2e-16	2e-16	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63
7	5650	1.51	2e-16	2e-16	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63
8	192666	2.89	2e-16	2e-16	1 x 50 keratin 24 [Source:HGNC Symbol;Acc:18527]
9	388533	2.2	2e-16	2e-16	1 x 49 keratinocyte differentiation-associated protein [Source:HGNC
10	3934	1.63	2e-16	2e-16	1 x 50 lipocalin 2 [Source:HGNC Symbol;Acc:6526]
11	4014	2.14	2e-16	2e-16	2 x 48 loricrin [Source:HGNC Symbol;Acc:6663]
12	137797	2.94	2e-16	2e-16	1 x 50 LY6/PLAUR domain containing 2 [Source:HGNC Symbol;Acc
13	84659	1.37	2e-16	2e-16	1 x 48 ribonuclease, RNase A family, 7 [Source:HGNC Symbol;Acc
14	6283	1.67	2e-16	2e-16	1 x 49 S100 calcium binding protein A12 [Source:HGNC Symbol;Acc
15	6278	1.91	2e-16	2e-16	1 x 49 S100 calcium binding protein A7 [Source:HGNC Symbol;Acc
16	338324	2.7	2e-16	2e-16	1 x 48 S100 calcium binding protein A7A [Source:HGNC Symbol;Acc
17	6286	2.8	2e-16	2e-16	1 x 50 S100 calcium binding protein P [Source:HGNC Symbol;Acc:1
18	5275	-1.97	2e-16	2e-16	1 x 50 serpin peptidase inhibitor, clade B (ovalbumin), member 13 [E
19	6317	-1.4	2e-16	2e-16	1 x 49 serpin peptidase inhibitor, clade B (ovalbumin), member 3 [Sc
20	6705	1.25	2e-16	2e-16	1 x 50 small proline-rich protein 2F [Source:HGNC Symbol;Acc:112

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	34.03	NULL	15 / 21	CC cornified envelope
2	28.48	NULL	4 / 10	MF RAGE receptor binding
3	26.71	NULL	18 / 42	BP keratinization
4	24.24	NULL	20 / 53	BP keratinocyte differentiation
5	19.71	NULL	17 / 76	BP epidermis development
6	19.29	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
7	17.31	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
8	15.56	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
9	15.33	NULL	5 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
10	15.18	NULL	8 / 19	BP peptide cross-linking
11	15.03	NULL	67 / 572	Disease GUDJ_psooriasis up
12	14.04	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
13	13.89	NULL	3 / 13	GSEA C2FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL
14	13.65	NULL	61 / 135	H.Tiss WIRTH_Mucosa
15	13.14	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
16	12.31	NULL	3 / 16	GSEA C2JAEGER_METASTASIS_DN
17	11.43	NULL	6 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
18	11.17	NULL	2 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
19	10.55	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
20	10.42	NULL	2 / 16	GSEA C2SESTO_RESPONSE_TO_UV_C7
21	10.01	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_U
22	9.84	NULL	2 / 17	Disease BCHETNIA_EBM up
23	9.65	NULL	1 / 13	GSEA C2HAHTOLA_CTCL_PATHOGENESIS
24	9.3	NULL	3 / 16	GSEA C2LEE_LIVER_CANCER_ACOX1_UP
25	9.19	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
26	9.09	NULL	1 / 9	GSEA C2SCHLOSSER_SERUM_RESPONSE_UP
27	8.95	NULL	3 / 12	BP cellular aldehyde metabolic process
28	8.87	NULL	1 / 15	GSEA C2KANG_FLUOROURACIL_RESISTANCE_DN
29	8.6	NULL	3 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HP131_DN
30	8.6	NULL	2 / 8	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
31	8.56	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_UP
32	8.55	NULL	2 / 13	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL
33	8.54	NULL	1 / 16	CC microvillus membrane
34	8.53	NULL	1 / 10	GSEA C2BROWNE_HCMV_INFECTION_12HR_UP
35	8.06	NULL	1 / 11	GSEA C2KEGG_DRUG_METABOLISM_CYTOCHROME_P450
36	8	NULL	2 / 9	GSEA C2MCLACHLAN_DENTAL_CARIES_DN
37	7.93	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
38	7.89	NULL	2 / 15	MF interleukin-1 receptor binding
39	7.67	NULL	3 / 13	GSEA C2HAN_SATB1_TARGETS_DN
40	7.65	NULL	1 / 12	GSEA C2RIZKI_TUMOR_INVASIVENESS_3D_DN



GW_075

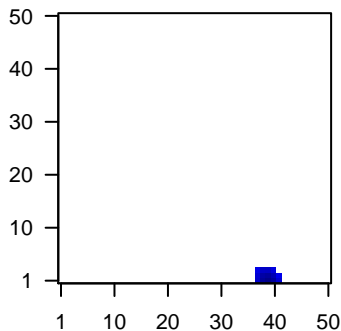
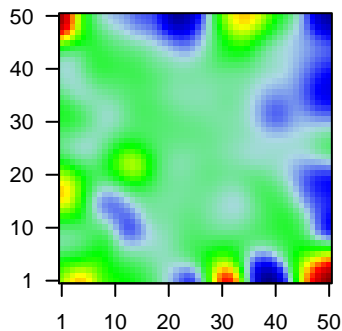
Local Summary

%DE = 0.86
 # metagenes = 14
 # genes = 236
 # genes in genesets = 209
 # genes with $fdr < 0.1 = 172$ (8 + / 164 -)
 # genes with $fdr < 0.05 = 94$ (4 + / 90 -)
 # genes with $fdr < 0.01 = 40$ (1 + / 39 -)

$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.52
 $\langle FC \rangle = -0.26$
 $\langle \text{shrinkage-t} \rangle = -9.28$
 $\langle p\text{-value} \rangle = 0.04$
 $\langle fdr \rangle = 0.72$

Profile

Spot



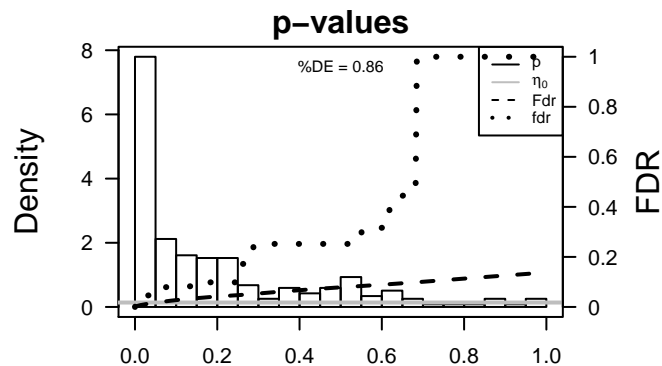
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	5900	-1.04	2e-10	4e-06	39 x 2 ral guanine nucleotide dissociation stimulator [Source:HGNC
2	84061	-0.86	1e-07	1e-05	39 x 1 magnesium transporter 1 [Source:HGNC Symbol;Acc:28880]
3	727956	-0.81	6e-07	3e-05	40 x 1 succinate dehydrogenase complex, subunit A, flavoprotein ps
4	728294	-0.78	2e-06	5e-05	40 x 1 D-2-hydroxyglutarate dehydrogenase [Source:HGNC Symbc
5	399900	-0.7	3e-06	2e-04	39 x 1
6	100132406	-0.72	9e-06	5e-04	39 x 1 neuroblastoma breakpoint family, member 10 [Source:HGNC
7	114785	-0.68	3e-05	5e-04	39 x 1 methyl-CpG binding domain protein 6 [Source:HGNC Symbc
8	1762	-0.66	4e-05	5e-04	40 x 1 dystrophia myotonica, WD repeat containing [Source:HGNC S
9	158399	-0.65	5e-05	7e-04	39 x 1 zinc finger protein 483 [Source:HGNC Symbol;Acc:23384]
10	641737	-0.6	7e-05	1e-03	40 x 1
11	90639	-0.63	1e-04	3e-03	40 x 1 cytochrome c oxidase assembly homolog 19 (S. cerevisiae) [S
12	5256	-0.58	4e-04	3e-03	40 x 1 phosphorylase kinase, alpha 2 (liver) [Source:HGNC Symbol;
13	6625	-0.56	5e-04	3e-03	39 x 3 small nuclear ribonucleoprotein 70kDa (U1) [Source:HGNC S
14	163882	-0.56	5e-04	3e-03	39 x 3 consortin, connexin sorting protein [Source:HGNC Symbol;Ac
15	3586	-0.52	6e-04	3e-03	40 x 1 interleukin 10 [Source:HGNC Symbol;Acc:5962]
16	100190986	-0.56	6e-04	3e-03	39 x 1
17	26040	-0.55	7e-04	3e-03	40 x 3 SET binding protein 1 [Source:HGNC Symbol;Acc:15573]
18	9612	-0.54	9e-04	3e-03	38 x 1 nuclear receptor corepressor 2 [Source:HGNC Symbol;Acc:7
19	9747	-0.49	9e-04	3e-03	39 x 1 family with sequence similarity 115, member A [Source:HGNC
20	100128288	-0.53	1e-03	3e-03	39 x 1

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-12.89	NULL	2 / 4	GSEA C2BIOCARTA_CYTOKINE_PATHWAY
2	-8.77	NULL	1 / 10	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_U
3	-8.32	NULL	1 / 11	GSEA C2FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP
4	-7.83	NULL	3 / 14	MMML C6SCIEJ_MMML 8
5	-7.59	NULL	1 / 13	GSEA C2REACTOME_P38MAPK_EVENTS
6	-7.29	NULL	1 / 14	GSEA C2ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN
7	-7.29	NULL	1 / 14	GSEA C2KEGG_COLORECTAL_CANCER
8	-7.29	NULL	1 / 14	GSEA C2KEGG_PANCREATIC_CANCER
9	-7.22	NULL	1 / 10	CC oligosaccharyltransferase complex
10	-7.01	NULL	1 / 15	GSEA C2REACTOME_SIGNALLING_TO_ERKS
11	-7.01	NULL	1 / 15	GSEA C2REACTOME_SIGNALLING_TO_RAS
12	-6.83	NULL	2 / 16	BP cognition
13	-6.76	NULL	1 / 16	GSEA C2POMEROY_MEDULLOBLASTOMA_PROGNOSIS_UP
14	-6.76	NULL	1 / 16	GSEA C2JIANG_HYPOXIA_CANCER
15	-6.76	NULL	1 / 16	GSEA C2BIOCARTA_RAS_PATHWAY
16	-6.76	NULL	1 / 16	GSEA C2REACTOME_SIGNALLING_BY_NGF
17	-6.76	NULL	1 / 16	GSEA C2REACTOME_TRKA_SIGNALLING_FROM_THE_PLASMA_MEMB
18	-6.72	NULL	1 / 5	GSEA C2BIOCARTA_INFLAM_PATHWAY
19	-6.28	NULL	2 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
20	-6.24	NULL	1 / 13	MF magnesium ion transmembrane transporter activity
21	-6.09	NULL	1 / 5	GSEA C2DONATO_CELL_CYCLE_TRETINOIN
22	-6.08	NULL	1 / 6	GSEA C2BUDHU_LIVER_CANCER_METASTASIS_UP
23	-6.08	NULL	1 / 6	GSEA C2SEIKE_LUNG_CANCER_POOR_SURVIVAL
24	-6.07	NULL	3 / 13	GSEA C2SPIRA_SMOKERS_LUNG_CANCER_DN
25	-5.99	NULL	1 / 14	BP magnesium ion transport
26	-5.6	NULL	2 / 14	BP cellular response to estradiol stimulus
27	-5.23	NULL	4 / 44	BP meiosis
28	-5.18	NULL	2 / 11	GSEA C2STEIN_ESRRA_TARGETS_DN
29	-5.18	NULL	1 / 8	GSEA C2BIOCARTA_ASBCCELL_PATHWAY
30	-5.18	NULL	1 / 15	BP 2-oxoglutarate metabolic process
31	-5.11	NULL	1 / 4	MMML C6SCIEJ_MMML 44
32	-5.11	NULL	1 / 12	miRNA target site 1249
33	-4.95	NULL	3 / 24	BP negative regulation of T cell proliferation
34	-4.91	NULL	2 / 13	GSEA C2BONOME_OVARIAN_CANCER_POOR_SURVIVAL_DN
35	-4.89	NULL	1 / 28	MF small GTPase regulator activity
36	-4.89	NULL	1 / 28	LymphonAVE_Immune response 1
37	-4.76	NULL	2 / 14	BP mitochondrion morphogenesis
38	-4.75	NULL	1 / 6	GSEA C2CAFFAREL_RESPONSE_TO_THC_24HR_3_UP
39	-4.7	NULL	1 / 7	GSEA C2LIU_CMYB_TARGETS_DN
40	-4.68	NULL	1 / 8	GSEA C2FAELT_B CLL_WITH_VH_REARRANGEMENTS_UP



GW_075

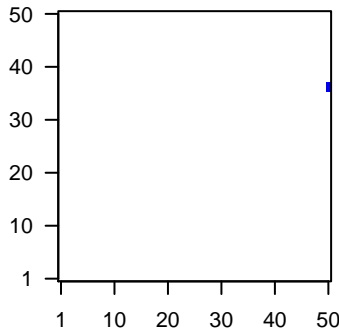
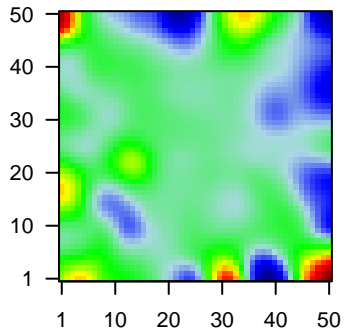
Local Summary

%DE = 0.4
 # metagenes = 2
 # genes = 71
 # genes in genesets = 71
 # genes with fdr < 0.1 = 16 (0 + / 16 -)
 # genes with fdr < 0.05 = 13 (0 + / 13 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)

<r> metagenes = 1
 <r> genes = 0.35
 <FC> = -0.17
 <shrinkage-t> = -6.08
 <p-value> = 0.1
 <fdr> = 0.78

Profile

Spot



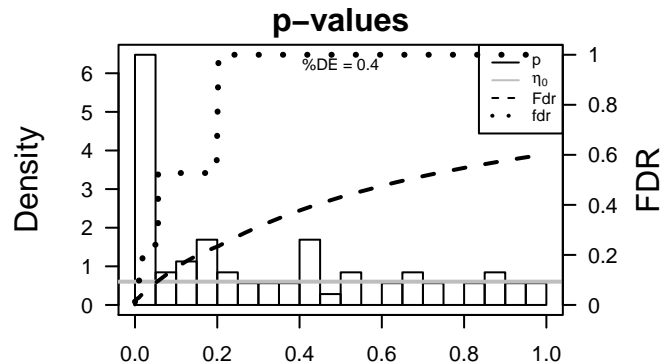
Local Genelist

Rank	ID	log(FC)	fdr	Description
		p-value		Metagene
1	4254	-0.66	5e-05	50 x 36 KIT ligand [Source:HGNC Symbol;Acc:6343]
2	4179	-0.58	3e-04	50 x 36 CD46 molecule, complement regulatory protein [Source:HGNC]
3	64393	-0.54	8e-04	50 x 37 zinc finger, matrin-type 3 [Source:HGNC Symbol;Acc:29983]
4	55556	-0.52	1e-03	50 x 37 enolase superfamily member 1 [Source:HGNC Symbol;Acc:3]
5	10159	-0.49	2e-03	50 x 36 ATPase, H+ transporting, lysosomal accessory protein 2 [Sou
6	57088	-0.45	5e-03	50 x 36 phospholipid scramblase 4 [Source:HGNC Symbol;Acc:1649]
7	91694	-0.45	6e-03	50 x 37 LON peptidase N-terminal domain and ring finger 1 [Source:]
8	7844	-0.44	6e-03	50 x 37 RNF103-CHMP3 readthrough [Source:HGNC Symbol;Acc:3]
9	23215	-0.44	7e-03	50 x 37 proline-rich coiled-coil 2C [Source:HGNC Symbol;Acc:2490]
10	64112	-0.43	8e-03	50 x 37 modulator of apoptosis 1 [Source:HGNC Symbol;Acc:16658]
11	23456	-0.43	8e-03	50 x 36 ATP-binding cassette, sub-family B (MDR/TAP), member 10
12	5431	-0.43	8e-03	50 x 37 polymerase (RNA) II (DNA directed) polypeptide B, 140kDa [
13	22828	-0.43	8e-03	50 x 37 SR-related CTD-associated factor 8 [Source:HGNC Symbol;
14	10194	-0.42	9e-03	50 x 36 teashirt zinc finger homeobox 1 [Source:HGNC Symbol;Acc:1
15	58155	-0.41	1e-02	50 x 36 polypyrimidine tract binding protein 2 [Source:HGNC Symbol;
16	55252	-0.4	1e-02	50 x 37 additional sex combs like 2 (Drosophila) [Source:HGNC Sym]
17	7763	-0.39	2e-02	50 x 36 zinc finger, AN1-type domain 5 [Source:HGNC Symbol;Acc:1
18	10099	-0.38	2e-02	50 x 37 tetraspanin 3 [Source:HGNC Symbol;Acc:17752]
19	51765	-0.36	3e-02	50 x 37 Serine/threonine-protein kinase MST4 [Source:UniProtKB/S
20	23505	-0.35	3e-02	50 x 37 transmembrane protein 131 [Source:HGNC Symbol;Acc:303]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-11.49	NULL	1 / 3	miRNA target-197
2	-10.76	NULL	1 / 8	miRNA target-9
3	-9.94	NULL	1 / 12	BP positive regulation of Ras protein signal transduction
4	-9.94	NULL	1 / 12	GSEA C2BIOCARTA_ERYTH_PATHWAY
5	-9.64	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
6	-9.55	NULL	1 / 13	GSEA C2BIOCARTA_IL17_PATHWAY
7	-9.19	NULL	1 / 14	GSEA C2AIYAR_COBRA1_TARGETS_DN
8	-8.87	NULL	1 / 15	GSEA C2BIOCARTA_BAD_PATHWAY
9	-8.58	NULL	1 / 16	GSEA C2RODRIGUES_NTN1_TARGETS_UP
10	-8.58	NULL	1 / 16	GSEA C2BIOCARTA_MCM_PATHWAY
11	-8.18	NULL	1 / 8	GSEA C2IZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN
12	-8.09	NULL	1 / 14	GSEA C2TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYT
13	-8.09	NULL	1 / 10	BP angiotensin maturation
14	-8.09	NULL	1 / 10	BP regulation of MAPK cascade
15	-8.08	NULL	1 / 18	BP embryonic hemopoiesis
16	-7.81	NULL	1 / 15	GSEA C2SEIDEN_ONCOGENESIS_BY_MET
17	-7.81	NULL	1 / 15	GSEA C2FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK
18	-7.81	NULL	1 / 15	GSEA C2ZHAN_MULTIPLE_MYELOMA_CD1_DN
19	-7.55	NULL	1 / 16	GSEA C2GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN
20	-7.53	NULL	1 / 2	MMML C6SCIEJ_MMML 38
21	-7.5	NULL	1 / 13	GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_T
22	-7.04	NULL	1 / 16	GSEA C2GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP
23	-6.95	NULL	1 / 11	GSEA C2IZUKA_LIVER_CANCER_PROGRESSION_L0_L1_UP
24	-6.91	NULL	1 / 19	BP regulation of complement activation
25	-6.8	NULL	1 / 14	MMML C6SCIEJ_MMML 30
26	-6.79	NULL	1 / 11	GSEA C2SU_PANCREAS
27	-6.77	NULL	1 / 12	Pathway AcBENTINK_e2f3.1
28	-6.5	NULL	1 / 12	BP apoptotic nuclear changes
29	-6.49	NULL	2 / 48	miRNA target-miR-200b
30	-6.4	NULL	1 / 22	BP complement activation, classical pathway
31	-6.3	NULL	2 / 22	BP intrinsic apoptotic signaling pathway in response to endoplasmic re
32	-6.19	NULL	2 / 39	miRNA target-miR-503-3p
33	-6.18	NULL	1 / 30	BP extrinsic apoptotic signaling pathway in absence of ligand
34	-6.18	NULL	1 / 30	BP neural crest cell migration
35	-6.16	NULL	1 / 13	GSEA C2LIU_TARGETS_OF_VMYB_VS_CMYB_UP
36	-6.1	NULL	2 / 12	BP nucleotide biosynthetic process
37	-6.09	NULL	1 / 14	GSEA C2SIMBULAN_UV_RESPONSE_NORMAL_DN
38	-5.97	NULL	2 / 46	BP cellular component disassembly involved in execution phase of apo
39	-5.96	NULL	2 / 30	miRNA target-miR-146-5p
40	-5.93	NULL	1 / 14	GSEA C2REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS



GW_075

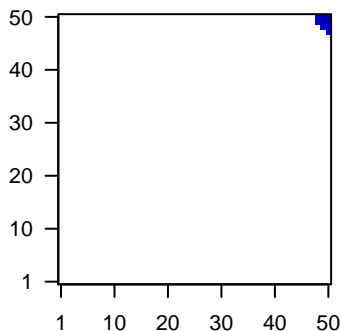
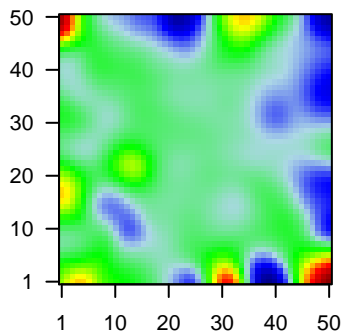
Local Summary

%DE = 0.57
 # metagenes = 9
 # genes = 159
 # genes in genesets = 158
 # genes with fdr < 0.1 = 65 (11 + / 54 -)
 # genes with fdr < 0.05 = 56 (9 + / 47 -)
 # genes with fdr < 0.01 = 37 (5 + / 32 -)

<r> metagenes = 0.98
 <r> genes = 0.29
 <FC> = -0.24
 <shrinkage-t> = -8.4
 <p-value> = 0
 <fdr> = 0.59

Profile

Spot



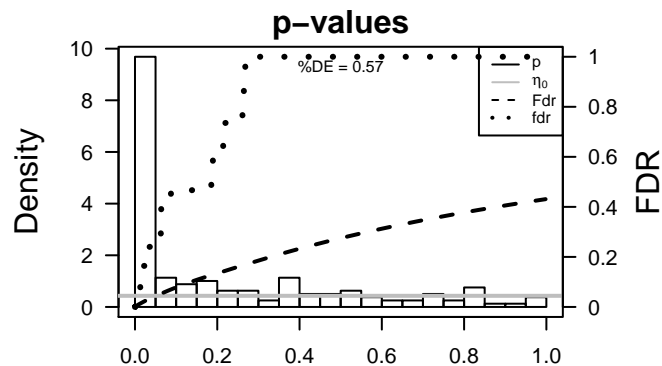
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	25975	1.36	2e-16	5e-15	EGF-like-domain, multiple 6 [Source:HGNC Symbol;Acc:322
2	3304	-1.41	2e-16	5e-15	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:52
3	3856	-1.57	2e-16	5e-15	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
4	26047	-1.31	9e-16	8e-14	contactin associated protein-like 2 [Source:HGNC Symbol;Ar
5	7546	-1.29	2e-15	4e-13	Zic family member 2 [Source:HGNC Symbol;Acc:12873]
6	139728	-1.26	8e-15	1e-11	pregnancy up-regulated nonubiquitous CaM kinase [Source:l
7	339512	-1.18	3e-13	1e-11	chromosome 1 open reading frame 110 [Source:HGNC Synt
8	4922	-1.18	4e-13	1e-09	neurotensin [Source:HGNC Symbol;Acc:8038]
9	3866	-1.09	2e-11	2e-08	keratin 15 [Source:HGNC Symbol;Acc:6421]
10	1056	-1.02	3e-10	3e-08	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
11	256764	1	8e-10	6e-08	WD repeat domain 72 [Source:HGNC Symbol;Acc:26790]
12	5625	-0.98	2e-09	7e-08	proline dehydrogenase (oxidase) 1 [Source:HGNC Symbol;Ar
13	2729	0.96	3e-09	7e-08	glutamate-cysteine ligase, catalytic subunit [Source:HGNC S
14	1857	-0.95	4e-09	7e-08	dishevelled segment polarity protein 3 [Source:HGNC Symbo
15	11166	-0.95	5e-09	5e-06	SRY (sex determining region Y)-box 21 [Source:HGNC Synt
16	79677	-0.87	7e-08	2e-05	structural maintenance of chromosomes 6 [Source:HGNC Sy
17	216	-0.82	5e-07	2e-05	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
18	84707	-0.8	8e-07	2e-05	brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
19	56963	-0.8	9e-07	3e-05	repulsive guidance molecule family member a [Source:HGNC
20	80896	-0.79	1e-06	2e-04	N-acetylneuraminate pyruvate lyase (dihydropicolinate synt

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-16.52	NULL	1 / 2	GSEA C2KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
2	-16.16	NULL	4 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
3	-14.78	NULL	2 / 7	GSEA C2MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
4	-13.36	NULL	2 / 10	GSEA C2HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
5	-11.61	NULL	4 / 13	GSEA C2KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
6	-10.32	NULL	2 / 10	GSEA C2CERVERA_SDHB_TARGETS_1_DN
7	-9.54	NULL	2 / 7	GSEA C2FREDERICK_PRKCI_TARGETS
8	-9.38	NULL	1 / 5	GSEA C2DASU_IL6_SIGNALING_UP
9	-9.22	NULL	2 / 14	GSEA C2AMBROSINI_FLAVOPIRIDOL_TREATMENT_TP53
10	-9.18	NULL	2 / 11	GSEA C2CONCANNON_APOPTOSIS_BY_EPOXOMICIN_UP
11	-8.88	NULL	5 / 15	GSEA C2KEGG_Glutathione_Metabolism
12	-8.57	NULL	3 / 11	MF glutathione binding
13	-8.57	NULL	3 / 11	GSEA C2KEGG_DRUG_Metabolism_Cytochrome_P450
14	-8.57	NULL	2 / 8	GSEA C2SATO_SILENCED_EPIGENETICALLY_IN_PANCREATIC_CANCE
15	-8.45	NULL	1 / 11	CC axolemma
16	-8.43	NULL	5 / 20	MF glutathione transferase activity
17	-8.43	NULL	1 / 6	GSEA C2SESTO_RESPONSE_TO_UV_CO
18	-8.43	NULL	1 / 6	GSEA C2BIOCARTA_TID_PATHWAY
19	-8.39	NULL	2 / 12	GSEA C2MOROSSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTRO
20	-8.35	NULL	2 / 9	GSEA C2BROWNE_HCMV_INFECTION_8HR_UP
21	-8.05	NULL	3 / 12	GSEA C2BROCKE_APOPTOSIS_REVERSED_BY_IL6
22	-8	NULL	1 / 4	GSEA C2L_TUMOR_ENDOTHELIAL_MARKERS_DN
23	-7.88	NULL	1 / 8	GSEA C2KEGG_Glycerolipid_Metabolism
24	-7.72	NULL	2 / 12	GSEA C2LEE_METASTASIS_AND_ALTERNATIVE_SPLICING_DN
25	-7.7	NULL	2 / 13	GSEA C2JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER
26	-7.7	NULL	1 / 7	GSEA C2WEINMANN_ADAPTATION_TO_HYPOXIA_UP
27	-7.65	NULL	2 / 16	GSEA C2TCGA_GLIOMASTOMA_COPY_NUMBER_UP
28	-7.59	NULL	1 / 11	Glio neurons_glio
29	-7.59	NULL	1 / 13	BP developmental pigmentation
30	-7.45	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
31	-7.45	NULL	1 / 6	GSEA C2KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
32	-7.37	NULL	1 / 14	BP transmission of nerve impulse
33	-7.37	NULL	1 / 14	GSEA C2SILIGAN_TARGETS_OF_EWS_FL11_FUSION_DN
34	-7.37	NULL	1 / 14	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_B
35	-7.28	NULL	1 / 14	GSEA C2WATANABE_COLON_CANCER_MSI_VS_MSS_UP
36	-7.13	NULL	1 / 8	GSEA C2BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN
37	-7.13	NULL	1 / 8	GSEA C2ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN
38	-7.13	NULL	1 / 8	GSEA C2CHANDRAN_METASTASIS_UP
39	-7.13	NULL	1 / 8	GSEA C2WU_APOPTOSIS_BY_CDKN1A_NOT_VIA_TP53
40	-7.13	NULL	1 / 8	GSEA C2KEGG_PRION_DISEASES



GW_075

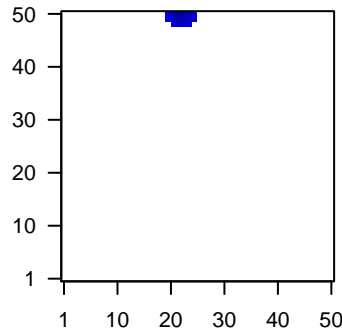
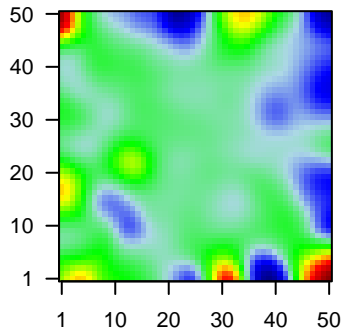
Local Summary

%DE = 0.63
 # metagenes = 16
 # genes = 209
 # genes in genesets = 205
 # genes with $fdr < 0.1$ = 82 (8 + / 74 -)
 # genes with $fdr < 0.05$ = 54 (5 + / 49 -)
 # genes with $fdr < 0.01$ = 20 (1 + / 19 -)

<r> metagenes = 0.97
 <r> genes = 0.26
 <FC> = -0.26
 <shrinkage-t> = -9.19
 <p-value> = 0.02
 <fdr> = 0.72

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	2353	-1.51	2e-16	9e-15	22 x 50 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:11142]
2	2354	-2.19	2e-16	9e-15	22 x 50 FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:11143]
3	150094	-1.24	2e-14	7e-11	22 x 50 salt-inducible kinase 1 [Source:HGNC Symbol;Acc:11142]
4	1958	-1.16	1e-12	2e-10	22 x 50 early growth response 1 [Source:HGNC Symbol;Acc:3238]
5	8553	-1.04	3e-12	3e-09	22 x 50 basic helix-loop-helix family, member e40 [Source:HGNC Symbol;Acc:11142]
6	7538	-1.06	5e-11	4e-09	22 x 50 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:12862]
7	23645	-1.05	9e-11	4e-07	22 x 50 protein phosphatase 1, regulatory subunit 15A [Source:HGNC Symbol;Acc:11142]
8	1843	-0.87	5e-09	4e-07	22 x 50 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3238]
9	3725	-0.93	9e-09	2e-06	22 x 50 jun proto-oncogene [Source:HGNC Symbol;Acc:6204]
10	3459	0.89	4e-08	6e-05	22 x 50 interferon gamma receptor 1 [Source:HGNC Symbol;Acc:543]
11	3726	-0.8	8e-07	7e-05	22 x 50 jun B proto-oncogene [Source:HGNC Symbol;Acc:6205]
12	467	-0.77	2e-06	7e-05	22 x 50 activating transcription factor 3 [Source:HGNC Symbol;Acc:71]
13	10972	-0.76	3e-06	7e-05	25 x 50 transmembrane emp24-like trafficking protein 10 (yeast) [Source:HGNC Symbol;Acc:11142]
14	163126	-0.75	3e-06	9e-05	25 x 49 EP300 interacting inhibitor of differentiation 2 [Source:HGNC Symbol;Acc:11142]
15	71	-0.68	5e-06	2e-04	24 x 50 actin, gamma 1 [Source:HGNC Symbol;Acc:144]
16	23301	-0.73	7e-06	2e-04	24 x 50 EH domain binding protein 1 [Source:HGNC Symbol;Acc:291]
17	7465	-0.72	1e-05	2e-04	23 x 50 WEE1 G2 checkpoint kinase [Source:HGNC Symbol;Acc:127]
18	57132	-0.71	1e-05	6e-04	22 x 50 charged multivesicular body protein 1B [Source:HGNC Symbol;Acc:11142]
19	58526	-0.69	2e-05	3e-03	21 x 50 MID1 interacting protein 1 [Source:HGNC Symbol;Acc:20715]
20	91612	-0.65	6e-05	8e-03	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:20715]

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-48.95	NULL	6 / 10	GSEA C2CHASSOT_SKIN_WOUND
2	-40.23	NULL	8 / 16	GSEA C2NAGASHIMA_EGF_SIGNALING_UP
3	-34.93	NULL	6 / 16	GSEA C2AMIT_SERUM_RESPONSE_40_MCF10A
4	-31.95	NULL	7 / 15	GSEA C2AMIT_EGF_RESPONSE_40_HELA
5	-30.43	NULL	5 / 24	TF Tissue/AQUERIZAS_Trachea
6	-28.72	NULL	5 / 16	GSEA C2AMIT_EGF_RESPONSE_40_MCF10A
7	-28.54	NULL	4 / 14	GSEA C2TIAN_TNF_SIGNALING_NOT_VIA_NFKB
8	-26.49	NULL	4 / 14	BP response to light stimulus
9	-26.25	NULL	3 / 15	BP response to corticosterone
10	-24.46	NULL	5 / 16	GSEA C2JZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
11	-24.13	NULL	3 / 11	GSEA C2AMIT_EGF_RESPONSE_20_HELA
12	-23.53	NULL	5 / 30	BP cellular response to hormone stimulus
13	-23.34	NULL	2 / 9	GSEA C2GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
14	-22.87	NULL	3 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
15	-22.38	NULL	7 / 16	GSEA C2AMIT_DELAYED_EARLY_GENES
16	-22.21	NULL	5 / 39	BP response to cAMP
17	-22.11	NULL	6 / 16	TF Tissue/AQUERIZAS_Pancreas
18	-21.79	NULL	4 / 30	BP cellular response to calcium ion
19	-21.67	NULL	2 / 5	miRNA target-101
20	-19.57	NULL	3 / 10	GSEA C2BIOCARTA_CDMAC_PATHWAY
21	-19.43	NULL	4 / 16	GSEA C2BIOCARTA_ETS_PATHWAY
22	-19.06	NULL	4 / 15	GSEA C2DIRMEIER_LMP1_RESPONSE_EARLY
23	-18.56	NULL	4 / 16	GSEA C2AMIT_EGF_RESPONSE_60_MCF10A
24	-18.38	NULL	4 / 14	GSEA C2BIOCARTA_IL2_PATHWAY
25	-18.14	NULL	4 / 39	TF Tissue/AQUERIZAS_Thyroid
26	-18.09	NULL	3 / 30	BP response to progesterone
27	-18.08	NULL	2 / 16	GSEA C2AMIT_EGF_RESPONSE_60_HELA
28	-17.99	NULL	2 / 10	GSEA C2REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCR
29	-17.98	NULL	3 / 12	GSEA C2BIOCARTA_CCR5_PATHWAY
30	-16.87	NULL	3 / 12	GSEA C2BIOCARTA_ARENRF2_PATHWAY
31	-16.78	NULL	1 / 5	GSEA C2TURJANSKI_MAPK11_TARGETS
32	-16.78	NULL	5 / 56	BP response to mechanical stimulus
33	-16.59	NULL	3 / 20	TF Tissue/AQUERIZAS_Adrenal cortex
34	-16.46	NULL	2 / 7	GSEA C2TURJANSKI_MAPK7_TARGETS
35	-16.4	NULL	2 / 8	GSEA C2YEMELYANOV_GR_TARGETS_DN
36	-16.34	NULL	4 / 19	MF R-SMAD binding
37	-15.97	NULL	4 / 16	GSEA C2AMIT_SERUM_RESPONSE_120_MCF10A
38	-15.93	NULL	8 / 62	TF Tissue/AQUERIZAS_Lung
39	-15.76	NULL	3 / 15	GSEA C2BROWNE_HCMV_INFECTION_30MIN_UP
40	-15.69	NULL	3 / 15	GSEA C2BIOCARTA_INSULIN_PATHWAY

p-values

