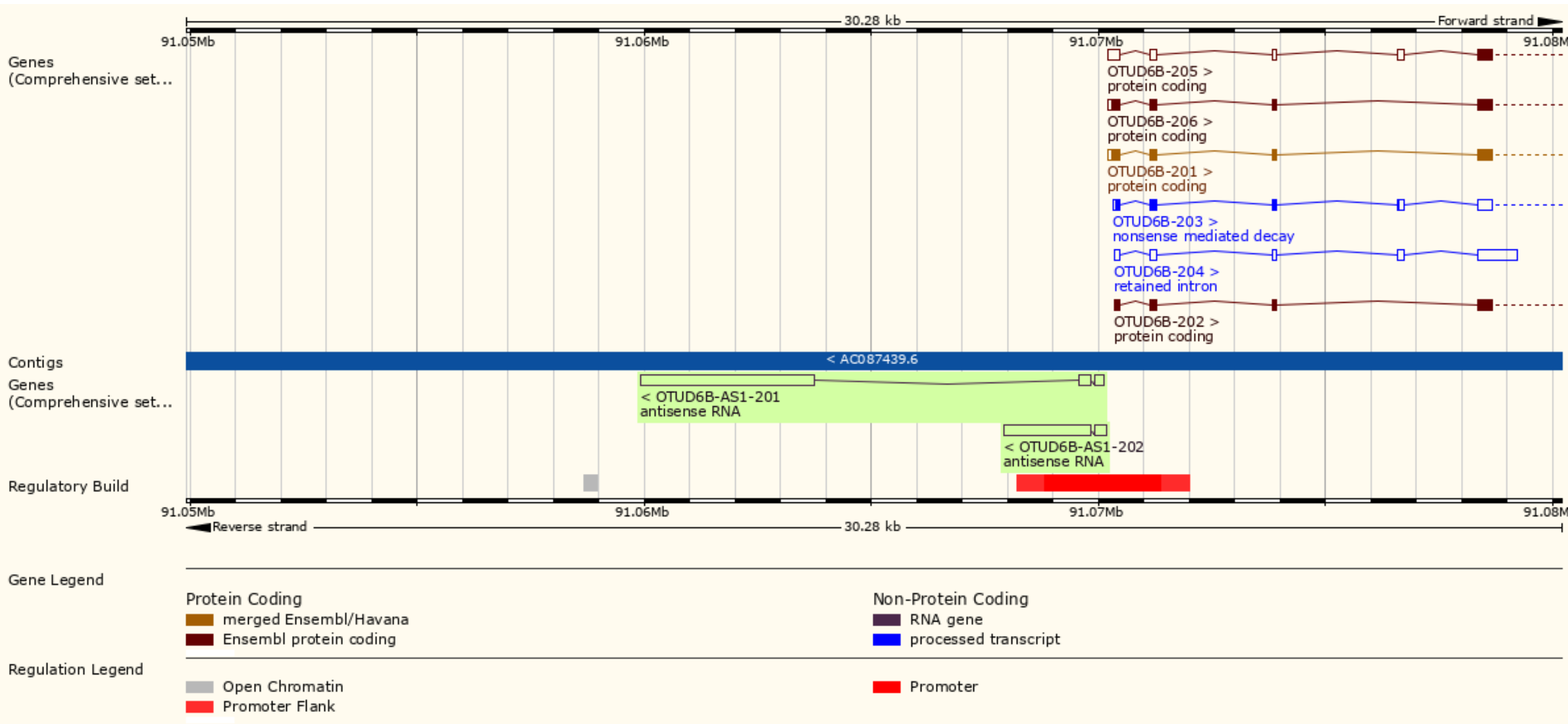


Clinically Relevant lncRNA candidates in four cancers

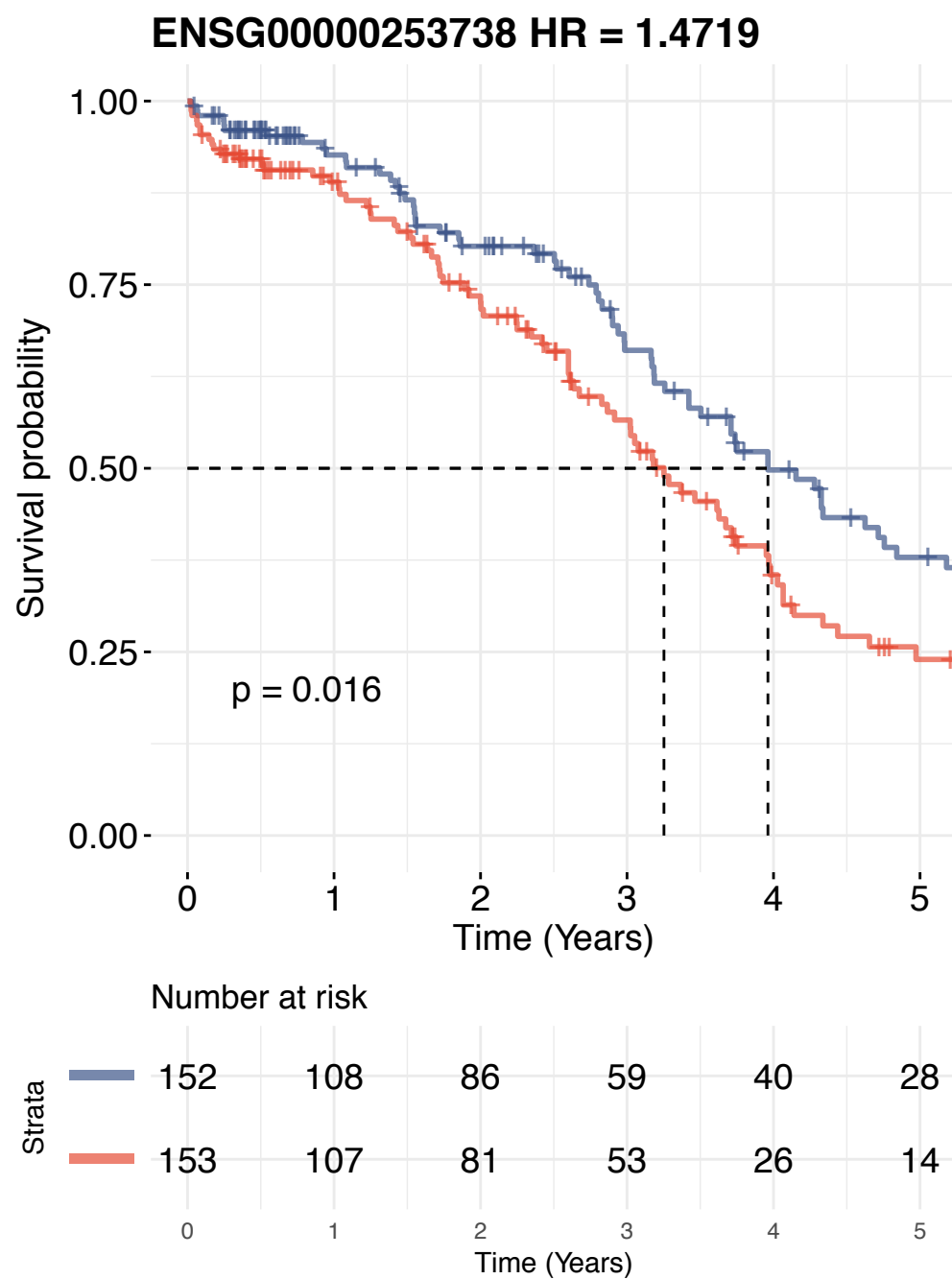
March 28th, 2018

(1) GS1-251I9.4 in OV

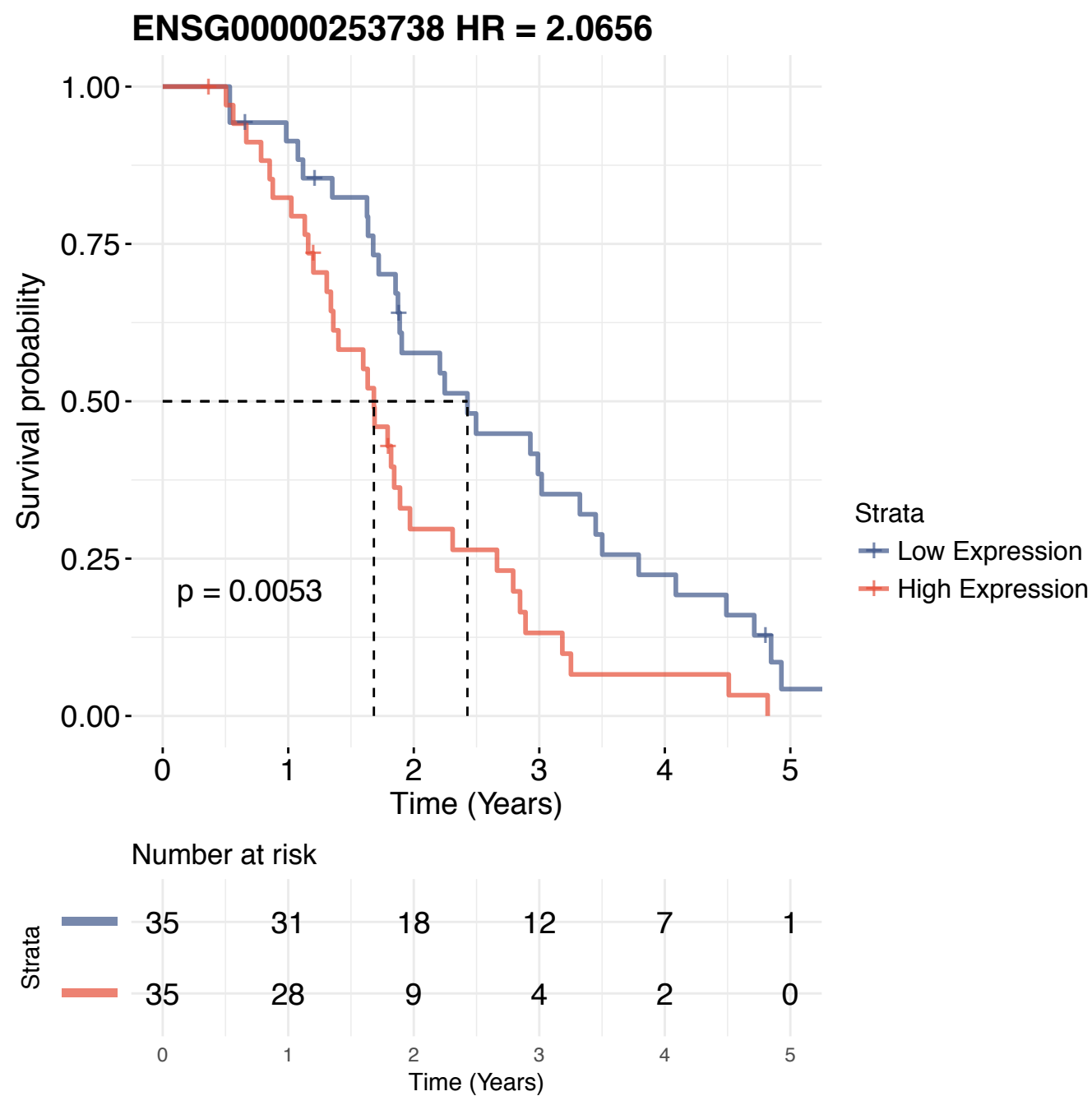
Antisense IncRNA to OTUD6B, a functional deubiquitinating enzyme



(1) GS1-25119.4 in OV



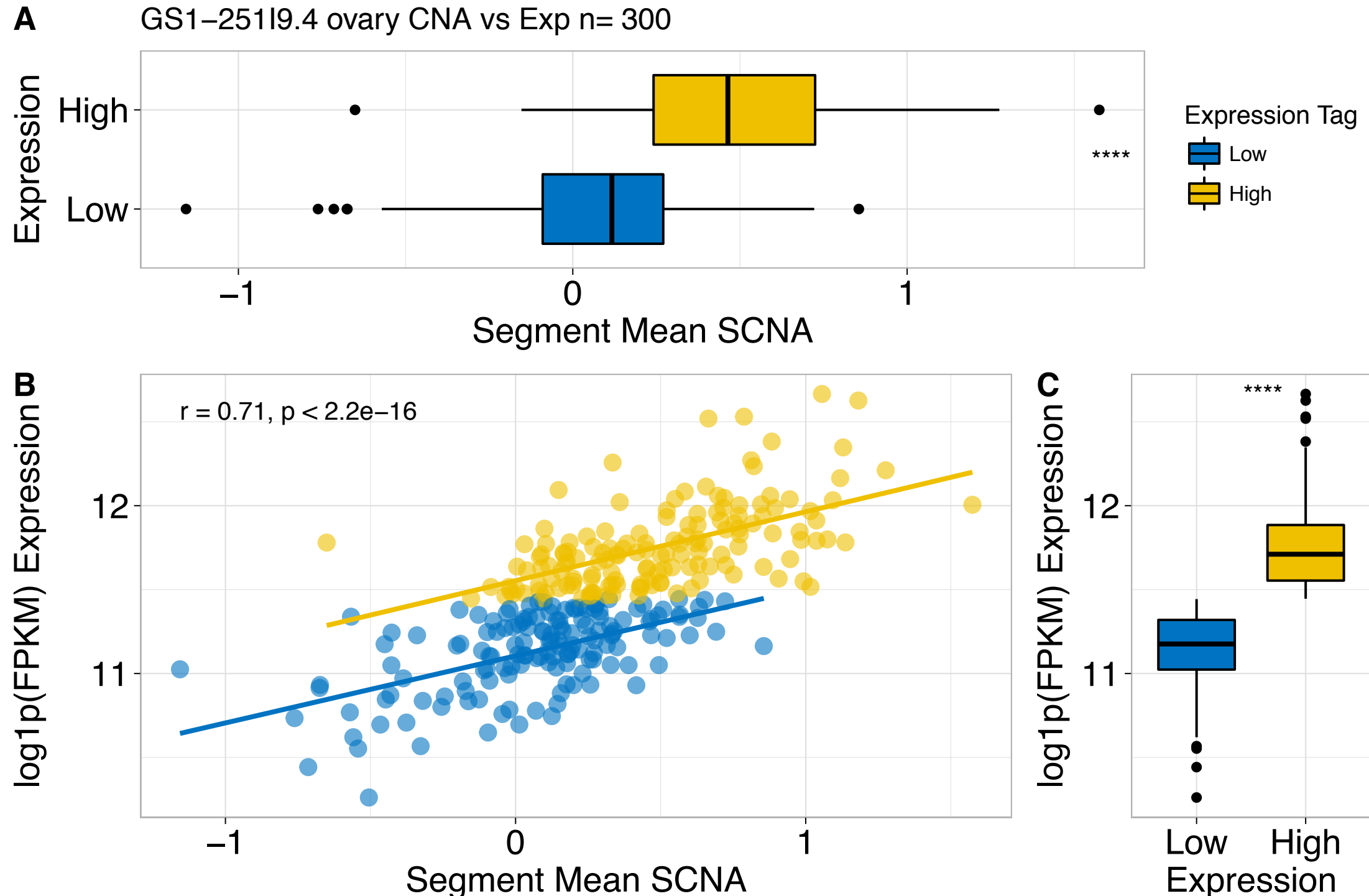
TCGA



PCAWG

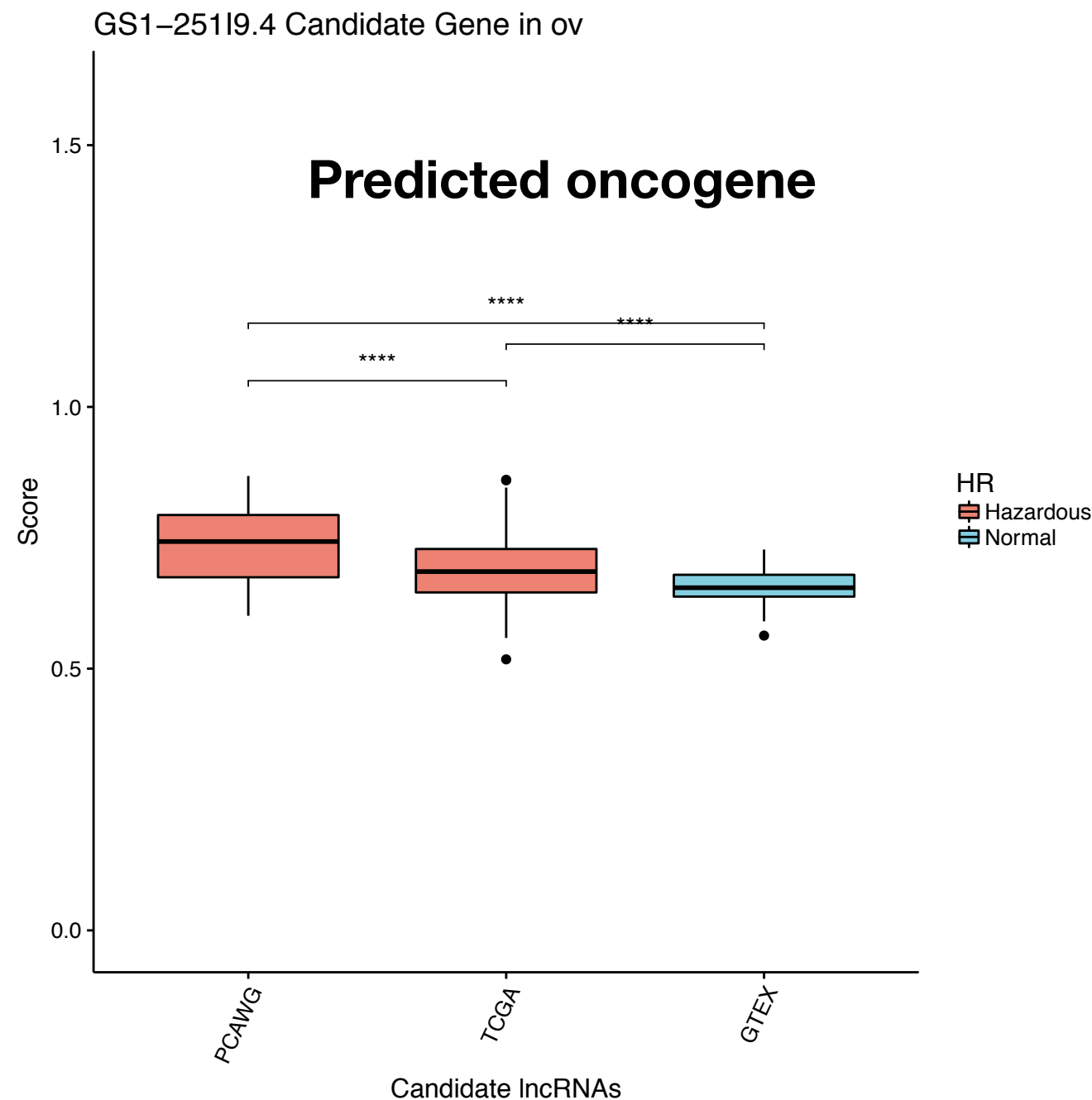
(1) GS1-251I9.4 in OV

- Too little methylation data to observe any trends however, expression is significantly positively associated with copy number amplification in genomic region

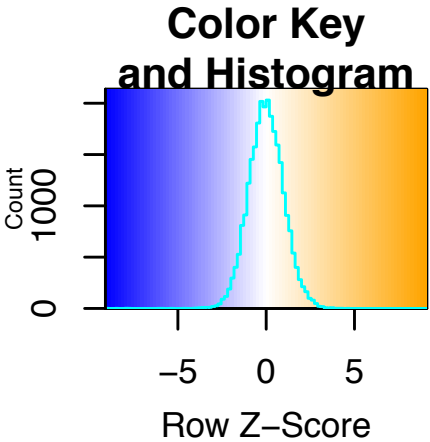


(1) GS1-25119.4 in OV

- Expression is significantly relatively higher in both TCGA and PCAWG cohorts compared to normal samples from GTEx, fallopian tubes would be more appropriate here but there are only 7 such samples thus, ovarian samples were used for comparison

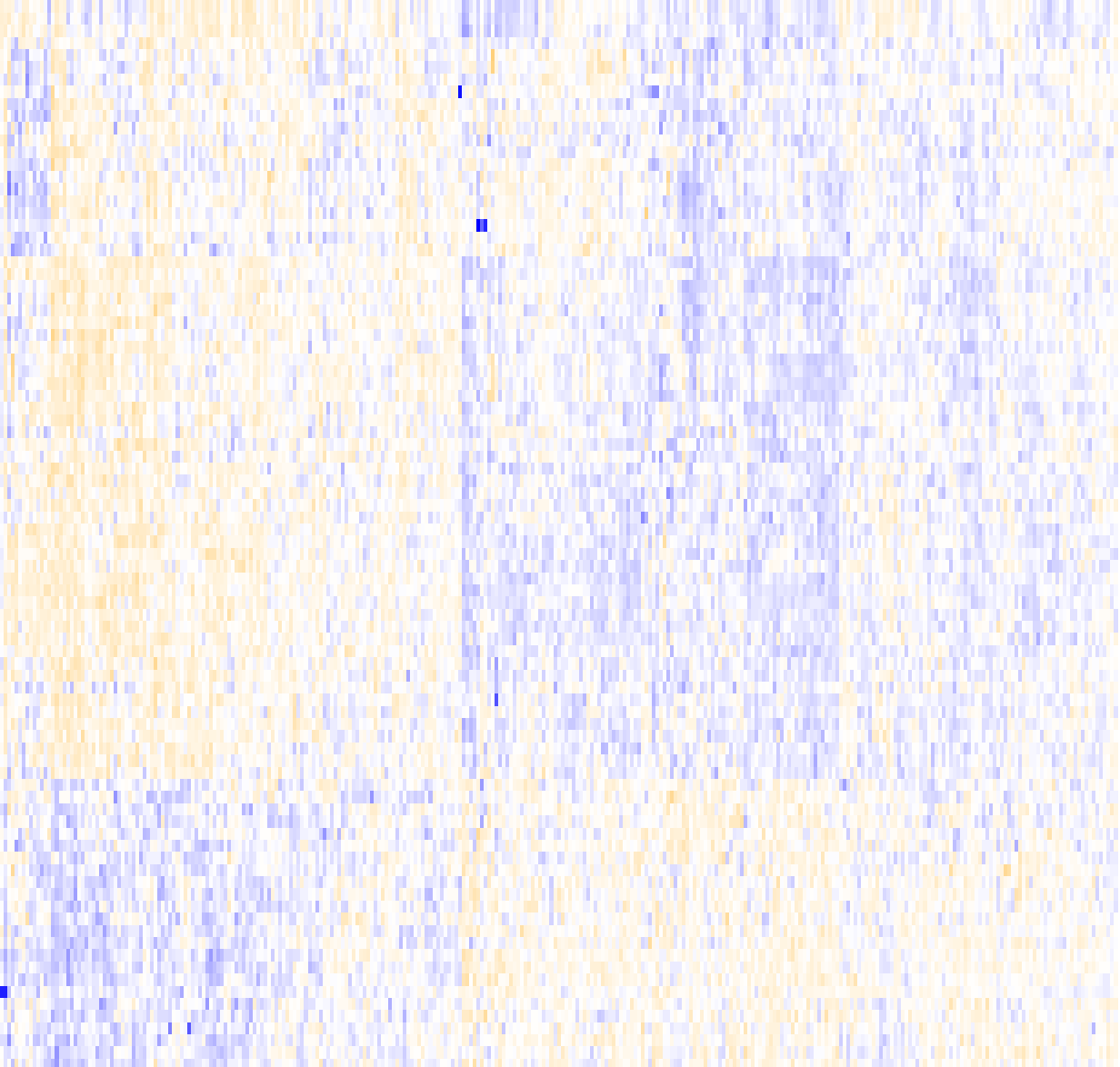
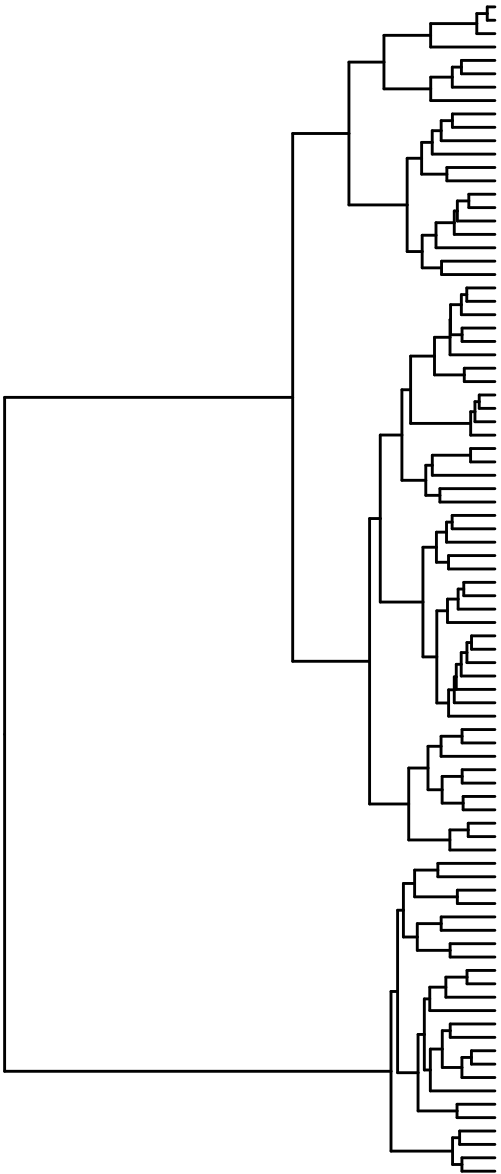
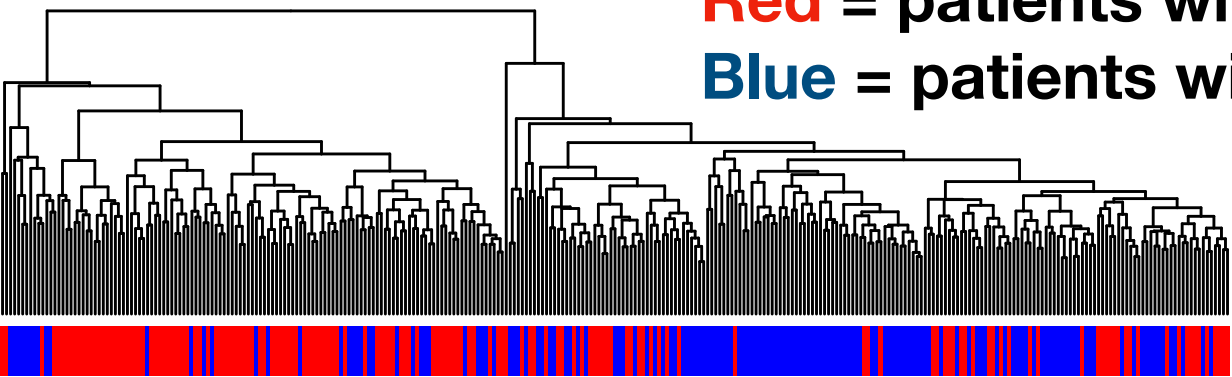


(1) GS1-25119.4 in OV



NSG00000253738 Ovarian serous cystadenocarcinoma

Red = patients with high lncRNA expression
Blue = patients with low lncRNA expression

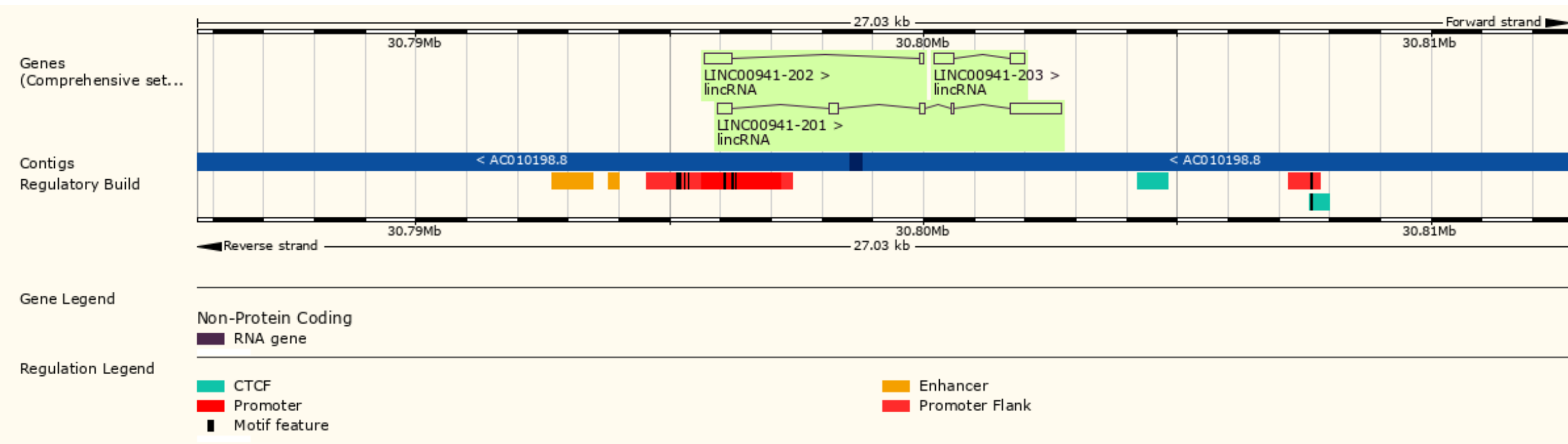


NSG00000228253
NSG00000198899
NSG00000198840
NSG00000140043
NSG00000175073
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NSG00000179041
NSG00000214954
NSG00000205133
NSG00000164830
NSG00000155099
NSG00000133872
NSG00000186343
NSG00000164953
NSG00000164823
NSG00000104320
NSG00000155100
NSG00000085719
NSG00000104413
NSG00000185728
NSG00000182197
NSG00000156467
NSG00000137547
NSG00000156170
NSG00000132541
NSG00000120533
NSG00000104325
NSG00000164751
NSG00000147586
NSG00000156831
NSG00000156795
NSG00000189376
NSG00000147687
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NSG00000163344
NSG00000104518
NSG00000186132
NSG00000145354
NSG00000120656
NSG00000185808
NSG00000154640
NSG00000173486
NSG00000163463
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NSG00000140990
NSG00000127540
NSG00000168569
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NSG00000054148
NSG00000175602
NSG00000131507
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NSG00000153140
NSG00000058729
NSG00000164182
NSG00000164172
NSG00000140319
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NSG00000166200
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NSG00000196814
NSG00000176225
NSG00000152223
NSG00000197037
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NSG00000136715
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NSG00000214655
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NSG00000127481
NSG00000116127
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Significantly co-expressed PCGs

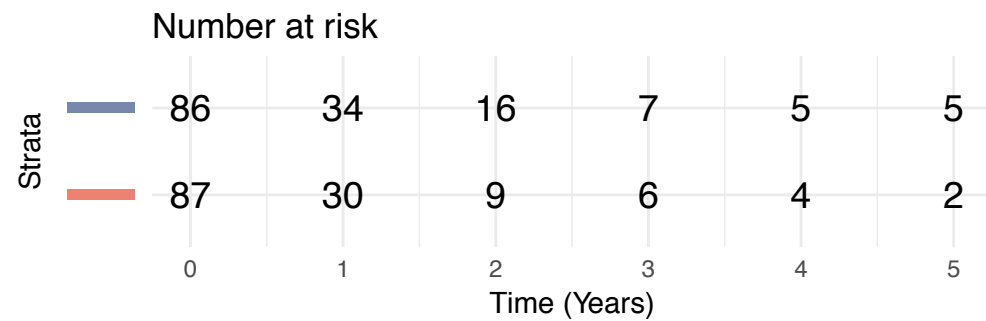
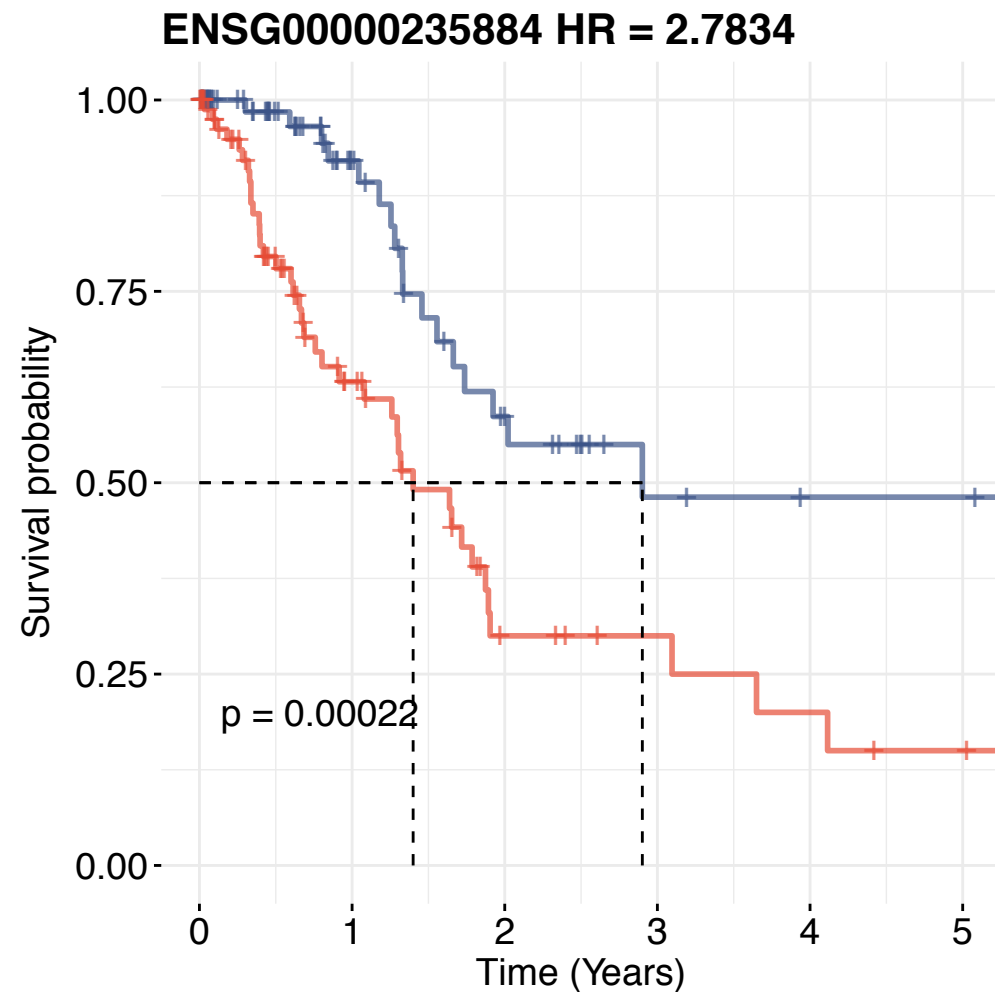
(2) LINC00941 PAAD

Intergenic lncRNA overlapping a promoter region downstream of an enhancer

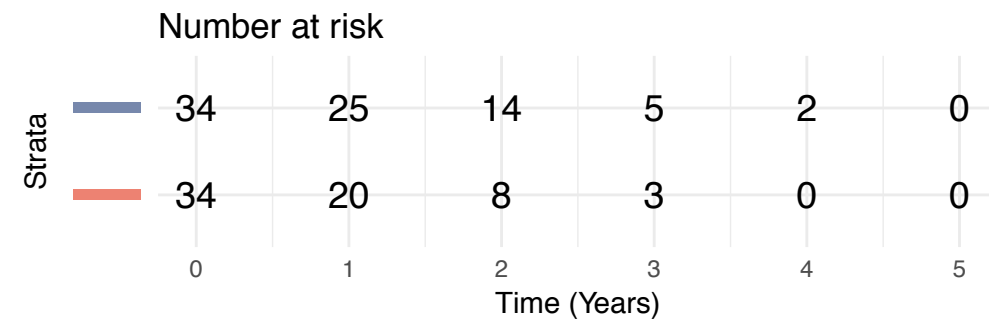
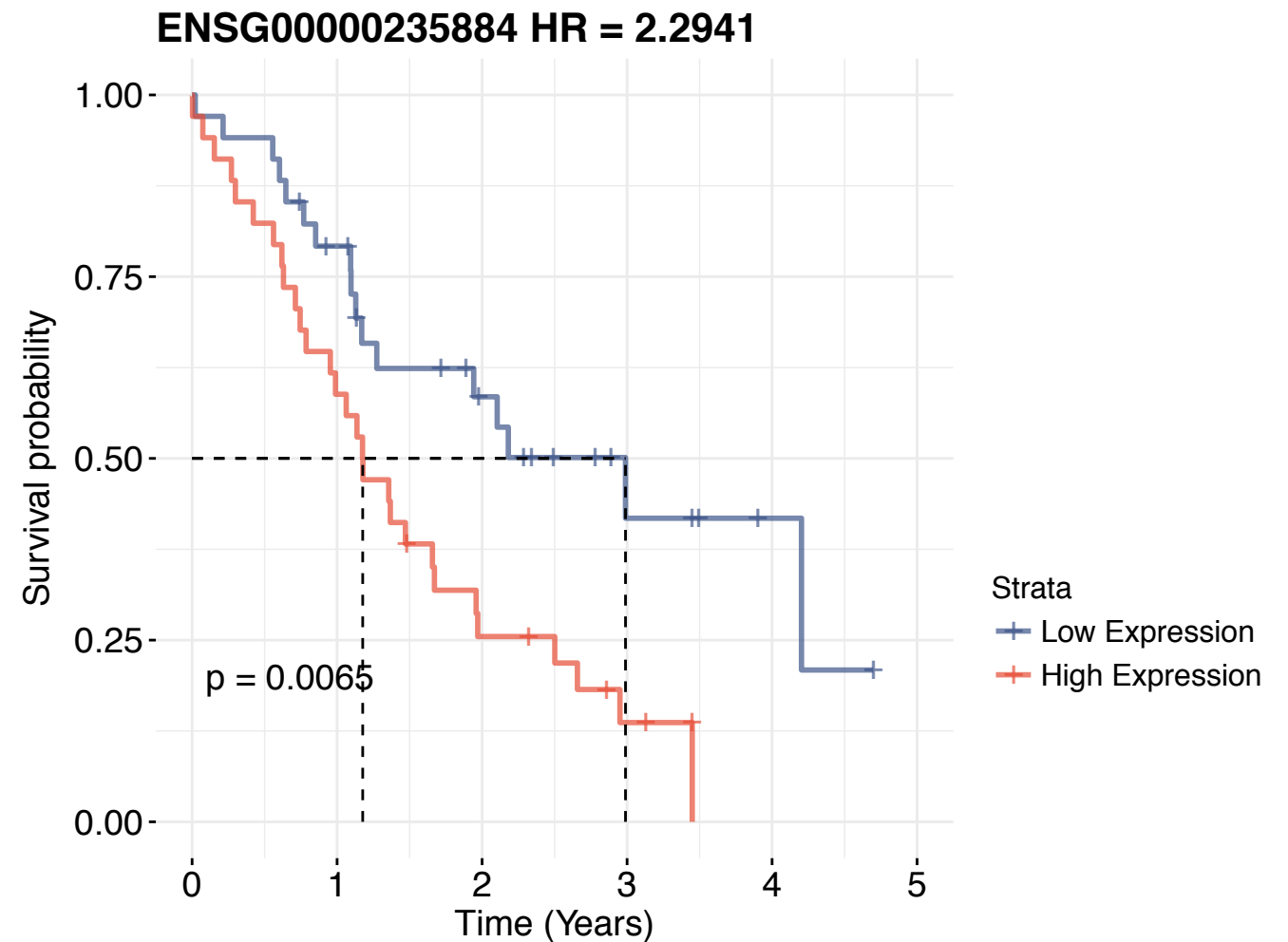


No PCGs nearby

(2) LINC00941 PAAD



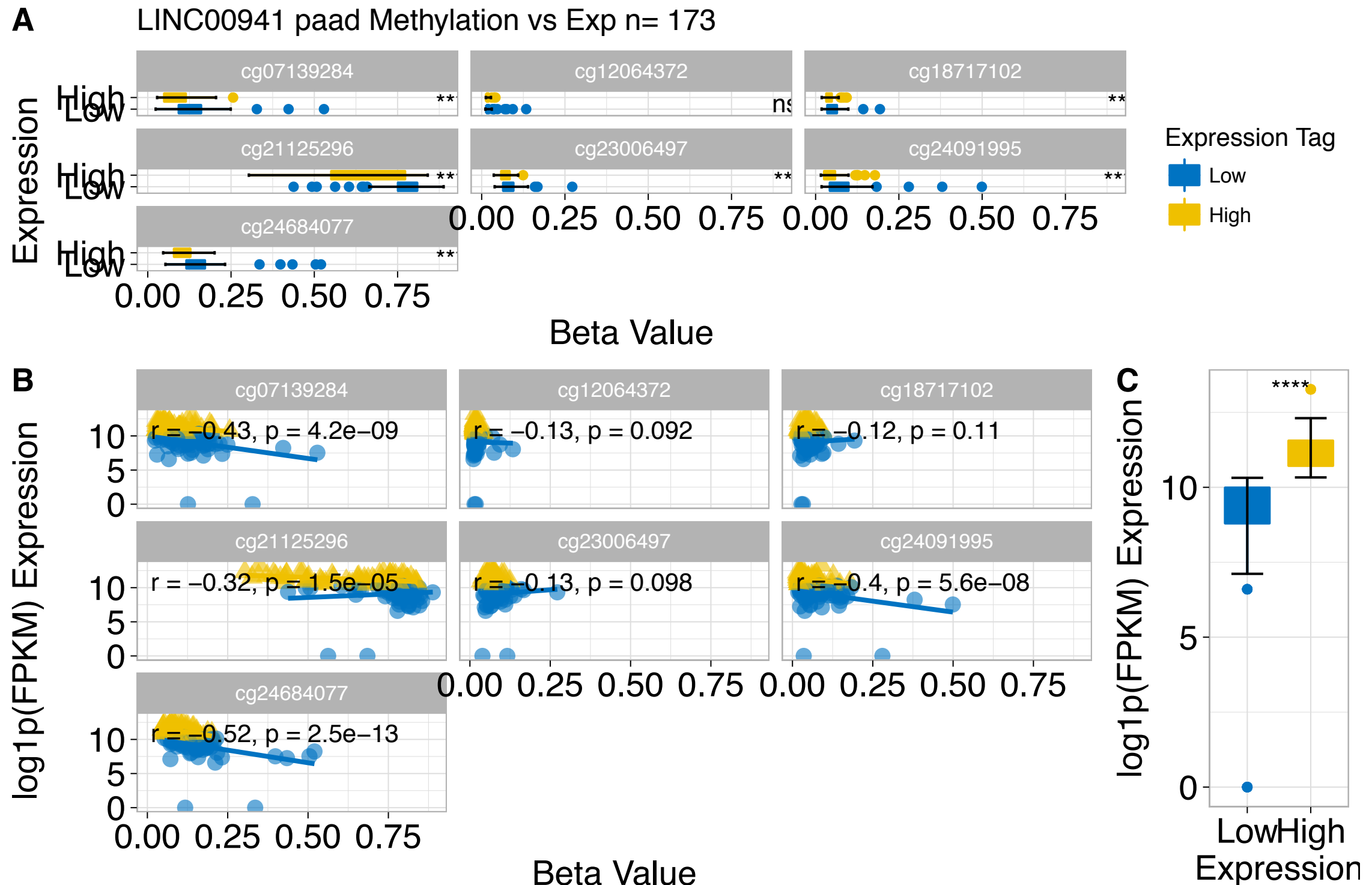
TCGA



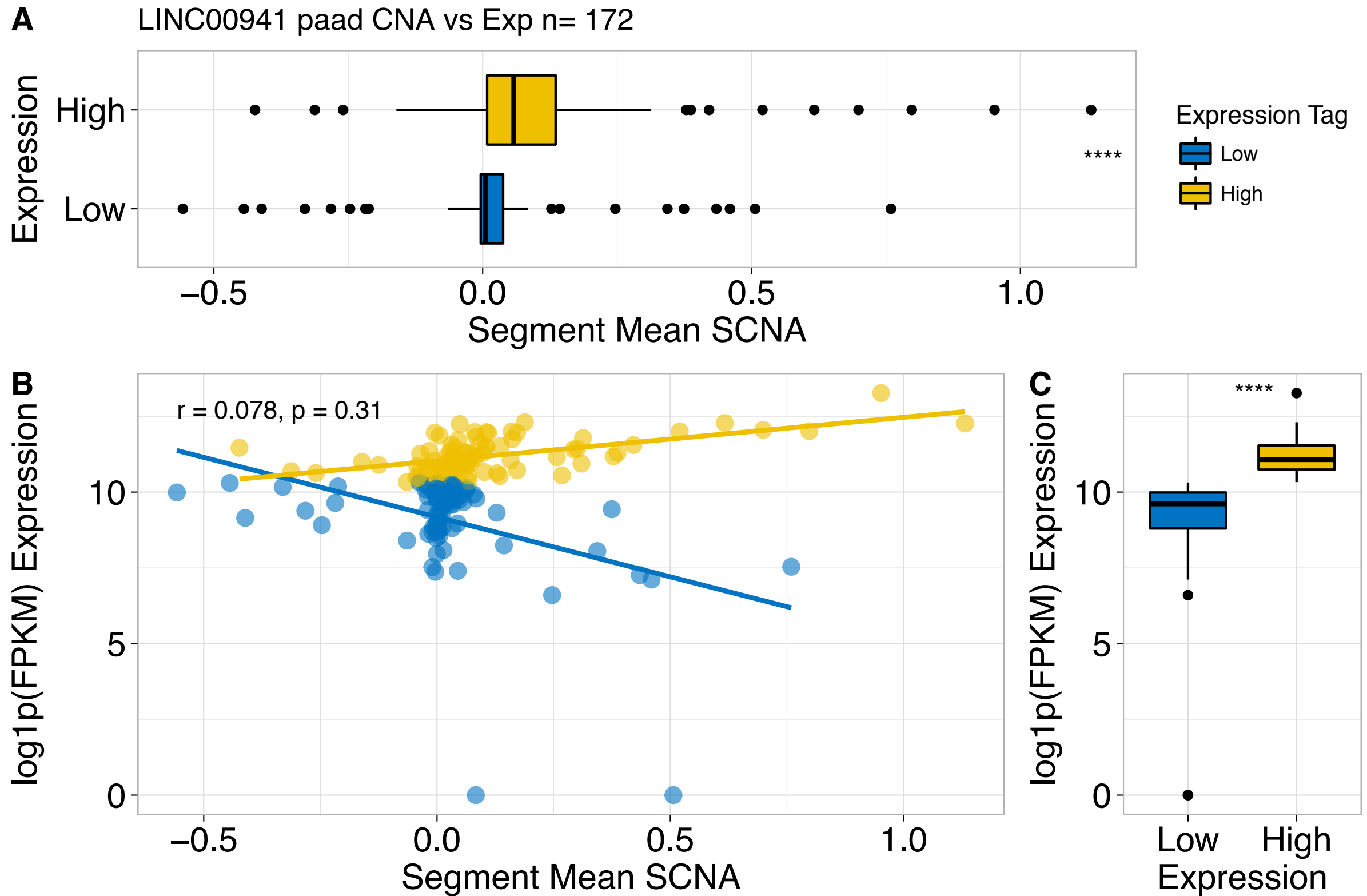
PCAWG

(2) LINC00941 PAAD

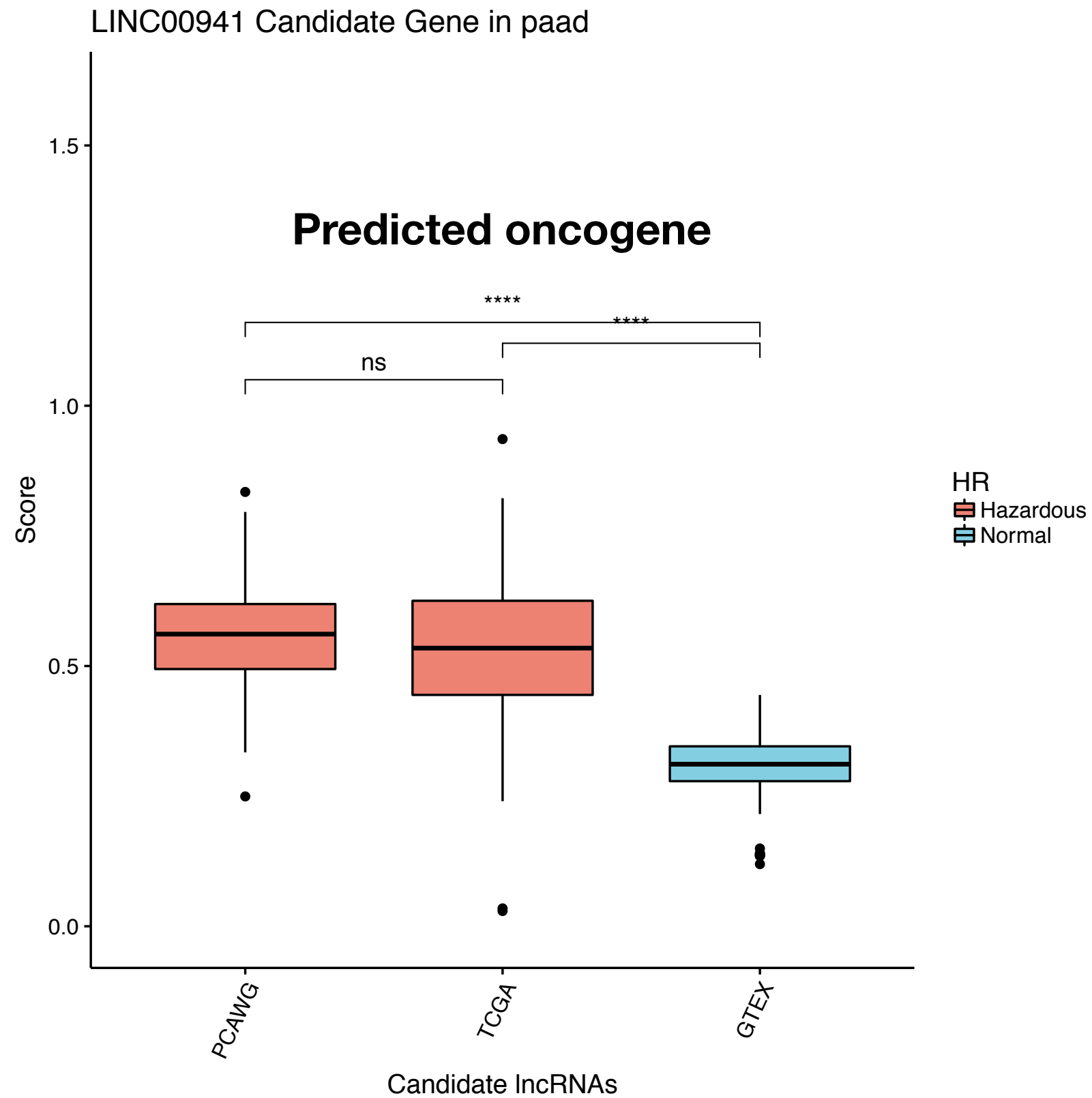
- Patients with low expression also have higher methylation of probes overlapping the lncRNA



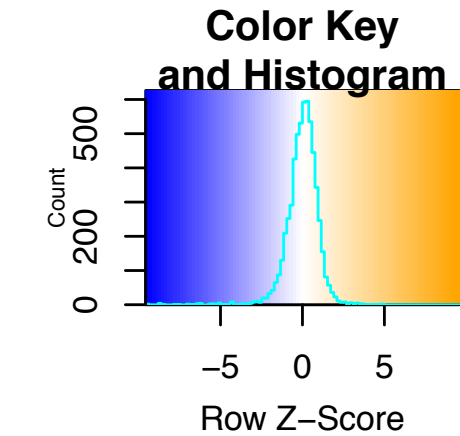
(2) LINC00941 PAAD



(2) LINC00941 PAAD

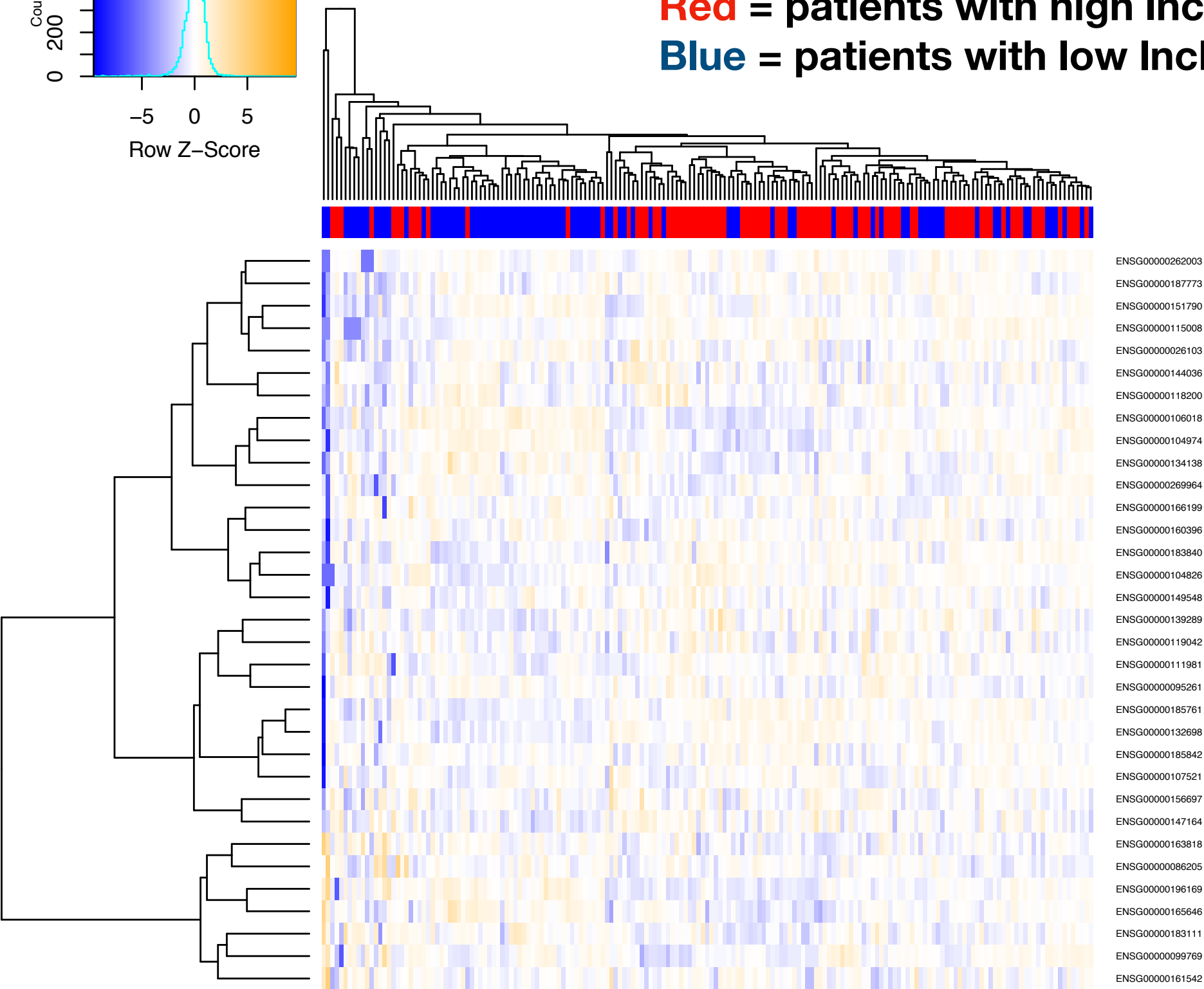


(2) LINC00941 PAAD



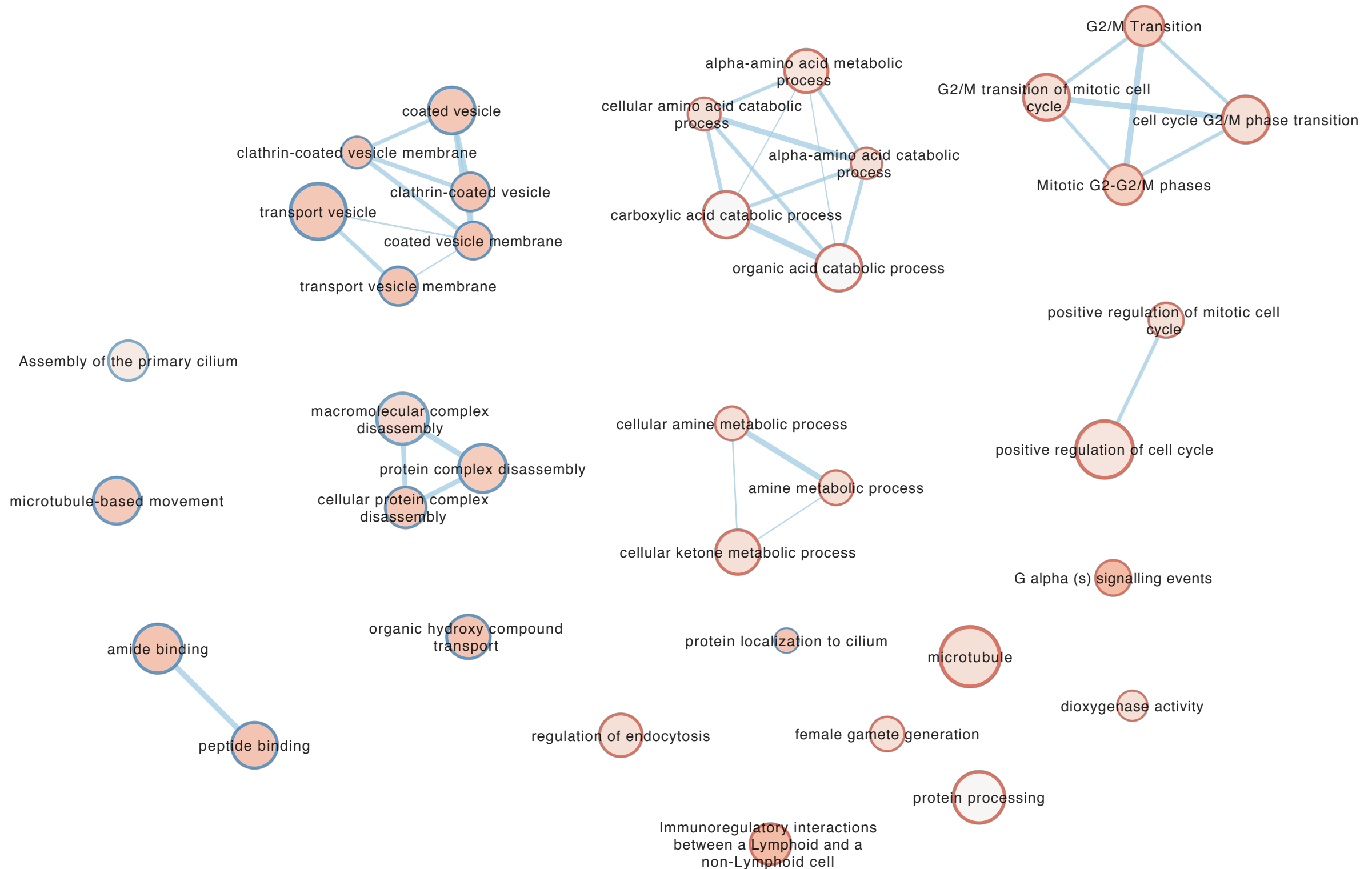
ENSG00000235884 Pancreatic adenocarcinoma

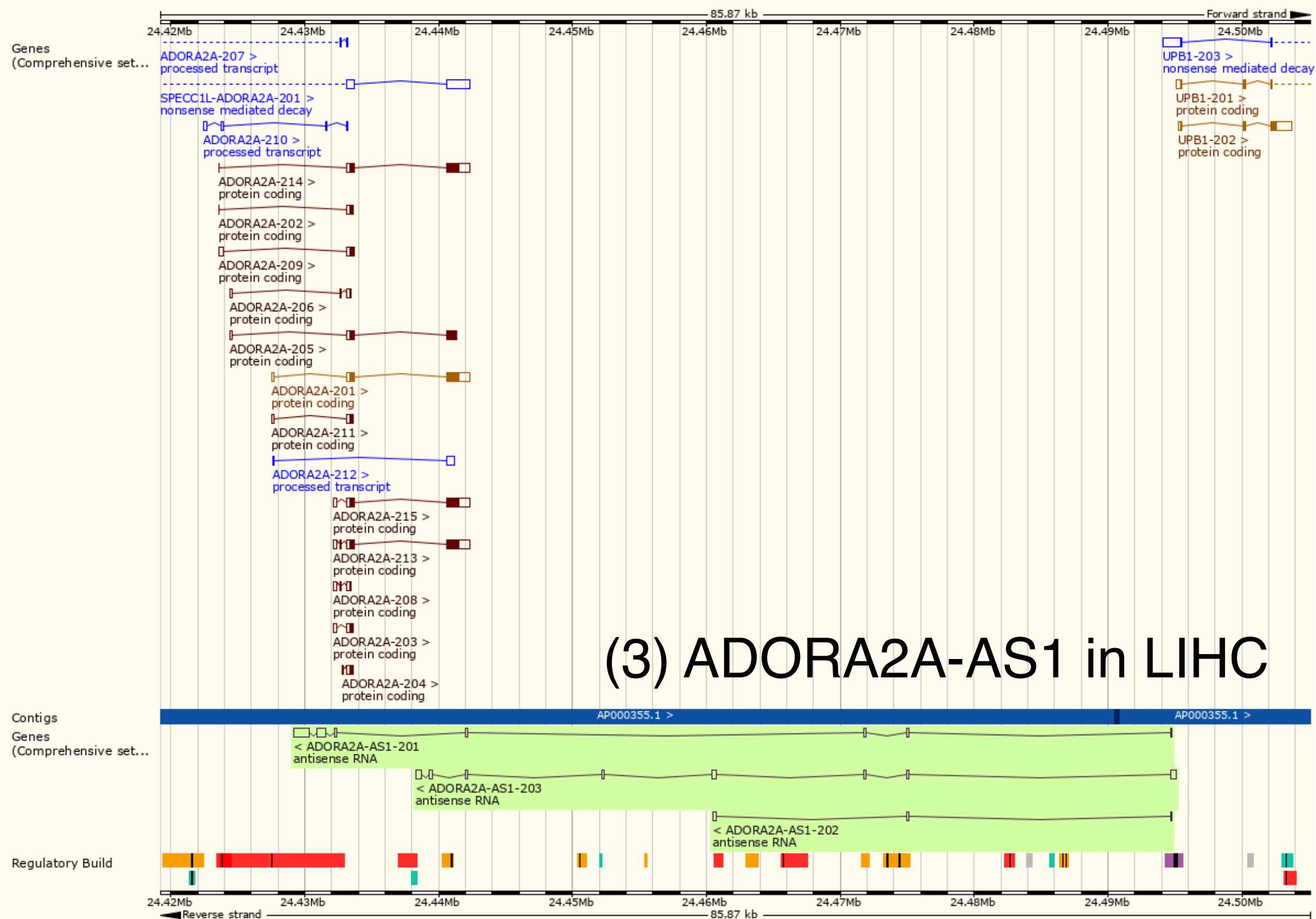
Red = patients with high lncRNA expression
Blue = patients with low lncRNA expression



Significantly co-expressed PCGs

LINC00941 PAAD positively associated pathways





(3) ADORA2A-AS1 in LIHC

Gene Legend

Protein Coding

- Ensembl protein coding
- merged Ensembl/Havana

Non-Protein Coding

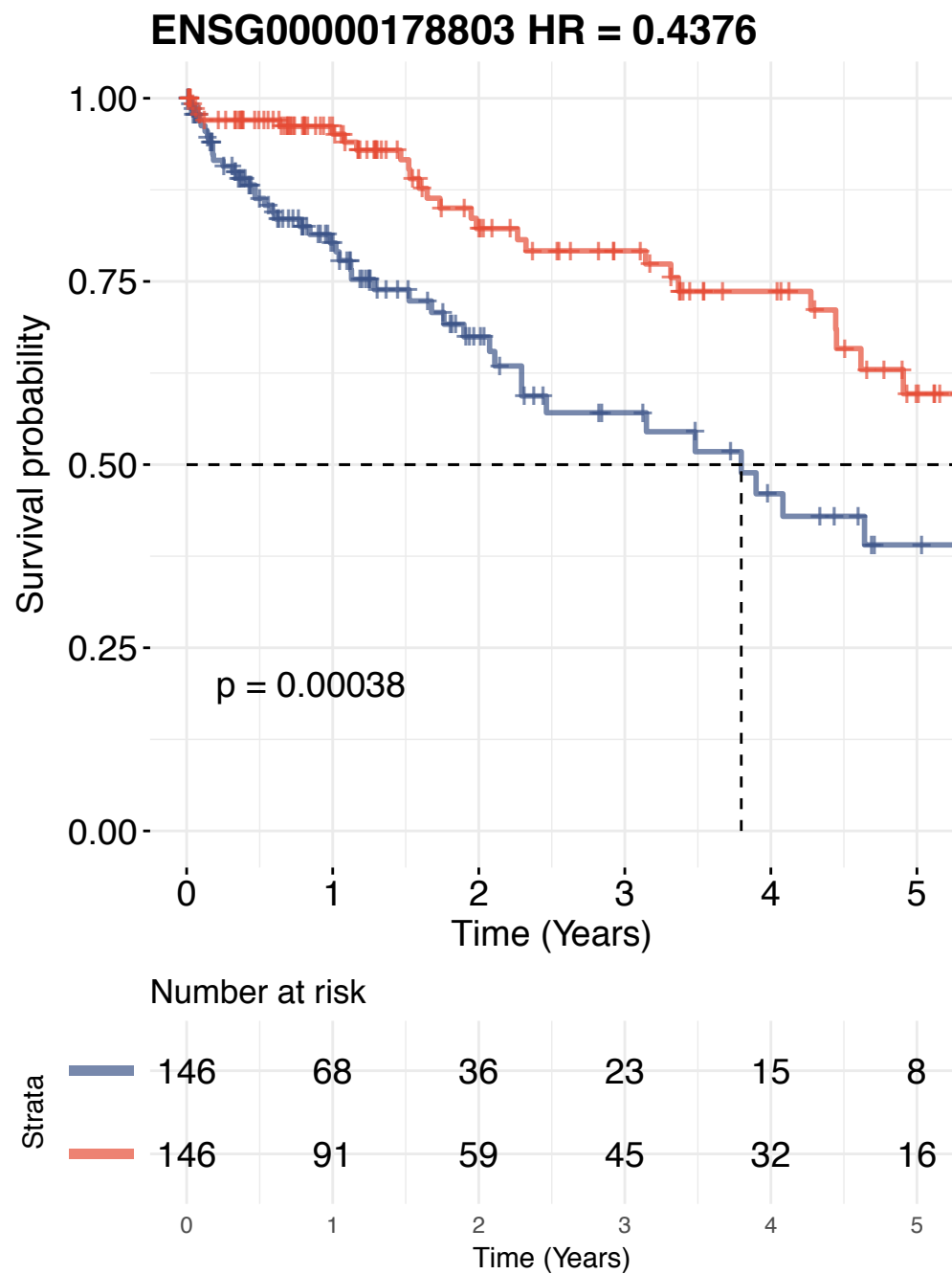
- RNA gene
- processed transcript

Regulation Legend

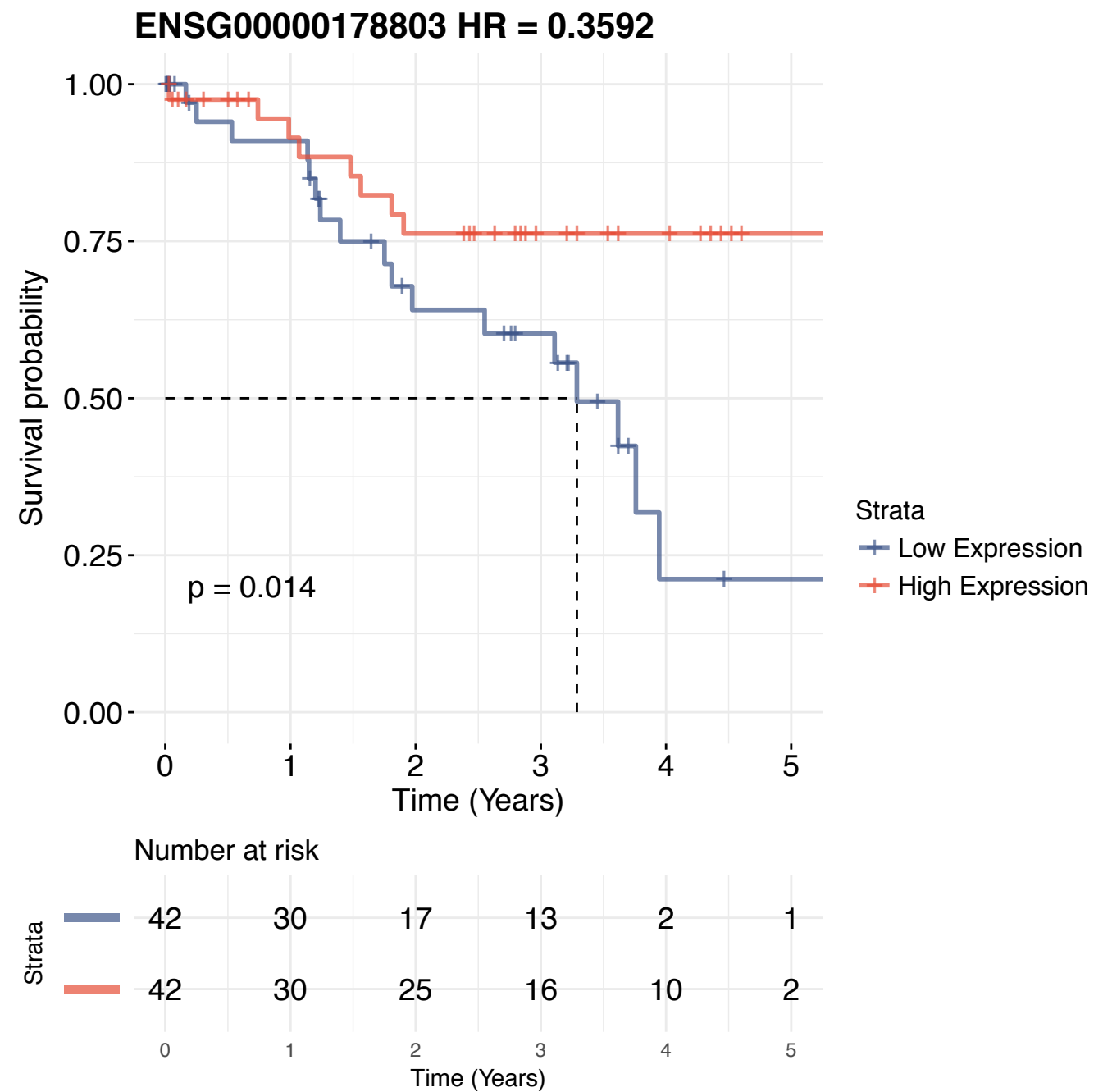
- CTCF
- Open Chromatin
- Promoter Flank
- Motif feature

- Enhancer
- Promoter
- Transcription Factor Binding Site

(3) ADORA2A-AS1 in LIHC



TCGA

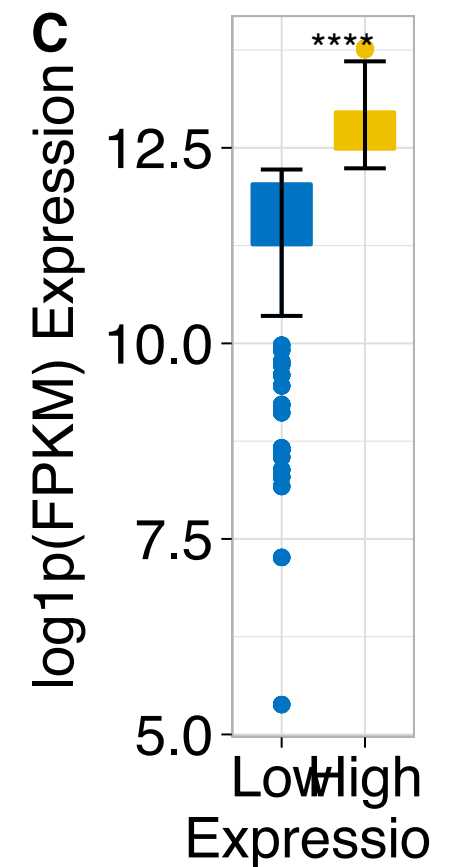
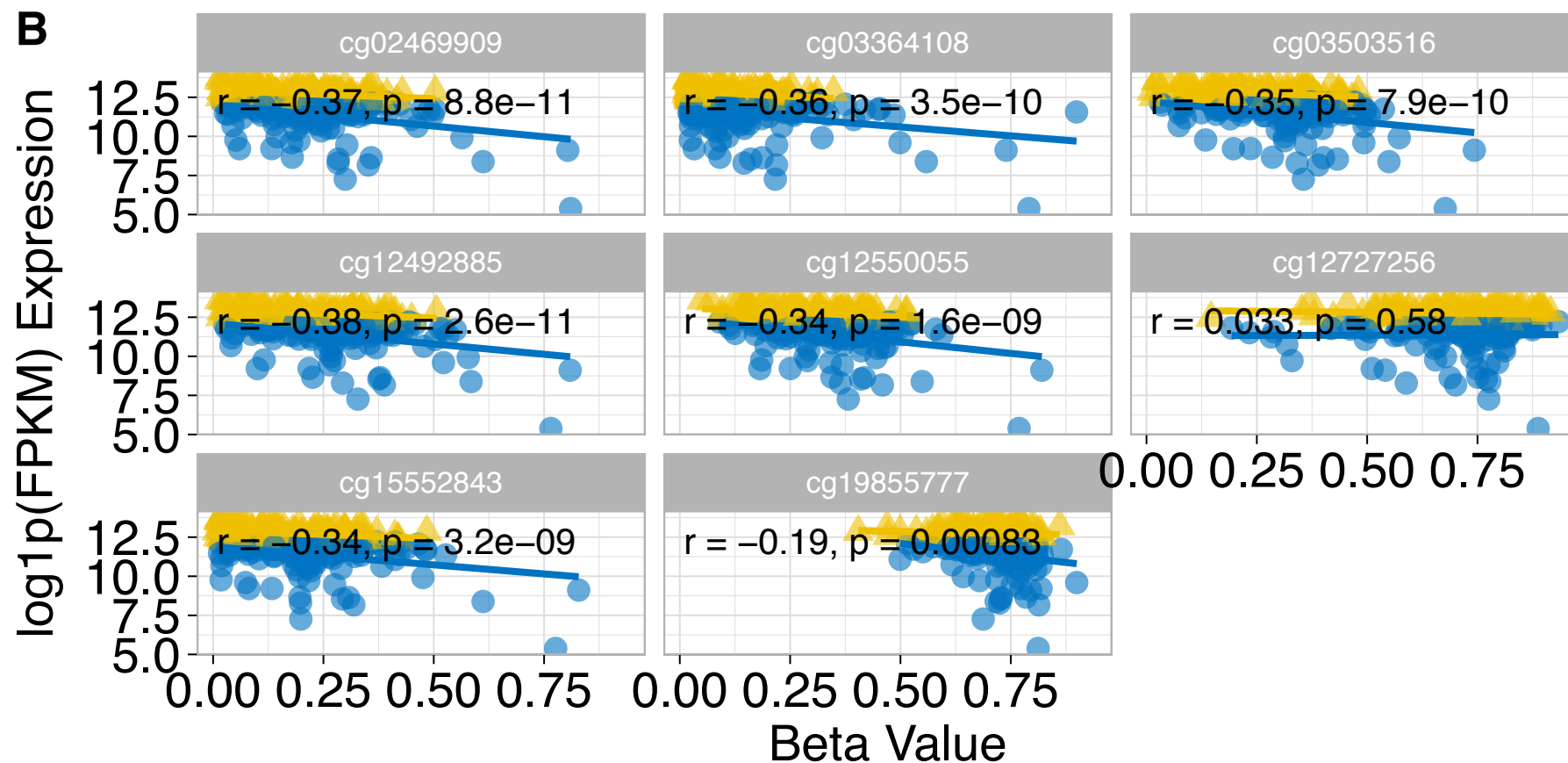
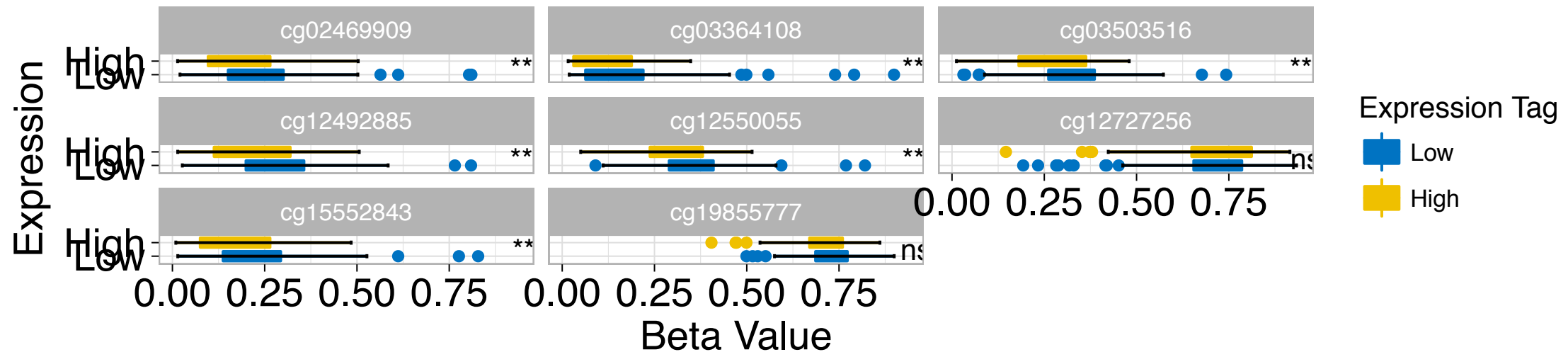


PCAWG

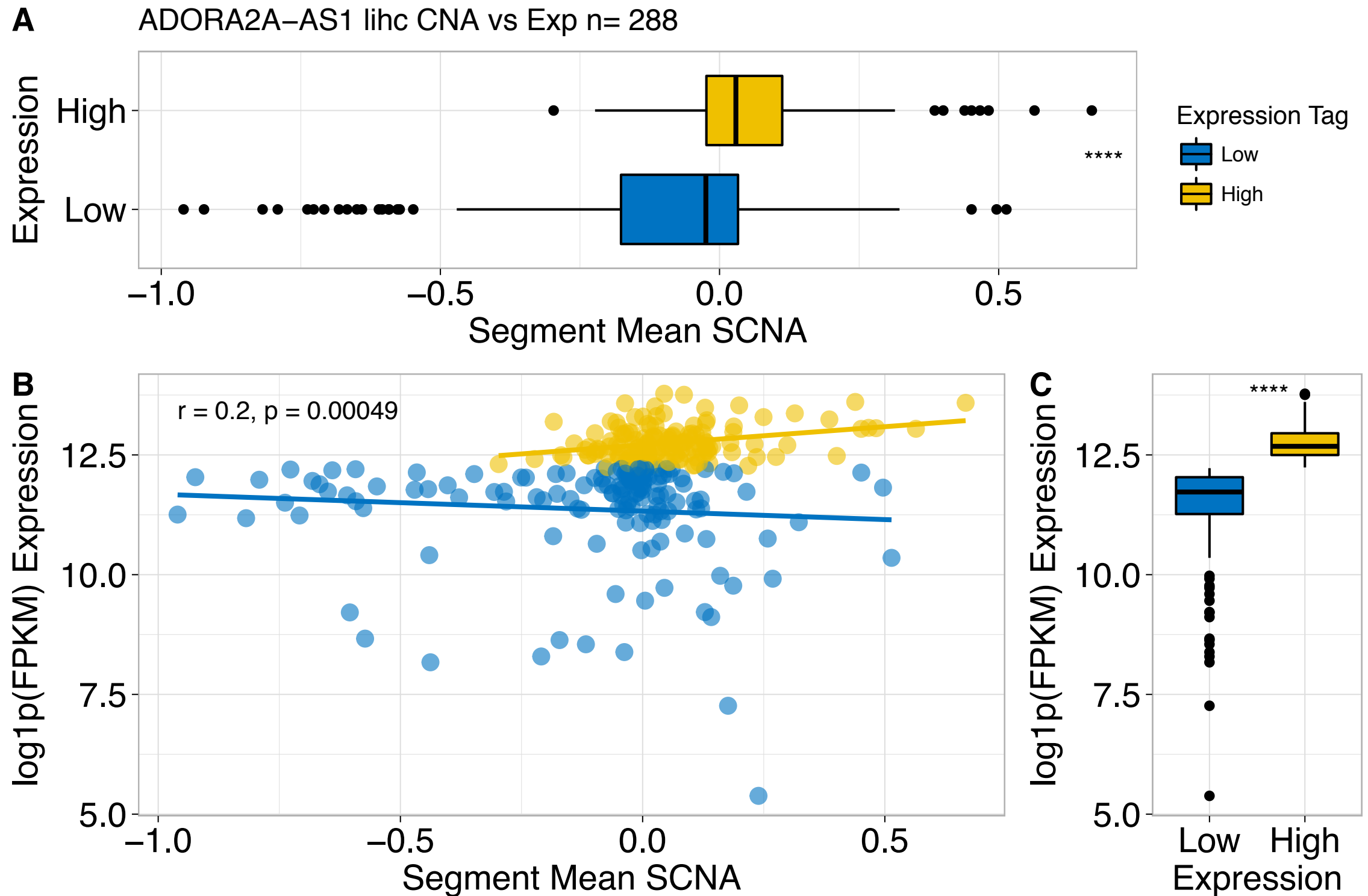
(3) ADORA2A-AS1 in LIHC

- Patients with low expression also have higher methylation of probes overlapping the lncRNA

A ADORA2A-AS1 lihc Methylation vs Exp n= 292

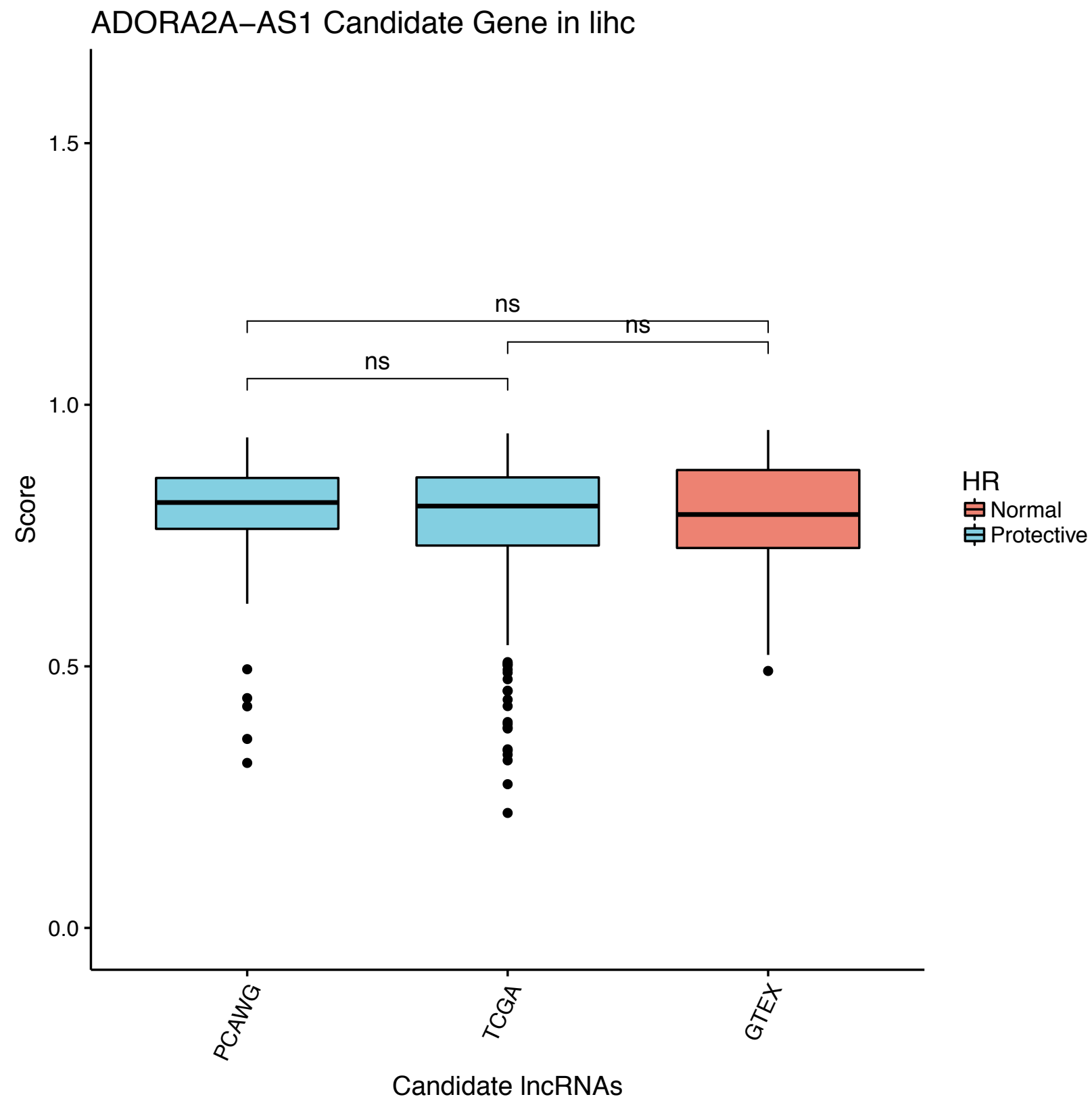


(3) ADORA2A-AS1 in LIHC

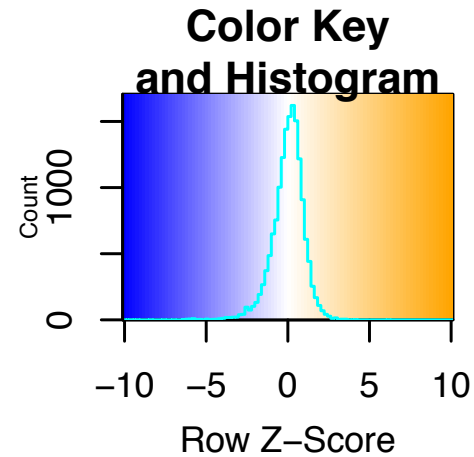


- Patients with low expression also have more copy number deletions

(3) ADORA2A-AS1 in LIHC

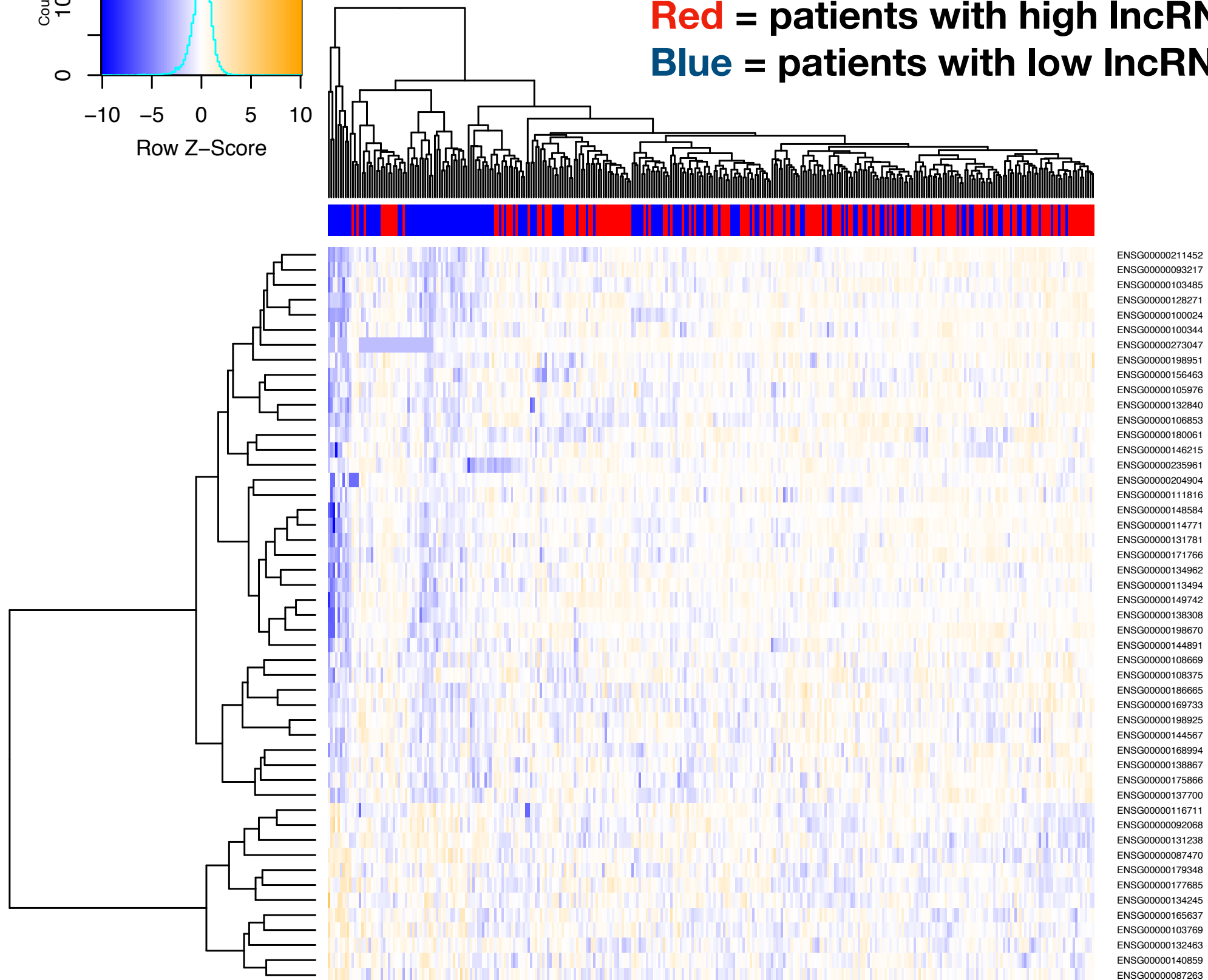


(3) ADORA2A-AS1 in LIHC



ENSG00000178803 Liver hepatocellular carcinoma

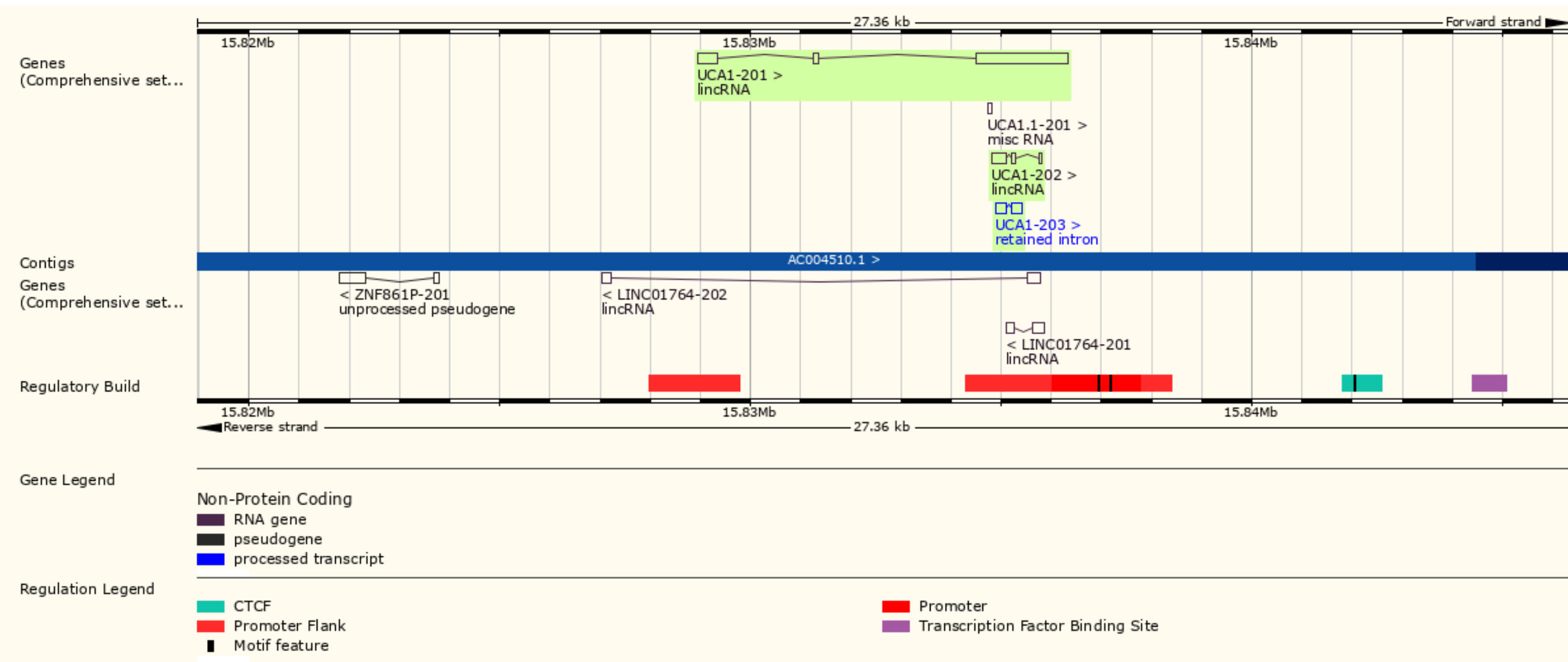
Red = patients with high lncRNA expression
Blue = patients with low lncRNA expression



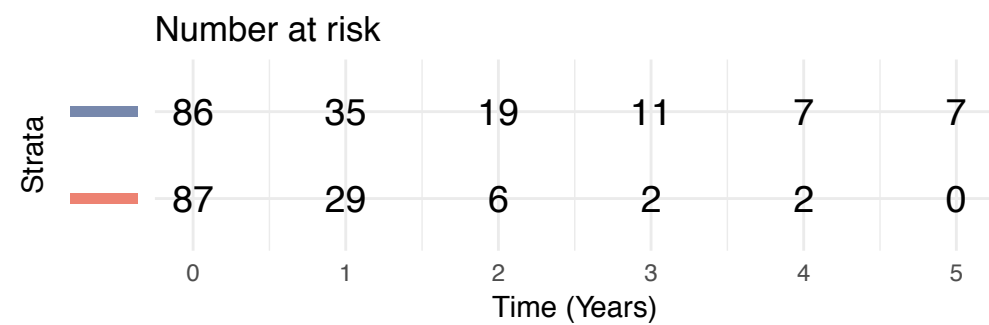
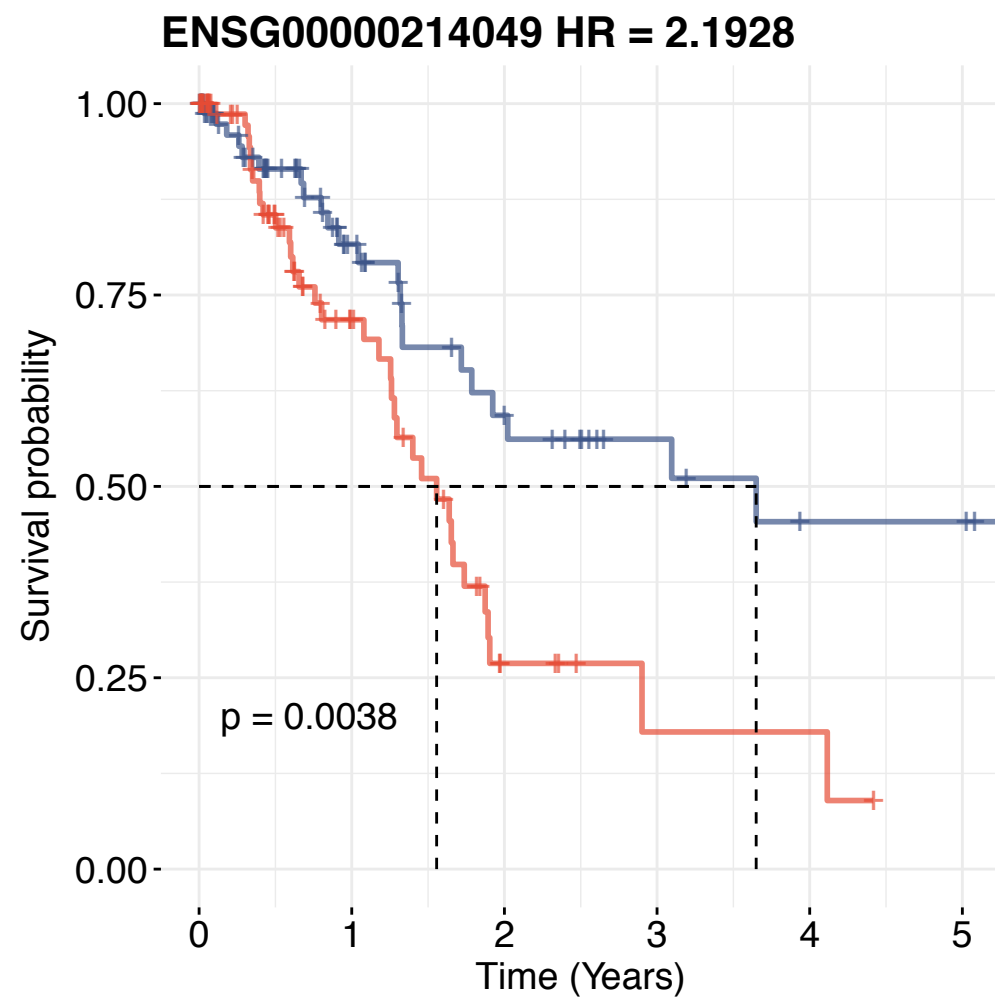
Significantly co-expressed PCGs

(4) UCA1 PAAD

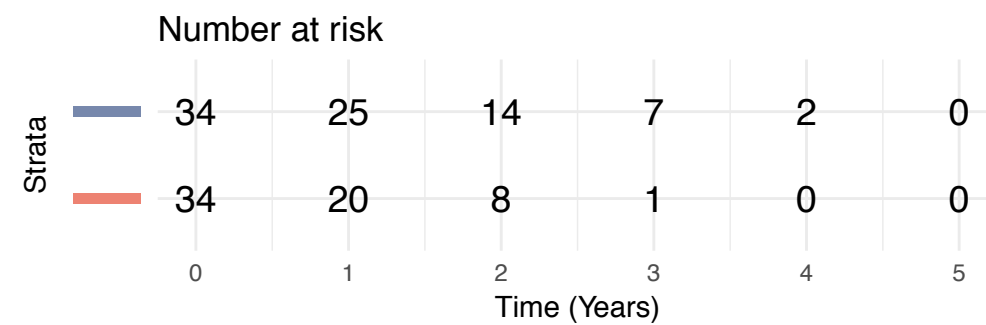
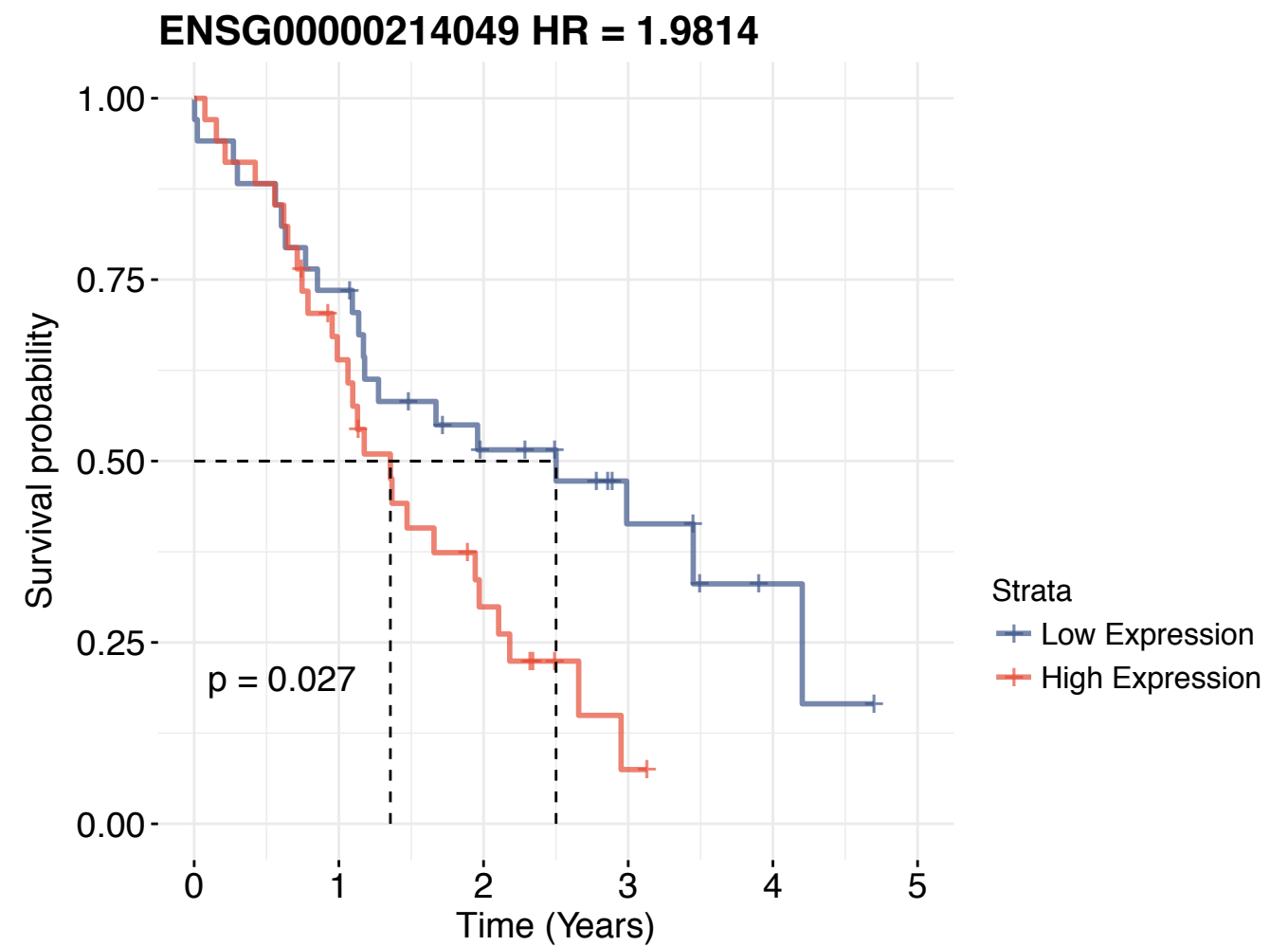
- Intergenic lncRNA overlapping promoter region



(4) UCA1 PAAD



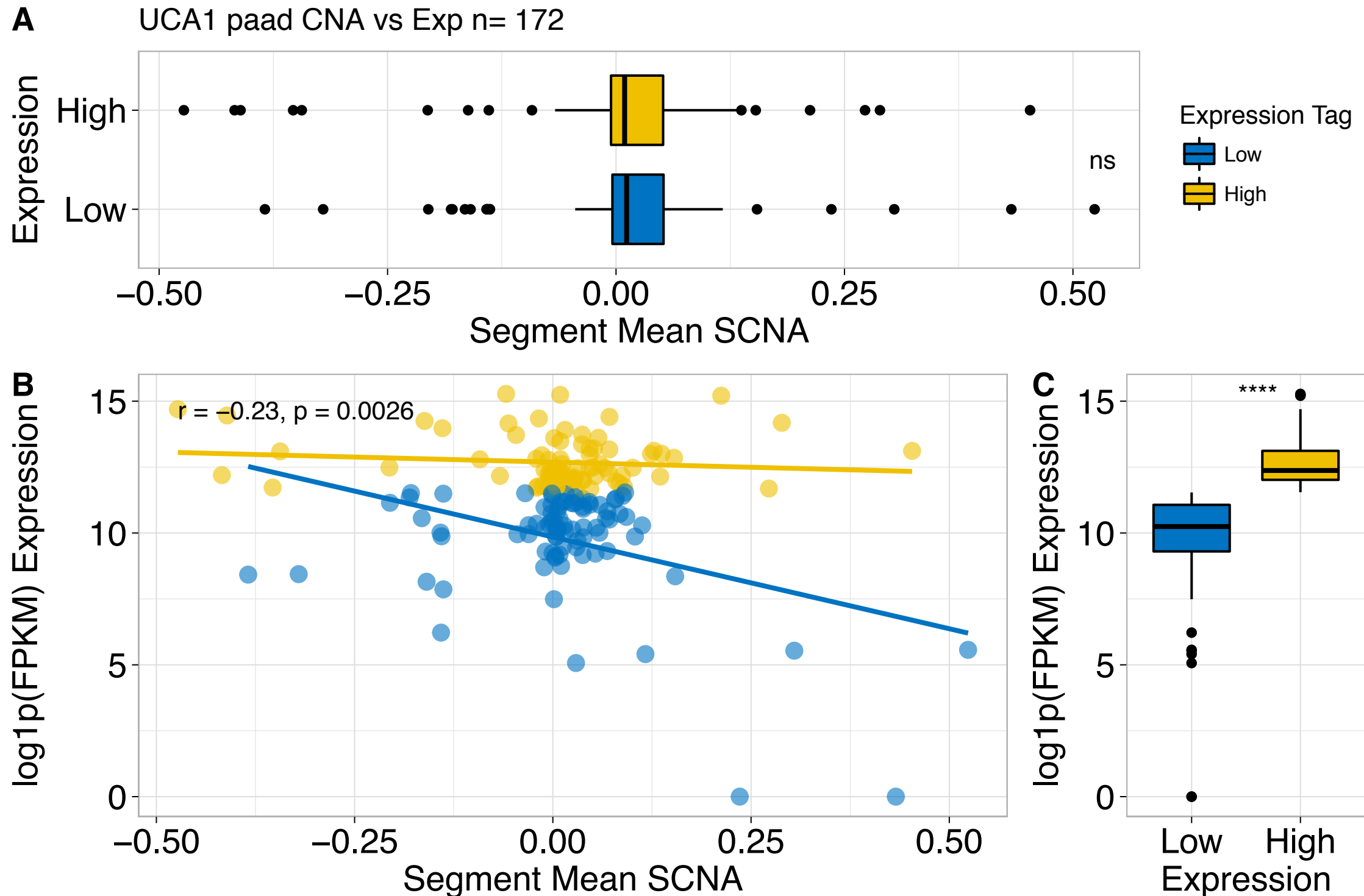
TCGA



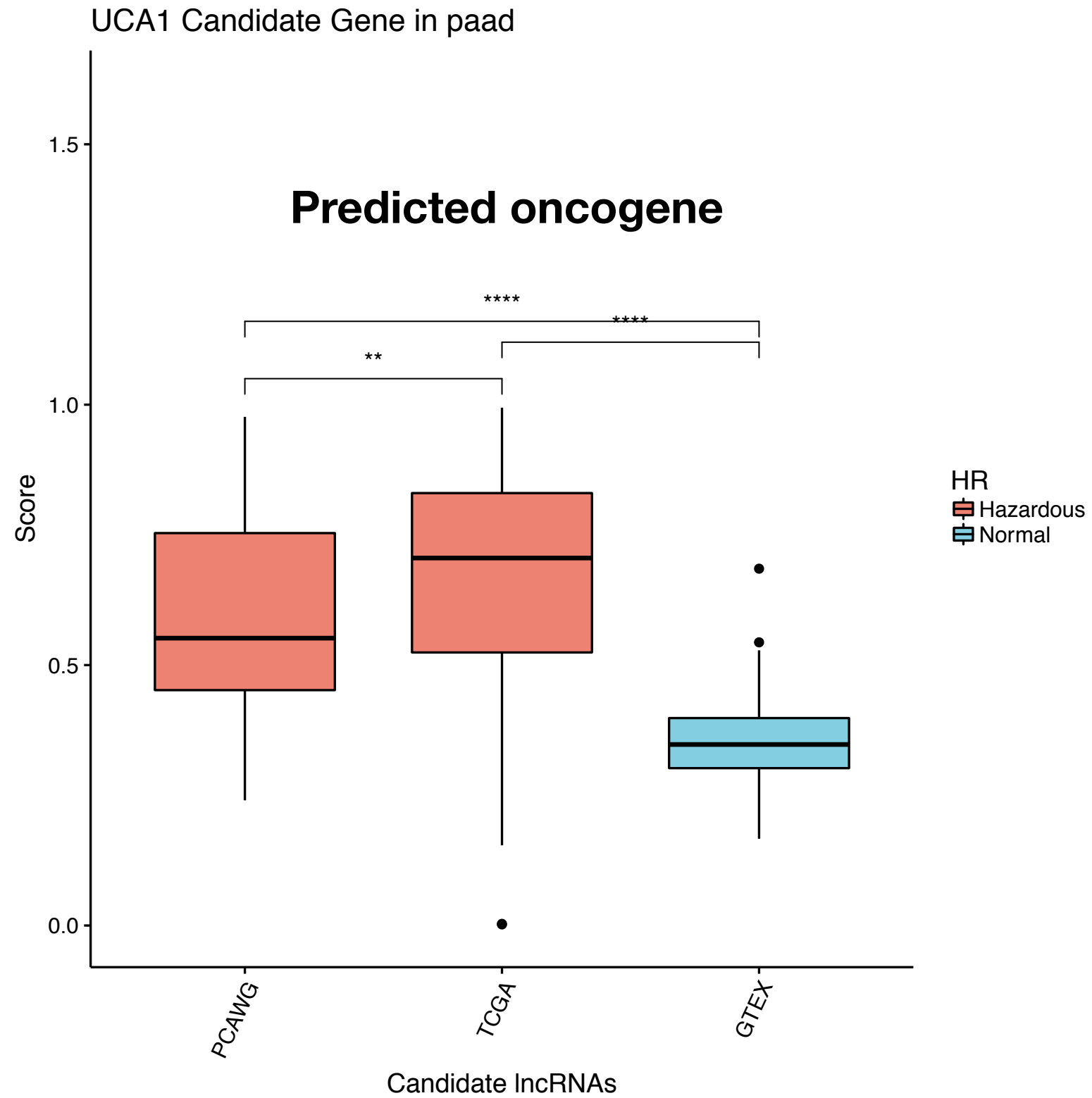
PCAWG

UCA1 PAAD

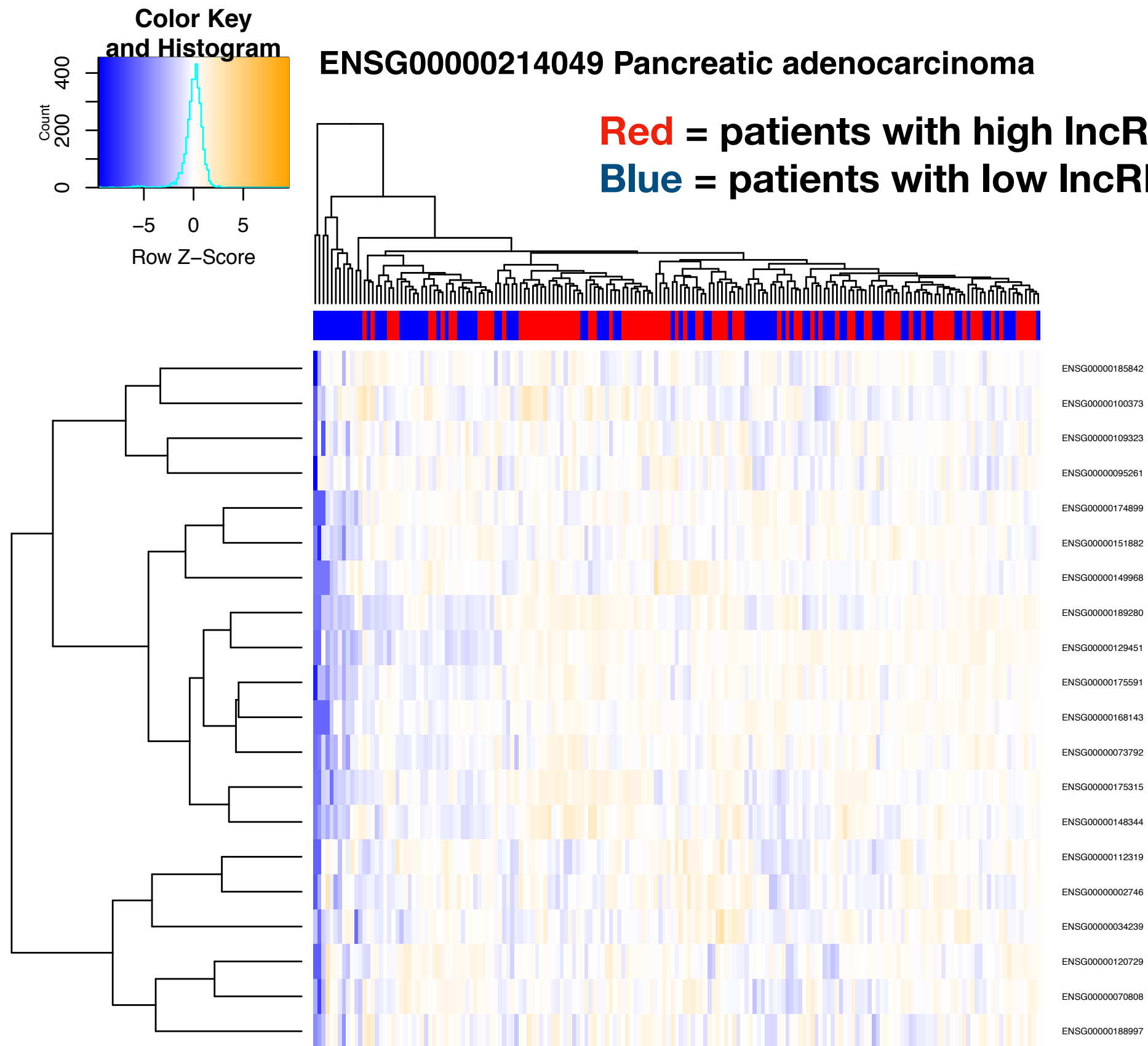
- Too little methylation data, no significant difference in copy number aberrations between low and high expressing patients



UCA1 PAAD

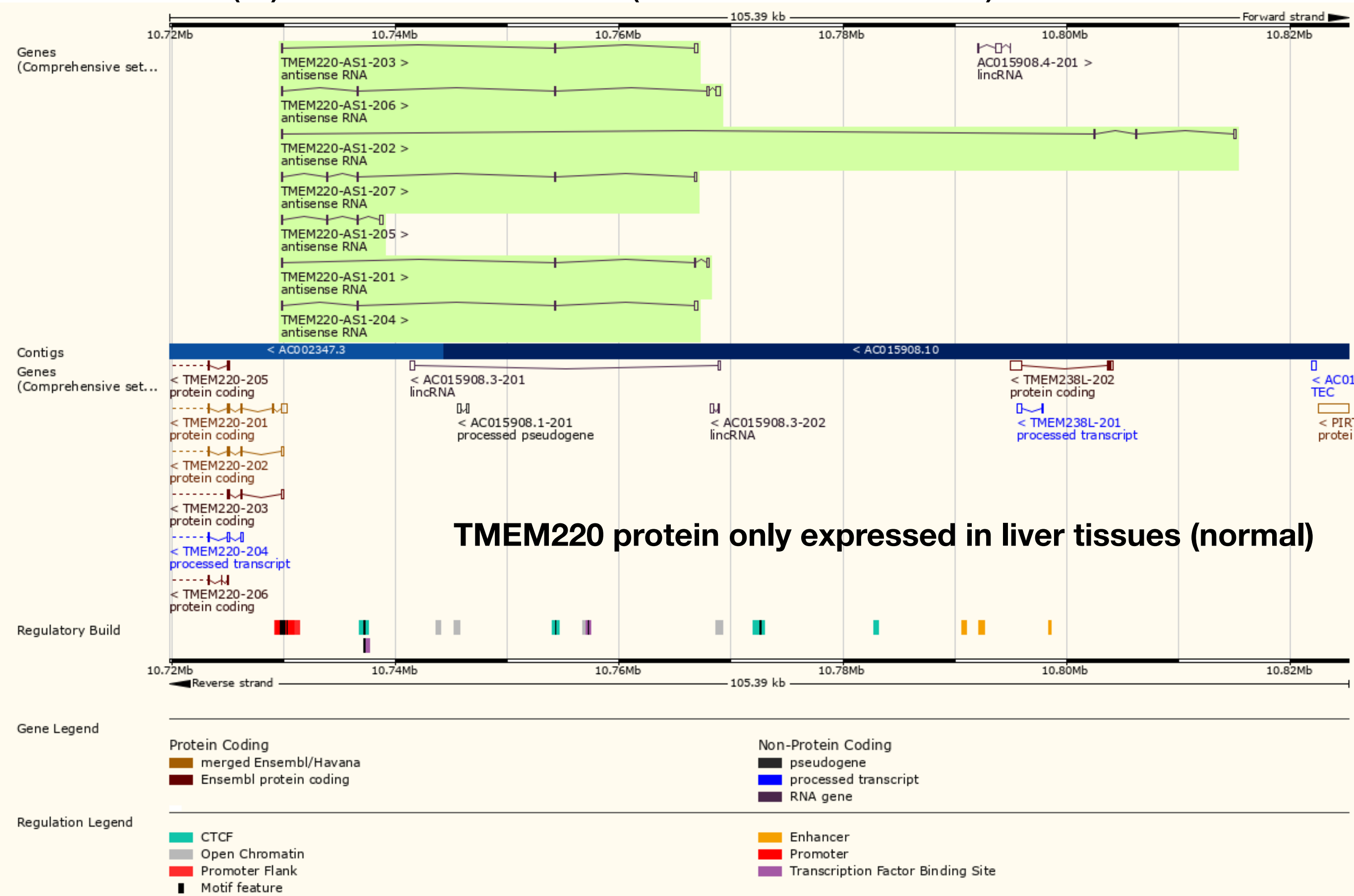


UCA1 PAAD

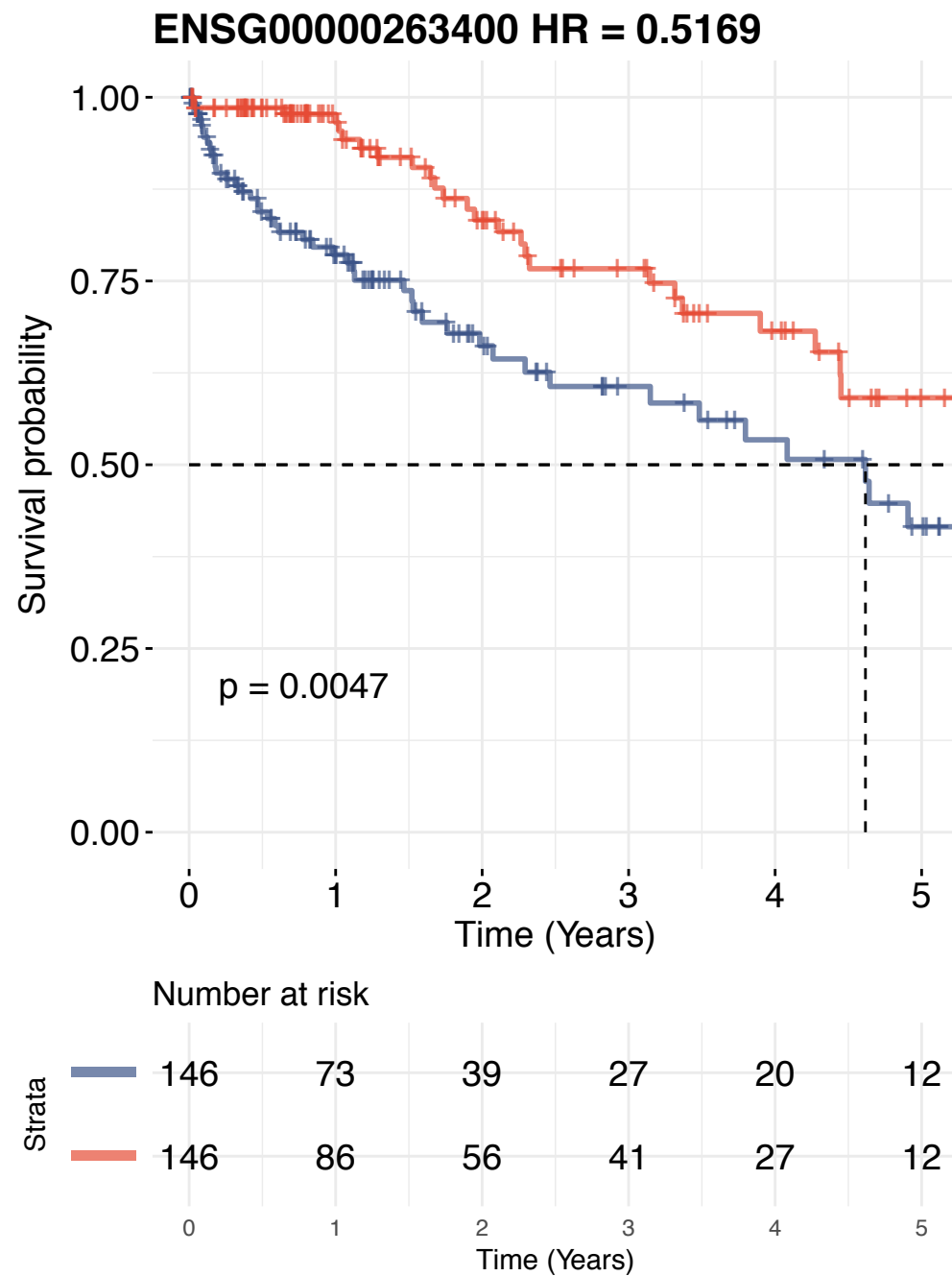


Significantly co-expressed PCGs

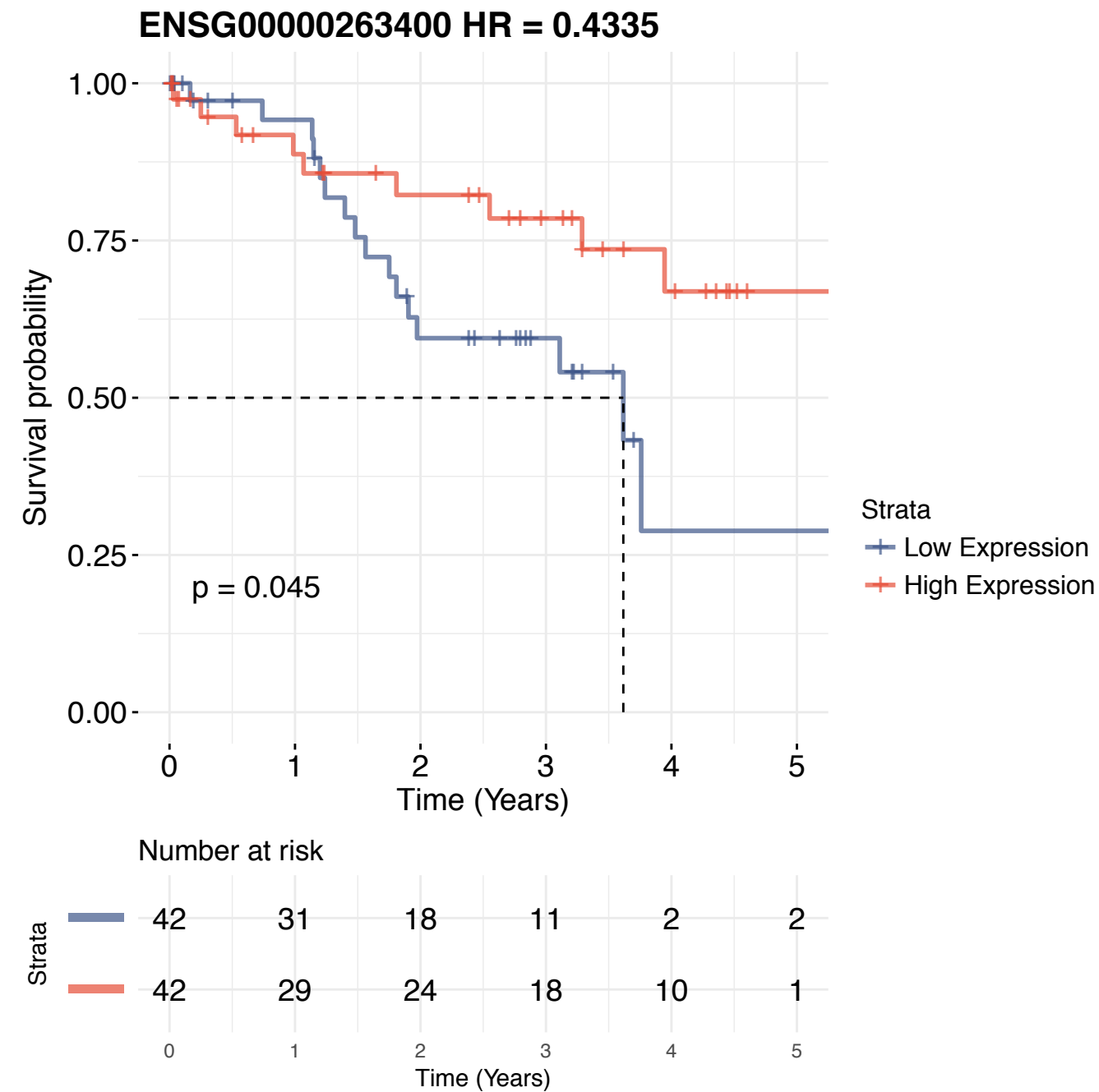
(5) CTC-297N7.5 (TMEM220-AS1) LIHC



(5) CTC-297N7.5 (TMEM220-AS1) LIHC



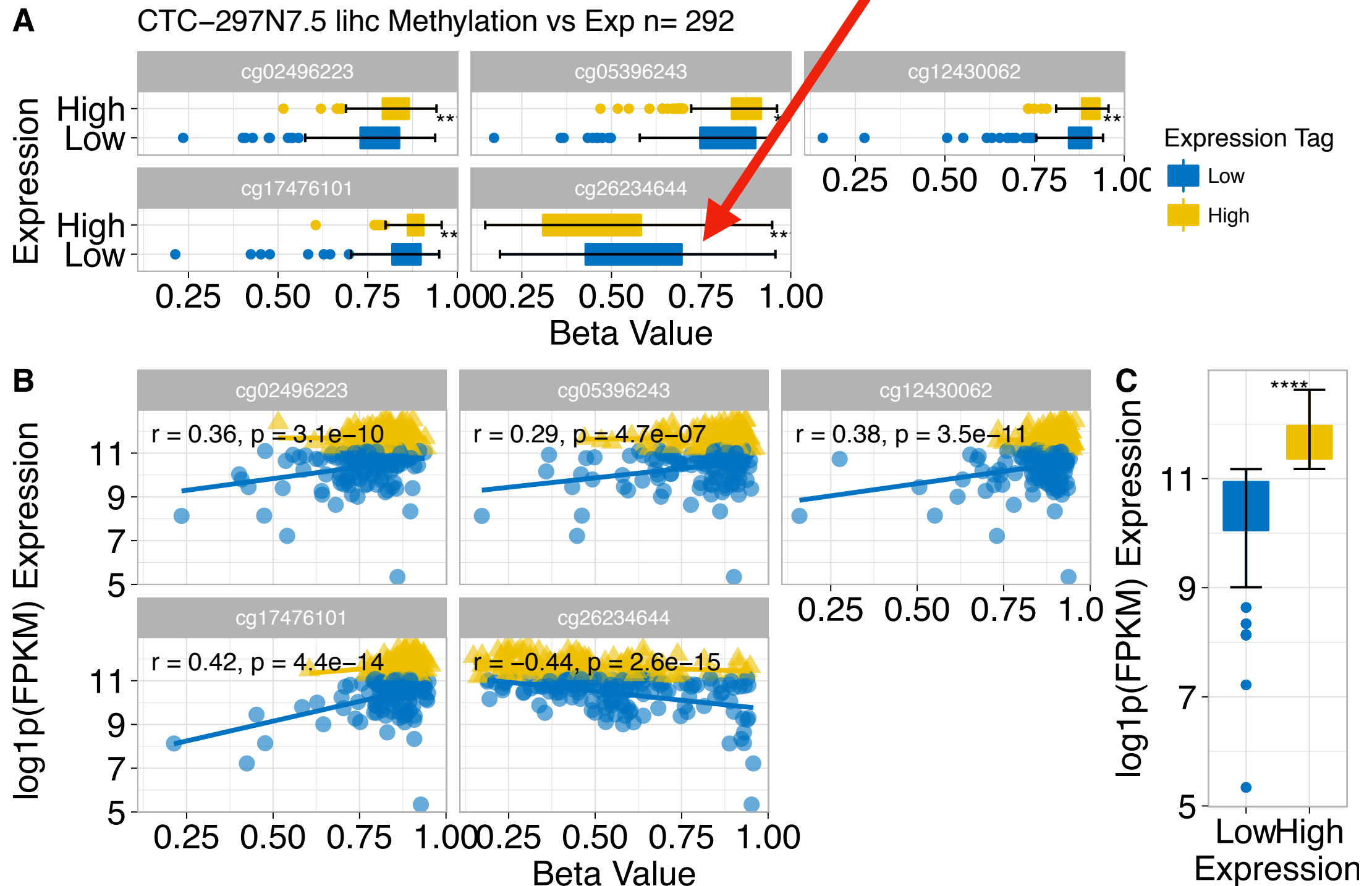
TCGA



PCAWG

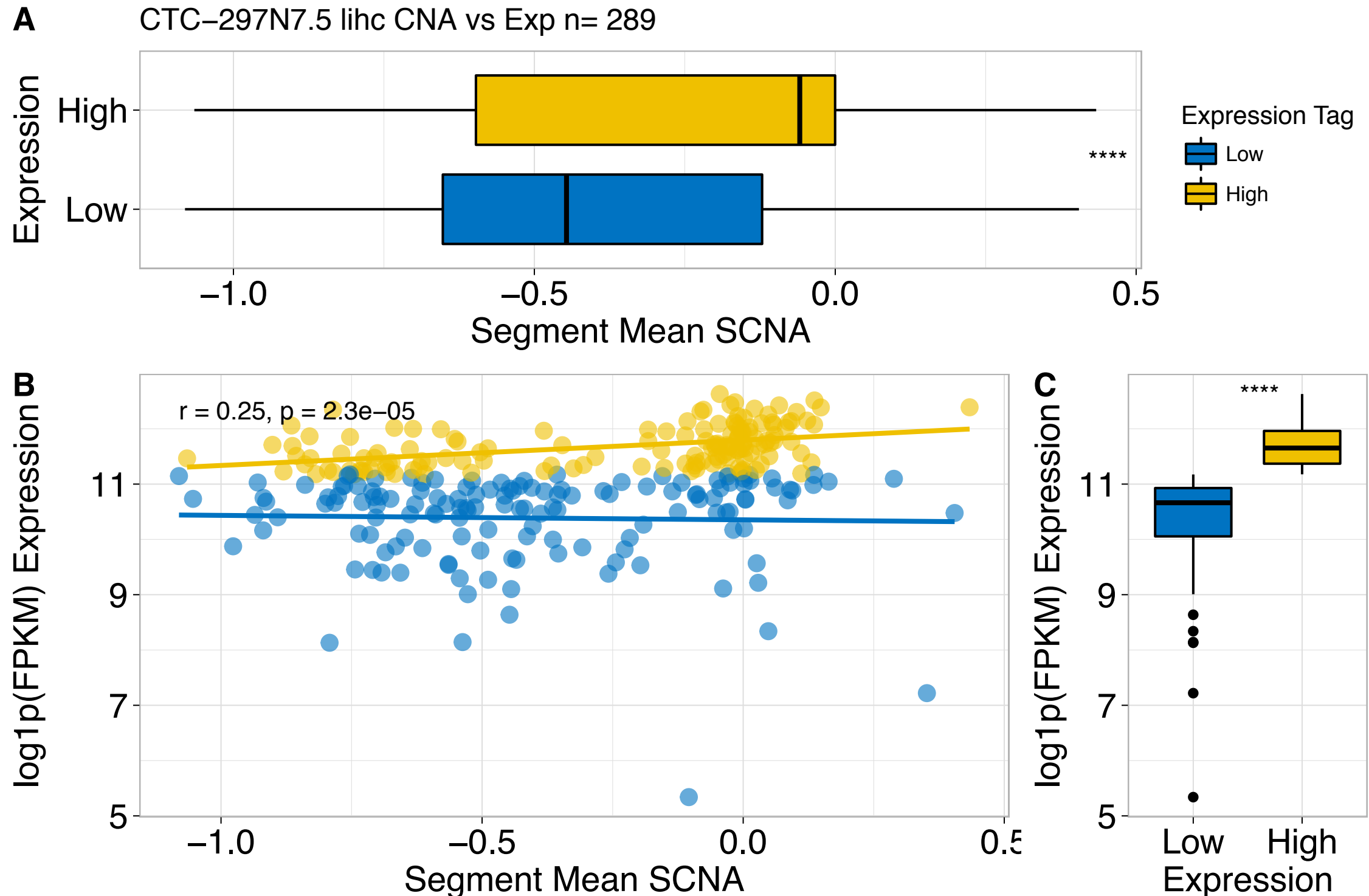
(5) CTC-297N7.5 (TMEM220-AS1) LIHC

- Patients with high expression also have higher methylation of probes overlapping the lncRNA except for probe cg26234644

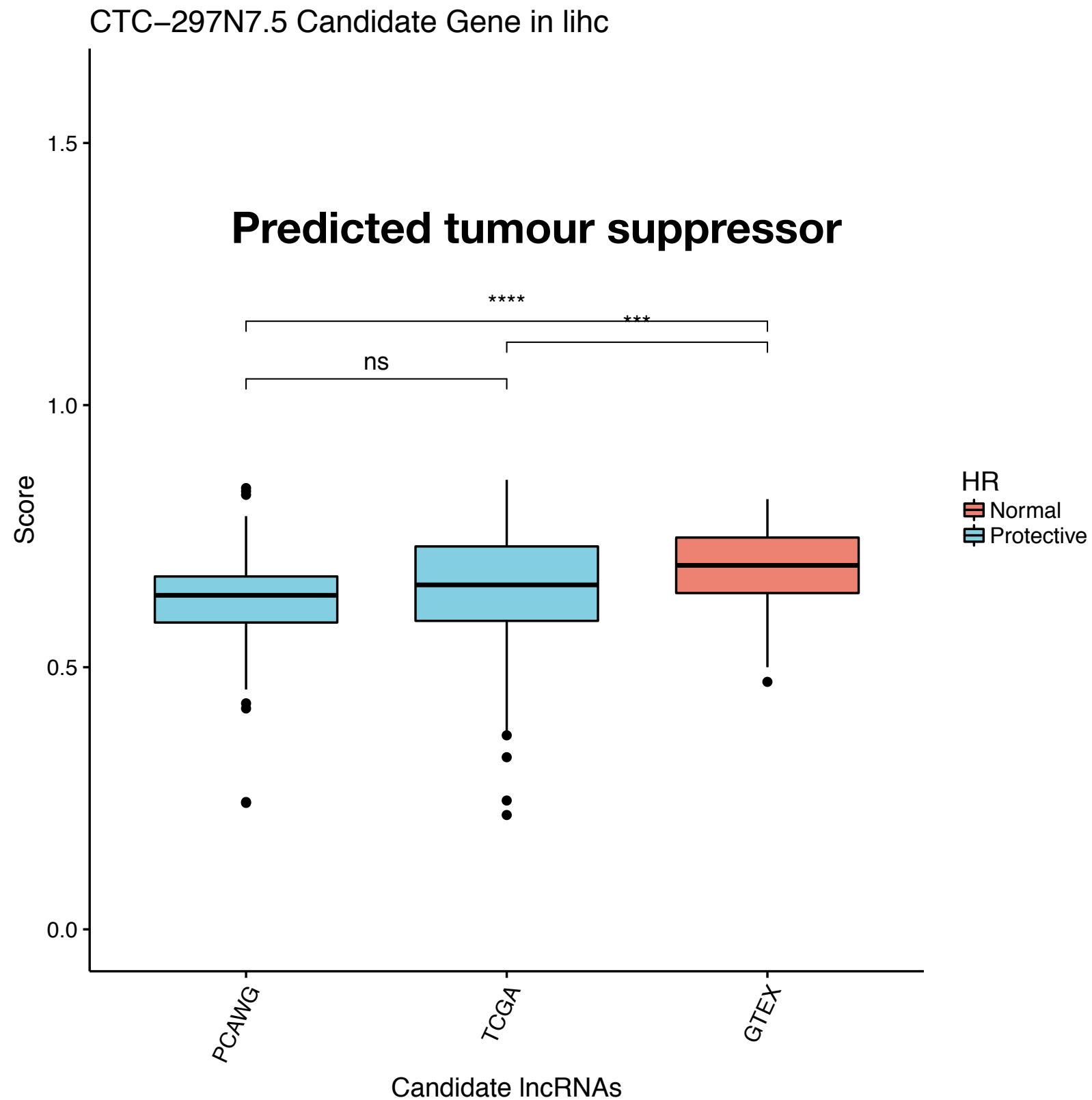


(5) CTC-297N7.5 (TMEM220-AS1) LIHC

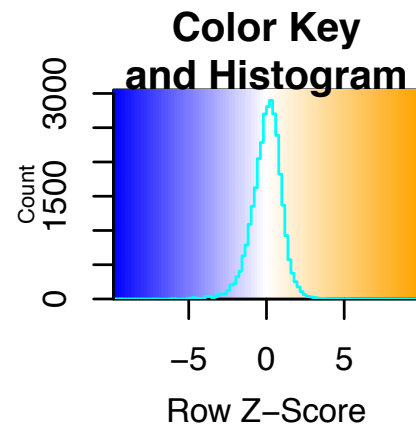
- Patients with low expression also have more copy number deletions of region



(5) CTC-297N7.5 (TMEM220-AS1) LIHC

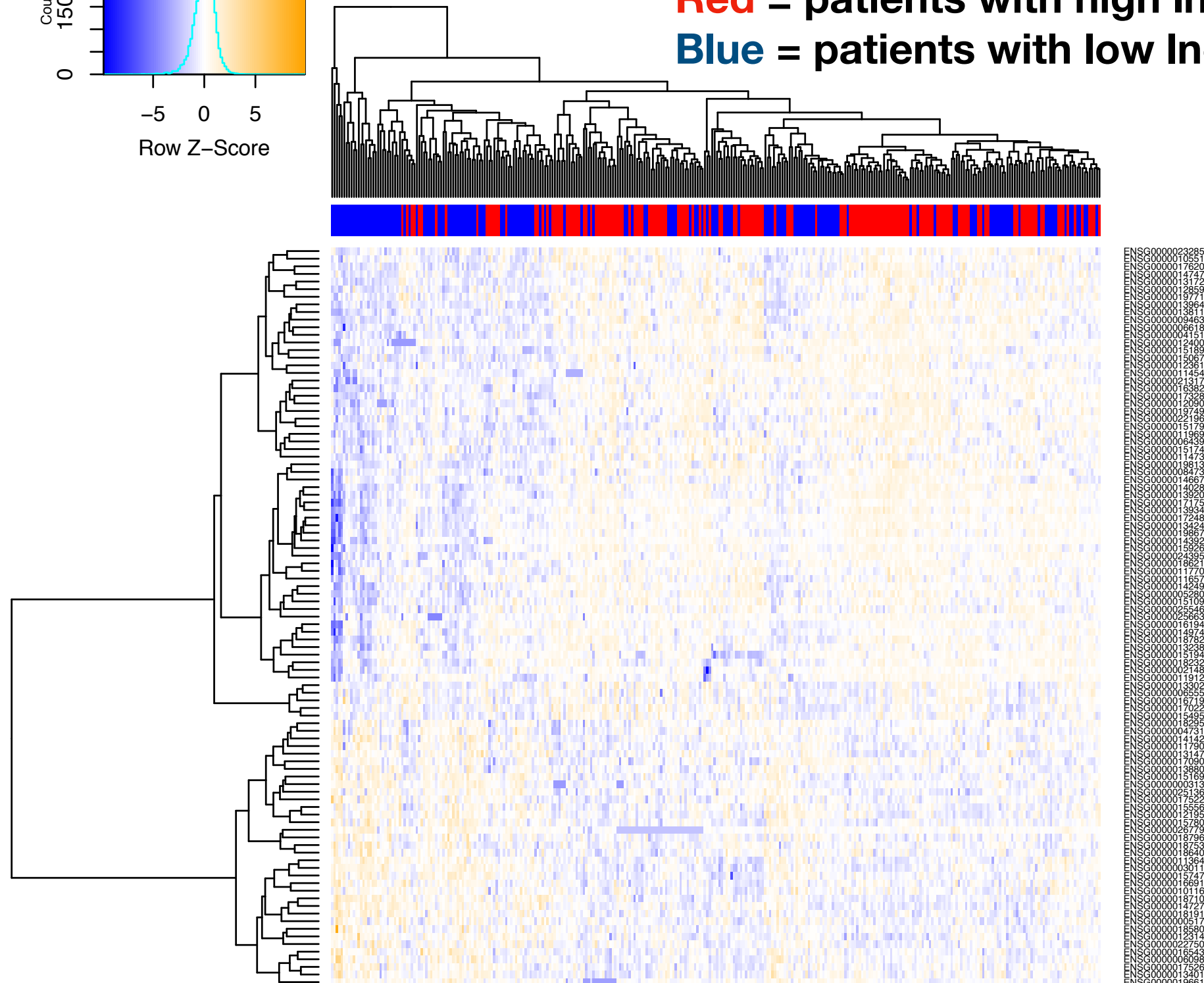


(5) CTC-297N7.5 (TMEM220-AS1) LIHC



NSG00000263400 Liver hepatocellular carcinoma

Red = patients with high lncRNA expression
Blue = patients with low lncRNA expression



Significantly co-expressed PCGs

(5) CTC-297N7.5 (TMEM220-AS1) LIHC

**Identification of four prognostic LncRNAs for survival prediction of patients with hepatocellular carcinoma.
Peer J. 2017**

Four lncRNAs (*RP11-322E11.5*, *RP11-150O12.3*, *AC093609.1*, ***CTC-297N7.9***) were found to be significantly and independently associated with survival of HCC patients.

Chromosome bands

67 way GERP
elements
Human cDNAs
(RefSeq/ENA)
Genes
(Comprehensive set...)

Contigs
Genes
(Comprehensive set...)

CCDS set

Human cDNAs
(RefSeq/ENA)

1KG All SNPs/indels

All phenotype-assoc...

SV - 1KG 3 - All
Regulatory Build

Age of Base
%GC

Variant Legend

- splice donor variant
- missense variant
- synonymous variant
- 5 prime UTR variant
- non coding transcript exon variant
- upstream gene variant
- intergenic variant
- stop gained
- splice region variant
- coding sequence variant
- 3 prime UTR variant
- intron variant
- regulatory region variant

Structural Variant L...

CNV

Regulation Legend

- CTCF
- Promoter
- Motif feature
- Open Chromatin
- Promoter Flank

Gene Legend

- Protein Coding
 - Ensembl protein coding
 - merged Ensembl/Havana
 - CCDS set
- Non-Protein Coding
 - processed transcript
 - RNA gene

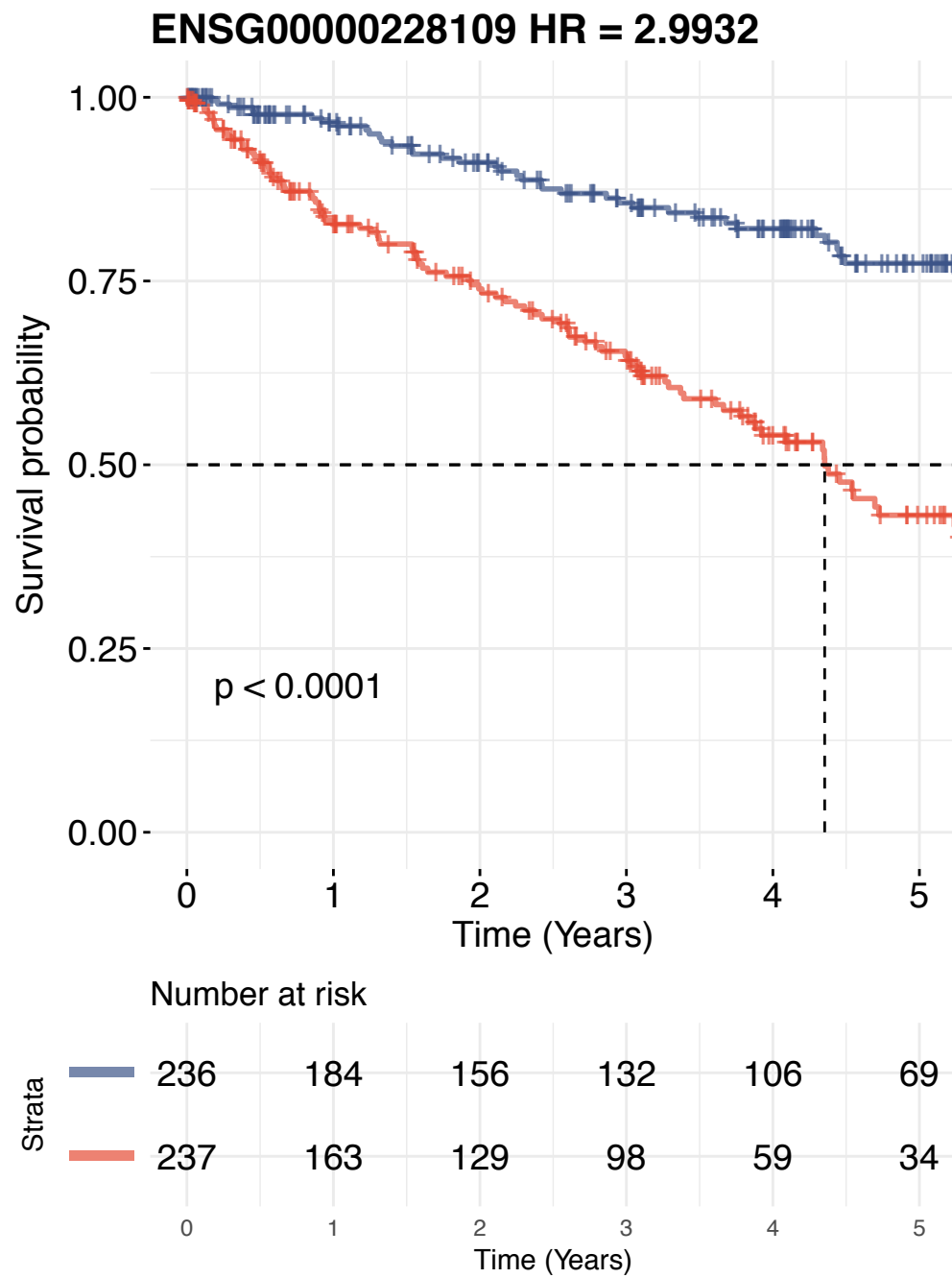
Age of Base Legend

- Human-specific base
- Appeared in mammals (paler = older)
- Appeared in primates (paler = older)

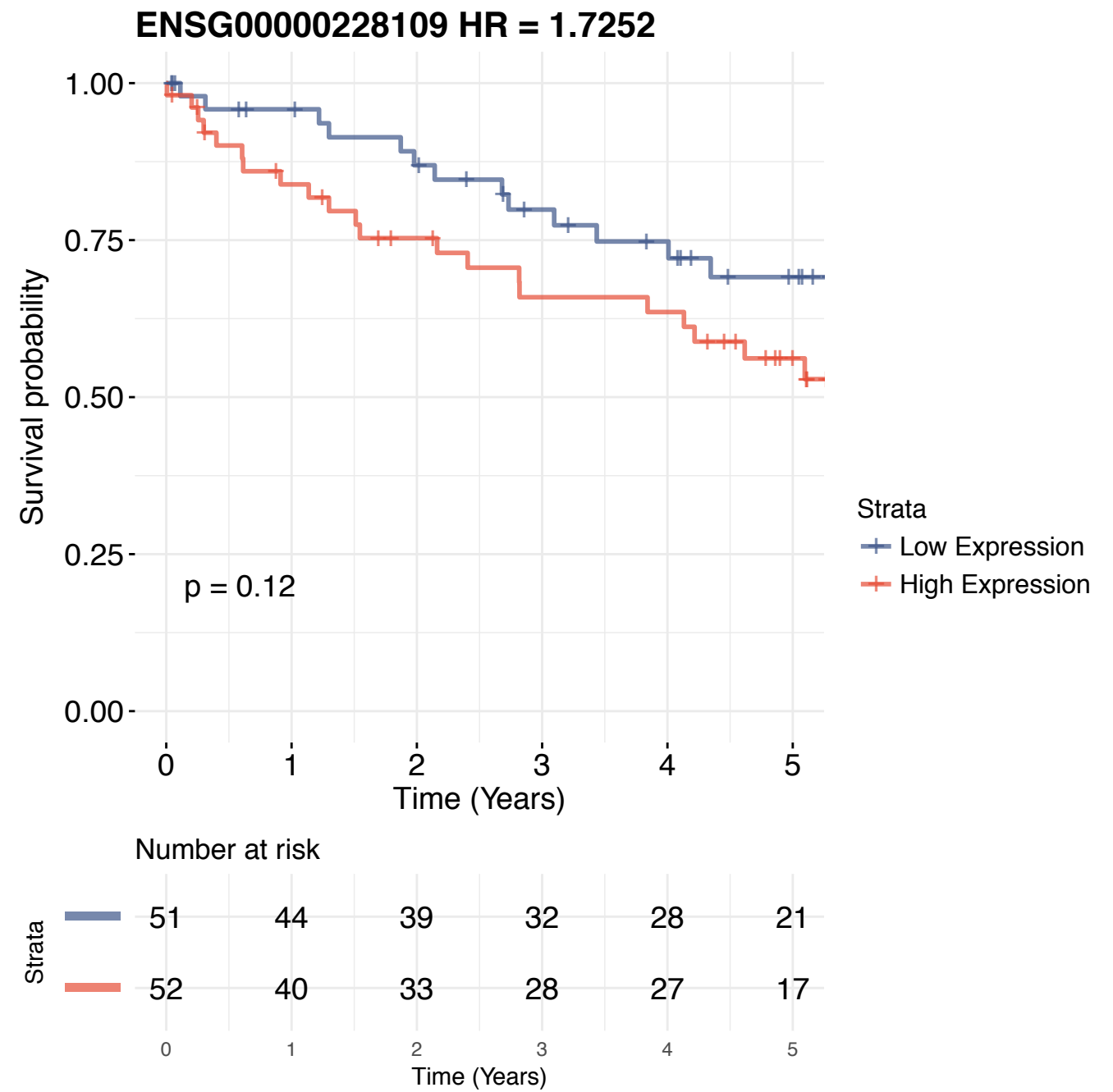
There are currently 604 tracks turned off.
Ensembl Homo sapiens version 91.38 (GRCh38.p10) Chromosome 3: 196,991,283 - 197,035,242

(6) MFI2-AS1 in KIRC

(6) MFI2-AS1 in KIRC



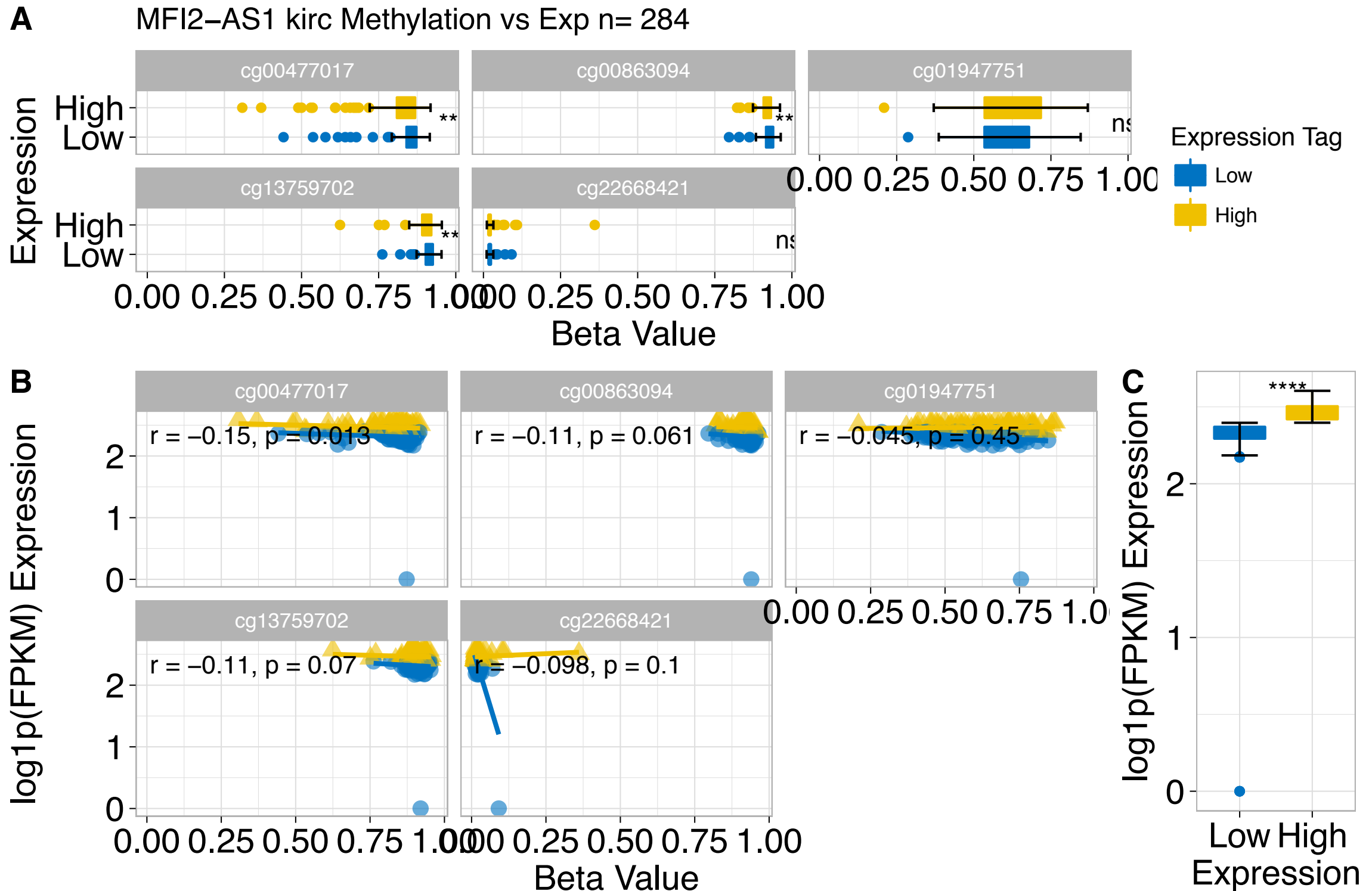
TCGA



PCAWG

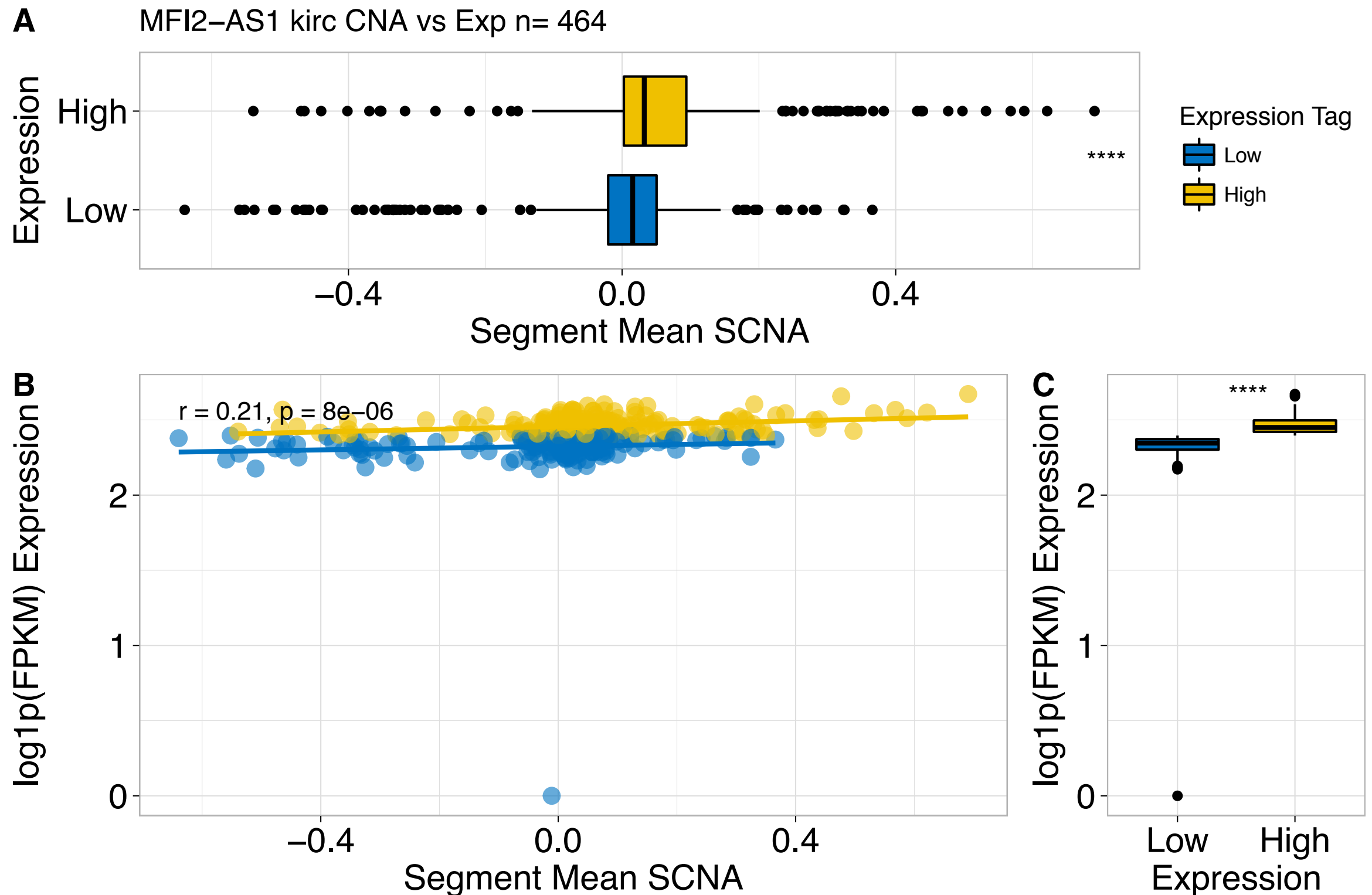
(6) MFI2-AS1 in KIRC

- Patients with low expression also have higher methylation of most probes overlapping gene

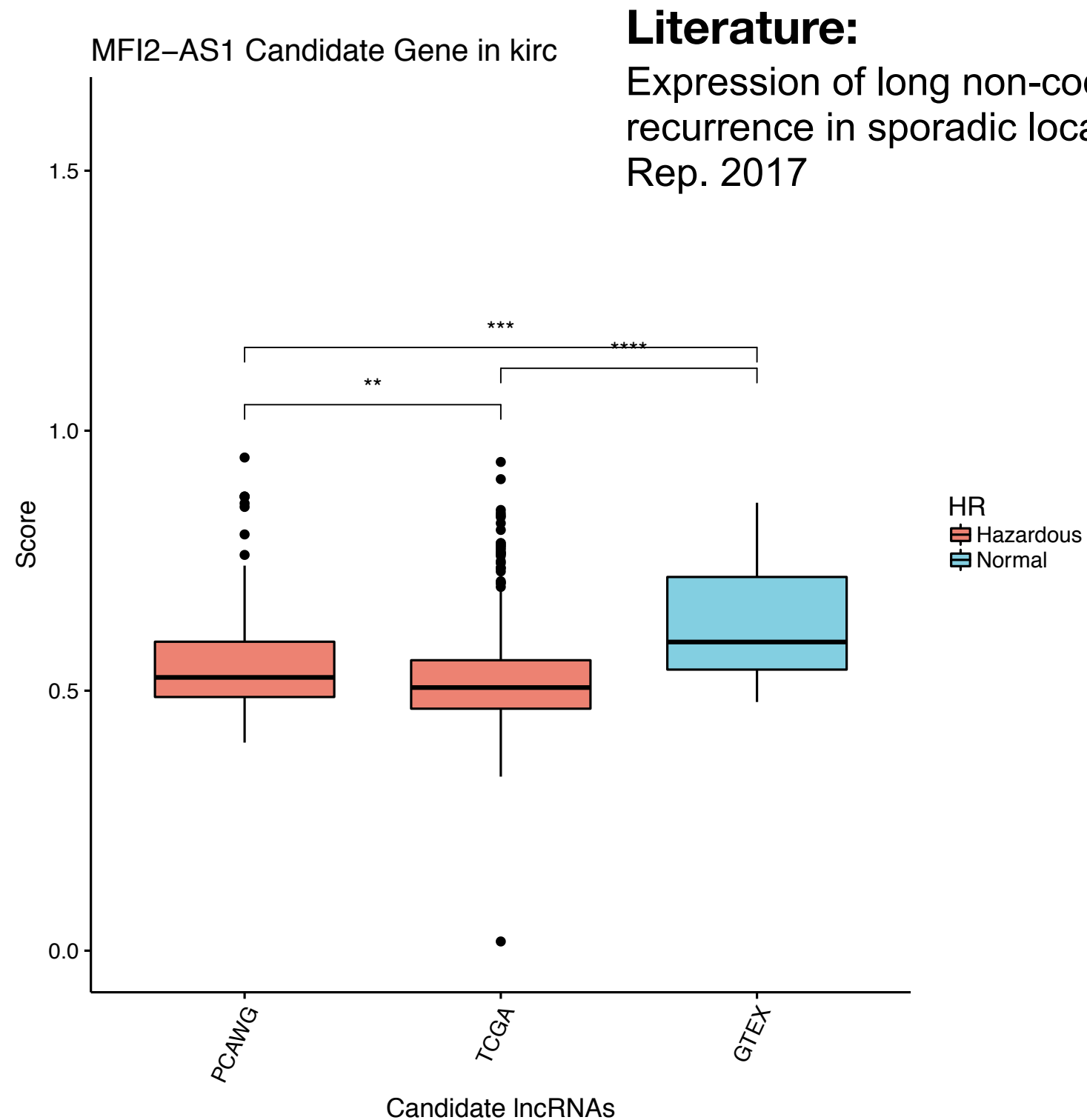


(6) MFI2-AS1 in KIRC

- Patients with high expression also have more copy number amplifications of region



(6) MFI2-AS1 in KIRC



Literature:

Expression of long non-coding RNA ***MFI2-AS1*** is a strong predictor of recurrence in sporadic localized clear-cell renal cell carcinoma. Sci Rep. 2017

Relatively lower expressed compared to GTEx but higher expression in cancer is associated with worse survival outcome

MFI2-AS1 KIRC

