

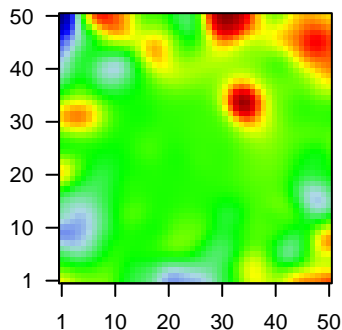
G7_mel

Global Summary

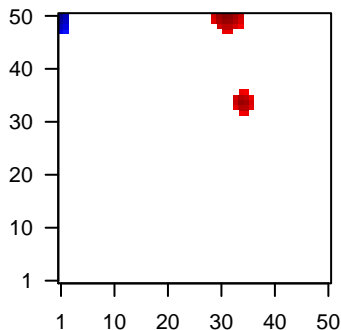
%DE = 0.21
 # genes with fdr < 0.2 = 2774 (1701 + / 1073 -)
 # genes with fdr < 0.1 = 2106 (1333 + / 773 -)
 # genes with fdr < 0.05 = 1674 (1083 + / 591 -)
 # genes with fdr < 0.01 = 1068 (682 + / 386 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.06
 <p-value> = 0.08
 <fdr> = 0.79

Profile



Regulated Spots

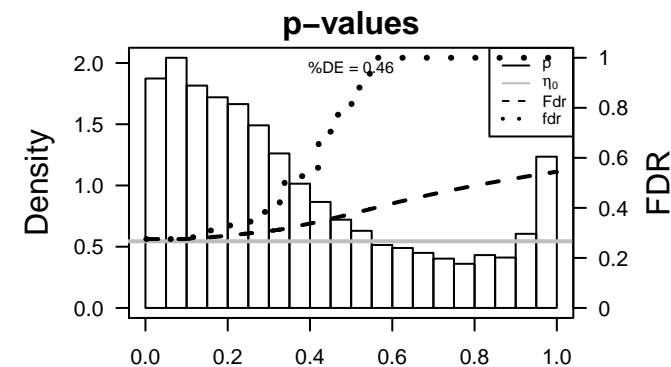
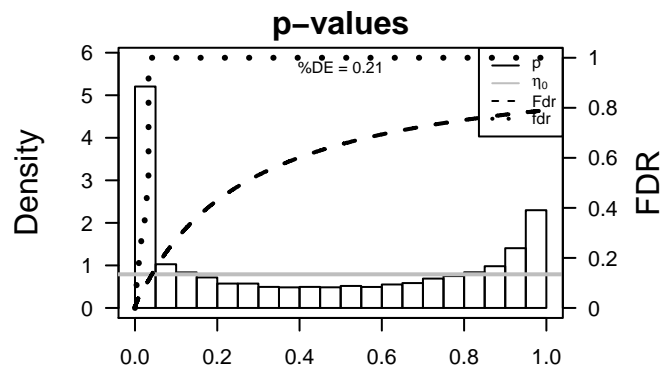


Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ANKRD10	-0.84	2e-16	1e-13	1 x 24 ankryrin repeat domain 10 [Source:HGNC Symbol;Acc:HGNC
2	ARL1	-1.43	2e-16	1e-13	25 x 49 ADP-ribosylation factor-like 1 [Source:HGNC Symbol;Acc:Hi
3	ATRX	-1.27	2e-16	1e-13	43 x 7 alpha thalassemia/mental retardation syndrome X-linked (So
4	BECN1	-1.5	2e-16	1e-13	49 x 15 beclin 1, autophagy related [Source:HGNC Symbol;Acc:HGN
5	BSCL2	-2.04	2e-16	1e-13	50 x 50 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:!
6	CTSC	-1.69	2e-16	1e-13	1 x 42 cathepsin C [Source:HGNC Symbol;Acc:HGNC:2528]
7	DAP3	-0.89	2e-16	1e-13	7 x 11 death associated protein 3 [Source:HGNC Symbol;Acc:HGNC
8	ELP2	-1.64	2e-16	1e-13	37 x 50 elongator acetyltransferase complex subunit 2 [Source:HGNC
9	F13A1	1.88	2e-16	1e-13	49 x 31 coagulation factor XIII, A1 polypeptide [Source:HGNC Symbc
10	GLB1	-1.41	2e-16	1e-13	40 x 50 galactosidase, beta 1 [Source:HGNC Symbol;Acc:HGNC:429
11	HAUS1	-1.62	2e-16	1e-13	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
12	LAMB2	-1.46	2e-16	1e-13	50 x 6 laminin, beta 2 (laminin S) [Source:HGNC Symbol;Acc:HGNC
13	MALSU1	-1.53	2e-16	1e-13	49 x 15 mitochondrial assembly of ribosomal large subunit 1 [Source:
14	MRE11A	-1.17	2e-16	1e-13	12 x 43 MRE11 meiotic recombination 11 homolog A (S. cerevisiae) [
15	NUP85	-1.56	2e-16	1e-13	1 x 50 nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
16	PDE4D	-1.51	2e-16	1e-13	3 x 8 phosphodiesterase 4D, cAMP-specific [Source:HGNC Symbc
17	PSME1	-1.05	2e-16	1e-13	8 x 20 proteasome (prosome, macropain) activator subunit 1 (PA28 ;
18	PTCD3	-1.43	2e-16	1e-13	48 x 50 pentatricopeptide repeat domain 3 [Source:HGNC Symbol;Ac
19	SNX14	-1.53	2e-16	1e-13	39 x 50 sorting nexin 14 [Source:HGNC Symbol;Acc:HGNC:14977]
20	ST6GALNAC1	-1.55	2e-16	1e-13	1 x 44 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-

Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.52	0.003	296	GSEA C2BORCZUK_MALIGNANT_MESOTHELIOMA_UP
2	5.31	0.003	373	GSEA C2/ECCHI_GASTRIC_CANCER_EARLY_UP
3	5.2	0.003	1326	GSEA C2DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_UP
4	5.17	0.003	100	GSEA C2SESTO_RESPONSE_TO_UV_CO
5	4.79	0.004	87	MF unfolded protein binding
6	4.75	0.004	1171	TF KIM_MYC targets
7	4.69	0.004	16	GSEA C2Y_AGING_MIDDLE_DN
8	4.6	0.005	687	BP gene expression
9	4.58	0.005	316	GSEA C2HSIAO_HOUSEKEEPING_GENES
10	4.49	0.005	416	GSEA C2SHEN_SMARCA2_TARGETS_UP
11	4.44	0.005	62	GSEA C2REACTOME_TRANSLATION
12	4.38	0.006	158	Brain Overlap_fetal_midbrain_Het
13	4.35	0.006	209	GSEA C2LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
14	4.33	0.006	8205	CC cytoplasm
15	4.3	0.006	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
16	4.26	0.006	197	GSEA C2WANG_TUMOR_INVASIVENESS_DN
17	4.24	0.006	65	GSEA C2SHEPARD_BMYB_TARGETS
18	4.21	0.006	270	GSEA C2BASAKI_YBX1_TARGETS_UP
19	4.12	0.007	155	GSEA C2SHEPARD_CRUSH_AND_BURN_MUTANT_DN
20	4.12	0.007	102	GSEA C2DAIRKEE_CANCER_PRONE_RESPONSE_BPA_E2
<i>Underexpressed</i>				
1	-5.81	0.002	135	GSEA C2WHITFIELD_CELL_CYCLE_G1_S
2	-5.16	0.003	15	BP lipid particle organization
3	-4.82	0.004	27	GSEA C2REACTOME_DNA_STRAND_ELONGATION
4	-4.75	0.004	29	BP DNA strand elongation involved in DNA replication
5	-4.62	0.005	43	GSEA C2PID_FANCONI_PATHWAY
6	-4.59	0.005	139	BP DNA replication
7	-4.46	0.005	10	BP intra-S DNA damage checkpoint
8	-4.27	0.006	335	Chr Chr 22
9	-4.27	0.006	11	BP mitotic G2 DNA damage checkpoint
10	-4.23	0.006	20	BP telomere maintenance via semi-conservative replication
11	-4.17	0.007	16	GSEA C2REACTOME_LAGGING_STRAND_SYNTHESIS
12	-3.92	0.008	58	GSEA C2WAKASUGI_HAVE_ZNF143_BINDING_SITES
13	-3.83	0.009	65	BP telomere maintenance
14	-3.81	0.009	32	GSEA C2REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
15	-3.8	0.009	7	GSEA C2S_INTERFERON_GAMMA_PATHWAY
16	-3.8	0.009	7	GSEA C2MYLYKANGAS_AMPLIFICATION_HOT_SPOT_25
17	-3.79	0.009	20	GSEA C2BIOCARTA_ATRBRCA_PATHWAY
18	-3.76	0.009	3897	Colon CaCes1_Colon
19	-3.72	0.009	61	GSEA C2BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL
20	-3.6	0.010	38	GSEA C2REACTOME_G2_M_CHECKPOINTS



G7_mel

Local Summary

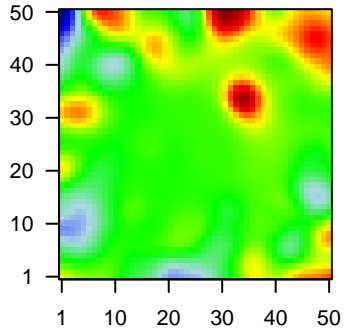
%DE = 0.87
 # metagenes = 16
 # genes = 49
 # genes in genesets = 48

 # genes with $fdr < 0.1$ = 34 (34 + / 0 -)
 # genes with $fdr < 0.05$ = 34 (34 + / 0 -)
 # genes with $fdr < 0.01$ = 34 (34 + / 0 -)

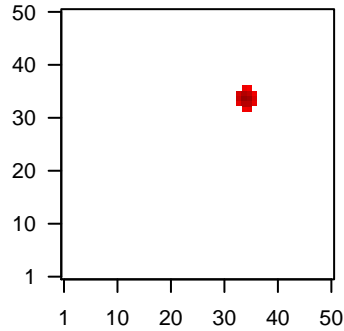
 $\langle r \rangle$ metagenes = 0.9
 $\langle r \rangle$ genes = 0.48

 $\langle FC \rangle$ = 0.78
 $\langle \text{shrinkage-t} \rangle$ = 11.92
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.3

Profile



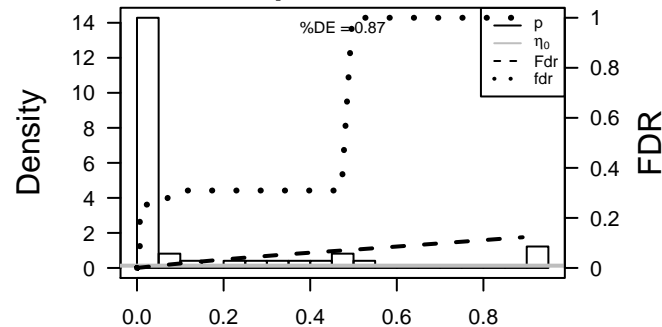
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HECW2	1.53	2e-11	5e-10	34 x 34 HECT, C2 and WW domain containing E3 ubiquitin protein lig
2	C9orf153	1.47	1e-10	1e-09	34 x 34 chromosome 9 open reading frame 153 [Source:HGNC Synt
3	PYGM	1.43	3e-10	1e-09	34 x 34 phosphorylase, glycogen, muscle [Source:HGNC Symbol;Acc
4	EBLN2	1.42	5e-10	1e-09	34 x 34 endogenous Bornavirus-like nucleoprotein 2 [Source:HGNC
5	HIST3H3	1.4	7e-10	1e-09	34 x 34 histone cluster 3, H3 [Source:HGNC Symbol;Acc:HGNC:477
6	MGST1	1.4	8e-10	2e-09	34 x 34 microsomal glutathione S-transferase 1 [Source:HGNC Synt
7	TRPM8	1.39	1e-09	9e-08	34 x 34 transient receptor potential cation channel, subfamily M, merr
8	PEX11G	1.29	2e-08	2e-07	34 x 34 peroxisomal biogenesis factor 11 gamma [Source:HGNC Syn
9	PRPH	1.24	5e-08	2e-07	34 x 34 peripherin [Source:HGNC Symbol;Acc:HGNC:9461]
10	MAGEA6	1.21	1e-07	2e-07	34 x 34 melanoma antigen family A6 [Source:HGNC Symbol;Acc:HGI
11	OR1411	1.2	1e-07	5e-06	34 x 34 olfactory receptor, family 14, subfamily I, member 1 [Source:l
12	ZNF792	1.11	1e-06	5e-06	34 x 34 zinc finger protein 792 [Source:HGNC Symbol;Acc:HGNC:24
13	PIK3AP1	1.09	2e-06	1e-05	34 x 34 phosphoinositide-3-kinase adaptor protein 1 [Source:HGNC
14	RAD51L3-RF	1.05	4e-06	1e-05	34 x 34
15	HIST1H3J	1.04	5e-06	3e-05	34 x 34 histone cluster 1, H3j [Source:HGNC Symbol;Acc:HGNC:477
16	LGI2	1	1e-05	3e-05	34 x 34 leucine-rich repeat LGI family, member 2 [Source:HGNC Syn
17	JAKMIP2	0.99	1e-05	3e-05	34 x 34 janus kinase and microtubule interacting protein 2 [Source:HC
18	HIST1H2AK	0.96	2e-05	3e-05	34 x 34 histone cluster 1, H2ak [Source:HGNC Symbol;Acc:HGNC:47
19	CCDC184	0.96	2e-05	3e-05	34 x 34 coiled-coil domain containing 184 [Source:HGNC Symbol;Acc
20	SUSD4	0.96	3e-05	1e-04	34 x 34 sushi domain containing 4 [Source:HGNC Symbol;Acc:HGNC

p-values



G7_mel

Local Summary

%DE = 0.74
 # metagenes = 19
 # genes = 181
 # genes in genesets = 181

 # genes with $fdr < 0.1$ = 97 (85 + / 12 -)
 # genes with $fdr < 0.05$ = 79 (68 + / 11 -)
 # genes with $fdr < 0.01$ = 43 (38 + / 5 -)

 $\langle r \rangle$ metagenes = 0.91
 $\langle r \rangle$ genes = 0.08

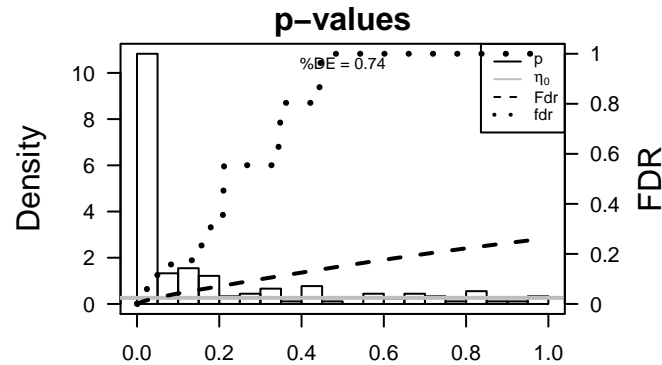
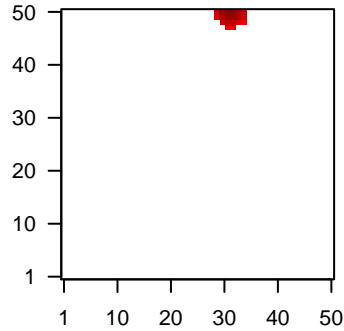
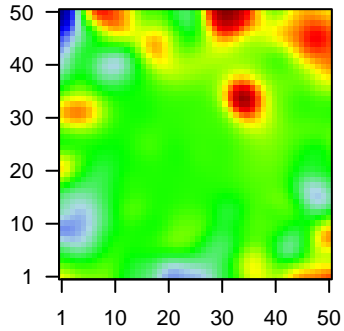
 $\langle FC \rangle$ = 0.31
 $\langle \text{shrinkage-t} \rangle$ = 5
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.59

Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	PRMT5	-1.48	9e-15	8e-08	34 x 50 protein arginine methyltransferase 5 [Source:HGNC Symbol;Acc:HGNC:10317]
2	UBE3D	1.37	2e-09	2e-07	33 x 50 ubiquitin protein ligase E3D [Source:HGNC Symbol;Acc:HGNC:10317]
3	COG3	1.31	1e-08	2e-07	30 x 50 component of oligomeric golgi complex 3 [Source:HGNC Symbol;Acc:HGNC:10317]
4	EIF3L	-0.54	1e-08	2e-07	31 x 47 eukaryotic translation initiation factor 3, subunit L [Source:HGNC Symbol;Acc:HGNC:10317]
5	ZNF613	1.28	2e-08	3e-06	31 x 49 zinc finger protein 613 [Source:HGNC Symbol;Acc:HGNC:25117]
6	PCBP4	1.23	7e-08	9e-06	33 x 50 poly(rC) binding protein 4 [Source:HGNC Symbol;Acc:HGNC:10317]
7	RSAD1	1.17	3e-07	1e-05	29 x 49 radical S-adenosyl methionine domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10317]
8	RBM41	1.14	6e-07	1e-05	34 x 50 RNA binding motif protein 41 [Source:HGNC Symbol;Acc:HGNC:10317]
9	BAAT	1.12	8e-07	1e-05	32 x 50 bile acid CoA:amino acid N-acyltransferase [Source:HGNC Symbol;Acc:HGNC:10317]
10	ULBP2	1.12	9e-07	3e-05	32 x 48 UL16 binding protein 2 [Source:HGNC Symbol;Acc:HGNC:10317]
11	HSPB9	1.08	2e-06	3e-05	30 x 50 heat shock protein, alpha-crystallin-related, B9 [Source:HGNC Symbol;Acc:HGNC:10317]
12	RBM22	1.05	3e-06	3e-05	34 x 49 RNA binding motif protein 22 [Source:HGNC Symbol;Acc:HGNC:10317]
13	CXXC5	1.07	3e-06	3e-05	31 x 50 CXXC finger protein 5 [Source:HGNC Symbol;Acc:HGNC:26117]
14	USP30	1.05	4e-06	3e-05	34 x 50 ubiquitin specific peptidase 30 [Source:HGNC Symbol;Acc:HGNC:10317]
15	TOR3A	1.05	4e-06	3e-04	33 x 48 torsin family 3, member A [Source:HGNC Symbol;Acc:HGNC:10317]
16	PCGF1	0.98	2e-05	3e-04	33 x 50 polycomb group ring finger 1 [Source:HGNC Symbol;Acc:HGNC:10317]
17	TPD52L2	0.97	2e-05	3e-04	34 x 50 tumor protein D52-like 2 [Source:HGNC Symbol;Acc:HGNC:10317]
18	NFXL1	0.97	2e-05	5e-04	33 x 48 nuclear transcription factor, X-box binding-like 1 [Source:HGNC Symbol;Acc:HGNC:10317]
19	FAH	0.91	5e-05	5e-04	29 x 50 fumarylacetoacetate hydrolase (fumarylacetoacetase) [Source:HGNC Symbol;Acc:HGNC:10317]
20	DHDDS	-0.91	6e-05	5e-04	34 x 50 dehydrodolichyl diphosphate synthase [Source:HGNC Symbol;Acc:HGNC:10317]

Profile

Spot



G7_mel

Local Summary

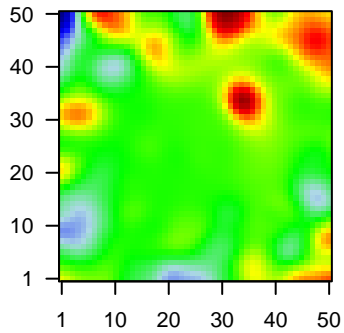
%DE = 0.73
 # metagenes = 8
 # genes = 181
 # genes in genesets = 180

 # genes with $fdr < 0.1$ = 105 (15 + / 90 -)
 # genes with $fdr < 0.05$ = 88 (13 + / 75 -)
 # genes with $fdr < 0.01$ = 57 (9 + / 48 -)

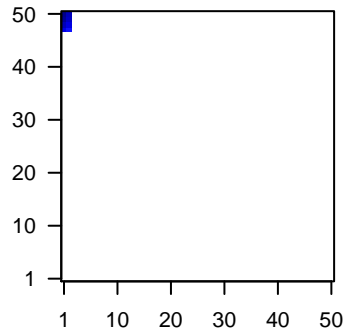
 $\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.27

 $\langle FC \rangle$ = -0.35
 $\langle \text{shrinkage-t} \rangle$ = -5.6
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.52

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	HAUS1	-1.62	2e-16	5e-15	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbc
2	NUP85	-1.56	2e-16	5e-15	1 x 50 nucleoporin 85kDa [Source:HGNC Symbol;Acc:HGNC:8734]
3	GMNN	-1.45	9e-14	2e-10	2 x 50 geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc
4	RFC5	-1.39	4e-12	3e-09	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S
5	GMPS	-1.31	6e-11	2e-08	1 x 48 guanine monphosphate synthase [Source:HGNC Symbol;Acc
6	HADH	-1.23	7e-10	2e-08	1 x 48 hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc
7	TIMM9	-1.27	1e-09	8e-07	1 x 47 translocase of inner mitochondrial membrane 9 homolog (yea
8	FTSJ2	-1.21	2e-08	3e-06	1 x 48 FtsJ RNA methyltransferase homolog 2 (E. coli) [Source:HGNC
9	MAD2L2	-1.18	8e-08	9e-06	2 x 50 MAD2 mitotic arrest deficient-like 2 (yeast) [Source:HGNC S
10	CKB	1.1	3e-07	3e-05	2 x 47 creatine kinase, brain [Source:HGNC Symbol;Acc:HGNC:199
11	TRMT11	1.11	1e-06	3e-05	1 x 47 tRNA methyltransferase 11 homolog (S. cerevisiae) [Source:t
12	PRMT3	-1.07	2e-06	3e-05	1 x 47 protein arginine methyltransferase 3 [Source:HGNC Symbol;/
13	CDC6	-1.06	3e-06	3e-05	1 x 50 cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
14	KNTC1	-1.05	3e-06	4e-05	1 x 50 kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
15	RFC4	-1	4e-06	9e-05	1 x 50 replication factor C (activator 1) 4, 37kDa [Source:HGNC Syn
16	ORC6	-0.94	6e-06	9e-05	1 x 50 origin recognition complex, subunit 6 [Source:HGNC Symbol;
17	CDC47L	-1	7e-06	1e-04	1 x 50 cell division cycle associated 7-like [Source:HGNC Symbol;A
18	ENOSF1	-0.99	1e-05	2e-04	1 x 48 enolase superfamily member 1 [Source:HGNC Symbol;Acc:H
19	HDGFRP3	-0.98	2e-05	2e-04	1 x 48
20	FEN1	-0.88	2e-05	2e-04	1 x 50 flap structure-specific endonuclease 1 [Source:HGNC Symbc

p-values

