

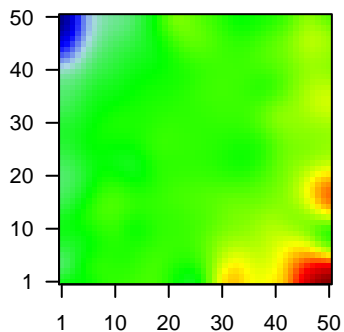
GW_026

Global Summary

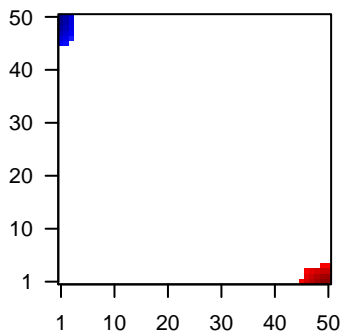
%DE = 0.15
 # genes with fdr < 0.2 = 2062 (1124 + / 938 -)
 # genes with fdr < 0.1 = 1681 (929 + / 752 -)
 # genes with fdr < 0.05 = 1454 (804 + / 650 -)
 # genes with fdr < 0.01 = 1024 (568 + / 456 -)
 # genes in genesets = 16332

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.08
 <fdr> = 0.85

Profile



Regulated Spots



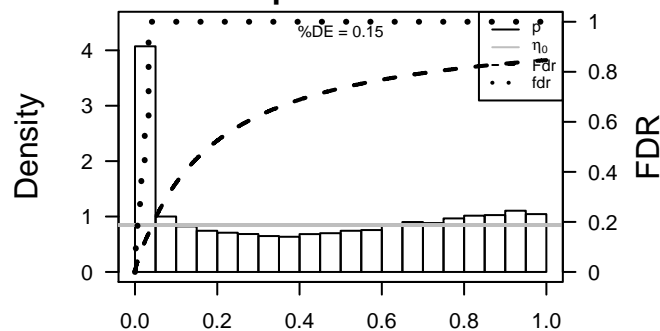
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	21	1.75	2e-16	2e-14	50 x 17 ATP-binding cassette, sub-family A (ABC1), member 3 [Source:HGNC Symbol;Acc:16299]
2	27299	1.74	2e-16	2e-14	49 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]
3	131	-2.45	2e-16	2e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	57016	-2.43	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase)
5	441282	-1.79	2e-16	2e-14	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC Symbol;Acc:16299]
6	8644	-1.89	2e-16	2e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:16299]
7	241	1.48	2e-16	2e-14	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC Symbol;Acc:16299]
8	341	1.81	2e-16	2e-14	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
9	348	1.75	2e-16	2e-14	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
10	22809	1.46	2e-16	2e-14	44 x 1 activating transcription factor 5 [Source:HGNC Symbol;Acc:71]
11	387695	-1.74	2e-16	2e-14	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Symbol;Acc:16299]
12	399948	1.83	2e-16	2e-14	50 x 15 colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3]
13	64073	-1.84	2e-16	2e-14	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Symbol;Acc:16299]
14	713	1.74	2e-16	2e-14	50 x 1 complement component 1, q subcomponent, B chain [Source:HGNC Symbol;Acc:16299]
15	714	1.84	2e-16	2e-14	50 x 1 complement component 1, q subcomponent, C chain [Source:HGNC Symbol;Acc:16299]
16	135398	2.22	2e-16	2e-14	1 x 40 chromosome 6 open reading frame 141 [Source:HGNC Symbol;Acc:16299]
17	733	1.55	2e-16	2e-14	48 x 18 complement component 8, gamma polypeptide [Source:HGNC Symbol;Acc:16299]
18	375791	-2	2e-16	2e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symbol;Acc:16299]
19	771	-1.47	2e-16	2e-14	1 x 44 carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371]
20	57172	1.54	2e-16	2e-14	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HGNC Symbol;Acc:16299]

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	19.95	NULL	417	H.Tiss WIRTH_Immune system
2	13.72	NULL	312	BP immune response
3	11.61	NULL	553	Cancer Lembcke_Colonc Inflammation
4	11.34	NULL	316	Cancer SPANG_BCL6-index2
5	11.13	NULL	274	Lymphoma SPANG_IL21 DN
6	10.07	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1
7	9.97	NULL	204	BP cytokine-mediated signaling pathway
8	9.87	NULL	15	CC MHC class II protein complex
9	9.76	NULL	60	BP interferon-gamma-mediated signaling pathway
10	9.68	NULL	47	BP antigen processing and presentation
11	9.43	NULL	74	BP regulation of immune response
12	9.07	NULL	51	BP type I interferon signaling pathway
13	8.7	NULL	265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
14	8.7	NULL	265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
15	8.7	NULL	265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
16	8.7	NULL	265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
17	8.41	NULL	162	CC external side of plasma membrane
18	8.16	NULL	60	BP T cell costimulation
19	7.88	NULL	22	Lymphoma GAVE_NFkB BL DN
20	7.82	NULL	84	BP T cell receptor signaling pathway
<i>Underexpressed</i>				
1	-30.76	NULL	135	H.Tiss WIRTH_Mucosa
2	-18.33	NULL	21	CC cornified envelope
3	-16.27	NULL	53	BP keratinocyte differentiation
4	-15.09	NULL	572	Disease GUDJ_psooriasis up
5	-14.96	NULL	42	BP keratinization
6	-14.61	NULL	76	BP epidermis development
7	-11.21	NULL	16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	-10.94	NULL	618	Chr Chr 4
9	-10.53	NULL	19	BP peptide cross-linking
10	-9.52	NULL	16	GSEA C2ONDER_CDH1_TARGETS_3_DN
11	-9.28	NULL	10	MF RAGE receptor binding
12	-8.64	NULL	16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
13	-8.15	NULL	10	BP cellular response to zinc ion
14	-7.85	NULL	15	GSEA C2WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
15	-7.38	NULL	186	MF structural molecule activity
16	-7.33	NULL	38	BP epithelial cell differentiation
17	-7.29	NULL	16	GSEA C2JAEGER_METASTASIS_DN
18	-7.11	NULL	7	MMML C6CIEJ_MMML 13
19	-7.07	NULL	15	BP negative regulation of growth
20	-6.97	NULL	386	Chr Chr 22

p-values



GW_026

Local Summary

%DE = 0.98
 # metagenes = 18
 # genes = 288
 # genes in genesets = 285

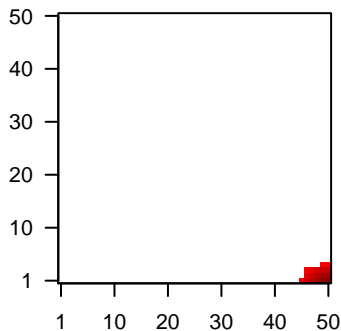
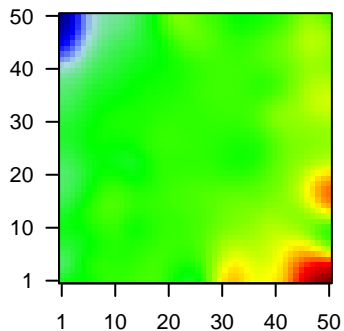
genes with $fdr < 0.1 = 275$ (274 + / 1 -)
 # genes with $fdr < 0.05 = 267$ (266 + / 1 -)
 # genes with $fdr < 0.01 = 251$ (250 + / 1 -)

<r> metagenes = 0.99
 <r> genes = 0.58

<FC> = 0.9
 <shrinkage-t> = 31.44
 <p-value> = 0
 <fdr> = 0.13

Profile

Spot



Local Genelist

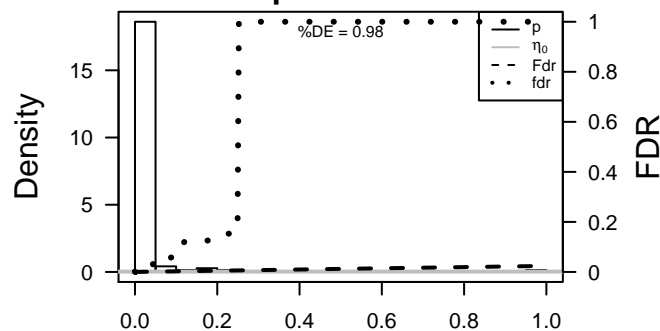
Rank	ID	log(FC)	fdr	p-value	Description
1	27299	1.74	2e-16	4e-17	49 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]
2	241	1.48	2e-16	4e-17	50 x 1 arachidonate 5-lipoxygenase-activating protein [Source:HGNC]
3	341	1.81	2e-16	4e-17	50 x 1 apolipoprotein C-I [Source:HGNC Symbol;Acc:607]
4	348	1.75	2e-16	4e-17	50 x 1 apolipoprotein E [Source:HGNC Symbol;Acc:613]
5	713	1.74	2e-16	4e-17	50 x 1 complement component 1, q subcomponent, B chain [Source]
6	714	1.84	2e-16	4e-17	50 x 1 complement component 1, q subcomponent, C chain [Source]
7	57172	1.54	2e-16	4e-17	49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG]
8	6363	1.6	2e-16	4e-17	50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc]
9	6364	1.84	2e-16	4e-17	46 x 1 chemokine (C-C motif) ligand 20 [Source:HGNC Symbol;Acc]
10	962	1.45	2e-16	4e-17	50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]
11	972	1.56	2e-16	4e-17	50 x 1 CD74 molecule, major histocompatibility complex, class II invr.
12	169044	1.94	2e-16	4e-17	45 x 1 collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298]
13	1436	1.74	2e-16	4e-17	50 x 1 colony stimulating factor 1 receptor [Source:HGNC Symbol;Ac]
14	4283	1.84	2e-16	4e-17	49 x 1 chemokine (C-X-C motif) ligand 9 [Source:HGNC Symbol;Ac]
15	1545	2.54	2e-16	4e-17	50 x 4 cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc]
16	5168	1.65	2e-16	4e-17	50 x 2 ectonucleotide pyrophosphatase/phosphodiesterase 2 [Sourc]
17	10875	1.74	2e-16	4e-17	50 x 1 fibrinogen-like 2 [Source:HGNC Symbol;Acc:3696]
18	2359	1.4	2e-16	4e-17	50 x 3 formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]
19	84868	1.42	2e-16	4e-17	50 x 1 hepatitis A virus cellular receptor 2 [Source:HGNC Symbol;Ac]
20	3109	1.44	2e-16	4e-17	50 x 1 major histocompatibility complex, class II, DM beta [Source:H]

Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	29.57	NULL	13 / 15	CC MHC class II protein complex
2	28.79	NULL	96 / 417	H.Tiss WIRTH_Immune system
3	23.49	NULL	56 / 312	BP immune response
4	23.36	NULL	97 / 553	Cancer Lembcke_Colonc Inflammation
5	19.6	NULL	44 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
6	19.6	NULL	44 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
7	19.6	NULL	44 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down
8	19.6	NULL	44 / 265	Glio wilscher_GBM_Verhaak-PNmut_expression_B_down
9	19.27	NULL	16 / 47	BP antigen processing and presentation
10	18.66	NULL	9 / 16	GSEA C27FARMER_BREAST_CANCER_CLUSTER_1
11	18.31	NULL	7 / 11	GSEA C27BIOCARTA_TCYTOTOXIC_PATHWAY
12	17.83	NULL	7 / 11	GSEA C27BIOCARTA_THELPER_PATHWAY
13	17.52	NULL	18 / 60	BP T cell costimulation
14	16.9	NULL	5 / 12	GSEA C2ZHAN_MULTIPLE_MYELOMA_DN
15	16.1	NULL	8 / 21	CC clathrin-coated endocytic vesicle membrane
16	15.57	NULL	8 / 13	Cancer GENTLES_modul18
17	15.47	NULL	7 / 15	GSEA C27FINAK_BREAST_CANCER_SDPD_SIGNATURE
18	15.36	NULL	2 / 4	GSEA C27REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
19	15.29	NULL	8 / 23	CC integral to luminal side of endoplasmic reticulum membrane
20	15.27	NULL	27 / 162	CC external side of plasma membrane
21	15.23	NULL	6 / 13	MMML C27SCIEJ_MMML_6
22	15.17	NULL	3 / 7	GSEA C27TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINEI
23	15.14	NULL	18 / 74	BP regulation of immune response
24	14.96	NULL	8 / 16	GSEA C27SU_THYMUS
25	14.61	NULL	3 / 5	GSEA C27WONG_ENDOMETRIAL_CANCER_LATE
26	14.58	NULL	6 / 8	Glio Donson-migration tethering and rolling-associated with LTS in HG
27	14.3	NULL	2 / 4	MMML C27SCIEJ_MMML_2
28	14.23	NULL	6 / 12	GSEA C27BIOCARTA_CTL_PATHWAY
29	13.95	NULL	6 / 15	Glio Donson-chemokines/cytokines-associated with LTS in HGA
30	13.78	NULL	6 / 13	GSEA C27BIOCARTA_IL17_PATHWAY
31	13.67	NULL	8 / 28	CC transport vesicle membrane
32	13.61	NULL	4 / 11	GSEA C27APPEL_IMATINIB_RESPONSE
33	13.24	NULL	18 / 84	BP T cell receptor signaling pathway
34	13.15	NULL	2 / 3	GSEA C27KEGG_VIRAL_MYOCARDITIS
35	13.11	NULL	2 / 7	GSEA C27TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINEI
36	13.09	NULL	3 / 6	GSEA C27SANA_RESPONSE_TO_IFNG_UP
37	12.75	NULL	5 / 11	GSEA C27WILENSKY_RESPONSE_TO_DARAPLADIB
38	12.65	NULL	8 / 32	CC ER to Golgi transport vesicle membrane
39	12.6	NULL	9 / 35	CC trans-Golgi network membrane
40	12.58	NULL	5 / 10	GSEA C27EE_DIFFERENTIATING_T_LYMPHOCYTE

p-values



GW_026

Local Summary

%DE = 0.97
 # metagenes = 17
 # genes = 233
 # genes in genesets = 227

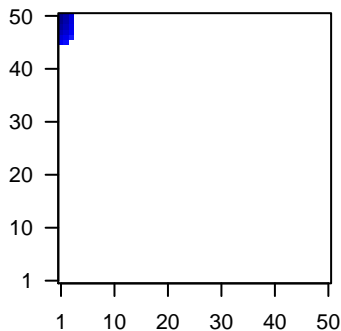
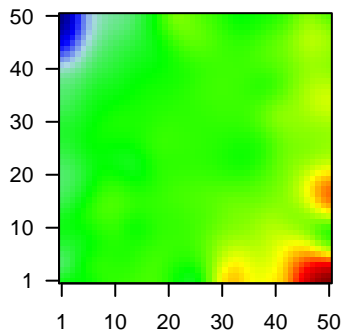
genes with $fdr < 0.1$ = 217 (3 + / 214 -)
 # genes with $fdr < 0.05$ = 216 (2 + / 214 -)
 # genes with $fdr < 0.01$ = 204 (1 + / 203 -)

$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.44

$\langle FC \rangle = -1.16$
 $\langle \text{shrinkage-t} \rangle = -40.98$
 $\langle p\text{-value} \rangle = 0$
 $\langle fdr \rangle = 0.12$

Profile

Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.45	2e-16	2e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	57016	-2.43	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member B10 (aldose reductase
3	441282	-1.79	2e-16	2e-17	1 x 49 aldo-keto reductase family 1, member B15 [Source:HGNC S
4	8644	-1.89	2e-16	2e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sym
5	387695	-1.74	2e-16	2e-17	1 x 49 chromosome 10 open reading frame 99 [Source:HGNC Synt
6	64073	-1.84	2e-16	2e-17	1 x 46 chromosome 19 open reading frame 33 [Source:HGNC Synt
7	375791	-2	2e-16	2e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Synt
8	84290	-1.62	2e-16	2e-17	1 x 50 calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
9	4680	-2.05	2e-16	2e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
10	9635	-2.69	2e-16	2e-17	1 x 46 chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
11	22802	-2.25	2e-16	2e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
12	84518	-1.93	2e-16	2e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
13	1382	-1.81	2e-16	2e-17	1 x 48 cellular retinoic acid binding protein 2 [Source:HGNC Symbol
14	49860	-2.34	2e-16	2e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
15	9547	-1.62	2e-16	2e-17	1 x 46 chemokine (C-X-C motif) ligand 14 [Source:HGNC Symbol;f
16	92196	-1.6	2e-16	2e-17	3 x 50 death associated protein-like 1 [Source:HGNC Symbol;Acc:2
17	1672	-2.07	2e-16	2e-17	1 x 50 defensin, beta 1 [Source:HGNC Symbol;Acc:2766]
18	414325	-1.66	2e-16	2e-17	1 x 48 defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
19	1673	-2.49	2e-16	2e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
20	9982	-3	2e-16	2e-17	1 x 47 fibroblast growth factor binding protein 1 [Source:HGNC Syml

Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-59.44	NULL	83 / 135	H.Tiss WIRTH_Mucosa
2	-41.64	NULL	18 / 21	CC cornified envelope
3	-34.06	NULL	24 / 53	BP keratinocyte differentiation
4	-33.16	NULL	97 / 572	Disease GUDJ_psooriasis up
5	-32.61	NULL	19 / 42	BP keratinization
6	-29.87	NULL	23 / 76	BP epidermis development
7	-23.2	NULL	5 / 10	MF RAGE receptor binding
8	-22.69	NULL	10 / 19	BP peptide cross-linking
9	-21.7	NULL	8 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
10	-17.25	NULL	3 / 8	GSEA C2LIU_CDX2_TARGETS_DN
11	-17.01	NULL	3 / 10	GSEA C2AUJLA_IL22_AND_IL17A_SIGNALING
12	-16.8	NULL	6 / 16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
13	-16.52	NULL	7 / 16	GSEA C2HUPER_BREAST_BASAL_VS_LUMINAL_UP
14	-15.01	NULL	6 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
15	-13.4	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
16	-13.11	NULL	7 / 15	GSEA C2WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
17	-12.78	NULL	6 / 13	BP negative regulation of peptidase activity
18	-12.54	NULL	23 / 186	MF structural molecule activity
19	-12.41	NULL	10 / 44	CC keratin filament
20	-12.24	NULL	4 / 15	GSEA C2CHANG_IMMORTALIZED_BY_HPV31_DN
21	-12.2	NULL	57 / 1182	CC extracellular region
22	-12.17	NULL	4 / 25	BP response to zinc ion
23	-12.06	NULL	4 / 14	GSEA C2CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_U
24	-11.72	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
25	-11.52	NULL	16 / 82	CC intermediate filament
26	-11.36	NULL	2 / 8	GSEA C2DORN_ADENOVIRUS_INFECTION_24HR_UP
27	-11.02	NULL	7 / 38	BP epithelial cell differentiation
28	-10.99	NULL	3 / 16	GSEA C2AMIT_SERUM_RESPONSE_480_MCF10A
29	-10.97	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_1
30	-10.96	NULL	10 / 52	BP negative regulation of endopeptidase activity
31	-10.84	NULL	4 / 15	GSEA C2ONDER_CDH1_TARGETS_2_DN
32	-10.61	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
33	-10.53	NULL	3 / 13	BP intermediate filament cytoskeleton organization
34	-10.48	NULL	4 / 27	BP response to bacterium
35	-10.42	NULL	3 / 10	GSEA C2SMID_BREAST_CANCER_ERBB2_UP
36	-10.29	NULL	5 / 16	GSEA C2COLDREN_GEFITINIB_RESISTANCE_DN
37	-10.09	NULL	4 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
38	-10.07	NULL	12 / 21	CC desmosome
39	-10.01	NULL	3 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
40	-9.94	NULL	4 / 16	GSEA C2ROY_WOUND_BLOOD_VESSEL_DN

p-values

