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SHORT COMMUNICATION

Genome-Wide Polyadenylation Maps Reveal Dynamic mRNA 3'-End Formation in the Failing Human Heart

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Running title: Alternative Polyadenylation in Human Hearts

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ABSTRACT

***Rationale*:** Alternative cleavage and polyadenylation (APA) of mRNA represents a layer of gene regulation that to date has remained unexplored in the heart. This phenomenon may be very relevant, as the positioning of the polyA tail in mRNAs influences the length of the 3'UTR, a critical determinant of gene expression.

***Objective*:** To investigate whether the 3'UTR length is regulated by APA in the human heart and whether this changes in the failing heart.

***Methods and Results*:** We used 3'end RNA-sequencing (e3'-Seq) to directly measure global patterns of APA in healthy and failing human heart specimens. By monitoring polyadenylation profiles in these hearts, we identified disease-specific APA signatures in numerous genes. Interestingly, many of the genes with shortened 3'UTRs in heart failure were enriched for functional groups such as 'RNA binding', while genes with longer 3'UTRs were enriched for 'cytoskeletal organization' and 'actin binding'. RNA sequencing in a larger series of human hearts revealed that these APA candidates are often differentially expressed in failing hearts, with an inverse correlation between 3'UTR length and the level of gene expression. Protein levels of the APA regulator, Poly(A)-Binding Protein Nuclear 1 were substantially downregulated in failing hearts.

***Conclusion*:** We provide genome-wide, high-resolution polyadenylation maps of the human heart and show that the 3'end formation of mRNA is dynamic in heart failure, suggesting that APA-mediated 3'UTR length modulation represents an additional layer of gene regulation in failing hearts.

Keywords:
Alternative polyadenylation, 3'UTR, heart failure, gene expression/regulation, human, RNA splicing cardiomyopathy.

Nonstandard Abbreviations and Acronyms:

APA	alternative polyadenylation
CS	cleavage site
DCM	dilated cardiomyopathy
PAS	polyadenylation signal
e3'-Seq	enhanced 3'end RNA-sequencing
3'-UTR	3'-untranslated region

INTRODUCTION

The poly(A)tail is found at the 3'-end of fully processed eukaryotic mRNAs and is crucial for mRNA stability and transport of mRNA from the nucleus to the cytoplasm. This poly(A)tail of about 200 adenosines is added by a tightly-coupled two-step process of mRNA cleavage and polyadenylation and is carried out by a surprisingly large multi-protein complex, which in humans constitutes of ~85 proteins[1]. It was recently discovered that about half of the human genes generate alternative mRNA isoforms that differ in length of their 3'UTR due to a process called alternative cleavage and polyadenylation (APA)[2]. Given the role of the 3'UTR in mRNA stability, shortening of the 3'UTR by APA may have a profound impact on gene expression. In fact, it has been shown that shorter mRNA isoforms of specific genes can produce ten-fold more protein, partly by escaping miRNA-mediated repression[3]. Although APA has already been described 30 years ago, the implementation of deep-sequencing techniques allowed only recently to better appreciate the extent of APA. The first transcriptome-wide studies on APA reported that proliferative cells (e.g. cancer cells) globally shift towards shorter mRNA isoforms, while differentiating cells generally lengthen their 3'UTR[3, 4]. The biological consequence of specific APA events was reported in cancer cells, where expression of the shorter isoform of the proto-oncogene IGF2BP1/IMP-1 caused oncogene transformation[3]. Altogether, these recent discoveries highlight APA as a widespread regulatory mechanism to control gene expression.

Here, we performed e3'-Seq to map and quantify 3'end-cleavage and poly(A)sites at the nucleotide resolution in healthy and failing human hearts. These polyadenylation profiles allowed us to identify disease-specific APA signatures in dozens of genes, indicating that APA-mediated 3'UTR length modulation represents an additional layer of gene regulation in the failing heart.

METHODS

Detailed methods are provided in the Online Supplement.

RESULTS

Global analysis of APA in the heart.

To reliably monitor genome-wide APA events, we developed an enhanced 3'-Seq protocol (e3'-seq) that improves 3'-mRNA cleavage site (CS) position mapping and quantification[5] (Suppl. Methods). A flow-chart of the e3'-Seq procedure and an example of 3'read mapping and CS identification is shown in Figures 1A-B and Online Figure I. We measured CSs in 5 control and 5 DCM hearts. In total we obtained information on the CS in 12.317 3'UTRs, of which ~50% contained two or more CS (Online Figure II). e3'-Seq data can be visualized directly in the UCSC browser; α-cardiac actin (ACTC1) is shown as an example in Figure 1C. ACTC1 has one CS, and the read distribution is similar between control and DCM samples. Strikingly, a CS is used that is located shortly after the stop codon, and not, as expected at the end of the 3'UTR. This may be highly relevant when one investigates the expression regulation of ACTC1 by miRNAs or RNA binding proteins.

We determined shortening versus lengthening of 3'UTRs based on CS_J scores, a metric which determines the center of mass of all reads mapping to CSs within a 3'UTR (Suppl. Methods). Based on these scores we examined the differences in APA in control and DCM hearts and identified 1370 transcripts with a shift in CS usage (Table II, Chi-Square test, $p<0.001$ after Bonferroni-correction for the number of 3'UTRs with more than 2 CS). In ~50% of these transcripts the shift is towards the distal CS. Equal proportions shifting towards the distal and the proximal CS indicates that there is no global shortening or lengthening of 3'UTRs in DCM and this is confirmed when calculating the proximal usage index (PUI) distribution per sample, which also revealed no significant difference in the global usage of proximal CS (Fig. 1D and Suppl. Methods).

Pathway analysis.

Enriched functional groups among the 1370 genes displaying altered APA were examined using the online tool PANTHER. Genes displaying 3'UTR shortening were mostly enriched for categories related to RNA binding, while genes that displayed 3'UTR lengthening were found in categories of 'actin binding' and 'structural constituent of cytoskeleton' (Table 1).

Candidate genes displaying altered APA in DCM.

Six genes displaying a clear shift in APA in DCM hearts are shown in Figure 2, Online Figure IV and X. These candidates were selected from Table III, based on: 1) their previously described functions in the heart (e.g Regulator of Calcineurin-1 (RCAN1)[6], CDC42 effector protein-3 (CDC42EP3))[7], or 2) their absolute difference of CS usage between control and DCM hearts (e.g small EDRK-rich factor 2 (SERF2) and Phosphatidylinositol Glycan K (PIGK), WEE1 G2-checkpoint kinase (Wee1) and Fibrosin-like 1 (FBRSL1)). CDC42EP3, PIGK, RCAN1 and Wee1 show significant 3'UTR shortening in DCM hearts, manifested by a prominent increase in the proximal CS usage relative to the distal one. FBRSL1 and SERF2 are two examples of transcripts with 3'UTR lengthening. 3'end qRT-PCR was used as an independent method to confirm the results of the e3'-Seq. As shown in Online Figure V, 3'end qRT-PCR confirmed the APA shifts in DCM hearts for CDC42EP3, PIGK, FBRSL1, SERF2 and Wee1, but the latter three did not reach statistical significance in this assay.

Effect of APA changes on gene expression.

To explore whether the observed APA changes may affect mRNA abundance of the corresponding genes, we used an extensive RNA-seq database of independent control hearts and DCM hearts (see Suppl. Methods). As shown in Figure 3A, we found significant upregulation of the genes with a shortened 3'UTR (i.e. PIGK and Wee1) and a downregulation of those with a longer 3'UTR (i.e. FBRSL1 and SERF2). Western blotting for FBRSL1 and SERF2 revealed that these two protein are also reduced at the protein level in DCM hearts (Online Figure VI). The mRNA expression of RCAN1 and CDC42EP3 were not different. For one of our main candidates, PIGK, we performed luciferase assays after subcloning the short and long 3'UTR fragment downstream of a Renilla cassette (Online Figure VII). Transfection of these constructs into H10 cells revealed that the 3'UTR shortening of PIGK enhanced Renilla luciferase, which is in line with the enhanced PIGK mRNA expression in DCM hearts where 3'UTR shortening is observed. Finally, when calculating the expression levels of the hundred most significantly changed APA genes, we show that almost 50% of the candidates with a shortened 3'UTR are upregulated in DCM. Visa versa, genes that display 3'UTR lengthening are more often downregulated than the ones with 3'UTR shortening (Online Figure VIII).

APA changes may be driven by disturbed expression of cleavage and polyadenylation factors.

Mechanisms that may underlie the altered APA in DCM hearts could be related to altered expression of cleavage and polyadenylation factors[1]. Therefore, we analyzed the expression levels of several of these factors and found that the expression of Poly(A)-Binding Protein Nuclear 1 (PABPN1) was downregulated not only on the mRNA level but also on the protein level (Figure 3B-C). Additionally, we also found that the mRNA expression of Cleavage and Polyadenylation-specific factor-4 (CPSF4) was down-regulated, while Cleavage and Polyadenylation Factor Subunit-11 (PCF11) was upregulated in DCM hearts (Online Figure IX).

DISCUSSION

In this study, we provide genome-wide, high-resolution polyadenylation maps of the human heart and show that in subsets of genes, 3'end formation of mRNA changes in failing hearts. For the vast majority of genes, the importance of APA remains unknown, but this work and that of others[8], indicate that APA shifts towards a proximal cleavage site (CS), resulting in shorter 3'UTRs, may contribute to an increased expression. Along the same lines, an APA shift towards a distal CS contributes to down-regulation of the mRNA. We did not find *global* shifts in 3'UTR length in failing hearts, but identified groups of genes where the 3'UTR ratio changed. Genes displaying 3'UTR shortening were mostly enriched for categories related to RNA binding, while the genes that displayed 3'UTR lengthening were found in categories of 'actin binding' and 'structural constituent of cytoskeleton'. Strikingly, we did not find APA shifts in genes important for contractile functions, suggesting that APA does not play an important role in these genes. Assuming that UTR length is inversely correlated with expression, the pathway analysis suggests that changes in APA patterns in DCM stimulate (post-)transcriptional regulation, while repressing genes involved in the structural cytoskeleton organization of the cell. As cardiac remodeling involves alterations in both processes, it is conceivable that many of the APA changes described in this study contribute to these aspects of heart failure.

This is the first study that directly measures global APA in the human heart. Park et al. analyzed mRNA isoforms in the hypertrophied mouse heart by microarrays and found global shortening of 3'UTRs, something that we did not observe in human hearts[9]. Nevertheless, microarray-based analysis of APA has serious limitations: it is restricted by the design of the array probes, which never cover the complete mRNA, and quantification of APA isoforms with more than two poly(A)sites is unreliable.

An important question regarding APA in heart failure relates to the mechanism that underlies the altered usage of poly(A)sites. We found disturbed mRNA expression in failing hearts of several genes that are involved in the 3'end-processing machinery. A main finding is the robust decrease of PABPN1 protein, as this gene has been identified as a suppressor of APA[5]. This suggests that the observed loss of PABPN1 in heart failure may have contributed to 3'UTR shortening of at least some candidates. Gene-targeting studies that directly examine the role of PABPN1 in the mouse heart would be important to further delineate its role in heart failure. Moreover, other factors, such as RNA binding proteins, splicing and transcriptional mechanisms and even histone modifications could all affect APA choices. The mechanism underlying 3'UTR lengthening in the failing heart remains elusive.

In conclusion, we show that the 3'-end formation of numerous mRNAs is altered in the failing heart, which is paralleled by a reduced expression of PABPN1. Interestingly, many of the genes with shortened 3'UTRs in DCM are involved in RNA binding, while the genes with 3'UTR lengthening appear involved in cytoskeletal organization.

This suggests that specific APA events fulfill a (patho-)biological function. Future studies that address the pathophysiological consequences of these APA changes are required to evaluate their role in the pathogenesis of heart failure and whether manipulation of APA can be considered a therapeutic option for heart failure.

Accession Codes.

3'-Seq bam-files are available at NCBI BioProject accession PRJNA288418.

DISCLOSURES

None.

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FIGURE LEGENDS

Figure 1. Quantifying the 3'ends of cardiac mRNAs. (A) Overview of e3'-Seq procedure. (B) e3'-Seq allows precise mapping of CS by identifying reads that align to the 3'end of transcripts (in blue), span the CS and cover the beginning of untemplated poly(A) tails (in red). The polyadenylation signal (PAS) and CS are indicated. (C) CS profiles, representing the number of reads supporting cleavage at each position along the transcript are visualized in the UCSC genome browser. This panel reveals one CS, proximal in the 3'UTR of ACTC1 in 5 control hearts (purple peaks) and 5 DCM hearts (blue peaks). Note the high evolutionary conservation at the beginning of the 3'UTR until the CS. (D) The proximal usage index (PUI) is similar in healthy and DCM hearts.

Figure 2. APA shifts in DCM. Three examples of transcripts with shifts in CS usage are shown. In the left panels the 3'UTRs of (A) CDC42EP3, (B) PIGK and (C) RCAN1 are depicted in a modified UCSC genome browser view. The peaks represent the CSs per sample (5 controls in blue and 5 DCMs in purple). The line above the peaks represents the transcript's last exon. In the right panels, fractions of distal and proximal CS usage are calculated in relation to total reads in the 3'UTR. A lower distal/proximal ratio in DCM hearts is indicative for a shorter transcript in DCM.

Figure 3. Expression of APA candidates and APA regulators in DCM. Scatterplots of mRNA expression of (A) APA candidates and (B) a potential regulator of alternative polyadenylation (PABPN1) from a comprehensive RNA-seq database. NPPA was included as a marker for DCM and HPRT1 as a control. *: p-values<1.0E-10, a Bonferroni correction was applied for the total number genes detected by the RNA-seq. (C) Western Blotting for PABPN1 in control and DCM hearts.

TABLE 1. Enriched functional groups in shortened and lengthened 3’UTRs

Shorter 3’UTR	# genes	Fold-enrichment	p-value
RNA binding	52	2.5	7.0E-07
mRNA binding	27	2.6	1.4E-03
Nucleic acid binding	157	1.44	1.9E-04
Protein binding	133	1.42	3.5E-03
Catalytic activity	246	1.35	8.5E-06

Longer 3’UTR	# genes	Fold-enrichment	p-value
Actin binding	21	3.4	2.7E-04
Cytoskeletal protein binding	26	3.1	1.5E-04
Structural constituent of cytoskeleton	52	1.9	1.0E-03

Novelty and Significance

What Is Known?

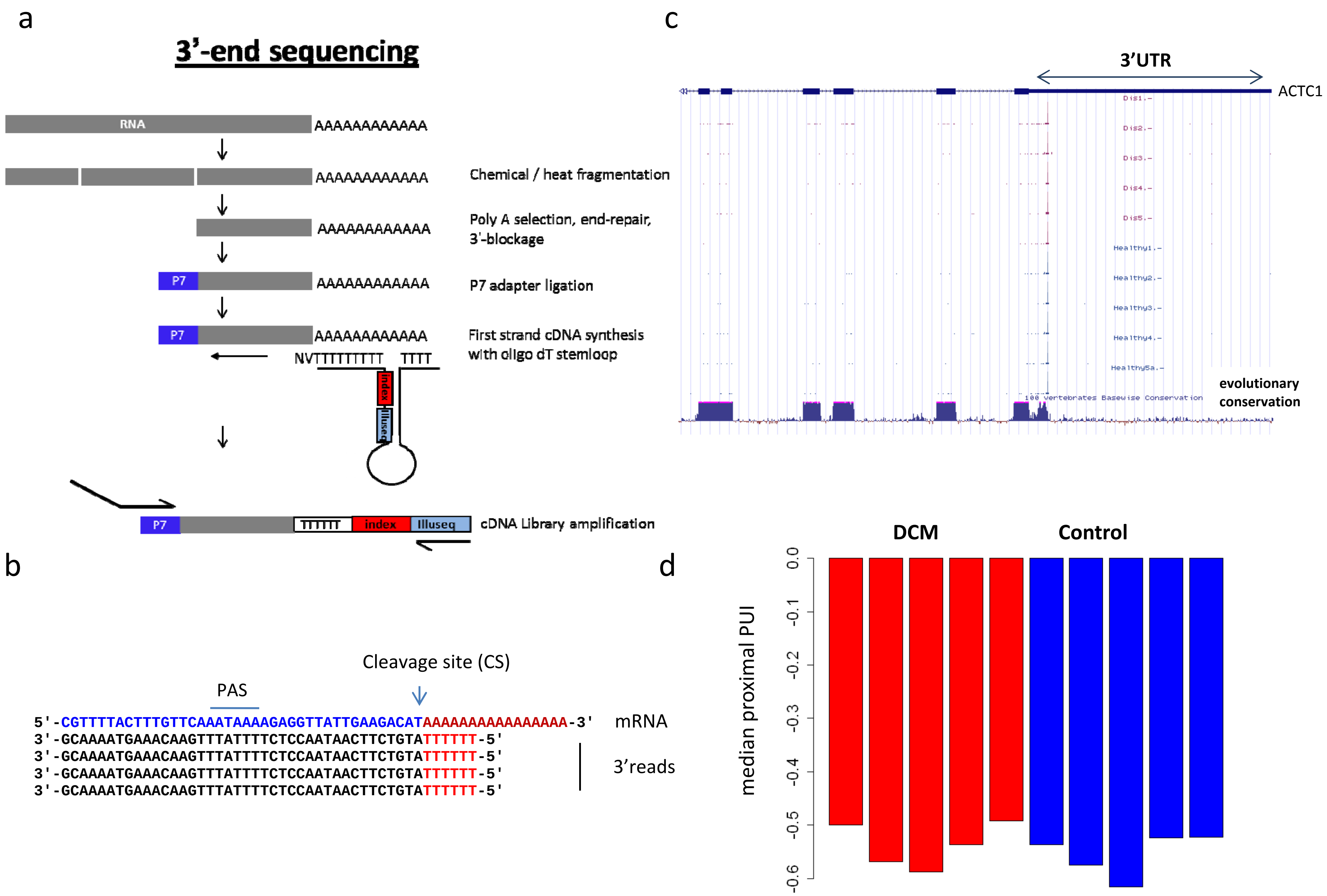
- The 3’UTR is a well-known hotspot for microRNAs and RNA binding protein interactions, and as such, is important for gene expression regulation.
- The polyadenylation machinery determines the length of the 3’UTR by precise positioning of the polyA tail.
- About half of the human genes generate alternative mRNA isoforms that differ in length at the 3’end by a process called alternative cleavage and polyadenylation (APA). However, in the human heart, APA is uncharted.

What New Information Does This Article Contribute?

- We performed 3’-end sequencing and provide genome-wide polyadenylation maps of healthy and failing hearts.
- Heart failure-specific APA signatures are present in numerous genes.
- We identified robust down-regulation of one of the main APA regulators, Poly(A)-Binding Protein Nuclear 1, in failing hearts.

Alternative cleavage and polyadenylation (APA) is emerging as an important layer of gene regulation. It was recently discovered that about half of the human genes generate alternative mRNA isoforms that differ in length of their 3’UTR due to this APA process. In this study, we provide genome-wide polyadenylation maps of the human heart and show that in subsets of genes, 3’end formation of mRNA alters in failing hearts. We found that changes in length of the 3’UTR inversely correlated with expression level of the affected genes in heart failure. As a putative mechanism underlying these APA changes we identified a robust down-regulation of Poly(A)-binding protein Nuclear 1 in failing hearts.

Figure 1


a
3'-end sequencing
RNA
AAAAAAAAAAAA
Chemical / heat fragmentation
Poly A selection, end-repair, 3'-blockage
P7
P7 adapter ligation
First strand cDNA synthesis with oligo dT stemloop
NVTTTTTTTTT
TTTT
index
Illuseq
TTTTTT
cDNA Library amplification
b
Cleavage site (CS)
PAS
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mRNA
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3'-GCAAAATGAAACAAGTTTATTTTCTCCAATAACTTCTGTATTTTTTT-5'
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Figure 2

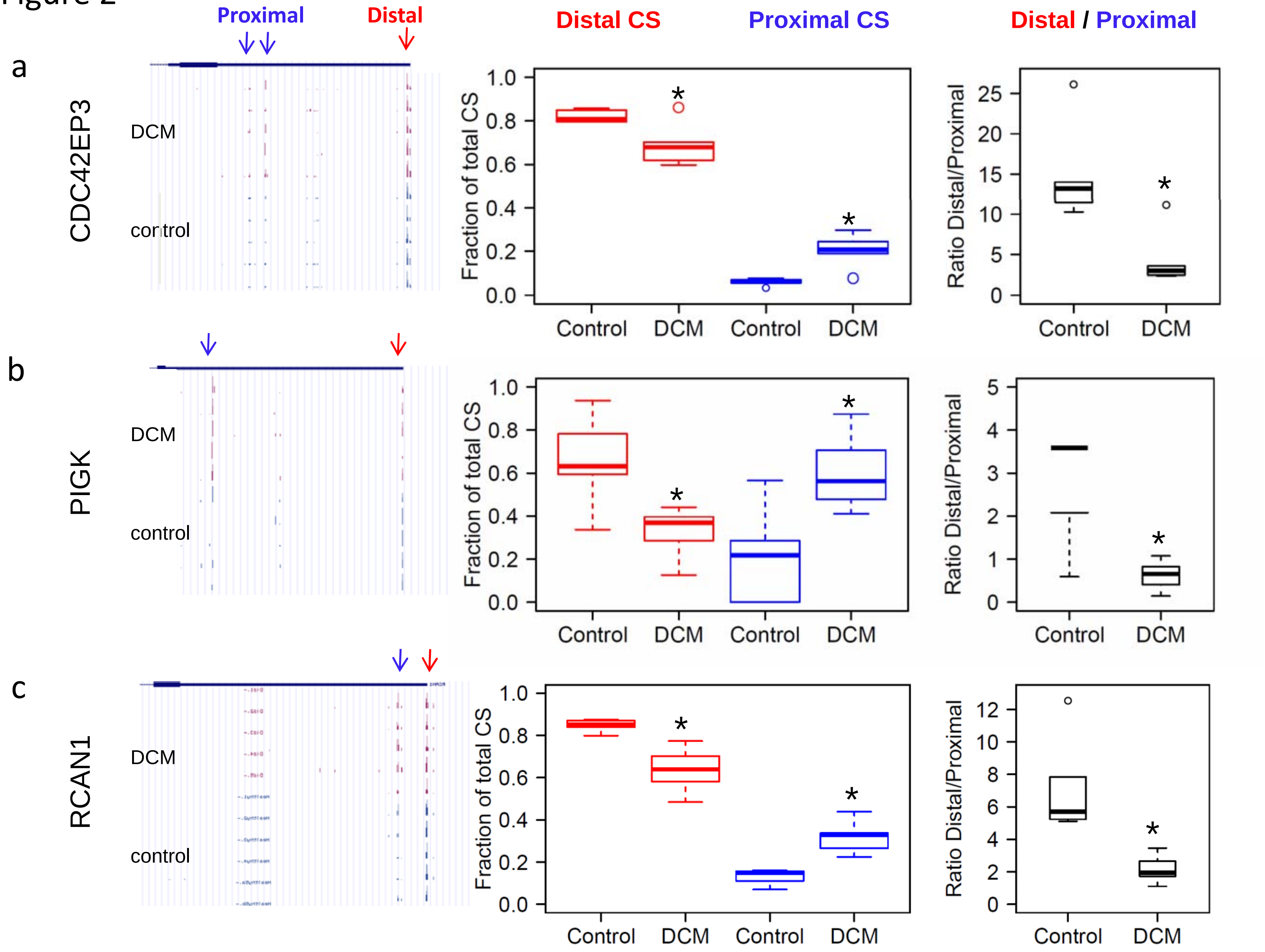
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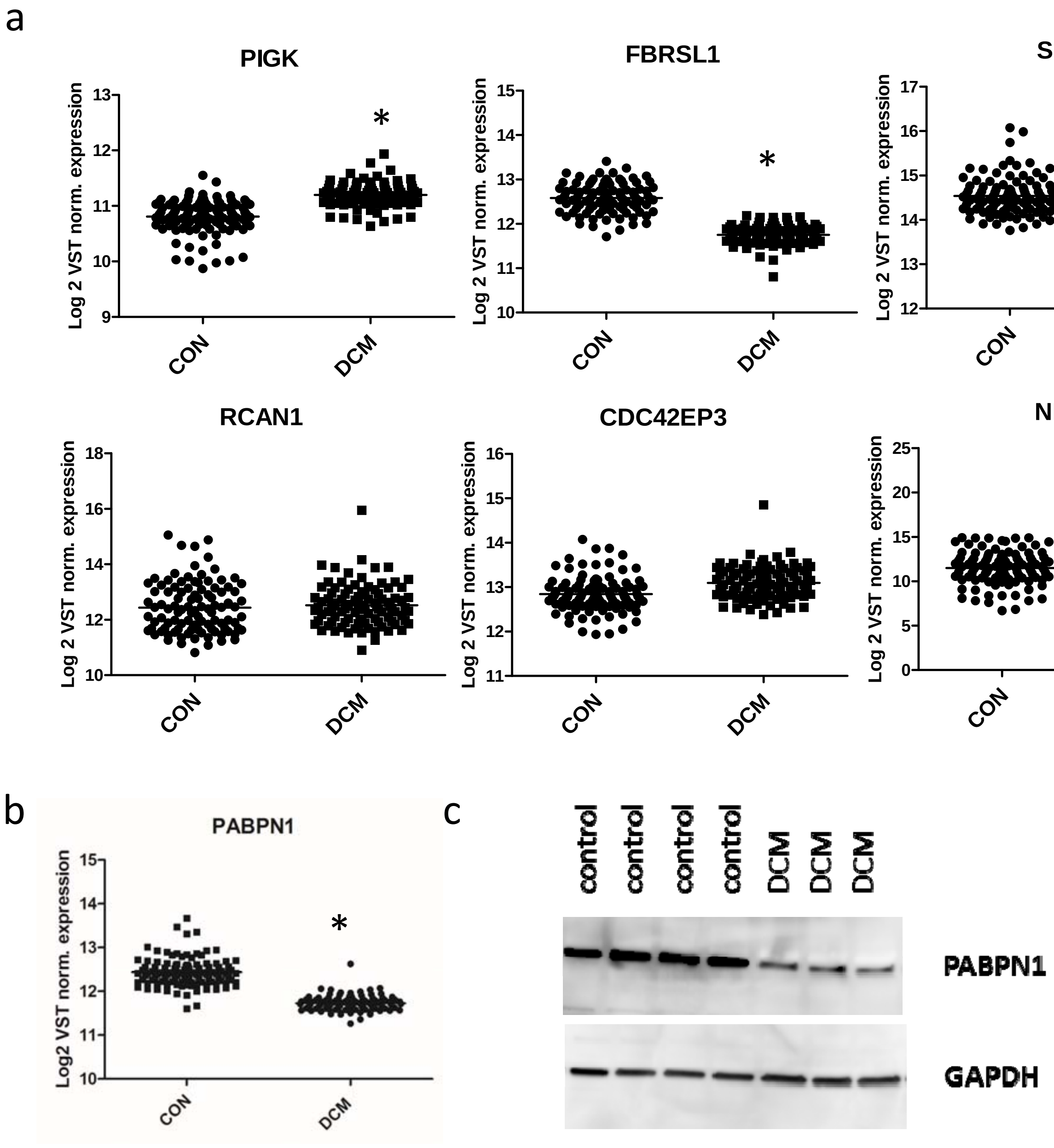
Figure 3


a
PIGK
FBRSL1
SERF2
Wee1
RCAN1
CDC42EP3
NPPA
HPRT1
Log 2 VST norm. expression
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b
PABPN1
Log2 VST norm. expression
CON
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c
control
control
control
control
DCM
DCM
DCM
PABPN1
GAPDH

Supplementary Methods

Human samples

Fresh left ventricular tissue from 5 patients with end-stage idiopathic dilated cardiomyopathy (DCM) were obtained during heart transplantation surgery (2 males/3 females, age 50±6 years, LV ejection fraction 21±6.5%). These tissues were obtained from the Sydney Heart Bank (Cris dos Remedios). As controls we used left ventricular (LV) tissue of non-failing donors (not used for transplantation due to logistic reasons) which had no history of cardiac abnormalities, normal ECG and normal ventricular function on echocardiography within 24 hours of heart transplantation. The average age of the control group was 55.8±8.9 years. The study protocol conformed with the Declaration of Helsinki and approved by the local Ethical Committee. All patients gave informed consent. Specific patient characteristics are provided in the table below.

Sample	**Age**	**M/F**	**LVEF**
Disease 1	47	m	20%
Disease 2	43	m	15%
Disease 3	60	f	25%
Disease 4	50	f	30%
Disease 5	52	f	15%
Healthy	61	f	
Healthy	57	m	
Healthy	65	f	
Healthy	46	f	
Healthy	50	f	

Construction of the 3'-seq libraries. Our improved 3'-Seq protocol is based on Jenal et al[1] and incorporates additional modifications described by Martin et al[2]. 5-10 µg of total RNA (Trizol; Life Technologies) was heat-fragmented for 12 minutes in 1x Fragmentation Buffer (Ambion) at 70°C to generate RNA fragments of ~100 nucleotides. Next, the 3'end poly(A) RNA fragments were selected using the Oligotex mRNA Kit (QIAGEN) and RNA was end-repaired with T4 polynucleotide kinase for 45 min. at 37°C following manufacturer's instructions. Afterwards, 3'ends were blocked for ligations by incubation with 1mM Cordycepin 5'-triphosphate (Sigma) and 10U of polyA polymerase (PAP, NEB) in 1xPAP buffer for 30 min. at 37°C. Next, a P7 RNA adapter (5'-CAAGCAGAAGACGGCAUACGAGAU-3') was ligated to the 5'end using 2 units of T4 RNA ligase I and 2.5uM of RNA adapter, for 4h at room temperature. Between each step, RNA was purified using Agencourt RNAClean XP magnetic beads (Beckman Coulter) following the manufacturer's instructions. At this point, RNA fragments were converted to cDNA employing the Superscript III RT kit (Life Technologies) and an anchored oligo(d)T stem loop primer containing a barcoded Illumina adaptor as previously described by Martin et al[2]. The use of this stem loop primer strategy for cDNA generation eliminates the poly(A) tail from the 3'end fragments, allowing direct readout of the CS position. Next, cDNA was purified twice with Agentcourt AMPure XP magnetic beads (Beckman Coulter) using a ratio 1.5:1 beads:sample. To generate the final 3'seq library, the cDNA with the correct adaptor sequences was enriched/amplified using Phusion DNA polymerase (Life Technologies) and primers P7 and Illumina_Truseq, for 12 cycles following manufacture's recommendations. Finally, the 3'seq library was size selected with AMPure XP magnetic beads by two rounds of purification with a ratio 1:1 beads:sample, before being sequenced on an Illumina HiSeq2000 system[1].

Analysis of 3'-Seq data. Sequenced reads start with a barcode followed by six Ts whose end marks the precise location where the poly(A) tail starts and therefore allow the mapping of the cleavage site (CS) with a nucleotide resolution. After trimming of barcode and six Ts, reads were aligned to the human genome (hg19) using TopHat. Up to two mismatches were allowed in the reads' seed region (the first 28 nt). As CS location often fluctuates around a major site, we merged reads from all samples and identified ''CS runs'' (that is, genomic intervals that contain multiple reads having distance below 10 nt between consecutive ones) and considered the local maxima of these runs as the CS locations. We required spacing of at least 50 nt between consecutive CSs (in case of lower spacing between CSs, the stronger, that is, the one supported by a higher number of reads, was chosen). Only CSs supported by at least 3 reads (at the location of the CS run maximum) in two independent samples were considered in subsequent analyses. The average length of the detected runs was 7 nt. Overall, 48,500 CS were detected. Priming of the oligo-dT primer to genomic regions that are A-rich ("internal priming") could lead to false call of CSs. To reduce such false calls we extracted genomic sequences of 50 nt centered at the location of the putative CSs, and filtered out a CS if that region contained a stretch of 10 nt of which at least 8 were As and the rest were Gs. 6,438 CSs were filtered by this step, leaving 42,062 CSs for subsequent analyses. To map CSs to genes and genomic regions (e.g, 3'UTR, introns, intergenic etc.), gene coordinates and annotations were extracted from the human Ensembl-Gene table of the UCSC browser[3]. To cover novel cleavage sites located downstream of current transcript annotations, we extended the 3'UTR of each transcript by 1000bp. The genomic coordinates of these CSs are provided in Table II. The statistics for the number of sequenced and mapped reads are shown in Table IV.

We searched for enriched sequence motifs, in the region 50nt upstream and downstream the CS. The most enriched sequence was the canonical AAUAAA polyadenylation signal, located 20-30 nt upstream of the

CS, but also previously described variants of this sequence were highly enriched (Figure III). The identification of polyadenylation signals at this location is a strong indicator for the precision and robustness of the 3'-Seq.

Differential usage of CS. In order to identify significant shifts in CS usage between samples, we first counted the number of reads in each CS run in each sample. Only runs mapping to the 3' UTRs were considered in the analysis. We next tested each transcript that contained more than one 3' UTR CS for relationship between peak levels (that is, CS usage) and disease state using chi-square tests. We used p=0.001, after Bonferroni correction for multiple testing as a cut-off for significance. All tests were carried out using R (http://www.r-project.org/). To determine whether a shift was towards proximal or distal CS, for each transcript in each condition, we calculated a weighted mean of CS index (weighting each CS [j] according to its reads coverage [w_j]):

$$\langle CS\_J \rangle = \sum_{j=1}^{n} w_j \times j.$$

A decrease in < *CS_J* > indicates 3' UTR shortening and vice versa.

PAS usage index (PUI). To quantify the relative usage of each PAS in a transcript in a certain condition, we defined the PAS usage index (PUI). For a given transcript with N CSs in the 3'UTR, the PUI of the j^{th} CS in a certain sample is defined by:

$$PUI_j = log_2\left(\frac{E_j}{\langle E \rangle}\right);\ j = 1..N,$$

where E_j is the level of the CS run associated with the j^{th} cleavage site, and <E> is the geometric mean of the levels of all the runs associated with the N cleavage sites. PUI distributions calculated over proximal CSs (by definition, for proximal CSs j=1) were compared between samples using the nonparametric Wilcoxon test. All transcripts which showed significant APA shift between the healthy and disease samples were included in this analysis. As a global measure for the usage of proximal CSs in a sample, we took the median of the distribution of proximal site PUIs in that sample, taking into account all transcript with more than one 3' UTR CS.

Quantitative 3'PCR

To validate the results obtained from the 3'Seq, first strand cDNA was synthesized using Superscript III reverse transcriptase (Invitrogen) according to the manufacturer's instructions with the P7-T25-VN oligo-dT primer. qRT-PCR was performed on a lightcycler 480 system II, with standard SYBR green protocols using the P7 primer and gene-specific proximal and distal forward primers located within 100 bp upstream of the cleavage site. Primer sequences are listed in table I. Due to the high AT-rich nucleotide content upstream of the distal CS of RCAN1, we were unable to design reliable primers to validate RCAN1 3'UTR shortening by 3'-PCR.

Pathway analysis. Analysis of enrichment of functional groups was conducted at PANTHERdb.org using 'Statistical Overrepresentation Test' in the 'Gene List Analysis' tool[4]. We compared genes with altered APA with a list of non-APA regulated cardiac expressed genes as the reference. Only functional groups containing at least 4 genes with altered APA and P<0.01 (after Bonferroni correction for the number of independent tests) are shown.

RNA-seq for gene expression analysis. Total RNA was extracted using TRIzol reagent from 107 control and 96 DCM hearts, and RNA-seq libraries were prepared with the TruSeq RNA Sample Preparation Kit (Illumina). Control heart samples were drawn from a set of non-diseased donor heart samples previously used for eQTL analysis.[5] Barcoded cDNA fragments of poly(A)+ RNA were subsequently sequenced on a HiSeq 2000 instrument from Illumina with 2 × 100 bp PE chemistry. Gene level quantification was performed using htseq-count and genome assembly GCRh37. Gene counts were normalized using variance-stabilization transformation (VST) and log2 transformed. VST is part of DESeq[6-8]. Cardiac biopsies were collected from different centers, but the methodology of RNA isolation, library preparation and RNA-seq was the same for all samples, as this was performed in the same lab. This novel RNA-seq database is currently being analyzed for a separate manuscript on alternative splicing.

Western Blotting. Myocardial tissue extracts in RIPA buffer of 4 control and 3 DCM hearts were separated on 10% SDS-PAGE gels and transferred to Immobilon-P membranes (Millipore). Primary antibodies used for protein detection were SERF2 (Abcam ab188264, dilution 1:250), FBRSL1 (Abcam ab111515, dilution 1:250), Wee1 (Thermo Scientific, PA5-15385, dilution 1:1000) and PABPN1 (Epitomics #2428-1, dilution 1:500). 40 µg protein was loaded per lane. GAPDH (Santa Cruz, SC365062, dilution 1:10.000) was used as a loading control.

Luciferase assays. A long (3437 bp) and a short (569 bp) fragment of the 3'UTR of PIGK were cloned into the psiCHECK-2 luciferase reporter (Promega) downstream of the Renilla luciferase, using XhoI/SalI and NotI restriction sites. The long fragment encompassed the (nearly) complete 3'UTR of PIGK, and we mutated the proximal APA site (Quickchange kit, ThermoFisher) to ensure that 3'UTR is fully transcribed of this construct. The short transcript encompasses the part of the 3'UTR that is formed when the proximal APA site is used. Primers used for cloning and mutagenesis are listed in Table I. We transfected a cardiomyocyte-like cell type, H10 cells with these psiCHECK2 constructs (Lipofectamine, Thermofisher), and after 48 hours, dual luciferase activity assays (Promega) were performed.

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Supplemental Figures

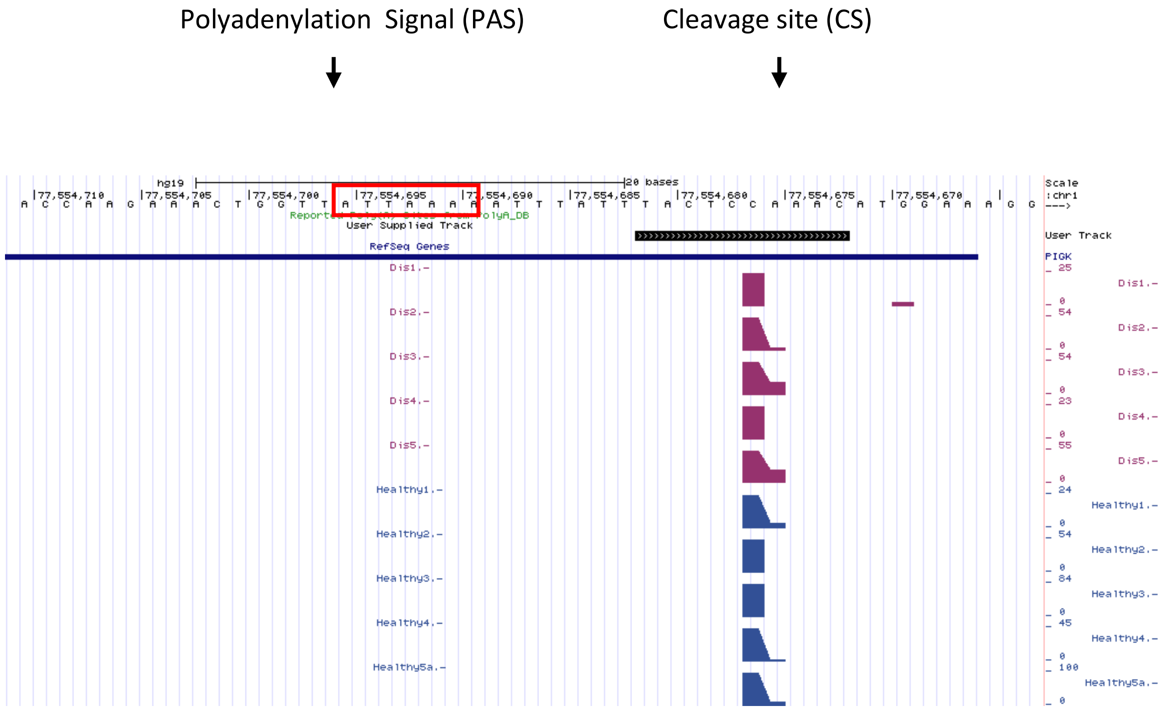


Figure I. UCSC genome browser view shows the polyadenylation signal and the distal cleavage site of PIGK. The tracks of 5 DCM (Dis, purple) and 5 control hearts (healthy, blue) are shown. The number of reads per sample are shown on the right.

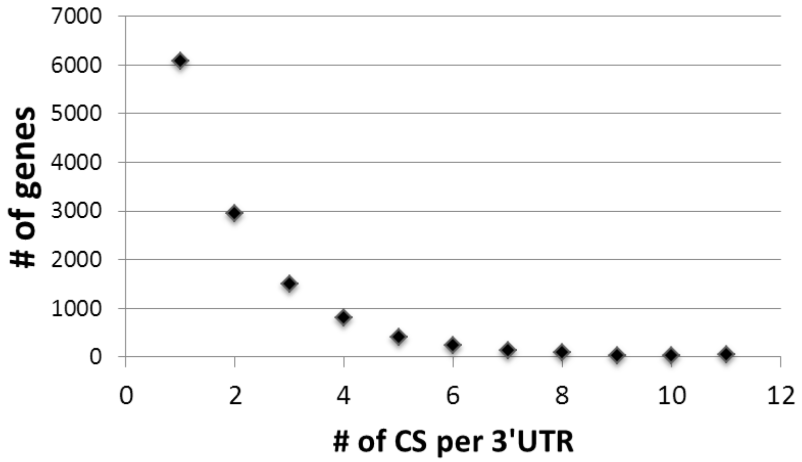


Figure II. Number of polyA sites or CS detected per 3'UTR. In total we obtained information on the CS of 12.317 genes in the heart, of which 6.070 genes contained one CS, and the rest contained 2 or more CS. The distribution of the number of CS in the 3'-Seq is shown.

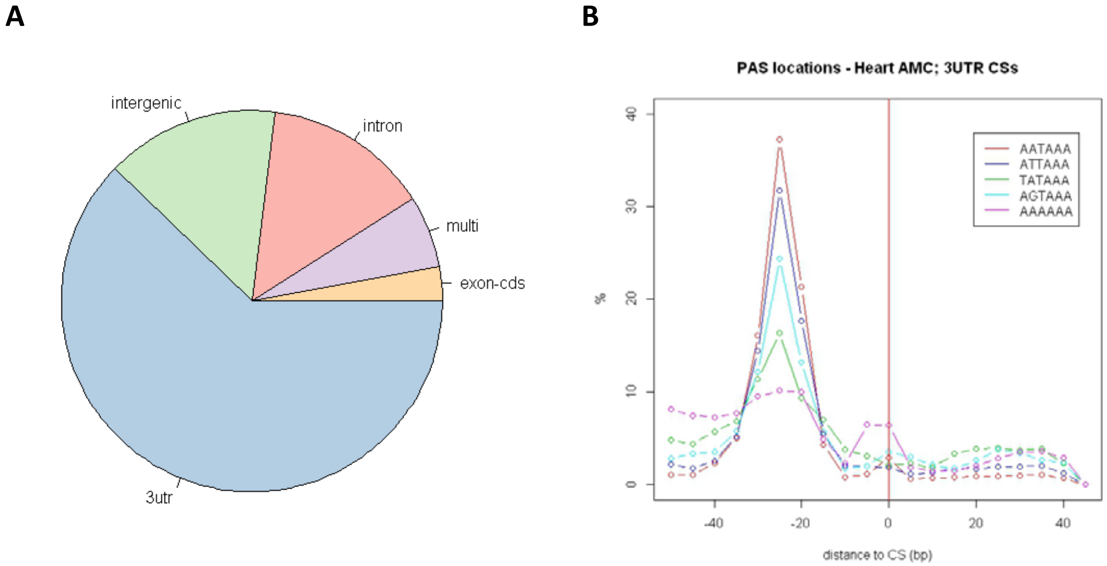


Figure III. Quantification of the 3'Seq. A) Distribution of the CS in the cardiac 3'-Seq datasets in genomic regions. CSs were highly enriched for 3'UTRs (61%; 25,856/42,062). B) The canonical PAS and its major variants were significantly enriched in the [-40bp, -10bp] region relative to the CSs. (Enrichment was calculated against the 2nd order markov random sequences as described by Jenal et al, 2013). The most enriched signal was the canonical PAS AATAAA, but also variants to this sequence were highly enriched, with ATTAAA being the second most prominent one. The sharp peak at position ~20 nt upstream of the CS provides a strong indication for the precision of the CS mapping by this 3'-Seq experiment.

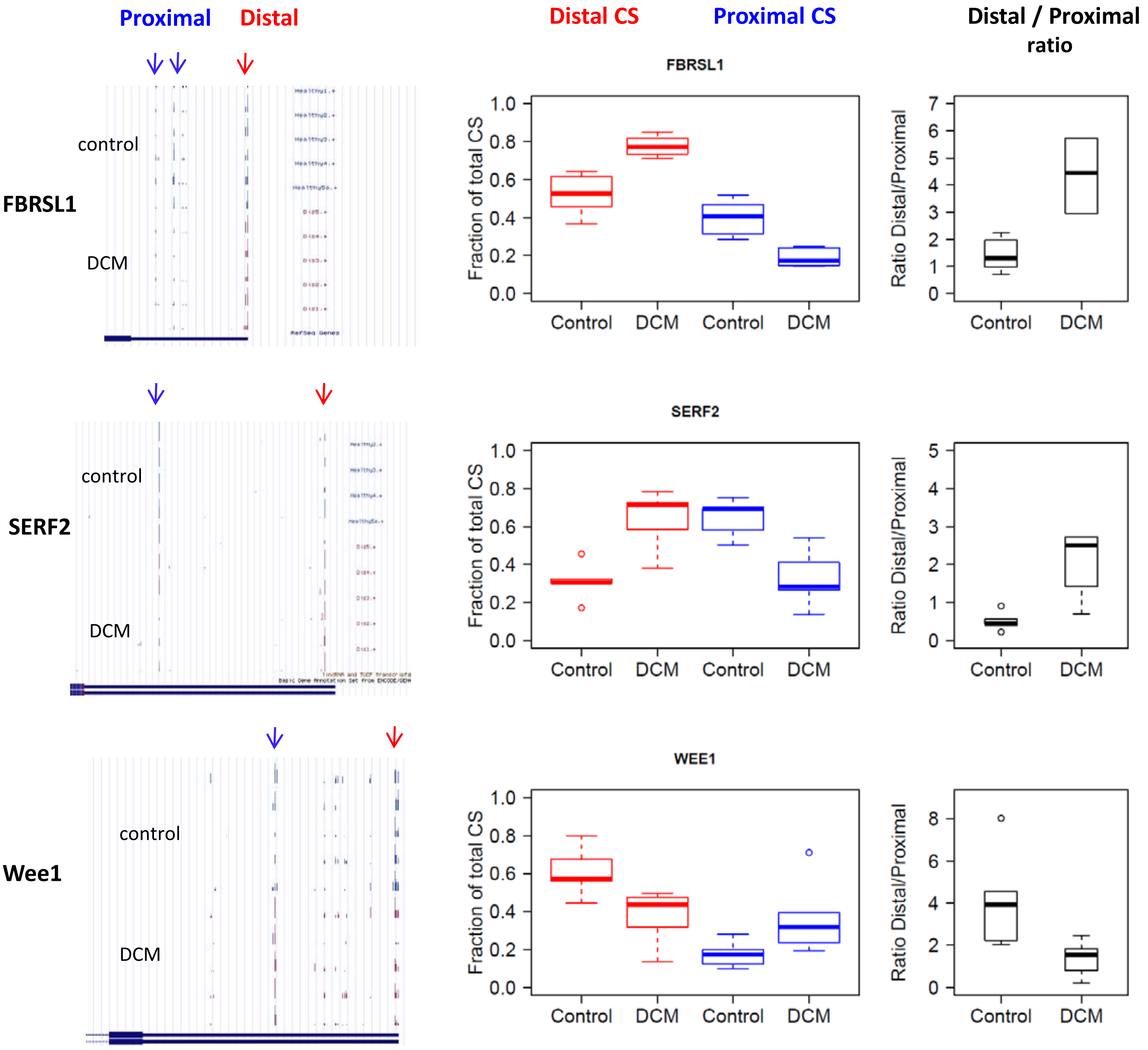


Figure IV. APA shifts in DCM. In the left panels the 3'UTRs of FBRSL1, SERF2 and Wee1 are depicted in a modified UCSC genome browser view. The peaks represent the CS usage per sample (5 healthy hearts in blue and 5 DCM hearts in purple). The blue horizontal line above the peaks represents the last exon of the transcript and covers the end of the open reading frame (thick line) and the 3'UTR (thinner line). In the panels on the right (Proximal CS, Distal CS and Distal/Proximal), the fraction of proximal and distal CS usage is calculated in relation to the total reads in the 3'UTR. A lower distal/proximal ratio in DCM hearts is indicative for a shorter transcript in DCM and vice versa.

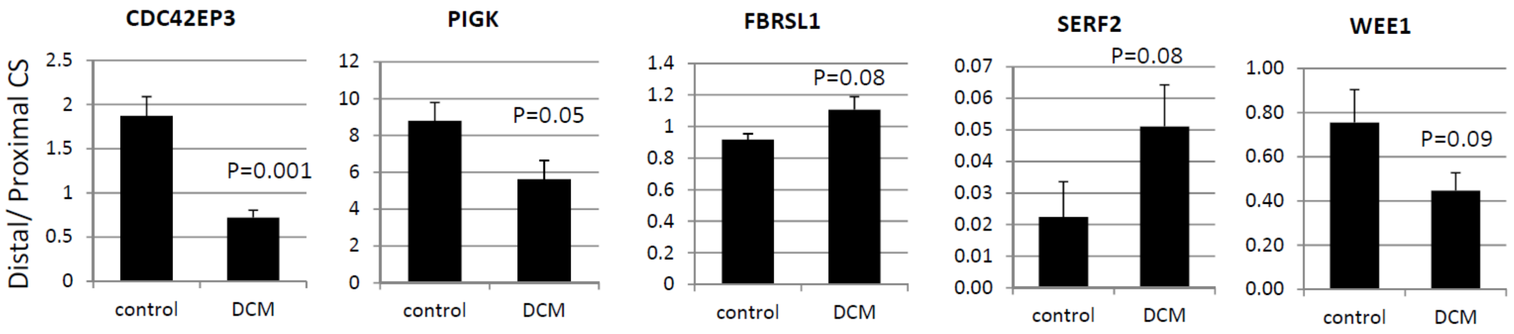


Figure V. 3'end qRT-PCR validates APA shifts in DCM hearts of CDC42EP3 and PIGK. RNA of 4 control hearts and 5 DCM hearts was reverse transcribed with the P7-T25-VN oligo dT primer. Quantitative PCR was performed with a reverse T7 primer and gene-specific forward primers, located within 100 basepairs of either the proximal or distal cleavage site (table I). The ratio of distal/proximal mRNA isoform expression per APA candidate is shown.

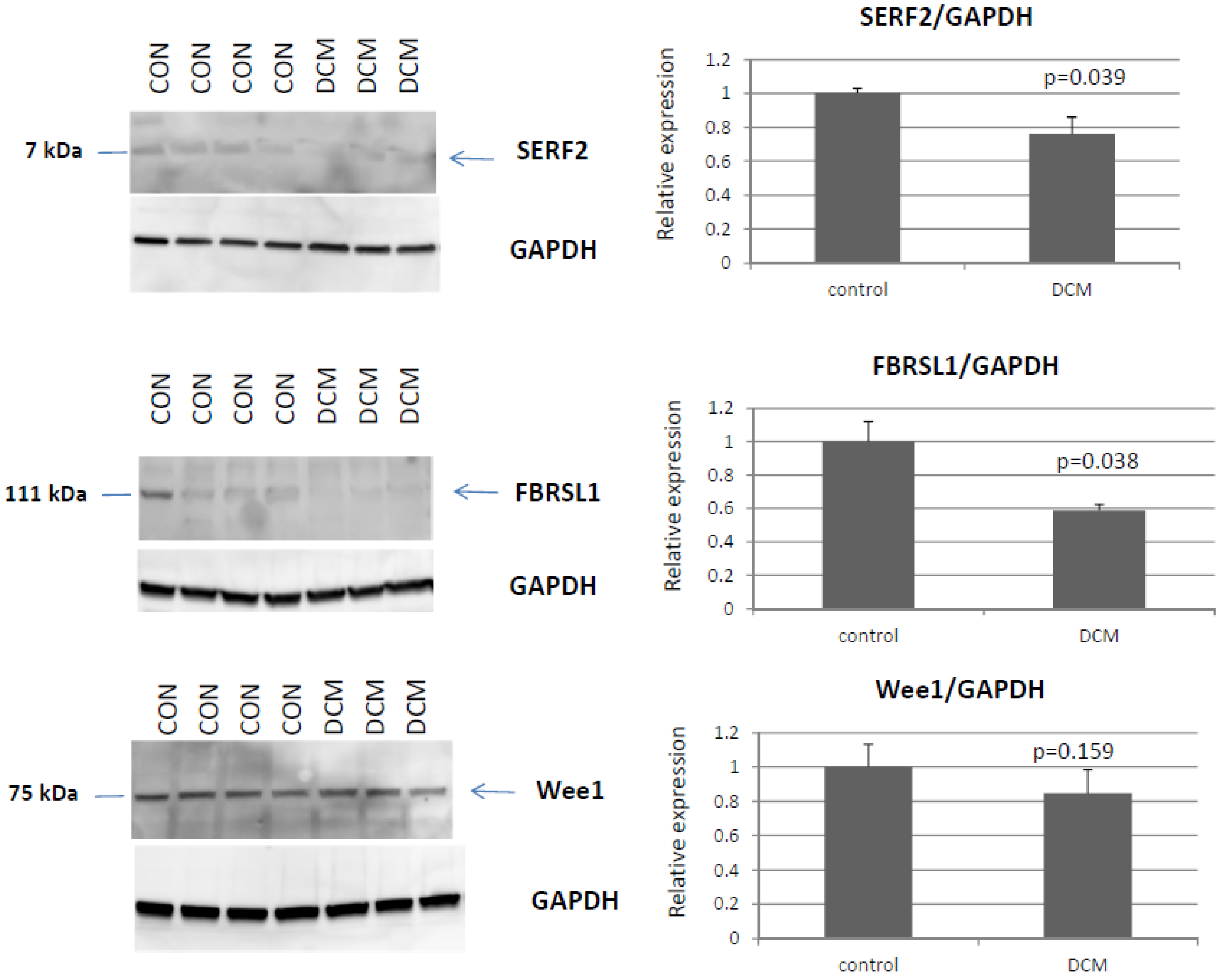


Figure VI. Western Blotting of SERF2, FBRSL1 and Wee1 in human heart lysates. Quantification revealed that SERF2 and FBRSL1 were significantly down-regulated in DCM hearts, while we did not observe a sigificant alteration for Wee1 protein, as its expression was more heterogenous between DCM hearts. Data are expressed as mean ± SEM. P-values comparing expression in control versus DCM hearts is calculated in student t-test.

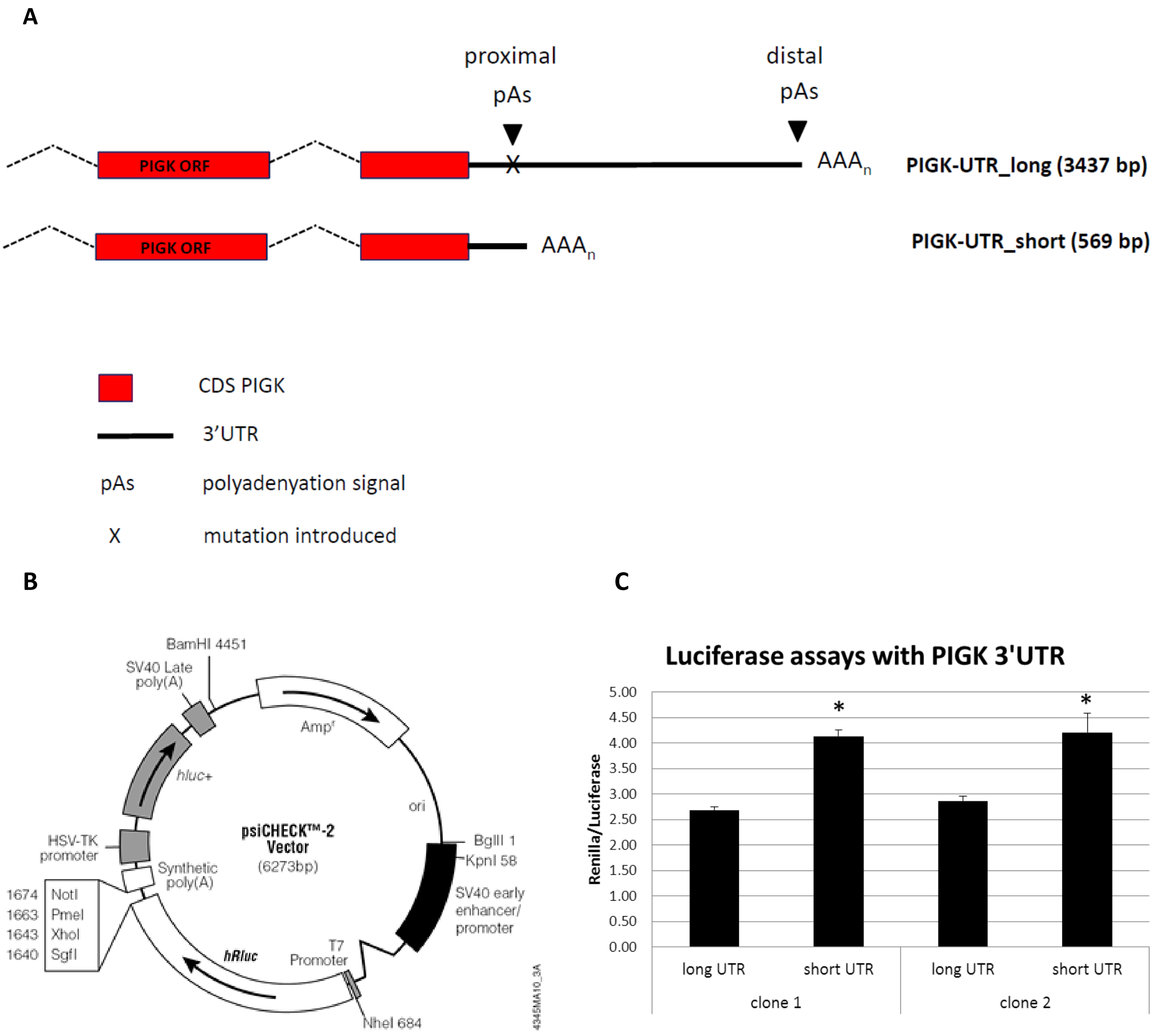


Figure VII. Luciferase assays using 3'UTR fragments of PIGK indicate increased expression when the 3'UTR has shortened. **A**. We cloned downstream to the Renilla luciferase in psiCHECK2 either the full length 3'UTR of PIGK (Long, 3437 bp) or the short 3'UTR that is formed when the proximal pAs is used (short, 569 bp). We mutated the proximal APA site in the long construct to ensure that the 3'UTR is fully transcribed. **B.** The psiCHECK2 vector is shown, where the 3'UTRs are cloned between NotI and XhoI sites of the multiple cloning sites. Note the luciferase firefly cassette (hluc+) that was used to normalize Renilla values for transfection efficiencies. **C.** Transfection of H10 cells (cardiomyocyte-like cells) in 24 well plates with 100 ng of the constructs revealed that 3'UTR shortening of PIGK enhanced expression of Renilla luciferase, which is in line with the enhanced PIGK mRNA expression in DCM hearts (Fig 3A), where shortening of the 3'UTR is observed (Fig 2). Two independent clones per contructs were used as indicated. Transfections and subsequent dual luciferase assays were performed in triplicate, and this experiment was performed twice. *p<0.05 in student t-test, compared to long UTR of the same clone.

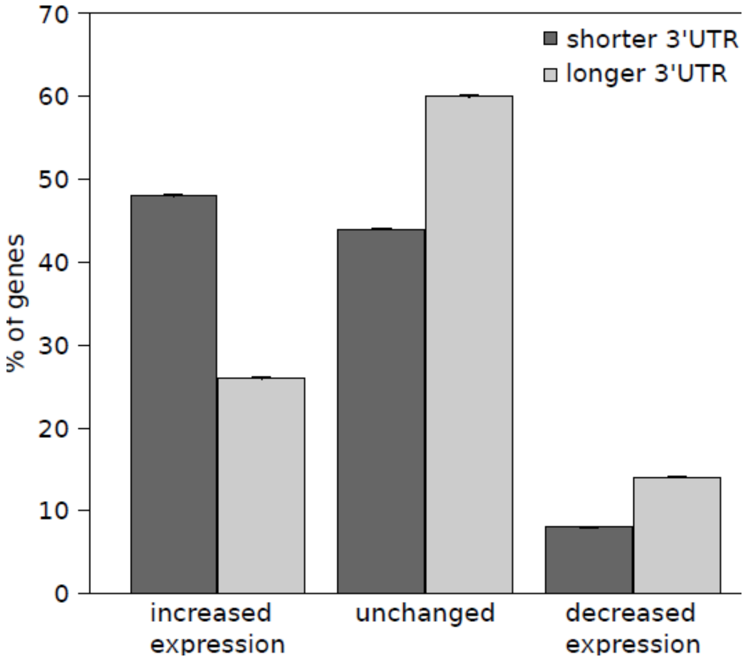


Figure VIII. mRNA expression changes in DCM compared to control hearts of the 50 most signficantly genes with 3'UTR shortening or 3'UTR lengthening. These 100 genes were selected on their corrected p-value for difference in APA usage in DCM hearts (Table I). Differentially expressed genes in the RNA seq of control versus DCM hearts are both statistically significant and have a fold-change >1.25 (Mann Whitney U test, corrected for multiple testing). The difference between the groups (i.e. shorter versus longer 3'UTR) is statistically significant; p=0.0049 (Chi-square test). Note that more genes are upregulated with a shortened 3'UTR than with a lengthened 3'UTR. Visa versa, genes that display 3'UTR lengthening are more often down-regulated in DCM.

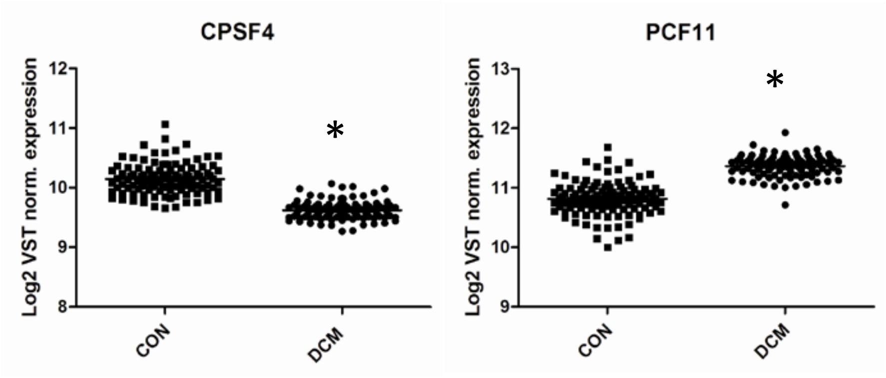
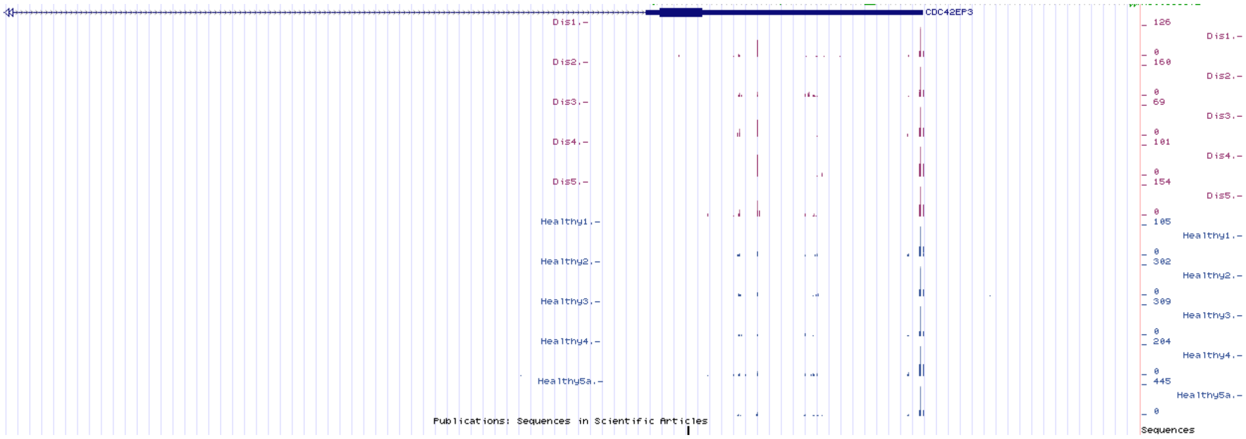


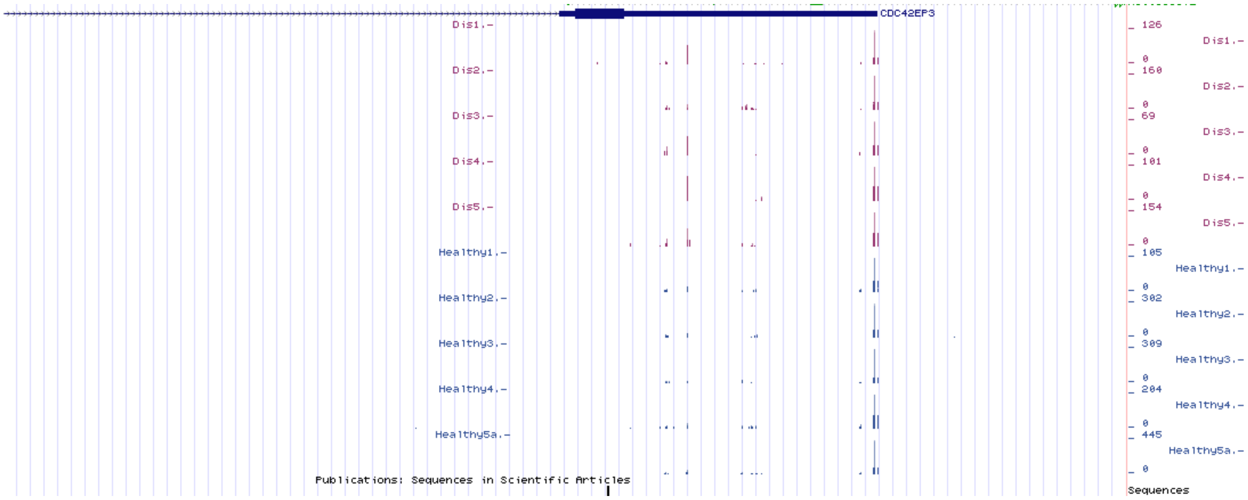
Figure IX. mRNA expression of potential regulators of APA in DCM

Scatterplots of mRNA expression of regulators of the 3'end formation machinery from a comprehensive RNA-seq database. *: p-values<1.0E-10. A Bonferroni correction was applied for the total number genes detected by the RNA-seq.

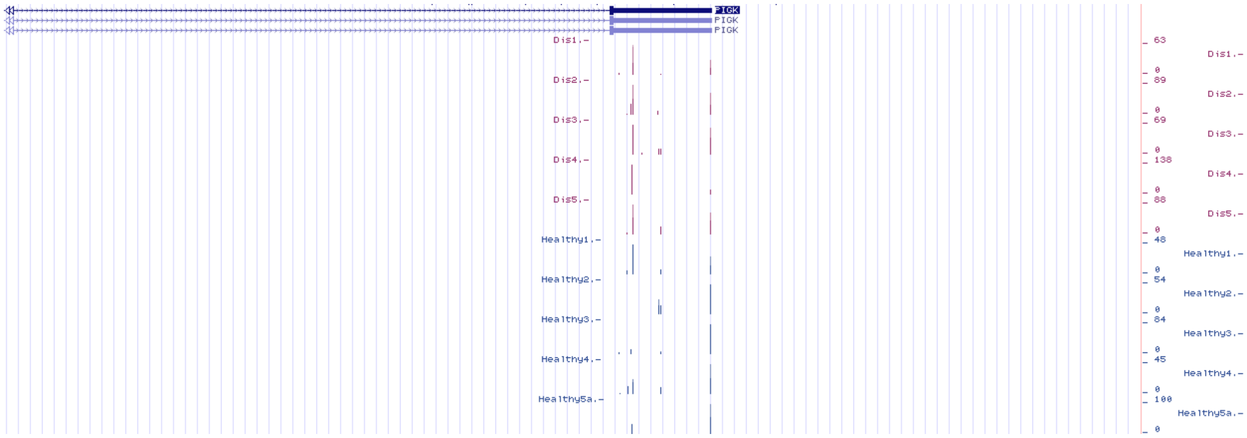
Genome browser view ACTC1



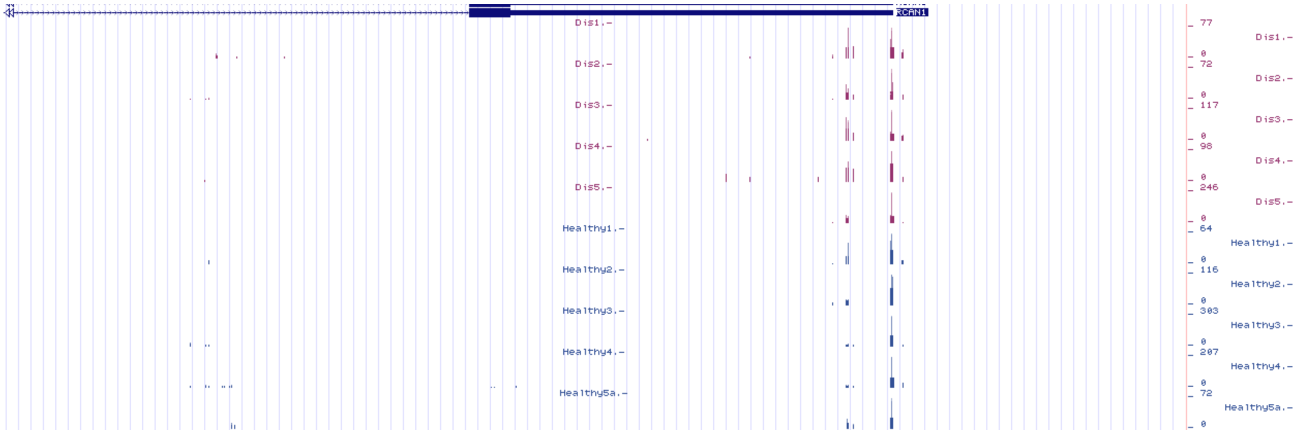
Genome browser view of CDC42EP3



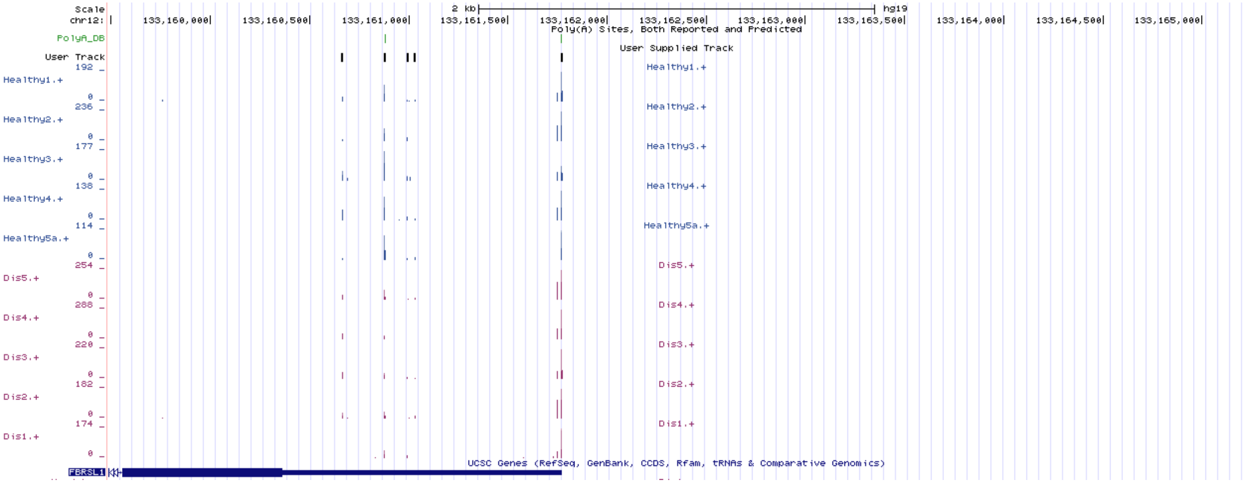
Genome browser view of PIGK



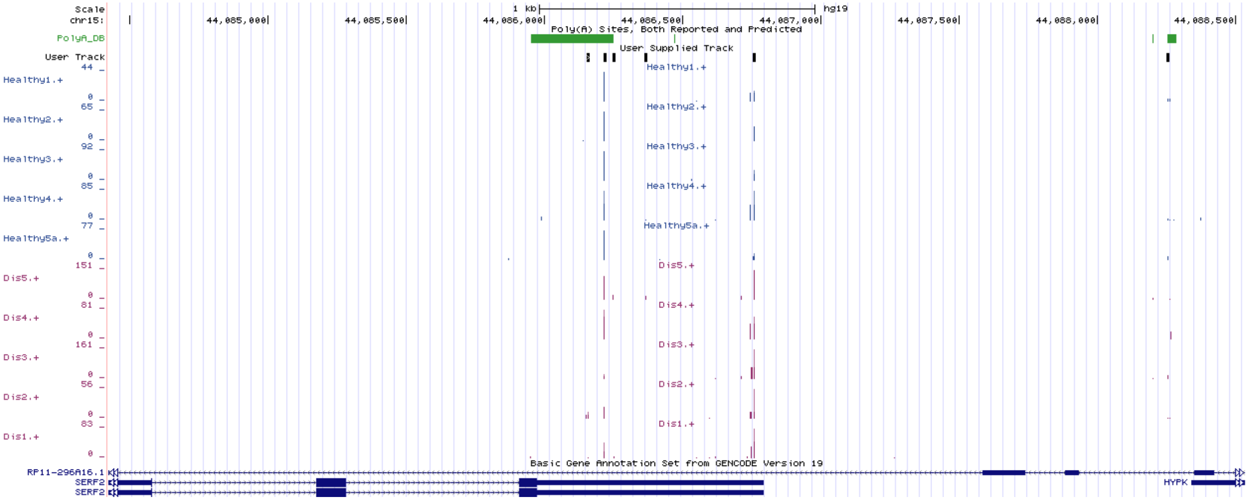
Genome browser view of RCAN1



Genome browser view of FBRSL1



Genome browser view of SERF2



Genome browser view of Wee1

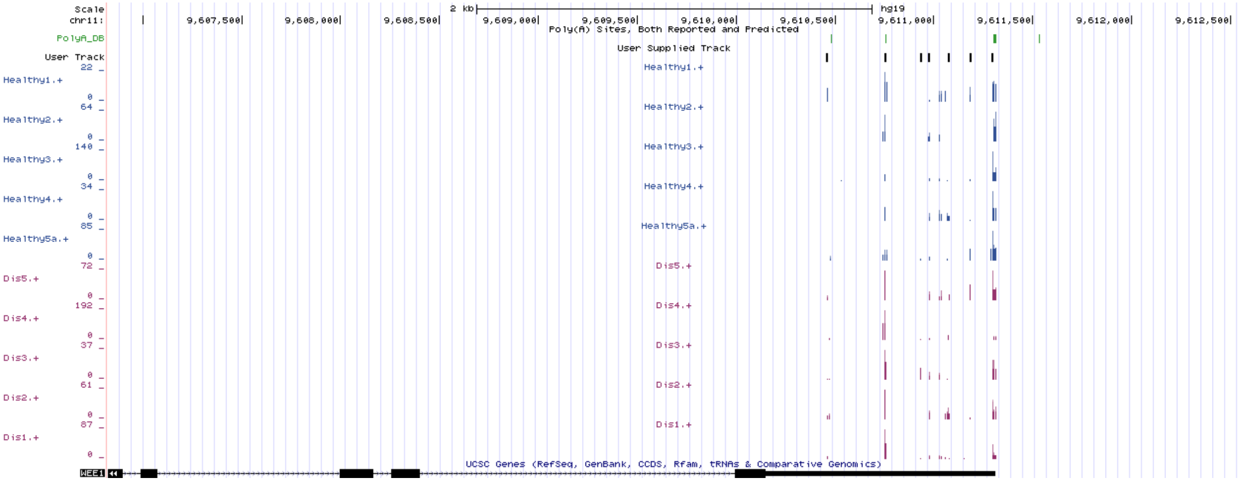


Figure X. Enlarged genome browser views of all APA tracks presented in this study.

Suppl. Table I: Primers used for 3'end sequencing and 3'PCR

Primer name	**Primer sequence (5'-> 3')**
P7	CAAGCAGAAGACGGCATACGAGAT
P7t25VN	CAAGCAGAAGACGGCATACGAGATTTTTTTTTTTTTTTTTTTTTTTTTVN
3seq_RT1	TTTTTTTTTTTTTTTTTTTGcagtAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTactgCTTTTTTVN
3seq_RT2	TTTTTTTTTTTTTTTTTTTGatcgAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTcgatCTTTTTTVN
3seq_RT3	TTTTTTTTTTTTTTTTTTTGtgacAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTgtcaCTTTTTTVN
3seq_RT4	TTTTTTTTTTTTTTTTTTTCgctaAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTtagcGTTTTTTVN
3seq_RT5	TTTTTTTTTTTTTTTTTTTGagctAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTagctCTTTTTTVN
3seq_RT6	TTTTTTTTTTTTTTTTTTTGctagAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTctagCTTTTTTVN
3seq_RT7	TTTTTTTTTTTTTTTTTTTCgatcAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTgatcGTTTTTTVN
3seq_RT8	TTTTTTTTTTTTTTTTTTTCtcgaAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTtcgaGTTTTTTVN
3seq_RT9	TTTTTTTTTTTTTTTTTTTGcgatAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTatcgCTTTTTTVN
3seq_RT10	TTTTTTTTTTTTTTTTTTTCactgAGATCGGAAGAGCGCTACACGACGCTCTTCCGATCTcagtGTTTTTTVN
Illumina_Truseq	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT
CDC42EP3_proximal_F	AGAGACTGTGGGCTACACCAC
CDC42EP3_distal_F	AGCATCATGTGGAAGAATGGGAAC
PIGK_proximal_F	TGTTGGACCACTTACATTGTAC
PIGK_distal_F	GGTTTAACTGTGTAGATCCTAG
RCAN_proximal_F	TGCCAAGTAACAATGCATGC
RCAN_distal_F	ACGGTACTTGGTAAGAGGGAG
Wee1_proximal_F	GGATGATGATTCTGTGGAGGTA
Wee1_distal_F	CATGTTTGCACTTGTCTTTGAC
FBRSL1_proximal_F	CCTCAGATCCTTCTCCAGAT
FBRSL1_distal_F	CACGGTGGACCCTGTTTGTT
NPPA_F1	AGTGGTTTGATGGTGACTTCC
NPPA_R	TCTGTCCATGGTGCTGAAG
GAPDH_F	AAGAGAGAGACCCTCACTGC
GAPDH_R	ATGGTACATGACAAGGTGCG
PIGK- 3’UTR cloning_F	acgtaCTCGAGGCGAATGAGACAGAGATCAG
PIGK-3’UTR cloning_short_R	tgcacGCGGCCGCTGCAGGATTCCATGAGTGAC
PIGK-3’UTR cloning_long_R	tgcacGCGGCCGCATGTGTAAATAGGGCAGGCA
PIGK-proxAPA mutagenesis-F	CTCATGGAATCCTGCAGCTTGGGTTAAAAGCAAAGATGAAAAATTGG
PIGK-proxAPA mutagenesis-R	CCAATTTTTCATCTTTGCTTTTAACCCAAGCTGCAGGATTCCATGAG

Suppl. Table II. Transcripts that show statistically significant APA changes between control versus DCM hearts (sorted on p-value).

Bonferroni correction was applied to the number of 3'UTRs analyzed that had more than 2 CS

geneid	sym	strand	3utrid	N.3utr.Peaks	mean.PAS.J.D	mean.PAS.J.H	SHIFT_direction	pval bonferroni corrected
8048	CSRP3	-	3utr_1	6	2,20	2,36	Shorter	4,15E-188
6262	RYR2	+	3utr_1	9	8,26	8,63	Shorter	1,78E-92
91612	CHURC1	+	3utr_1	4	1,92	1,38	Longer	4,43E-87
506	ATP5B	-	3utr_1	2	1,92	1,87	Longer	2,96E-83
1278	COL1A2	+	3utr_1	4	3,37	3,10	Longer	4,56E-83
10284	SAP18	+	3utr_1	6	3,48	3,06	Longer	3,80E-75
6678	SPARC	-	3utr_1	4	3,50	3,64	Shorter	7,21E-72
203068	TUBB	+	3utr_1	2	1,17	1,12	Longer	1,09E-68
10529	NEBL	-	3utr_1	10	7,99	8,24	Shorter	5,61E-65
5500	PPP1CB	+	3utr_3	4	1,86	2,05	Shorter	1,03E-63
1345	COX6C	-	3utr_3	4	1,44	1,07	Longer	2,92E-63
813	CALU	+	3utr_1	6	4,75	5,40	Shorter	1,83E-60
92906	HNRPLL	-	3utr_1	6	3,32	3,00	Longer	8,07E-59
5569	PKIA	+	3utr_1	6	4,17	4,12	Longer	3,31E-58
6710	SPTB	-	3utr_1	3	1,96	2,37	Shorter	3,03E-57
6138	RPL15	+	3utr_1	3	1,49	1,41	Longer	2,49E-55
1827	RCAN1	-	3utr_2	3	1,73	1,91	Shorter	4,02E-55
10776	ARPP19	-	3utr_1	4	2,00	2,45	Shorter	3,51E-54
7111	TMOD1	+	3utr_1	4	3,02	3,43	Shorter	1,40E-53
56172	ANKH	-	3utr_1	5	2,07	2,19	Shorter	1,82E-52
163	AP2B1	+	3utr_1	3	1,53	2,02	Shorter	1,85E-52
10272	FSTL3	+	3utr_1	3	1,22	1,95	Shorter	2,45E-51
57666	FBRSL1	+	3utr_1	5	4,05	3,41	Longer	2,52E-51
7078	TIMP3	+	3utr_1	6	5,64	5,50	Longer	6,28E-51
23242	COBL	-	3utr_5	5	2,86	2,83	Longer	7,06E-51
6500	SKP1	-	3utr_1	5	2,39	2,60	Shorter	1,12E-50
10891	PPARGC1A	-	3utr_2	4	3,70	3,95	Shorter	8,33E-50
2632	GBE1	-	3utr_1	2	1,59	1,35	Longer	4,47E-49
64795	RMND5A	+	3utr_1	3	2,09	2,21	Shorter	1,78E-48
7077	TIMP2	-	3utr_1	6	5,52	5,30	Longer	8,69E-48
10231	RCAN2	-	3utr_1	3	2,63	2,79	Shorter	9,00E-47
9827	RGP1	+	3utr_1	5	4,72	3,94	Longer	2,02E-46
27129	HSPB7	-	3utr-extend	3	1,05	1,09	Shorter	2,25E-44
4976	OPA1	+	3utr_1	10	7,09	7,20	Shorter	1,20E-43
119504	ANAPC16	+	3utr_1	6	4,06	3,62	Longer	1,40E-43
23433	RHOQ	+	3utr_2	9	5,23	5,38	Shorter	2,94E-43
26994	RNF11	+	3utr_1	4	3,00	2,42	Longer	6,32E-43
2181	ACSL3	+	3utr_1	4	3,37	2,52	Longer	1,18E-42
5862	RAB2A	+	3utr_1	5	4,13	4,24	Shorter	1,27E-42
5048	PAFAH1B1	+	3utr_1	4	3,08	3,64	Shorter	9,34E-42
966	CD59	-	3utr_2	10	5,12	5,33	Shorter	1,50E-41
10772	SRSF10	-	3utr_1	3	2,00	1,34	Longer	2,72E-41
1153	CIRBP	+	3utr_1	3	2,06	2,03	Longer	3,96E-41
5515	PPP2CA	-	3utr_1	8	1,24	1,25	Shorter	4,26E-41
7465	WEE1	+	3utr_2	6	3,83	4,89	Shorter	5,04E-41
155435	RBM33	+	3utr_3	3	2,67	2,33	Longer	7,32E-41
439921	MXRA7	-	3utr_1	4	3,44	3,19	Longer	1,49E-40
3032	HADHB	+	3utr_1	3	1,91	1,82	Longer	3,14E-40
10602	CDC42EP3	-	3utr_1	6	4,11	4,46	Shorter	3,92E-40
5208	PFKFB2	+	3utr_1	2	1,98	1,92	Longer	3,95E-40
130827	TMEM182	+	3utr_1	6	4,79	4,59	Longer	1,73E-39
11343	MGLL	-	3utr_1	7	6,30	5,88	Longer	4,43E-39
7057	THBS1	+	3utr_1	4	2,25	1,68	Longer	7,22E-39
5175	PECAM1	-	3utr	4	3,41	3,23	Longer	1,44E-37
1523	CUX1	+	3utr_1	6	4,55	5,11	Shorter	4,22E-37
1213	CLTC	+	3utr_2	6	4,02	3,81	Longer	1,62E-36
6400	SEL1L	-	3utr_1	4	2,70	2,86	Shorter	3,54E-36
5052	PRDX1	-	3utr_1	2	1,57	1,44	Longer	8,38E-36
57226	LYRM2	-	3utr_5	4	2,80	2,03	Longer	8,50E-36
8417	STX7	-	3utr_1	5	2,68	1,78	Longer	2,54E-35
7145	TNS1	-	3utr_1	4	3,96	3,86	Longer	7,11E-35
220988	HNRNPA3	+	3utr_1	6	2,46	3,06	Shorter	7,18E-35
6523	SLC5A1	+	3utr_1	5	2,25	2,52	Shorter	8,86E-35
10026	PIGK	-	3utr_1	4	2,12	3,20	Shorter	1,82E-34
6517	SLC2A4	+	3utr_2	4	2,87	2,68	Longer	3,74E-34
64854	USP46	-	3utr_1	5	3,29	2,80	Longer	5,52E-34

92140	MTDH	+	3utr_1	2	1,48	1,82	Shorter	1,19E-33
192670	EIF2C4	+	3utr_1	7	5,05	4,42	Longer	1,26E-33
8886	DDX18	+	3utr_1	3	2,37	2,76	Shorter	3,18E-33
7375	USP4	-	3utr_1	5	2,12	2,50	Shorter	4,29E-33
5573	PRKAR1A	+	3utr_1	9	8,26	8,48	Shorter	4,34E-33
ENSG000002	no	-	3utr	6	5,52	5,52	Shorter	4,51E-33
9948	WDR1	-	3utr_1	3	1,90	1,78	Longer	9,96E-33
1508	CTSB	-	3utr_1	5	2,22	2,12	Longer	1,19E-32
4026	LPP	+	3utr_2	6	4,35	4,62	Shorter	1,65E-32
1979	EIF4EBP2	+	3utr_1	5	3,50	4,02	Shorter	2,22E-32
9411	ARHGAP29	-	3utr_2	7	3,20	3,98	Shorter	2,60E-32
518	ATP5G3	-	3utr_1	4	2,01	2,00	Longer	3,49E-32
1994	ELAVL1	-	3utr_1	4	2,00	2,01	Shorter	4,46E-32
57129	MRPL47	-	3utr_1	3	1,77	1,42	Longer	6,63E-32
152137	CCDC50	+	3utr_1	6	4,58	4,45	Longer	1,01E-31
9702	CEP57	+	3utr_4	3	1,70	2,60	Shorter	1,48E-31
80306	MED28	+	3utr_1	5	4,04	4,37	Shorter	1,80E-31
5350	PLN	+	3utr-extend	5	4,09	4,27	Shorter	3,32E-31
55255	WDR41	-	3utr_3	4	2,48	2,03	Longer	5,09E-31
3183	HNRNPC	-	3utr_1	4	1,22	1,32	Shorter	7,91E-31
5606	MAP2K3	+	3utr_2	2	1,21	1,70	Shorter	8,47E-31
3915	LAMC1	+	3utr_2	4	3,35	3,13	Longer	9,73E-31
23281	MTUS2	+	3utr_1	2	1,84	1,17	Longer	1,01E-30
5478	PPIA	+	3utr_2	2	1,09	1,33	Shorter	1,14E-30
9444	QKI	+	3utr_3	12	4,92	5,09	Shorter	1,73E-30
2947	GSTM3	-	3utr_1	4	2,08	1,60	Longer	2,08E-30
10944	C11orf58	+	3utr_2	5	2,95	3,21	Shorter	2,64E-30
23543	RBFOX2	-	3utr_1	7	6,19	6,61	Shorter	3,50E-30
2982	GUCY1A3	+	3utr_3	5	3,26	2,50	Longer	4,03E-30
148534	TMEM56	+	3utr_1	6	3,44	3,83	Shorter	4,72E-30
1808	DPYSL2	+	3utr_2	4	2,20	2,38	Shorter	7,09E-30
821	CANX	+	3utr_2	8	6,53	6,51	Longer	1,22E-29
253017	TECRL	-	3utr_1	2	1,09	1,02	Longer	1,37E-29
81669	CCNL2	-	3utr_1	3	1,65	1,74	Shorter	1,65E-29
29103	DNAJC15	+	3utr_1	3	2,17	1,73	Longer	1,90E-29
25932	CLIC4	+	3utr_1	3	1,27	1,30	Shorter	4,91E-29
26190	FBXW2	-	3utr_2	5	1,98	2,34	Shorter	5,25E-29
515	ATP5F1	+	3utr_1	2	1,46	1,18	Longer	6,28E-29
8085	MLL2	-	3utr	2	1,13	1,44	Shorter	9,24E-29
10346	TRIM22	+	3utr_1	2	1,92	1,81	Longer	1,17E-28
90139	TSPAN18	+	3utr_1	3	2,79	2,68	Longer	1,36E-28
51747	LUC7L3	+	3utr_5	4	2,68	2,96	Shorter	1,67E-28
219931	TPCN2	+	3utr_2	3	2,19	2,87	Shorter	1,92E-28
5160	PDHA1	+	3utr_2	5	2,98	2,99	Shorter	2,19E-28
129446	XIRP2	+	3utr-extend	4	3,79	3,51	Longer	3,03E-28
221395	GPR116	-	3utr_1	4	2,89	3,04	Shorter	3,17E-28
10728	PTGES3	-	3utr_1	2	1,86	1,56	Longer	3,98E-28
6566	SLC16A1	-	3utr_1	5	3,22	3,20	Longer	5,18E-28
7072	TIA1	-	3utr_1	6	4,06	4,43	Shorter	8,27E-28
338657	CCDC84	+	3utr_1	2	1,06	1,33	Shorter	1,01E-27
441024	MTHFD2L	+	3utr_1	3	1,60	2,18	Shorter	1,17E-27
5833	PCYT2	-	3utr_1	5	1,81	1,78	Longer	1,27E-27
7750	ZMYM2	+	3utr_4	5	1,84	2,29	Shorter	1,31E-27
6647	SOD1	+	3utr_1	4	2,39	2,14	Longer	1,32E-27
10380	BPNT1	-	3utr_1	3	1,89	2,59	Shorter	1,39E-27
27295	PDLIM3	-	3utr_1	5	2,81	3,25	Shorter	2,19E-27
55692	LUC7L	-	3utr_1	2	1,92	1,73	Longer	2,31E-27
23011	RAB21	+	3utr_1	7	2,83	2,71	Longer	4,08E-27
23327	NEDD4L	+	3utr_1	5	3,51	3,28	Longer	5,78E-27
55837	EAPP	-	3utr_1	2	1,35	1,14	Longer	6,31E-27
3983	ABLIM1	-	3utr_1	4	3,99	3,99	Shorter	7,12E-27
22808	MRAS	+	3utr_1	4	3,37	3,52	Shorter	7,75E-27
10135	NAMPT	-	3utr_1	2	1,12	1,34	Shorter	7,91E-27
2626	GATA4	+	3utr_2	2	2,00	1,93	Longer	9,18E-27
23350	U2SURP	+	3utr_3	4	2,35	2,63	Shorter	1,13E-26
84236	RHBDD1	+	3utr_2	2	1,54	1,99	Shorter	1,40E-26
55122	AKIRIN2	-	3utr_1	3	2,35	2,23	Longer	1,88E-26
4060	LUM	-	3utr_1	3	1,06	1,15	Shorter	1,88E-26
6767	ST13	-	3utr_1	6	2,34	2,25	Longer	2,13E-26

5230	PGK1	+	3utr_1	4	1,05	1,09	Shorter	3,32E-26
824	CAPN2	+	3utr_1	3	2,01	2,02	Shorter	4,84E-26
410	ARSA	-	3utr_1	3	1,55	2,08	Shorter	5,24E-26
9774	BCLAF1	-	3utr_1	5	3,07	2,66	Longer	5,37E-26
9019	MPZL1	+	3utr_2	2	1,93	1,81	Longer	8,06E-26
57125	PLXDC1	-	3utr_1	2	1,08	1,26	Shorter	8,33E-26
8473	OGT	+	3utr_2	3	2,50	2,70	Shorter	8,86E-26
7453	WARS	-	3utr_1	4	3,23	3,51	Shorter	8,97E-26
9716	AQR	-	3utr_1	3	1,85	2,48	Shorter	1,12E-25
8125	ANP32A	-	3utr_1	4	2,53	2,61	Shorter	2,36E-25
1845	DUSP3	-	3utr_1	6	5,85	5,83	Longer	2,53E-25
5094	PCBP2	+	3utr_5	5	1,12	1,23	Shorter	2,69E-25
1390	CREM	+	3utr_2	4	2,64	3,13	Shorter	3,06E-25
154810	AMOTL1	+	3utr_1	3	2,60	2,21	Longer	3,26E-25
140885	SIRPA	+	3utr_1	2	1,82	1,65	Longer	5,53E-25
26505	CNNM3	+	3utr_1	3	1,46	2,20	Shorter	6,99E-25
5648	MASP1	-	3utr_4	8	5,99	5,72	Longer	1,44E-24
55208	DCUN1D2	-	3utr_1	3	2,96	2,87	Longer	1,73E-24
55075	UACA	-	3utr_1	4	1,49	1,76	Shorter	1,95E-24
23741	EID1	+	3utr_1	4	1,63	1,39	Longer	2,16E-24
54472	TOLLIP	-	3utr_1	3	2,03	1,80	Longer	2,80E-24
5164	PDK2	+	3utr_2	2	1,05	1,17	Shorter	3,04E-24
753	C18orf1	+	3utr_1	4	2,89	3,32	Shorter	3,10E-24
10169	SERF2	+	3utr_1	3	1,70	1,41	Longer	4,17E-24
8467	SMARCA5	+	3utr_1	3	1,77	2,02	Shorter	6,63E-24
90268	FAM105B	+	3utr_2	2	1,01	1,58	Shorter	8,28E-24
6648	SOD2	-	3utr_1	5	3,50	3,61	Shorter	1,14E-23
64397	ZFP106	-	3utr_1	5	4,90	4,96	Shorter	1,15E-23
64393	ZMAT3	-	3utr_1	3	2,64	2,14	Longer	1,29E-23
9318	COPS2	-	3utr_1	6	2,84	3,70	Shorter	1,42E-23
56998	CTNNBIP1	-	3utr_1	4	2,27	2,59	Shorter	1,42E-23
50807	ASAP1	-	3utr_1	3	2,96	2,84	Longer	1,67E-23
1634	DCN	-	3utr_1	6	3,04	3,07	Shorter	1,75E-23
55366	LGR4	-	3utr_1	3	1,94	2,05	Shorter	2,40E-23
23002	DAAM1	+	3utr_3	8	6,64	5,70	Longer	2,64E-23
29990	PILRB	+	3utr_1	2	1,58	1,24	Longer	2,84E-23
5154	PDGFA	-	3utr_1	2	1,92	1,77	Longer	3,05E-23
23484	LEPROTL1	+	3utr_1	3	2,74	2,50	Longer	3,28E-23
9406	ZRANB2	-	3utr_1	4	3,77	3,20	Longer	3,99E-23
283377	SPRYD4	+	3utr_1	2	1,89	1,57	Longer	4,06E-23
84188	FAR1	+	3utr_2	3	2,05	2,22	Shorter	4,12E-23
1072	CFL1	-	3utr_3	2	1,23	1,36	Shorter	4,38E-23
7415	VCP	-	3utr_1	3	2,57	2,43	Longer	4,39E-23
80323	CCDC68	-	3utr_1	2	1,90	1,47	Longer	6,04E-23
139231	FAM199X	+	3utr_1	3	2,73	2,69	Longer	9,48E-23
3454	IFNAR1	+	3utr_1	4	2,62	2,45	Longer	1,04E-22
94056	SYAP1	+	3utr_1	3	1,73	1,21	Longer	1,09E-22
3021	H3F3B	-	3utr_1	5	2,65	3,03	Shorter	2,17E-22
79647	AKIRIN1	+	3utr_2	3	2,45	2,91	Shorter	2,22E-22
10473	HMGN4	+	3utr_1	2	1,70	1,88	Shorter	2,39E-22
553115	PEF1	-	3utr_1	2	1,69	1,86	Shorter	2,85E-22
2805	GOT1	-	3utr_1	3	2,81	2,73	Longer	3,11E-22
167838	TXLNB	-	3utr_1	3	2,92	3,00	Shorter	4,02E-22
51014	TMED7	-	3utr_1	4	3,25	3,82	Shorter	4,24E-22
6427	SRSF2	-	3utr_1	3	2,35	2,15	Longer	4,66E-22
57608	KIAA1462	-	3utr_1	4	3,23	3,71	Shorter	4,83E-22
221477	C6orf89	+	3utr_1	7	2,83	2,87	Shorter	6,23E-22
137886	UBXN2B	+	3utr-extend	3	1,65	1,94	Shorter	6,69E-22
29117	BRD7	-	3utr_1	2	1,51	1,31	Longer	6,96E-22
8428	STK24	-	3utr_1	5	3,74	3,53	Longer	7,62E-22
10988	METAP2	+	3utr_1	2	1,13	1,22	Shorter	1,36E-21
57538	ALPK3	+	3utr_1	3	2,25	2,26	Shorter	1,92E-21
377	ARF3	-	3utr_2	3	2,36	2,23	Longer	2,12E-21
63976	PRDM16	+	3utr_1	5	3,12	3,60	Shorter	2,55E-21
27069	GHITM	+	3utr_1	9	4,22	3,97	Longer	2,55E-21
9877	ZC3H11A	+	3utr_2	2	1,93	1,84	Longer	2,70E-21
775	CACNA1C	+	3utr_3	7	3,42	3,31	Longer	3,20E-21
91775	FAM55C	+	3utr_1	5	2,02	2,42	Shorter	3,22E-21
5768	QSOX1	+	3utr_2	3	1,42	1,11	Longer	3,26E-21

6619	SNAPC3	+	3utr_3	4	1,45	2,16	Shorter	4,01E-21
152926	PPM1K	-	3utr_1	5	2,33	1,57	Longer	4,11E-21
11034	DSTN	+	3utr_1	4	3,20	3,05	Longer	4,12E-21
27032	ATP2C1	+	3utr_1	4	2,49	2,84	Shorter	5,19E-21
375449	MAST4	+	3utr_5	3	2,51	2,76	Shorter	5,38E-21
83856	FSD1L	+	3utr_3	2	1,33	1,93	Shorter	6,16E-21
10146	G3BP1	+	3utr_4	6	5,31	5,38	Shorter	6,85E-21
54960	GEMIN8	-	3utr_1	3	1,32	1,94	Shorter	7,45E-21
7334	UBE2N	-	3utr_2	4	2,05	2,06	Shorter	7,46E-21
9874	TLK1	-	3utr_1	5	2,34	2,38	Shorter	7,63E-21
5087	PBX1	+	3utr_1	4	3,77	3,95	Shorter	9,36E-21
6137	RPL13	+	3utr_1	4	1,15	1,11	Longer	1,05E-20
53981	CPSF2	+	3utr_2	5	2,84	3,37	Shorter	1,40E-20
65055	REEP1	-	3utr_1	3	2,34	1,58	Longer	1,43E-20
55703	POLR3B	+	3utr_1	3	2,57	1,79	Longer	1,50E-20
23	ABCF1	+	3utr_1	3	1,61	1,47	Longer	1,57E-20
55176	SEC61A2	+	3utr_4	3	2,00	1,44	Longer	1,64E-20
9158	FIBP	-	3utr_1	2	1,36	1,07	Longer	1,69E-20
54870	QRICH1	-	3utr_1	4	3,58	3,47	Longer	1,93E-20
2040	STOM	-	3utr_1	2	1,46	1,53	Shorter	2,45E-20
55740	ENAH	-	3utr_1	6	5,29	5,04	Longer	2,46E-20
8837	CFLAR	+	3utr_5	8	5,70	5,85	Shorter	2,48E-20
57132	CHMP1B	+	3utr_1	5	3,07	3,63	Shorter	2,52E-20
659	BMPR2	+	3utr_2	7	5,85	6,22	Shorter	2,55E-20
8239	USP9X	+	3utr_1	7	2,06	2,17	Shorter	2,88E-20
5000	ORC4	-	3utr_1	3	1,13	1,79	Shorter	2,88E-20
4128	MAOA	+	3utr_1	2	1,99	1,98	Longer	2,93E-20
91807	MYLK3	-	3utr_1	7	4,37	4,22	Longer	2,94E-20
7328	UBE2H	-	3utr_1	3	2,93	2,89	Longer	3,13E-20
83637	ZMIZ2	+	3utr_2	2	1,22	1,44	Shorter	3,14E-20
283464	GXYLT1	-	3utr_1	3	1,90	2,35	Shorter	3,58E-20
7026	NR2F2	+	3utr_1	5	3,08	3,61	Shorter	3,82E-20
64710	NUCKS1	-	3utr_1	10	7,58	7,65	Shorter	4,96E-20
4774	NFIA	+	3utr_1	3	2,39	2,37	Longer	5,94E-20
7468	WHSC1	+	3utr_4	3	1,72	2,10	Shorter	6,32E-20
55183	RIF1	+	3utr_3	4	1,73	2,83	Shorter	6,63E-20
57224	NHSL1	-	3utr_1	3	2,01	2,27	Shorter	6,92E-20
90624	LYRM7	+	3utr_1	4	3,92	3,84	Longer	8,17E-20
55973	BCAP29	+	3utr_3	5	3,18	3,32	Shorter	1,02E-19
55742	PARVA	+	3utr_3	10	6,85	6,57	Longer	1,09E-19
8724	SNX3	-	3utr_1	3	2,00	2,26	Shorter	1,19E-19
11149	BVES	-	3utr_1	4	2,62	2,48	Longer	1,24E-19
6885	MAP3K7	-	3utr_1	4	3,16	3,00	Longer	1,64E-19
51573	GDE1	-	3utr_1	4	3,38	3,43	Shorter	1,87E-19
29890	RBM15B	+	3utr_1	2	1,14	1,00	Longer	1,88E-19
11030	RBPMS	+	3utr_3	5	4,69	4,66	Longer	1,91E-19
1282	COL4A1	-	3utr_1	4	2,70	2,10	Longer	1,94E-19
83931	STK40	-	3utr_1	3	1,57	2,13	Shorter	2,14E-19
1462	VCAN	+	3utr_2	7	5,51	5,66	Shorter	2,15E-19
400961	PAIP2B	-	3utr_1	3	1,08	1,21	Shorter	2,21E-19
64432	MRPS25	-	3utr_3	2	1,39	1,20	Longer	2,31E-19
54708	mrt-05	+	3utr_1	4	3,01	2,79	Longer	2,88E-19
5834	PYGB	+	3utr_1	3	2,90	2,86	Longer	2,99E-19
9604	RNF14	+	3utr_2	4	3,95	3,83	Longer	3,03E-19
7326	UBE2G1	-	3utr_1	3	1,75	2,08	Shorter	3,28E-19
84191	FAM96A	-	3utr_1	2	1,78	1,92	Shorter	3,30E-19
1501	CTNND2	-	3utr_1	3	2,04	1,90	Longer	3,51E-19
128240	APOA1BP	+	3utr_1	3	1,64	1,47	Longer	3,92E-19
9445	ITM2B	+	3utr_1	6	1,90	1,93	Shorter	4,45E-19
5101	PCDH9	-	3utr_1	2	1,91	1,64	Longer	6,03E-19
8943	AP3D1	-	3utr_1	4	3,77	3,92	Shorter	7,20E-19
414	ARSD	-	3utr_1	2	1,96	1,68	Longer	8,43E-19
1289	COL5A1	+	3utr_1	4	2,28	2,65	Shorter	8,92E-19
23001	WDFY3	-	3utr_1	5	3,33	3,26	Longer	9,25E-19
55031	USP47	+	3utr_5	8	5,17	4,54	Longer	1,51E-18
79991	OBFC1	-	3utr_1	4	2,31	2,33	Shorter	1,51E-18
1983	EIF5	+	3utr_1	8	3,26	3,95	Shorter	1,58E-18
64412	GZF1	+	3utr_1	4	2,78	3,39	Shorter	1,59E-18
84248	FYTTD1	+	3utr_2	3	2,89	2,77	Longer	1,93E-18

3638	INSIG1	+	3utr_1	3	2,99	2,85	Longer	2,18E-18
667	DST	-	3utr_1	4	2,76	2,88	Shorter	2,21E-18
51340	CRNKL1	-	3utr_1	3	2,47	2,40	Longer	2,39E-18
488	ATP2A2	+	3utr_2	4	3,39	3,43	Shorter	2,49E-18
5563	PRKAA2	+	3utr_1	6	4,08	4,55	Shorter	2,59E-18
166	AES	-	3utr_1	2	1,48	1,42	Longer	3,83E-18
79876	UBA5	+	3utr_2	4	2,72	2,41	Longer	4,04E-18
2752	GLUL	-	3utr_1	3	1,97	1,99	Shorter	4,05E-18
509	ATP5C1	+	3utr_3	2	1,96	1,92	Longer	4,45E-18
10527	IPO7	+	3utr_2	5	2,44	2,88	Shorter	4,84E-18
10336	PCGF3	+	3utr_2	3	2,76	2,91	Shorter	5,63E-18
54205	CYCS	-	3utr_1	5	3,77	3,82	Shorter	5,65E-18
219771	CCNY	+	3utr_1	4	1,10	1,20	Shorter	6,10E-18
9464	HAND2	-	3utr_1	7	3,24	3,61	Shorter	6,11E-18
151242	PPP1R1C	+	3utr_2	5	2,68	3,10	Shorter	7,83E-18
3688	ITGB1	-	3utr_1	2	1,19	1,13	Longer	8,56E-18
8566	PDXK	+	3utr_2	6	3,91	3,63	Longer	8,84E-18
25972	UNC50	+	3utr_1	2	1,69	2,00	Shorter	9,15E-18
3281	HSBP1	+	3utr_1	3	1,52	1,46	Longer	9,82E-18
2909	ARHGAP35	+	3utr	3	2,72	2,82	Shorter	1,02E-17
83987	CCDC8	-	3utr_1	3	1,89	2,09	Shorter	1,23E-17
27067	STAU2	-	3utr_1	2	1,45	1,76	Shorter	1,29E-17
9761	MLEC	+	3utr_1	4	3,62	3,77	Shorter	1,41E-17
7323	UBE2D3	-	3utr_1	6	3,40	3,62	Shorter	1,46E-17
23705	CADM1	-	3utr_2	5	3,25	4,04	Shorter	1,53E-17
23216	TBC1D1	+	3utr_3	2	1,32	1,12	Longer	1,62E-17
55666	NPLOC4	-	3utr_1	2	1,53	1,79	Shorter	1,67E-17
23111	SPG20	-	3utr_1	3	1,90	1,86	Longer	1,84E-17
10768	AHCYL1	+	3utr_1	5	2,68	2,87	Shorter	1,88E-17
10060	ABCC9	-	3utr_1	5	4,29	4,54	Shorter	1,94E-17
23499	MACF1	+	3utr_7	3	2,61	2,40	Longer	1,97E-17
51520	LARS	-	3utr_1	2	1,17	1,32	Shorter	2,41E-17
8165	AKAP1	+	3utr_1	3	2,80	2,66	Longer	2,86E-17
83988	NCALD	-	3utr_1	4	2,54	2,50	Longer	3,24E-17
55109	AGGF1	+	3utr_2	3	1,81	2,38	Shorter	3,28E-17
633	BGN	+	3utr_1	2	2,00	1,99	Longer	3,99E-17
4289	MKLN1	+	3utr_3	5	4,37	4,24	Longer	4,02E-17
10075	HUWE1	-	3utr_1	2	1,73	1,55	Longer	4,47E-17
64848	YTHDC2	+	3utr_3	3	2,36	2,39	Shorter	4,67E-17
3423	IDS	-	3utr_1	5	4,32	4,22	Longer	4,72E-17
10625	IVNS1ABP	-	3utr_1	6	3,34	2,91	Longer	4,81E-17
23660	ZKSCAN5	+	3utr_1	3	1,99	1,89	Longer	5,00E-17
55193	PBRM1	-	3utr_1	3	2,72	2,85	Shorter	5,84E-17
2260	FGFR1	-	3utr_1	6	2,41	2,38	Longer	7,19E-17
9946	CRYZL1	-	3utr_1	3	2,11	2,36	Shorter	7,41E-17
79780	CCDC82	-	3utr_1	3	2,05	2,28	Shorter	7,57E-17
122704	MRPL52	+	3utr_1	2	1,33	1,08	Longer	8,32E-17
253782	CERS6	+	3utr-extend	2	1,05	1,34	Shorter	8,36E-17
4719	NDUFS1	-	3utr_1	5	2,30	2,60	Shorter	8,36E-17
2273	FHL1	+	3utr_1	5	4,40	4,14	Longer	9,11E-17
51318	MRPL35	+	3utr_1	6	2,89	3,07	Shorter	9,24E-17
3643	INSR	-	3utr_1	6	5,37	5,31	Longer	1,11E-16
26520	TIMM9	-	3utr_1	3	1,65	1,75	Shorter	1,21E-16
9360	PPIG	+	3utr_4	2	1,56	1,22	Longer	1,32E-16
22931	RAB18	+	3utr_1	5	2,76	2,64	Longer	1,34E-16
4627	MYH9	-	3utr_1	3	2,40	2,52	Shorter	1,56E-16
3767	KCNJ11	-	3utr_1	2	1,07	1,44	Shorter	1,71E-16
2318	FLNC	+	3utr_1	4	3,87	3,87	Shorter	1,82E-16
81545	FBXO38	+	3utr_1	3	1,10	1,31	Shorter	1,82E-16
10632	ATP5L	+	3utr_1	3	1,02	1,03	Shorter	2,26E-16
90102	PHLDB2	+	3utr_3	3	1,38	1,63	Shorter	2,35E-16
678	ZFP36L2	-	3utr_1	2	2,00	1,88	Longer	2,58E-16
11231	SEC63	-	3utr_1	4	2,20	1,95	Longer	2,71E-16
83660	TLN2	+	3utr_2	3	2,41	2,69	Shorter	2,88E-16
116254	C6orf72	+	3utr_2	3	2,44	2,75	Shorter	3,16E-16
84064	HDHD2	-	3utr_1	2	1,97	1,88	Longer	3,24E-16
80218	NAA50	-	3utr_1	7	3,59	3,55	Longer	3,33E-16
202333	CMYA5	+	3utr_1	4	3,80	3,72	Longer	3,49E-16
689	BTF3	+	3utr_2	3	1,98	1,84	Longer	3,58E-16

55745	MUDENG	+	3utr_3	3	2,64	2,14	Longer	3,63E-16
91369	ANKRD40	-	3utr_1	4	3,63	3,83	Shorter	3,96E-16
1182	CLCN3	+	3utr_1	4	3,78	3,89	Shorter	4,00E-16
19	ABCA1	-	3utr_1	3	2,94	2,39	Longer	4,12E-16
1947	EFNB1	+	3utr_1	2	1,46	1,24	Longer	4,64E-16
81034	SLC25A32	-	3utr_1	2	1,41	1,69	Shorter	5,06E-16
6558	SLC12A2	+	3utr_1	3	2,81	2,46	Longer	5,21E-16
10749	KIF1C	+	3utr_1	6	2,24	2,23	Longer	5,40E-16
10241	CALCOCO2	+	3utr_1	6	3,34	3,61	Shorter	5,94E-16
29090	C18orf55	+	3utr_1	3	2,50	1,90	Longer	6,12E-16
57159	TRIM54	+	3utr_1	2	1,73	1,65	Longer	6,27E-16
2332	FMR1	+	3utr_2	3	2,20	2,47	Shorter	6,66E-16
1428	CRYM	-	3utr_1	3	2,94	2,87	Longer	6,83E-16
26060	APPL1	+	3utr_2	5	3,92	4,32	Shorter	7,07E-16
8678	BECN1	-	3utr_1	3	2,97	2,94	Longer	7,61E-16
6482	ST3GAL1	-	3utr_1	2	1,85	1,94	Shorter	8,11E-16
ENSG000002	no	-	3utr	2	1,02	1,31	Shorter	8,34E-16
1654	DDX3X	+	3utr_2	3	2,49	2,42	Longer	8,87E-16
54915	YTHDF1	-	3utr_1	2	1,66	1,84	Shorter	9,34E-16
4090	SMAD5	+	3utr_1	2	1,94	1,99	Shorter	9,94E-16
23468	CBX5	-	3utr_1	5	2,75	2,31	Longer	1,19E-15
34	ACADM	+	3utr_5	4	3,01	3,04	Shorter	1,30E-15
56255	TMX4	-	3utr_1	3	2,53	2,26	Longer	1,30E-15
6168	RPL37A	+	3utr_1	5	1,06	1,07	Shorter	1,32E-15
55847	CISD1	+	3utr_1	6	3,69	4,24	Shorter	1,37E-15
4999	ORC2	-	3utr_1	3	2,11	1,95	Longer	1,43E-15
57604	KIAA1456	+	3utr_1	2	1,71	1,34	Longer	1,49E-15
10001	MED6	-	3utr_2	2	1,57	1,18	Longer	1,54E-15
1974	EIF4A2	+	3utr_1	2	1,28	1,39	Shorter	1,58E-15
7707	ZNF148	-	3utr_1	6	3,09	3,29	Shorter	1,61E-15
4969	OGN	-	3utr_1	4	3,44	2,98	Longer	1,69E-15
283131	NEAT1	+	3utr	11	5,41	5,67	Shorter	1,73E-15
4329	ALDH6A1	-	3utr_1	7	3,40	4,29	Shorter	1,78E-15
8540	AGPS	+	3utr_2	2	1,94	1,26	Longer	1,84E-15
81614	NIPA2	-	3utr_1	3	1,71	2,22	Shorter	1,84E-15
92259	MRPS36	+	3utr_1	7	4,19	4,04	Longer	1,97E-15
60492	CCDC90B	-	3utr_1	3	2,33	2,48	Shorter	2,11E-15
5537	PPP6C	-	3utr_1	7	3,13	3,18	Shorter	2,27E-15
26135	SERBP1	-	3utr_1	4	2,33	2,26	Longer	2,37E-15
10105	PPIF	+	3utr_1	2	1,14	1,44	Shorter	2,75E-15
1678	TIMM8A	-	3utr_1	3	1,51	1,70	Shorter	2,80E-15
64327	LMBR1	-	3utr_1	5	2,63	3,76	Shorter	2,87E-15
2926	GRSF1	-	3utr_1	6	3,68	3,32	Longer	2,89E-15
339487	ZBTB8OS	-	3utr_1	2	1,50	1,19	Longer	2,91E-15
54499	TMCO1	-	3utr_1	6	2,14	2,34	Shorter	3,01E-15
79875	THSD4	+	3utr_4	4	3,83	3,87	Shorter	3,16E-15
22927	HABP4	+	3utr_1	2	1,60	1,33	Longer	3,17E-15
134265	AFAP1L1	+	3utr_2	3	1,63	1,97	Shorter	3,59E-15
23029	RBM34	-	3utr_1	2	1,42	1,12	Longer	4,25E-15
729	C6	-	3utr_1	3	1,43	1,22	Longer	5,16E-15
64344	HIF3A	+	3utr_9	3	1,95	2,28	Shorter	6,36E-15
7320	UBE2B	+	3utr_1	5	3,88	3,80	Longer	6,41E-15
817	CAMK2D	-	3utr_1	5	3,01	3,10	Shorter	6,81E-15
55924	C1orf183	-	3utr_2	4	3,37	2,82	Longer	7,09E-15
9470	EIF4E2	+	3utr_3	2	1,35	1,67	Shorter	7,33E-15
11156	PTP4A3	+	3utr-extend	2	1,05	1,14	Shorter	7,33E-15
22822	PHLDA1	-	3utr_1	9	6,15	6,59	Shorter	7,41E-15
10611	PDLIM5	+	3utr_4	5	3,80	3,68	Longer	7,78E-15
3069	HDLBP	-	3utr_1	2	1,04	1,11	Shorter	8,82E-15
1454	CSNK1E	-	3utr_1	4	3,22	2,86	Longer	8,89E-15
7422	VEGFA	+	3utr_2	4	3,51	3,49	Longer	1,13E-14
9209	LRRFIP2	-	3utr_1	3	2,46	2,68	Shorter	1,22E-14
466	ATF1	+	3utr_2	3	1,90	2,45	Shorter	1,24E-14
23731	C9orf5	-	3utr_1	6	5,74	5,64	Longer	1,26E-14
51021	MRPS16	-	3utr_2	3	2,76	2,62	Longer	1,28E-14
1837	DTNA	+	3utr_3	2	1,33	1,03	Longer	1,33E-14
112399	EGLN3	-	3utr_1	5	2,58	2,83	Shorter	1,52E-14
286451	YIPF6	+	3utr_1	3	1,90	2,15	Shorter	1,53E-14
10627	MYL12A	+	3utr-extend	4	1,17	1,08	Longer	1,60E-14

80830	APOL6	+	3utr_1	3	2,52	1,81	Longer	1,88E-14
22874	PLEKHA6	-	3utr_1	3	2,01	1,34	Longer	2,13E-14
2115	ETV1	-	3utr_1	6	3,97	4,05	Shorter	2,19E-14
25828	TXN2	-	3utr_1	3	2,32	2,56	Shorter	2,20E-14
754	PTTG1IP	-	3utr_1	2	2,00	1,99	Longer	2,22E-14
2673	GFPT1	-	3utr_1	6	4,54	4,91	Shorter	2,29E-14
51247	PAIP2	+	3utr_1	3	2,90	2,72	Longer	2,55E-14
4659	PPP1R12A	-	3utr_4	2	1,67	1,05	Longer	2,79E-14
119032	C10orf32	+	3utr_1	6	3,60	4,40	Shorter	3,13E-14
5993	RFX5	-	3utr_1	2	1,04	1,31	Shorter	3,19E-14
3712	IVD	+	3utr_1	3	2,32	2,26	Longer	3,24E-14
998	CDC42	+	3utr_1	4	2,37	1,56	Longer	3,31E-14
55023	PHIP	-	3utr_1	4	2,98	2,90	Longer	3,43E-14
79770	TXNDC15	+	3utr_1	4	2,87	3,09	Shorter	3,78E-14
6747	SSR3	-	3utr_1	5	3,63	3,82	Shorter	3,88E-14
30001	ERO1L	-	3utr_1	3	1,80	1,86	Shorter	3,97E-14
5439	POLR2J	-	3utr_1	2	1,01	1,10	Shorter	4,19E-14
11078	TRIOBP	+	3utr_3	4	2,44	2,48	Shorter	4,24E-14
10488	CREB3	+	3utr_1	2	1,26	1,05	Longer	4,90E-14
57404	CYP20A1	+	3utr_2	5	3,17	2,69	Longer	6,01E-14
51729	WBP11	-	3utr_1	2	1,50	1,71	Shorter	6,20E-14
51465	UBE2J1	-	3utr_1	5	2,97	2,94	Longer	6,52E-14
11155	LDB3	+	3utr-extend	4	2,74	3,07	Shorter	7,03E-14
29095	ORMDL2	+	3utr_1	3	1,48	1,19	Longer	7,24E-14
51409	HEMK1	+	3utr_2	2	1,01	1,18	Shorter	7,43E-14
137964	AGPAT6	+	3utr_2	3	1,98	2,21	Shorter	7,78E-14
3749	KCNC4	+	3utr_3	3	2,40	2,37	Longer	7,93E-14
6711	SPTBN1	+	3utr_2	8	5,09	5,35	Shorter	8,14E-14
9694	TTC35	+	3utr-extend	3	1,50	1,20	Longer	8,33E-14
23369	PUM2	-	3utr_1	2	1,65	1,29	Longer	8,47E-14
4601	MXI1	+	3utr_1	3	2,41	2,15	Longer	8,66E-14
29079	MED4	-	3utr_2	3	1,26	1,28	Shorter	8,80E-14
63035	BCORL1	+	3utr_1	2	1,95	1,78	Longer	9,64E-14
54431	DNAJC10	+	3utr_2	6	4,45	4,08	Longer	1,31E-13
26263	FBXO22	+	3utr_2	3	2,11	2,54	Shorter	1,35E-13
5876	RABGGTB	+	3utr_2	3	2,51	2,06	Longer	1,45E-13
84869	CBR4	-	3utr_2	2	1,04	1,28	Shorter	1,50E-13
1627	DBN1	-	3utr_1	3	2,62	2,13	Longer	1,54E-13
647087	C7orf73	+	3utr_1	5	1,97	2,01	Shorter	1,58E-13
152007	GLIPR2	+	3utr_2	3	2,12	1,85	Longer	1,67E-13
7381	UQCRB	-	3utr_2	2	1,95	1,60	Longer	1,68E-13
11309	SLCO2B1	+	3utr_2	3	2,30	2,67	Shorter	1,74E-13
65983	GRAMD3	+	3utr_3	4	2,25	2,44	Shorter	1,77E-13
55529	TMEM55A	-	3utr_1	4	2,46	3,05	Shorter	1,77E-13
51705	EMCN	-	3utr_1	5	2,78	2,22	Longer	1,83E-13
4919	ROR1	+	3utr_2	3	2,67	2,54	Longer	2,15E-13
1277	COL1A1	-	3utr_1	5	3,56	3,30	Longer	2,18E-13
2580	GAK	-	3utr_1	2	2,00	1,97	Longer	2,21E-13
2824	GPM6B	-	3utr_1	2	1,68	1,27	Longer	2,24E-13
7402	UTRN	+	3utr_2	2	1,97	1,81	Longer	2,28E-13
23786	BCL2L13	+	3utr_2	3	1,86	1,58	Longer	2,71E-13
125150	ZSWIM7	-	3utr_1	2	1,48	1,27	Longer	2,76E-13
9913	SUPT7L	-	3utr_1	4	2,19	2,13	Longer	2,92E-13
375056	MIA3	+	3utr_2	4	3,45	3,14	Longer	2,94E-13
10299	mrt-06	+	3utr_2	3	2,56	1,90	Longer	3,06E-13
324	APC	+	3utr_2	4	2,85	2,22	Longer	3,07E-13
23091	ZC3H13	-	3utr_1	2	1,34	1,52	Shorter	3,25E-13
4905	NSF	+	3utr_1	2	1,99	1,77	Longer	3,77E-13
57210	SLC45A4	-	3utr_1	2	1,96	1,80	Longer	3,81E-13
9667	SAFB2	-	3utr_1	2	1,75	1,62	Longer	3,82E-13
57198	ATP8B2	+	3utr	2	1,45	1,76	Shorter	3,84E-13
55254	TMEM39A	-	3utr_1	4	2,36	2,61	Shorter	3,99E-13
9218	VAPA	+	3utr_1	4	2,33	2,23	Longer	4,16E-13
23471	TRAM1	-	3utr_1	3	2,84	2,96	Shorter	4,52E-13
9958	USP15	+	3utr_4	3	1,99	1,54	Longer	4,77E-13
10313	RTN3	+	3utr_1	3	1,67	1,71	Shorter	5,04E-13
9926	LPGAT1	-	3utr_1	3	2,72	2,36	Longer	5,09E-13
4191	MDH2	+	3utr_1	4	3,15	3,08	Longer	5,60E-13
79646	PANK3	-	3utr_1	3	2,96	2,88	Longer	5,97E-13

55669	MFN1	+	3utr_1	2	1,82	1,94	Shorter	6,29E-13
51020	HDDC2	-	3utr_1	3	1,98	2,03	Shorter	6,43E-13
23408	SIRT5	+	3utr_2	5	2,10	2,13	Shorter	6,73E-13
8743	TNFSF10	-	3utr_1	2	1,28	1,71	Shorter	7,21E-13
4660	PPP1R12B	+	3utr_2	7	3,70	4,21	Shorter	7,45E-13
153222	C5orf41	+	3utr_2	4	3,26	3,31	Shorter	7,84E-13
4691	NCL	-	3utr_1	4	3,61	3,67	Shorter	8,02E-13
56894	AGPAT3	+	3utr_1	4	3,07	3,07	Longer	8,15E-13
51230	PHF20	+	3utr_4	4	3,40	3,67	Shorter	8,24E-13
1108	CHD4	-	3utr_1	3	1,31	1,67	Shorter	8,40E-13
6184	RPN1	-	3utr_1	4	3,13	2,71	Longer	8,42E-13
23014	FBXO21	-	3utr_1	4	2,22	2,53	Shorter	8,48E-13
2885	GRB2	-	3utr_1	4	2,46	2,55	Shorter	8,57E-13
22879	MON1B	+	3utr_1	2	1,80	1,45	Longer	8,62E-13
1605	DAG1	+	3utr_2	2	1,97	2,00	Shorter	8,74E-13
84706	GPT2	+	3utr_1	2	1,32	1,67	Shorter	9,37E-13
6925	TCF4	-	3utr_1	4	3,06	2,85	Longer	9,44E-13
6304	SATB1	-	3utr_1	4	2,89	2,85	Longer	1,02E-12
8945	BTRC	+	3utr_1	3	2,82	2,83	Shorter	1,03E-12
55914	ERBB2IP	+	3utr_1	3	1,98	2,03	Shorter	1,06E-12
2257	FGF12	-	3utr_1	8	5,24	5,46	Shorter	1,07E-12
28958	CCDC56	-	3utr_2	2	1,47	1,09	Longer	1,08E-12
3184	HNRNPD	-	3utr_1	4	3,15	2,93	Longer	1,12E-12
8905	AP1S2	-	3utr_1	2	1,21	1,31	Shorter	1,12E-12
27327	TNRC6A	+	3utr_3	4	3,23	2,97	Longer	1,17E-12
1453	CSNK1D	-	3utr_1	3	2,73	2,85	Shorter	1,23E-12
57184	C15orf17	-	3utr_1	3	2,70	2,81	Shorter	1,32E-12
3257	HPS1	-	3utr_11	2	1,72	1,43	Longer	1,50E-12
948	CD36	+	3utr_2	4	3,29	3,44	Shorter	1,60E-12
80011	FAM192A	-	3utr_1	5	2,36	2,91	Shorter	1,61E-12
9631	NUP155	-	3utr_1	3	1,98	2,51	Shorter	1,63E-12
114799	ESCO1	-	3utr-extend	3	1,17	1,70	Shorter	1,64E-12
64786	TBC1D15	+	3utr_4	3	1,79	1,95	Shorter	1,67E-12
51271	UBAP1	+	3utr_2	2	1,60	1,36	Longer	1,86E-12
8609	KLF7	-	3utr_1	5	3,62	3,24	Longer	1,94E-12
51012	SLMO2	-	3utr_1	3	1,63	1,97	Shorter	1,96E-12
10558	SPTLC1	-	3utr_1	2	1,71	1,55	Longer	2,18E-12
58499	ZNF462	+	3utr_2	3	2,04	2,43	Shorter	2,20E-12
10492	SYNCRIP	-	3utr_1	4	3,50	3,73	Shorter	2,38E-12
1545	CYP1B1	-	3utr_2	5	3,13	2,97	Longer	2,42E-12
51097	SCCPDH	+	3utr_1	4	2,70	2,56	Longer	2,51E-12
171024	SYNPO2	+	3utr_1	5	1,11	1,07	Longer	2,51E-12
84649	DGAT2	+	3utr_1	2	1,69	1,29	Longer	2,52E-12
196394	AMN1	-	3utr_1	4	1,71	2,12	Shorter	2,90E-12
317649	EIF4E3	-	3utr_1	5	2,47	2,36	Longer	2,97E-12
30835	CD209	-	3utr_1	2	1,60	1,90	Shorter	3,15E-12
258010	SVIP	-	3utr_2	4	2,37	2,30	Longer	3,25E-12
84640	USP38	+	3utr_2	3	1,93	1,87	Longer	3,60E-12
7572	ZNF24	-	3utr_1	3	2,39	2,28	Longer	4,00E-12
4841	NONO	+	3utr_1	2	1,98	1,90	Longer	4,00E-12
55684	C9orf86	+	3utr_2	3	1,17	1,56	Shorter	4,08E-12
23012	STK38L	+	3utr_3	5	2,89	3,00	Shorter	4,34E-12
4134	MAP4	-	3utr_1	3	2,88	2,83	Longer	4,62E-12
56203	LMOD3	-	3utr_1	3	1,37	1,47	Shorter	4,79E-12
9412	MED21	+	3utr_2	2	1,11	1,56	Shorter	5,50E-12
7529	YWHAB	+	3utr_1	5	2,89	2,87	Longer	5,84E-12
7337	UBE3A	-	3utr_1	5	3,82	3,64	Longer	6,15E-12
528	ATP6V1C1	+	3utr_1	5	2,70	3,24	Shorter	6,41E-12
22990	PCNX	+	3utr_2	5	2,86	3,74	Shorter	6,69E-12
ENSG000002	no	-	3utr	2	1,41	1,93	Shorter	7,14E-12
123	PLIN2	-	3utr_2	2	1,91	1,70	Longer	7,18E-12
65258	MPPE1	-	3utr_1	3	2,35	2,13	Longer	7,29E-12
311	ANXA11	-	3utr_1	4	2,72	3,16	Shorter	7,74E-12
283337	ZNF740	+	3utr_1	3	2,42	2,70	Shorter	8,95E-12
441478	NRARP	-	3utr_1	3	1,37	1,95	Shorter	9,53E-12
3309	HSPA5	-	3utr_1	2	1,03	1,08	Shorter	1,00E-11
50862	RNF141	-	3utr_1	3	1,91	1,69	Longer	1,04E-11
1622	DBI	+	3utr_1	2	1,88	2,00	Shorter	1,05E-11
6923	TCEB2	-	3utr_1	2	1,03	1,00	Longer	1,07E-11

89122	TRIM4	-	3utr_1	2	1,58	1,14	Longer	1,18E-11
905	CCNT2	+	3utr_2	2	1,49	1,96	Shorter	1,22E-11
23604	DAPK2	-	3utr_1	2	1,41	1,24	Longer	1,26E-11
4076	CAPRIN1	+	3utr_2	5	2,24	1,62	Longer	1,27E-11
7528	YY1	+	3utr_1	6	3,23	2,76	Longer	1,28E-11
29967	LRP12	-	3utr_1	3	2,64	2,81	Shorter	1,29E-11
196528	ARID2	+	3utr_3	4	2,87	2,00	Longer	1,29E-11
11155	LDB3	+	3utr_4	6	5,80	5,78	Longer	1,29E-11
221078	NSUN6	-	3utr_1	3	2,23	2,78	Shorter	1,30E-11
3964	LGALS8	+	3utr_3	5	3,37	3,62	Shorter	1,36E-11
117178	SSX2IP	-	3utr_1	4	2,23	3,00	Shorter	1,38E-11
57506	MAVS	+	3utr_2	6	4,58	4,83	Shorter	1,43E-11
7170	TPM3	-	3utr_2	4	1,43	1,32	Longer	1,49E-11
127253	TYW3	+	3utr_1	2	1,10	1,34	Shorter	1,54E-11
6546	SLC8A1	-	3utr_1	2	2,00	1,99	Longer	1,56E-11
79939	SLC35E1	-	3utr_1	4	3,37	2,87	Longer	1,74E-11
85476	GFM1	+	3utr_3	5	2,31	2,45	Shorter	1,75E-11
3480	IGF1R	+	3utr_1	3	1,95	1,80	Longer	1,82E-11
571	BACH1	+	3utr_1	2	1,27	1,60	Shorter	1,99E-11
6659	SOX4	+	3utr_1	5	2,77	2,90	Shorter	2,23E-11
394	ARHGAP5	+	3utr_1	8	5,47	5,57	Shorter	2,44E-11
58487	CREBZF	-	3utr_1	6	3,03	2,93	Longer	2,85E-11
84886	C1orf198	-	3utr_1	4	3,63	3,70	Shorter	3,03E-11
254170	FBXO33	-	3utr_1	2	1,13	1,58	Shorter	3,09E-11
7520	XRCC5	+	3utr_1	4	3,75	3,74	Longer	3,17E-11
3192	HNRNPU	-	3utr_1	4	2,31	2,08	Longer	3,55E-11
126792	B3GALT6	+	3utr_1	3	2,00	2,14	Shorter	3,76E-11
89797	NAV2	+	3utr_1	3	2,82	2,97	Shorter	3,78E-11
5194	PEX13	+	3utr_2	4	2,53	2,81	Shorter	3,84E-11
7447	VSNL1	+	3utr_1	6	3,58	3,63	Shorter	4,49E-11
51501	C11orf73	+	3utr_1	2	1,64	1,33	Longer	4,57E-11
89910	UBE3B	+	3utr_2	2	1,95	1,82	Longer	4,58E-11
163131	ZNF780B	-	3utr_1	3	1,88	2,21	Shorter	5,22E-11
9991	PTBP3	-	3utr_1	4	2,96	2,71	Longer	5,41E-11
10193	RNF41	-	3utr_1	2	1,69	1,82	Shorter	5,68E-11
55266	TMEM19	+	3utr_2	4	2,34	2,03	Longer	5,77E-11
996	CDC27	-	3utr_1	7	5,12	5,36	Shorter	5,94E-11
6515	SLC2A3	-	3utr_1	2	1,92	1,98	Shorter	6,02E-11
159090	FAM122B	-	3utr_1	3	1,99	1,94	Longer	6,05E-11
10466	COG5	-	3utr_1	4	3,31	3,41	Shorter	6,36E-11
7082	TJP1	-	3utr_1	4	2,94	3,03	Shorter	6,95E-11
22826	DNAJC8	-	3utr_1	2	1,94	1,99	Shorter	7,06E-11
8310	ACOX3	-	3utr_1	5	3,37	3,63	Shorter	7,64E-11
80856	KIAA1715	-	3utr_1	3	2,47	1,81	Longer	7,77E-11
88	ACTN2	+	3utr_1	7	2,72	2,66	Longer	7,81E-11
7106	TSPAN4	+	3utr_1	2	1,98	1,85	Longer	8,44E-11
7107	GPR137B	+	3utr_2	2	1,96	1,83	Longer	8,65E-11
9200	PTPLA	-	3utr_1	3	2,11	2,21	Shorter	8,66E-11
2355	FOSL2	+	3utr_1	4	3,21	3,04	Longer	8,74E-11
51028	VPS36	-	3utr_1	4	2,85	2,73	Longer	8,90E-11
8682	PEA15	+	3utr_1	2	1,98	1,95	Longer	8,92E-11
390980	ZNF805	+	3utr_1	2	1,46	1,02	Longer	9,87E-11
81563	C1orf21	+	3utr_1	6	3,40	3,45	Shorter	1,02E-10
5935	RBM3	+	3utr_1	2	1,01	1,00	Longer	1,09E-10
8545	CGGBP1	-	3utr_1	4	2,80	2,87	Shorter	1,15E-10
5527	PPP2R5C	+	3utr_7	6	3,38	3,34	Longer	1,25E-10
7321	UBE2D1	+	3utr_1	2	1,09	1,13	Shorter	1,29E-10
6443	SGCB	-	3utr_1	5	4,78	4,64	Longer	1,31E-10
25852	ARMC8	+	3utr_2	2	1,49	1,71	Shorter	1,32E-10
5130	PCYT1A	-	3utr_2	2	1,99	1,97	Longer	1,32E-10
79660	PPP1R3B	-	3utr_1	2	2,00	1,95	Longer	1,33E-10
57003	CCDC47	-	3utr_1	3	2,47	2,34	Longer	1,36E-10
8427	ZNF282	+	3utr_2	2	1,45	1,18	Longer	1,39E-10
10659	CELF2	+	3utr_3	6	4,96	4,94	Longer	1,41E-10
3655	ITGA6	+	3utr_2	2	1,12	1,26	Shorter	1,45E-10
1601	DAB2	-	3utr_1	3	2,31	2,11	Longer	1,50E-10
8614	STC2	-	3utr_1	3	1,36	1,64	Shorter	1,50E-10
4291	MLF1	+	3utr_3	2	1,10	1,18	Shorter	1,54E-10
23545	ATP6V0A2	+	3utr_3	3	1,27	1,62	Shorter	1,57E-10

8560	DEGS1	+	3utr_1	2	1,95	1,83	Longer	1,65E-10
4052	LTBP1	+	3utr_1	4	3,19	3,15	Longer	1,75E-10
1183	CLCN4	+	3utr_1	3	1,93	2,26	Shorter	1,89E-10
4053	LTBP2	-	3utr_1	4	3,27	2,95	Longer	2,09E-10
1073	CFL2	-	3utr_1	6	4,16	4,38	Shorter	2,09E-10
6638	SNRPN	+	3utr_1	2	1,00	1,01	Shorter	2,12E-10
138050	HGSNAT	+	3utr_2	2	1,25	1,12	Longer	2,24E-10
5663	PSEN1	+	3utr_3	2	1,94	1,61	Longer	2,33E-10
54796	BNC2	-	3utr_1	2	1,26	1,75	Shorter	2,46E-10
79139	DERL1	-	3utr_1	4	3,27	2,92	Longer	2,47E-10
80232	WDR26	-	3utr_1	6	5,13	5,14	Shorter	2,63E-10
54976	C20orf27	-	3utr_1	2	1,79	1,94	Shorter	2,64E-10
291	SLC25A4	+	3utr_1	2	1,02	1,01	Longer	2,69E-10
950	SCARB2	-	3utr_1	6	3,51	3,60	Shorter	2,69E-10
2222	FDFT1	+	3utr_3	5	4,00	3,98	Longer	2,84E-10
28231	SLCO4A1	+	3utr_1	3	1,94	2,03	Shorter	2,85E-10
10061	ABCF2	-	3utr_2	3	1,23	1,48	Shorter	2,86E-10
55852	TEX2	-	3utr_1	2	1,50	1,33	Longer	2,98E-10
23313	KIAA0930	-	3utr_1	3	1,66	1,44	Longer	3,14E-10
1629	DBT	-	3utr_1	5	3,21	3,17	Longer	3,38E-10
79665	DHX40	+	3utr_2	2	1,94	2,00	Shorter	3,39E-10
140739	UBE2F	+	3utr_3	6	2,70	3,16	Shorter	3,69E-10
2997	GYS1	-	3utr_1	2	2,00	1,98	Longer	3,73E-10
5480	PPIC	-	3utr_1	3	2,07	2,24	Shorter	3,80E-10
27125	AFF4	-	3utr_1	2	1,96	1,74	Longer	3,97E-10
156	ADRBK1	+	3utr_1	2	2,00	1,99	Longer	3,98E-10
1385	CREB1	+	3utr_3	3	2,83	2,93	Shorter	4,59E-10
57459	GATAD2B	-	3utr_1	4	2,63	2,39	Longer	4,96E-10
11170	FAM107A	-	3utr_1	4	1,56	1,58	Shorter	5,37E-10
202052	DNAJC18	-	3utr_2	2	1,39	1,00	Longer	5,39E-10
10580	SORBS1	-	3utr_1	2	2,00	1,99	Longer	5,63E-10
6605	SMARCE1	-	3utr_1	3	1,80	1,95	Shorter	5,91E-10
126298	IRGQ	-	3utr_1	3	1,98	1,95	Longer	6,12E-10
5787	PTPRB	-	3utr_1	8	2,65	2,54	Longer	6,14E-10
125704	FAM69C	-	3utr_1	2	1,82	1,44	Longer	6,57E-10
4008	LMO7	+	3utr_2	6	3,38	3,42	Shorter	6,64E-10
221264	AKD1	-	3utr_6	2	1,82	1,31	Longer	6,65E-10
116983	ACAP3	-	3utr_1	2	1,46	1,32	Longer	6,68E-10
8496	PPFIBP1	+	3utr_3	4	2,81	2,75	Longer	6,70E-10
81858	SHARPIN	-	3utr_1	2	1,78	1,92	Shorter	7,13E-10
80335	WDR82	-	3utr_1	4	3,87	3,95	Shorter	7,18E-10
166785	MMAA	+	3utr_1	2	1,99	1,88	Longer	7,54E-10
6434	TRA2B	-	3utr_1	4	2,70	2,70	Shorter	7,96E-10
64400	AKTIP	-	3utr_1	3	2,06	1,49	Longer	9,15E-10
22871	NLGN1	+	3utr_2	3	2,09	2,09	Longer	9,26E-10
56984	PSMG2	+	3utr_1	2	1,98	1,90	Longer	9,29E-10
ENSG000002	no	-	3utr	2	1,33	1,78	Shorter	1,03E-09
80198	MUS81	+	3utr_1	2	1,75	2,00	Shorter	1,04E-09
202018	TAPT1	-	3utr_1	3	1,71	1,35	Longer	1,08E-09
10971	YWHAQ	-	3utr_1	3	1,25	1,46	Shorter	1,10E-09
81566	CSRNP2	-	3utr_1	3	2,10	2,66	Shorter	1,10E-09
91624	NEXN	+	3utr-extend	2	1,61	1,80	Shorter	1,11E-09
5685	PSMA4	+	3utr_1	3	2,65	2,42	Longer	1,14E-09
22982	DIP2C	-	3utr_1	3	1,96	2,03	Shorter	1,17E-09
400	ARL1	-	3utr_1	4	2,12	2,29	Shorter	1,33E-09
57472	CNOT6	+	3utr_1	3	1,80	1,92	Shorter	1,34E-09
6812	STXBP1	+	3utr_1	2	1,97	1,85	Longer	1,40E-09
51150	SDF4	-	3utr_1	2	1,99	1,94	Longer	1,47E-09
11100	HNRNPUL1	+	3utr_1	6	3,99	4,09	Shorter	1,48E-09
5562	PRKAA1	-	3utr_1	5	3,33	3,32	Longer	1,49E-09
79850	FAM57A	+	3utr-extend	2	1,31	1,85	Shorter	1,53E-09
4238	MFAP3	+	3utr_1	2	1,18	1,62	Shorter	1,73E-09
259217	HSPA12A	-	3utr_1	2	1,73	1,99	Shorter	1,82E-09
284273	ZADH2	-	3utr_1	6	2,69	2,98	Shorter	1,88E-09
84187	TMEM164	+	3utr_1	3	2,14	1,99	Longer	1,94E-09
84327	ZBED3	-	3utr_1	3	2,08	1,97	Longer	1,95E-09
9725	TMEM63A	-	3utr_1	2	1,84	1,99	Shorter	1,99E-09
84230	LRRC8C	+	3utr_2	3	2,69	2,67	Longer	2,02E-09
55591	VEZT	+	3utr_7	3	2,03	1,83	Longer	2,17E-09

2730	GCLM	-	3utr_1	2	1,71	1,23	Longer	2,18E-09
5519	PPP2R1B	-	3utr_3	2	1,32	1,78	Shorter	2,25E-09
8887	TAX1BP1	+	3utr_1	7	3,71	3,65	Longer	2,30E-09
253017	TECRL	-	3utr_2	5	2,49	2,52	Shorter	2,38E-09
11154	AP4S1	+	3utr_2	2	1,22	1,00	Longer	2,39E-09
26986	PABPC1	-	3utr_1	2	1,98	1,90	Longer	2,41E-09
4776	NFATC4	+	3utr_2	2	1,00	1,20	Shorter	2,49E-09
7170	TPM3	-	3utr_1	2	1,56	1,88	Shorter	2,60E-09
57513	CASKIN2	-	3utr_1	2	1,94	2,00	Shorter	2,72E-09
8611	PPAP2A	-	3utr_1	3	2,73	2,60	Longer	2,78E-09
4833	NME4	+	3utr_1	3	2,23	2,36	Shorter	2,80E-09
55504	TNFRSF19	+	3utr_3	3	2,13	2,41	Shorter	2,86E-09
114907	FBXO32	-	3utr_1	4	3,80	3,77	Longer	2,87E-09
26002	MOXD1	-	3utr_1	2	1,99	1,90	Longer	2,93E-09
55186	SLC25A36	+	3utr_2	4	3,91	3,89	Longer	3,02E-09
6612	SUMO3	-	3utr_1	4	3,92	3,96	Shorter	3,12E-09
5411	PNN	+	3utr_3	5	3,84	3,19	Longer	3,12E-09
25963	TMEM87A	-	3utr_1	2	1,92	1,99	Shorter	3,14E-09
65084	TMEM135	+	3utr_2	3	1,86	2,49	Shorter	3,29E-09
147179	WIPF2	+	3utr_2	2	1,70	1,87	Shorter	3,35E-09
23198	PSME4	-	3utr_1	3	2,55	2,47	Longer	3,35E-09
100526835	FPGT-TNNI3K	+	3utr_1	2	1,82	1,98	Shorter	3,62E-09
54602	NDFIP2	+	3utr_1	6	3,75	3,88	Shorter	4,04E-09
103910	MYL12B	+	3utr_1	2	1,16	1,21	Shorter	4,27E-09
55326	AGPAT5	+	3utr_1	3	1,32	1,16	Longer	4,31E-09
7957	EPM2A	-	3utr_1	4	3,09	3,20	Shorter	4,36E-09
79980	DSN1	-	3utr_1	2	1,53	1,92	Shorter	4,40E-09
80755	AARSD1	-	3utr_6	3	2,43	2,54	Shorter	4,42E-09
1267	CNP	+	3utr_1	2	1,06	1,23	Shorter	4,59E-09
91607	SLFN11	-	3utr_1	2	1,76	1,91	Shorter	4,67E-09
894	CCND2	+	3utr_1	3	2,99	2,99	Shorter	4,73E-09
9481	SLC25A27	+	3utr_1	2	1,80	1,93	Shorter	4,74E-09
23137	SMC5	+	3utr_1	2	1,98	1,92	Longer	4,75E-09
11337	GABARAP	-	3utr_1	3	2,97	2,99	Shorter	4,76E-09
51569	UFM1	+	3utr_1	5	3,46	3,11	Longer	4,76E-09
11325	DDX42	+	3utr_1	2	1,74	1,61	Longer	4,80E-09
196441	ZFC3H1	-	3utr_1	2	1,65	1,34	Longer	5,01E-09
1977	EIF4E	-	3utr_1	4	2,28	1,93	Longer	5,02E-09
6217	RPS16	-	3utr_1	3	2,98	2,96	Longer	5,30E-09
24138	IFIT5	+	3utr_1	5	2,82	2,93	Shorter	5,50E-09
473	RERE	-	3utr_1	4	3,95	3,92	Longer	5,53E-09
90806	ANGEL2	-	3utr_1	2	1,69	1,85	Shorter	5,62E-09
10253	SPRY2	-	3utr_1	2	1,61	1,97	Shorter	5,91E-09
2635	GBP3	-	3utr_1	2	1,93	1,50	Longer	5,94E-09
3799	KIF5B	-	3utr_1	4	3,73	3,76	Shorter	6,13E-09
10049	DNAJB6	+	3utr_3	2	1,99	1,97	Longer	6,17E-09
9266	CYTH2	+	3utr_2	2	1,09	1,27	Shorter	6,28E-09
55333	SYNJ2BP	-	3utr_1	5	4,07	3,73	Longer	6,32E-09
4204	MECP2	-	3utr_1	5	4,05	3,56	Longer	6,39E-09
51121	RPL26L1	+	3utr_1	2	1,18	1,32	Shorter	6,56E-09
9901	SRGAP3	-	3utr_1	2	1,44	1,78	Shorter	6,58E-09
11315	PARK7	+	3utr_1	2	1,06	1,02	Longer	7,40E-09
815	CAMK2A	-	3utr_1	4	2,87	3,47	Shorter	8,25E-09
29068	ZBTB44	-	3utr_1	5	3,09	3,50	Shorter	8,28E-09
65056	GPBP1	+	3utr_1	4	1,39	1,52	Shorter	8,79E-09
49855	SCAPER	-	3utr_1	2	1,14	1,62	Shorter	9,98E-09
4082	MARCKS	+	3utr_1	3	2,02	2,03	Shorter	1,06E-08
79134	TMEM185B	-	3utr_1	4	3,21	3,59	Shorter	1,08E-08
6208	RPS14	-	3utr_1	2	1,98	2,00	Shorter	1,14E-08
10152	ABI2	+	3utr_4	4	3,88	3,73	Longer	1,15E-08
4677	NARS	-	3utr_1	5	4,86	4,80	Longer	1,15E-08
889	KRIT1	-	3utr_1	2	1,10	1,20	Shorter	1,19E-08
79685	SAP30L	+	3utr_1	2	1,34	1,11	Longer	1,22E-08
91746	YTHDC1	-	3utr_1	3	2,19	2,17	Longer	1,24E-08
25	ABL1	+	3utr_1	2	1,71	1,89	Shorter	1,27E-08
94239	H2AFV	-	3utr_1	3	2,73	2,13	Longer	1,27E-08
2957	GTF2A1	-	3utr_1	2	1,48	1,89	Shorter	1,31E-08
55670	PEX26	+	3utr_1	2	1,77	2,00	Shorter	1,37E-08
151742	PPM1L	+	3utr_2	5	3,31	3,80	Shorter	1,39E-08

8451	CUL4A	+	3utr_1	6	5,11	4,83	Longer	1,43E-08
9444	QKI	+	3utr_2	4	3,22	3,22	Longer	1,50E-08
2395	FXN	+	3utr_1	4	1,95	2,40	Shorter	1,59E-08
3572	IL6ST	-	3utr_1	5	3,78	3,93	Shorter	1,64E-08
25978	CHMP2B	+	3utr_1	3	1,92	2,24	Shorter	1,76E-08
25898	RCHY1	-	3utr_1	4	2,60	2,31	Longer	1,81E-08
6045	RNF2	+	3utr_1	2	1,60	1,93	Shorter	1,83E-08
730	C7	+	3utr_1	2	1,34	1,66	Shorter	1,83E-08
374291	NDUFS7	+	3utr_1	2	1,99	1,97	Longer	1,84E-08
619279	ZNF704	-	3utr_1	4	3,56	3,22	Longer	1,84E-08
6431	SRSF6	+	3utr_1	4	1,70	1,76	Shorter	1,87E-08
4957	ODF2	+	3utr_5	2	1,13	1,27	Shorter	1,89E-08
10494	STK25	-	3utr_1	3	1,63	1,83	Shorter	1,90E-08
6303	SAT1	+	3utr_2	2	1,97	1,90	Longer	1,92E-08
5162	PDHB	-	3utr_1	5	3,54	3,70	Shorter	1,92E-08
23141	ANKLE2	-	3utr_1	3	2,26	2,00	Longer	1,97E-08
9782	MATR3	+	3utr_1	2	1,81	1,95	Shorter	1,98E-08
114883	OSBPL9	+	3utr_3	3	2,09	1,99	Longer	2,02E-08
7799	PRDM2	+	3utr_2	2	1,74	1,36	Longer	2,02E-08
55603	FAM46A	-	3utr_1	4	3,80	3,84	Shorter	2,03E-08
3992	FADS1	-	3utr_1	2	2,00	1,97	Longer	2,03E-08
165918	RNF168	-	3utr_1	3	1,47	1,89	Shorter	2,05E-08
57217	TTC7A	+	3utr_2	3	2,39	1,96	Longer	2,08E-08
54989	ZNF770	-	3utr_1	2	2,00	1,97	Longer	2,08E-08
9532	BAG2	+	3utr_1	4	1,77	1,73	Longer	2,10E-08
819	CAMLG	+	3utr_1	2	1,05	1,00	Longer	2,10E-08
5360	PLTP	-	3utr_1	2	1,01	1,04	Shorter	2,16E-08
57148	RALGAPB	+	3utr_3	3	2,59	2,54	Longer	2,24E-08
1293	COL6A3	-	3utr_1	2	1,84	1,92	Shorter	2,34E-08
83693	HSDL1	-	3utr_1	4	2,01	2,55	Shorter	2,45E-08
79607	FAM118B	+	3utr_1	3	1,75	2,15	Shorter	2,62E-08
63877	FAM204A	-	3utr_1	2	1,46	1,07	Longer	2,63E-08
54664	TMEM106B	+	3utr_3	4	3,68	3,45	Longer	2,69E-08
54532	USP53	+	3utr_2	2	1,36	1,79	Shorter	2,79E-08
29097	CNIH4	+	3utr_1	3	1,28	1,13	Longer	2,91E-08
60559	SPCS3	+	3utr_1	4	3,42	3,50	Shorter	2,97E-08
26985	AP3M1	-	3utr_1	4	3,15	2,70	Longer	2,99E-08
10827	FAM114A2	-	3utr_1	4	2,61	2,19	Longer	3,02E-08
57763	ANKRA2	-	3utr_1	2	1,20	1,60	Shorter	3,12E-08
10144	FAM13A	-	3utr_1	2	1,38	1,07	Longer	3,16E-08
8031	NCOA4	+	3utr_1	2	1,99	2,00	Shorter	3,37E-08
51312	SLC25A37	+	3utr_1	2	1,76	1,99	Shorter	3,37E-08
440574	MINOS1	+	3utr_1	3	1,08	1,04	Longer	3,40E-08
84897	TBRG1	+	3utr_2	3	1,86	1,50	Longer	3,52E-08
51031	GLOD4	-	3utr_1	3	1,31	1,55	Shorter	3,69E-08
10480	EIF3M	+	3utr_4	2	1,78	1,38	Longer	3,87E-08
1540	CYLD	+	3utr_5	2	1,14	1,41	Shorter	3,90E-08
9852	EPM2AIP1	-	3utr_1	3	2,75	2,72	Longer	3,92E-08
5058	PAK1	-	3utr_1	2	1,91	1,62	Longer	3,99E-08
222068	TMED4	-	3utr_1	2	1,82	1,91	Shorter	4,02E-08
800	CALD1	+	3utr_2	4	2,99	2,97	Longer	4,04E-08
9683	N4BP1	-	3utr_1	2	1,88	1,98	Shorter	4,11E-08
4811	NID1	-	3utr_1	3	2,42	2,18	Longer	4,13E-08
145173	B3GALTL	+	3utr_1	3	2,02	2,04	Shorter	4,20E-08
57690	TNRC6C	+	3utr_2	2	1,99	1,88	Longer	4,38E-08
23443	SLC35A3	+	3utr_1	2	1,05	1,20	Shorter	4,43E-08
55654	TMEM127	-	3utr_1	2	1,06	1,17	Shorter	4,51E-08
23243	ANKRD28	-	3utr_1	2	1,71	1,42	Longer	4,64E-08
2593	GAMT	-	3utr_2	2	1,94	1,48	Longer	4,85E-08
58986	TMEM8A	-	3utr_1	3	1,66	1,81	Shorter	4,88E-08
84864	MINA	-	3utr_1	2	1,90	1,52	Longer	4,98E-08
64123	ELTD1	-	3utr_1	2	1,75	1,56	Longer	5,56E-08
9929	JOSD1	-	3utr_1	2	1,03	1,07	Shorter	5,68E-08
130507	UBR3	+	3utr_1	6	5,48	5,44	Longer	5,80E-08
7172	TPMT	-	3utr_1	2	1,54	1,78	Shorter	6,15E-08
8237	USP11	+	3utr_1	2	1,31	1,03	Longer	6,25E-08
7434	VIPR2	-	3utr_1	2	1,66	1,46	Longer	6,28E-08
1965	EIF2S1	+	3utr_1	3	2,29	1,72	Longer	6,29E-08
9191	DEDD	-	3utr_1	3	1,64	2,20	Shorter	6,37E-08

25909	AHCTF1	-	3utr_1	2	1,33	1,12	Longer	6,38E-08
7168	TPM1	+	3utr_3	2	1,77	1,37	Longer	6,61E-08
54737	MPHOSPH8	+	3utr_3	2	1,97	1,86	Longer	7,21E-08
55102	ATG2B	-	3utr_1	2	1,18	1,46	Shorter	7,23E-08
27	ABL2	-	3utr_1	2	1,35	1,18	Longer	7,35E-08
81611	ANP32E	-	3utr_1	3	2,57	2,41	Longer	7,35E-08
ENSG000002	no	-	3utr	2	1,17	1,06	Longer	7,41E-08
135138	PACRG	+	3utr_1	2	1,53	1,84	Shorter	7,56E-08
1316	KLF6	-	3utr_1	2	1,00	1,03	Shorter	7,68E-08
9581	PREPL	-	3utr_2	4	2,95	2,96	Shorter	8,28E-08
1676	DFFA	-	3utr_1	2	1,18	1,05	Longer	8,52E-08
6251	RSU1	-	3utr_1	3	2,31	2,25	Longer	8,82E-08
142	PARP1	-	3utr_1	4	3,27	3,38	Shorter	9,00E-08
1314	COPA	-	3utr_1	2	1,03	1,07	Shorter	9,03E-08
2107	ETF1	-	3utr_1	4	2,62	2,44	Longer	9,24E-08
5576	PRKAR2A	-	3utr_1	5	4,54	4,61	Shorter	9,69E-08
27037	TRMT2A	-	3utr_1	2	1,49	1,12	Longer	1,00E-07
221496	LEMD2	-	3utr_1	2	1,47	1,31	Longer	1,00E-07
29083	GTPBP8	+	3utr_1	3	2,00	2,00	Longer	1,01E-07
57088	PLSCR4	-	3utr_1	2	1,62	1,95	Shorter	1,02E-07
10206	TRIM13	+	3utr_1	2	1,97	1,89	Longer	1,02E-07
10491	CRTAP	+	3utr_1	5	1,40	1,57	Shorter	1,02E-07
81533	ITFG1	-	3utr_1	3	2,64	2,58	Longer	1,03E-07
8503	PIK3R3	-	3utr_1	3	2,19	1,80	Longer	1,06E-07
10328	COX4NB	-	3utr_1	4	3,05	3,32	Shorter	1,07E-07
84826	SFT2D3	+	3utr_1	2	1,99	1,61	Longer	1,07E-07
5887	RAD23B	+	3utr_2	4	2,31	2,63	Shorter	1,08E-07
84726	PRRC2B	+	3utr_3	5	2,59	2,50	Longer	1,17E-07
148423	C1orf52	-	3utr_1	3	1,84	2,53	Shorter	1,22E-07
80212	CCDC92	-	3utr_3	3	2,80	2,80	Shorter	1,25E-07
64841	GNPNAT1	-	3utr_1	4	2,88	3,16	Shorter	1,25E-07
10138	YAF2	-	3utr_1	7	3,96	4,06	Shorter	1,27E-07
283989	TSEN54	+	3utr_2	2	1,65	1,32	Longer	1,28E-07
8766	RAB11A	+	3utr_1	5	2,95	3,00	Shorter	1,30E-07
23065	KIAA0090	-	3utr_1	2	1,78	1,47	Longer	1,31E-07
25939	SAMHD1	-	3utr_1	4	1,77	1,91	Shorter	1,35E-07
23593	HEBP2	+	3utr_1	2	1,13	1,03	Longer	1,37E-07
9147	NEMF	-	3utr_8	2	1,43	1,02	Longer	1,42E-07
6777	STAT5B	-	3utr_1	3	2,28	1,98	Longer	1,46E-07
127262	TPRG1L	+	3utr_1	2	1,99	1,97	Longer	1,47E-07
8675	STX16	+	3utr_3	5	3,49	3,78	Shorter	1,48E-07
6670	SP3	-	3utr_1	2	1,41	1,79	Shorter	1,50E-07
29091	STXBP6	-	3utr_1	4	1,97	1,76	Longer	1,54E-07
5150	PDE7A	-	3utr_1	3	1,15	1,31	Shorter	1,56E-07
6397	SEC14L1	+	3utr_1	2	1,60	1,14	Longer	1,57E-07
22926	ATF6	+	3utr_2	2	1,55	1,95	Shorter	1,58E-07
25994	HIGD1A	-	3utr_2	5	2,98	3,03	Shorter	1,63E-07
6599	SMARCC1	-	3utr_1	2	1,24	1,12	Longer	1,66E-07
92370	ACPL2	+	3utr_3	2	1,73	1,57	Longer	1,80E-07
3840	KPNA4	-	3utr_1	4	3,30	3,47	Shorter	1,81E-07
23082	PPRC1	+	3utr_1	2	1,20	1,59	Shorter	1,97E-07
55676	SLC30A6	+	3utr-extend	2	1,46	1,92	Shorter	2,03E-07
2746	GLUD1	-	3utr_1	3	2,00	1,98	Longer	2,06E-07
7188	TRAF5	+	3utr_1	2	1,67	1,24	Longer	2,07E-07
23095	KIF1B	+	3utr_1	3	2,84	2,67	Longer	2,11E-07
7979	SHFM1	-	3utr_7	2	1,99	1,91	Longer	2,14E-07
7468	WHSC1	+	3utr_3	3	2,03	1,58	Longer	2,18E-07
8301	PICALM	-	3utr_1	3	1,19	1,14	Longer	2,25E-07
8674	VAMP4	-	3utr_1	2	1,50	1,77	Shorter	2,26E-07
23291	FBXW11	-	3utr_1	4	2,82	3,13	Shorter	2,26E-07
10099	TSPAN3	-	3utr_1	3	2,94	2,98	Shorter	2,28E-07
7581	ZNF33A	+	3utr_2	2	1,97	1,75	Longer	2,31E-07
2817	GPC1	+	3utr_1	3	2,81	2,81	Shorter	2,49E-07
29980	DONSON	-	3utr_2	3	2,07	1,85	Longer	2,60E-07
51704	GPRC5B	-	3utr_1	2	1,23	1,35	Shorter	2,66E-07
9570	GOSR2	+	3utr_2	7	3,37	3,47	Shorter	2,75E-07
4205	MEF2A	+	3utr_1	4	2,91	3,04	Shorter	2,82E-07
9537	TP53I11	-	3utr_2	3	2,95	2,98	Shorter	2,89E-07
10752	CHL1	+	3utr_2	2	1,97	1,60	Longer	3,06E-07

4801	NFYB	-	3utr_1	7	3,82	3,63	Longer	3,07E-07
54947	LPCAT2	+	3utr_1	3	2,36	2,42	Shorter	3,09E-07
79577	CDC73	+	3utr_2	5	2,85	2,93	Shorter	3,14E-07
84079	ANKRD27	-	3utr_1	2	1,53	1,75	Shorter	3,28E-07
1635	DCTD	-	3utr_1	3	2,88	2,91	Shorter	3,38E-07
27067	STAU2	-	3utr_2	3	2,10	1,92	Longer	3,42E-07
22875	ENPP4	+	3utr_1	3	2,89	2,76	Longer	3,56E-07
51103	NDUFAF1	-	3utr_1	2	1,89	1,97	Shorter	3,73E-07
84912	SLC35B4	-	3utr_1	2	1,60	1,98	Shorter	3,75E-07
11056	DDX52	-	3utr_1	3	1,82	2,08	Shorter	3,78E-07
253461	ZBTB38	+	3utr_1	3	2,05	2,01	Longer	4,04E-07
4684	NCAM1	+	3utr_2	5	4,53	4,61	Shorter	4,14E-07
128077	LIX1L	+	3utr_1	3	2,05	1,83	Longer	4,17E-07
56888	KCMF1	+	3utr_1	5	1,73	1,74	Shorter	4,17E-07
8178	ELL	-	3utr_1	4	2,56	2,64	Shorter	4,52E-07
378	ARF4	-	3utr_1	2	1,98	1,95	Longer	4,57E-07
9330	GTF3C3	-	3utr_1	4	2,42	3,03	Shorter	4,76E-07
23036	ZNF292	+	3utr_3	3	2,15	2,16	Shorter	4,97E-07
5867	RAB4A	+	3utr_1	4	3,04	2,90	Longer	5,23E-07
127495	LRRC39	-	3utr_1	3	1,77	2,08	Shorter	5,32E-07
51109	RDH11	-	3utr_1	3	1,69	2,15	Shorter	5,36E-07
348093	RBPMS2	-	3utr_1	4	3,82	3,85	Shorter	5,58E-07
23261	CAMTA1	+	3utr_1	2	1,89	1,99	Shorter	5,63E-07
10923	SUB1	+	3utr_1	2	1,42	1,53	Shorter	5,63E-07
9112	MTA1	+	3utr_1	2	2,00	1,98	Longer	5,95E-07
9559	VPS26A	+	3utr_1	2	1,67	1,21	Longer	6,20E-07
23132	RAD54L2	+	3utr-extend	2	1,14	1,44	Shorter	6,26E-07
10806	SDCCAG8	+	3utr_1	2	1,12	1,55	Shorter	6,54E-07
57492	ARID1B	+	3utr_2	2	1,76	1,44	Longer	6,56E-07
6444	SGCD	+	3utr_4	4	2,27	2,03	Longer	6,87E-07
367	AR	+	3utr_3	4	2,75	2,98	Shorter	6,98E-07
862	RUNX1T1	-	3utr_1	2	1,06	1,16	Shorter	7,02E-07
7871	SLMAP	+	3utr-extend	3	1,47	1,38	Longer	7,54E-07
93621	MRFAP1	+	3utr_1	4	2,97	3,07	Shorter	8,23E-07
781	CACNA2D1	-	3utr_1	2	1,97	2,00	Shorter	8,28E-07
84962	AJUBA	-	3utr_1	3	1,88	2,00	Shorter	8,34E-07
5213	PFKM	+	3utr_4	2	1,96	1,87	Longer	8,66E-07
411	ARSB	-	3utr_1	2	1,83	1,97	Shorter	8,66E-07
113251	LARP4	+	3utr_2	3	2,17	2,66	Shorter	8,88E-07
55735	DNAJC11	-	3utr_1	2	1,88	1,94	Shorter	9,25E-07
22823	MTF2	+	3utr_2	2	1,75	1,39	Longer	9,47E-07
84961	FBXL20	-	3utr_1	3	2,64	2,37	Longer	9,58E-07
80169	CTC1	-	3utr_1	3	2,43	2,44	Shorter	9,75E-07
310	ANXA7	-	3utr_1	2	1,08	1,14	Shorter	9,88E-07
57644	MYH7B	+	3utr_1	3	1,92	1,97	Shorter	1,05E-06
10129	FRY	+	3utr_1	3	2,86	2,92	Shorter	1,06E-06
5318	PKP2	-	3utr_1	3	2,88	2,85	Longer	1,06E-06
5257	PHKB	+	3utr_2	5	3,20	3,06	Longer	1,10E-06
3831	KLC1	+	3utr_2	4	2,05	1,88	Longer	1,11E-06
51124	IER3IP1	-	3utr_1	2	1,98	1,95	Longer	1,13E-06
5774	PTPN3	-	3utr_1	2	1,53	1,73	Shorter	1,23E-06
6840	SVIL	-	3utr_1	3	2,39	2,42	Shorter	1,26E-06
4711	NDUFB5	+	3utr_1	4	2,85	2,78	Longer	1,39E-06
55588	MED29	+	3utr_1	3	1,80	1,80	Longer	1,42E-06
4892	NRAP	-	3utr_1	2	1,05	1,03	Longer	1,42E-06
7067	THRA	+	3utr_2	2	1,87	1,95	Shorter	1,43E-06
55291	PPP6R3	+	3utr_2	3	2,71	2,79	Shorter	1,44E-06
10417	SPON2	-	3utr_1	2	1,88	1,98	Shorter	1,50E-06
80315	CPEB4	+	3utr_1	4	2,89	3,12	Shorter	1,50E-06
5939	RBMS2	+	3utr_2	5	4,53	4,63	Shorter	1,51E-06
4149	MAX	-	3utr_2	3	2,65	2,65	Shorter	1,52E-06
1488	CTBP2	-	3utr_1	2	1,03	1,11	Shorter	1,54E-06
10948	STARD3	+	3utr_2	2	1,74	1,25	Longer	1,66E-06
7360	UGP2	+	3utr_5	2	2,00	1,99	Longer	1,80E-06
26097	CHTOP	+	3utr_3	4	1,30	1,26	Longer	1,81E-06
57606	SLAIN2	+	3utr_3	4	2,19	2,17	Longer	1,83E-06
58477	SRPRB	+	3utr_1	4	2,70	2,70	Longer	1,84E-06
5879	RAC1	+	3utr_1	4	3,05	3,08	Shorter	1,89E-06
51011	FAHD2A	+	3utr_1	2	1,13	1,03	Longer	2,02E-06

4043	LRPAP1	-	3utr_1	3	1,12	1,06	Longer	2,09E-06
5203	PFDN4	+	3utr_1	4	2,09	2,17	Shorter	2,10E-06
5337	PLD1	-	3utr_1	3	1,95	1,73	Longer	2,12E-06
25874	BRP44	-	3utr_1	3	1,22	1,24	Shorter	2,15E-06
114971	PTPMT1	+	3utr_1	3	2,13	2,03	Longer	2,23E-06
54629	FAM63B	+	3utr_1	3	2,69	2,88	Shorter	2,27E-06
29883	CNOT7	-	3utr_1	2	1,44	1,71	Shorter	2,32E-06
8897	MTMR3	+	3utr_1	5	3,07	3,42	Shorter	2,40E-06
27102	EIF2AK1	-	3utr_1	4	2,95	3,02	Shorter	2,46E-06
55870	ASH1L	-	3utr_1	2	1,92	1,99	Shorter	2,50E-06
8924	HERC2	-	3utr_1	3	2,53	2,38	Longer	2,52E-06
734	OSGIN2	+	3utr_2	5	2,49	2,45	Longer	2,63E-06
10579	TACC2	+	3utr_2	3	2,85	2,90	Shorter	2,64E-06
6385	SDC4	-	3utr_1	4	3,83	3,86	Shorter	2,68E-06
135293	PM20D2	+	3utr_1	2	2,00	1,82	Longer	2,71E-06
224	ALDH3A2	+	3utr_1	5	2,63	2,52	Longer	2,78E-06
51110	LACTB2	-	3utr_2	2	1,33	1,46	Shorter	2,79E-06
22856	CHSY1	-	3utr_1	2	1,83	1,61	Longer	2,80E-06
55207	ARL8B	+	3utr_3	3	2,32	2,23	Longer	2,92E-06
9960	USP3	+	3utr_4	2	1,66	1,89	Shorter	2,94E-06
6197	RPS6KA3	-	3utr_1	4	2,67	3,16	Shorter	2,94E-06
81542	TMX1	+	3utr_2	3	2,07	1,82	Longer	2,94E-06
51105	PHF20L1	+	3utr_4	3	2,76	2,69	Longer	3,10E-06
8079	MLF2	-	3utr_1	3	2,87	2,95	Shorter	3,16E-06
83930	STARD3NL	+	3utr_1	2	1,68	1,82	Shorter	3,26E-06
863	CBFA2T3	-	3utr_1	3	2,60	2,71	Shorter	3,35E-06
2050	EPHB4	-	3utr_1	2	1,94	1,77	Longer	3,52E-06
23017	FAIM2	-	3utr_1	2	1,47	1,22	Longer	3,55E-06
5793	PTPRG	+	3utr_2	2	1,11	1,55	Shorter	3,58E-06
23265	EXOC7	-	3utr_1	4	2,88	2,75	Longer	3,60E-06
51496	CTDSPL2	+	3utr_1	2	1,50	1,11	Longer	3,62E-06
5824	PEX19	-	3utr_1	3	2,12	1,97	Longer	3,66E-06
8829	NRP1	-	3utr_1	5	3,53	3,91	Shorter	3,67E-06
10365	KLF2	+	3utr-extend	3	1,36	1,56	Shorter	3,67E-06
126669	SHE	-	3utr_1	2	1,81	1,50	Longer	3,70E-06
284106	CISD3	+	3utr_1	5	2,94	2,98	Shorter	3,80E-06
92999	ZBTB47	+	3utr_1	3	2,35	2,50	Shorter	4,02E-06
253782	CERS6	+	3utr_1	4	3,36	3,72	Shorter	4,16E-06
10425	ARIH2	+	3utr_2	2	1,45	1,20	Longer	4,21E-06
8050	PDHX	+	3utr_1	2	1,07	1,03	Longer	4,23E-06
54751	FBLIM1	+	3utr_2	2	1,96	1,89	Longer	4,29E-06
55251	PCMTD2	+	3utr_1	4	2,24	2,17	Longer	4,48E-06
444	ASPH	-	3utr_11	2	1,69	1,98	Shorter	4,56E-06
23637	RABGAP1	+	3utr_2	2	1,83	1,95	Shorter	4,65E-06
51132	RLIM	-	3utr_1	2	1,68	1,81	Shorter	4,71E-06
127829	ARL8A	-	3utr_1	3	2,88	2,94	Shorter	4,78E-06
9784	SNX17	+	3utr-extend	3	1,07	1,02	Longer	4,89E-06
51100	SH3GLB1	+	3utr_1	3	1,91	1,84	Longer	4,92E-06
133522	PPARGC1B	+	3utr_1	3	2,75	2,83	Shorter	5,15E-06
757	TMEM50B	-	3utr_3	3	2,90	2,96	Shorter	5,21E-06
3182	HNRNPAB	+	3utr_1	4	3,96	3,96	Longer	5,27E-06
91147	TMEM67	+	3utr_6	5	2,50	2,99	Shorter	5,32E-06
5955	RCN2	+	3utr_1	2	1,61	1,15	Longer	5,37E-06
23548	TTC33	-	3utr_1	2	1,17	1,27	Shorter	5,38E-06
58494	JAM2	+	3utr_3	3	2,17	2,54	Shorter	5,55E-06
9813	KIAA0494	-	3utr_2	2	1,87	1,81	Longer	5,70E-06
9980	DOPEY2	+	3utr_2	2	1,76	1,93	Shorter	5,80E-06
114926	C8orf40	+	3utr_1	2	1,92	1,63	Longer	5,94E-06
8027	STAM	+	3utr_1	3	2,40	2,68	Shorter	6,10E-06
26225	ARL5A	-	3utr_3	6	3,75	3,70	Longer	6,30E-06
65988	ZNF747	-	3utr_2	4	2,08	2,57	Shorter	6,47E-06
60488	MRPS35	+	3utr_2	2	1,91	1,64	Longer	6,55E-06
2589	GALNT1	+	3utr_2	4	2,09	2,13	Shorter	6,66E-06
84168	ANTXR1	+	3utr_4	2	1,19	1,06	Longer	6,89E-06
3703	STT3A	+	3utr_2	3	2,75	2,44	Longer	6,93E-06
1312	COMT	+	3utr_3	3	1,97	2,05	Shorter	7,03E-06
220929	ZNF438	-	3utr_1	2	1,32	1,06	Longer	7,12E-06
143098	MPP7	-	3utr_1	3	2,08	2,45	Shorter	7,33E-06
5305	PIP4K2A	-	3utr_1	3	2,03	1,92	Longer	7,50E-06

6643	SNX2	+	3utr_2	2	1,73	1,58	Longer	7,55E-06
84838	ZNF496	-	3utr_1	3	2,25	2,00	Longer	7,73E-06
80262	C16orf70	+	3utr_2	3	1,87	2,07	Shorter	7,73E-06
84056	KATNAL1	-	3utr_1	5	4,61	4,69	Shorter	7,90E-06
2327	FMO2	+	3utr_1	5	3,56	3,37	Longer	7,99E-06
57120	GOPC	-	3utr_3	4	3,51	3,42	Longer	8,01E-06
9139	CBFA2T2	+	3utr_2	3	2,76	2,93	Shorter	8,02E-06
6935	ZEB1	+	3utr_3	3	2,00	2,00	Longer	8,12E-06
6310	ATXN1	-	3utr_1	3	2,86	2,60	Longer	8,48E-06
5033	P4HA1	-	3utr_1	2	1,12	1,30	Shorter	8,67E-06
340061	TMEM173	-	3utr_1	3	2,89	2,97	Shorter	8,90E-06
387	RHOA	-	3utr_1	3	2,88	2,89	Shorter	9,02E-06
7879	RAB7A	+	3utr_1	3	2,94	2,88	Longer	9,05E-06
11014	KDELR2	-	3utr_2	6	3,86	3,98	Shorter	9,23E-06
64771	C6orf106	-	3utr_1	4	3,84	3,82	Longer	9,34E-06
285381	DPH3	-	3utr_1	4	2,67	2,94	Shorter	9,37E-06
501	ALDH7A1	-	3utr_1	4	2,29	2,10	Longer	9,52E-06
348235	SKA2	-	3utr_1	7	4,60	4,57	Longer	9,62E-06
23585	TMEM50A	+	3utr_1	4	2,71	2,50	Longer	9,68E-06
84193	SETD3	-	3utr_1	2	1,56	1,79	Shorter	9,77E-06
10618	TGOLN2	-	3utr_1	3	2,98	2,99	Shorter	9,78E-06
2631	GBAS	+	3utr_2	2	1,79	1,76	Longer	9,90E-06
55187	VPS13D	+	3utr_2	4	3,12	3,19	Shorter	1,01E-05
131870	NUDT16	+	3utr_1	4	2,72	2,68	Longer	1,01E-05
58476	TP53INP2	+	3utr_1	3	2,88	2,95	Shorter	1,03E-05
51526	C20orf111	-	3utr_1	3	1,76	1,72	Longer	1,03E-05
1953	MEGF6	-	3utr_1	2	1,06	1,33	Shorter	1,05E-05
7430	EZR	-	3utr_1	3	2,96	2,93	Longer	1,06E-05
10933	MORF4L1	+	3utr_3	2	1,04	1,08	Shorter	1,08E-05
9512	PMPCB	+	3utr_3	2	1,98	1,76	Longer	1,09E-05
427	ASAH1	-	3utr_1	5	3,99	3,86	Longer	1,13E-05
80213	TM2D3	-	3utr_3	3	1,85	2,10	Shorter	1,13E-05
1727	CYB5R3	-	3utr_1	2	1,96	1,98	Shorter	1,18E-05
4781	NFIB	-	3utr_1	3	2,69	2,90	Shorter	1,21E-05
5502	PPP1R1A	-	3utr_2	2	1,02	1,04	Shorter	1,23E-05
6046	BRD2	+	3utr_3	2	1,01	1,00	Longer	1,24E-05
828	CAPS	+	3utr_1	2	1,77	1,36	Longer	1,29E-05
26128	KIAA1279	+	3utr_1	2	1,98	1,89	Longer	1,29E-05
3030	HADHA	-	3utr_1	3	2,04	2,03	Longer	1,31E-05
11282	MGAT4B	-	3utr_1	2	1,95	1,89	Longer	1,33E-05
171023	ASXL1	+	3utr_3	4	3,01	3,04	Shorter	1,34E-05
6272	SORT1	-	3utr_1	4	3,77	3,65	Longer	1,35E-05
2521	FUS	+	3utr_3	2	1,03	1,08	Shorter	1,44E-05
3181	HNRNPA2B1	-	3utr_1	5	2,20	2,18	Longer	1,46E-05
84337	ELOF1	-	3utr_1	2	1,99	1,93	Longer	1,47E-05
2289	FKBP5	-	3utr_1	4	3,70	3,65	Longer	1,47E-05
3337	DNAJB1	-	3utr_1	2	1,87	1,74	Longer	1,51E-05
8773	SNAP23	+	3utr_1	4	3,38	3,53	Shorter	1,55E-05
51560	RAB6B	-	3utr_1	3	2,53	2,75	Shorter	1,58E-05
91875	TTC5	-	3utr_1	3	2,53	2,24	Longer	1,59E-05
63933	CCDC90A	-	3utr_1	2	1,12	1,23	Shorter	1,62E-05
55832	CAND1	+	3utr_1	5	2,35	2,01	Longer	1,62E-05
66008	TRAK2	-	3utr_1	5	4,35	4,42	Shorter	1,63E-05
57446	NDRG3	-	3utr_1	3	2,55	2,82	Shorter	1,64E-05
9217	VAPB	+	3utr_1	2	1,40	1,25	Longer	1,65E-05
51154	MRTO4	+	3utr_1	3	2,38	2,01	Longer	1,66E-05
4023	LPL	+	3utr_2	2	1,99	2,00	Shorter	1,66E-05
116151	C20orf108	+	3utr_1	5	3,29	3,71	Shorter	1,70E-05
8575	PRKRA	-	3utr_1	3	2,03	2,03	Shorter	1,73E-05
65977	PLEKHA3	+	3utr_2	2	1,99	1,96	Longer	1,76E-05
4194	MDM4	+	3utr_2	6	5,81	5,89	Shorter	1,79E-05
2622	GAS8	+	3utr_3	2	1,75	1,44	Longer	1,84E-05
4673	NAP1L1	-	3utr_1	3	1,02	1,02	Longer	1,84E-05
1490	CTGF	-	3utr_1	2	1,99	1,98	Longer	1,85E-05
90861	HN1L	+	3utr_1	4	2,58	2,91	Shorter	1,88E-05
10130	PDIA6	-	3utr_1	3	2,10	2,12	Shorter	1,92E-05
223082	ZNRF2	+	3utr_1	2	1,86	1,50	Longer	2,01E-05
8303	SNN	+	3utr_1	2	1,36	1,56	Shorter	2,07E-05
23049	SMG1	-	3utr_1	2	1,86	1,94	Shorter	2,07E-05

3156	HMGCR	+	3utr_2	2	1,65	1,34	Longer	2,09E-05
ENSG000002	no	-	3utr	3	2,84	2,88	Shorter	2,11E-05
400916	CHCHD10	-	3utr_1	3	2,98	2,97	Longer	2,14E-05
23683	PRKD3	-	3utr_1	4	2,69	2,39	Longer	2,29E-05
334	APLP2	+	3utr_3	4	3,95	3,94	Longer	2,30E-05
23387	SIK3	-	3utr_1	2	1,57	1,76	Shorter	2,30E-05
22948	CCT5	+	3utr_3	4	2,52	2,45	Longer	2,36E-05
23362	PSD3	-	3utr_1	2	1,92	2,00	Shorter	2,39E-05
1123	CHN1	-	3utr_1	2	1,20	1,43	Shorter	2,40E-05
1615	DARS	-	3utr_1	3	2,13	2,19	Shorter	2,41E-05
3925	STMN1	-	3utr_2	2	1,03	1,10	Shorter	2,42E-05
3939	LDHA	+	3utr_4	2	1,64	1,44	Longer	2,45E-05
114823	LENG8	+	3utr_1	3	2,94	2,98	Shorter	2,54E-05
123722	FSD2	-	3utr_1	4	2,19	2,30	Shorter	2,57E-05
26269	FBXO8	-	3utr_1	2	1,91	1,99	Shorter	2,63E-05
9419	CRIPT	+	3utr_1	4	2,42	2,97	Shorter	2,64E-05
55173	MRPS10	-	3utr_1	3	2,92	2,96	Shorter	2,67E-05
23250	ATP11A	+	3utr_2	3	2,30	1,90	Longer	2,67E-05
7134	TNNC1	-	3utr_1	2	1,95	1,94	Longer	2,76E-05
55256	ADI1	-	3utr_1	3	2,10	2,05	Longer	2,79E-05
388969	C2orf68	-	3utr_1	2	1,19	1,07	Longer	2,86E-05
23596	OPN3	-	3utr_2	2	1,13	1,39	Shorter	2,88E-05
4140	MARK3	+	3utr_1	4	2,25	2,10	Longer	2,89E-05
10133	OPTN	+	3utr_1	4	1,82	1,87	Shorter	2,90E-05
6150	MRPL23	+	3utr_1	2	1,95	2,00	Shorter	2,97E-05
9690	UBE3C	+	3utr_3	3	2,84	2,81	Longer	2,98E-05
80314	EPC1	-	3utr_6	2	1,33	1,73	Shorter	3,01E-05
79568	C2orf47	+	3utr_1	2	1,97	1,61	Longer	3,03E-05
6801	STRN	-	3utr_1	6	3,88	4,00	Shorter	3,05E-05
11160	ERLIN2	+	3utr_2	4	2,11	2,12	Shorter	3,17E-05
6319	SCD	+	3utr_1	2	1,87	1,95	Shorter	3,17E-05
55341	LSG1	-	3utr_1	2	1,62	1,19	Longer	3,17E-05
80273	GRPEL1	-	3utr-extend	2	1,23	1,56	Shorter	3,25E-05
677	ZFP36L1	-	3utr_1	2	1,97	2,00	Shorter	3,33E-05
10964	IFI44L	+	3utr_1	5	3,04	2,92	Longer	3,38E-05
170463	SSBP4	+	3utr_2	2	1,94	1,76	Longer	3,40E-05
7553	ZNF7	+	3utr_3	2	1,46	1,09	Longer	3,45E-05
23208	SYT11	+	3utr_1	3	2,03	1,80	Longer	3,46E-05
9563	H6PD	+	3utr_1	6	5,75	5,78	Shorter	3,56E-05
2720	GLB1	-	3utr_1	2	1,07	1,15	Shorter	3,56E-05
9520	NPEPPS	+	3utr_6	2	1,98	1,93	Longer	3,59E-05
25871	C3orf17	-	3utr_1	3	1,26	1,36	Shorter	3,65E-05
26528	DAZAP1	+	3utr_2	2	1,49	1,27	Longer	3,71E-05
51133	KCTD3	+	3utr_1	2	1,76	1,99	Shorter	3,90E-05
51	ACOX1	-	3utr_1	4	2,33	2,52	Shorter	3,90E-05
54800	KLHL24	+	3utr_2	4	3,76	3,73	Longer	3,90E-05
63915	MUTED	-	3utr_1	2	1,12	1,33	Shorter	4,05E-05
5110	PCMT1	+	3utr_5	2	1,99	1,98	Longer	4,08E-05
10351	ABCA8	-	3utr_1	2	1,86	1,95	Shorter	4,16E-05
3267	AGFG1	+	3utr_1	4	2,94	3,15	Shorter	4,18E-05
11051	NUDT21	-	3utr_1	5	3,73	3,81	Shorter	4,32E-05
30845	EHD3	+	3utr_1	2	1,39	1,73	Shorter	4,36E-05
5728	PTEN	+	3utr_1	5	3,34	2,81	Longer	4,36E-05
23466	CBX6	-	3utr_1	3	2,80	2,79	Longer	4,37E-05
23164	MPRIP	+	3utr_3	3	2,07	2,07	Longer	4,39E-05
51088	KLHL5	+	3utr_2	4	2,54	2,58	Shorter	4,49E-05
9491	PSMF1	+	3utr_1	4	2,18	2,11	Longer	4,59E-05
6356	CCL11	+	3utr_1	3	2,27	2,04	Longer	4,69E-05
6990	DYNLT3	-	3utr_2	2	1,75	1,36	Longer	4,72E-05
7095	SEC62	+	3utr_4	5	4,43	4,50	Shorter	4,75E-05
92822	ZNF276	+	3utr_1	2	1,27	1,67	Shorter	4,76E-05
6345	SRL	-	3utr_1	3	2,19	2,62	Shorter	4,84E-05
57649	PHF12	-	3utr_1	3	2,86	2,94	Shorter	5,00E-05
79809	TTC21B	-	3utr_2	2	1,12	1,39	Shorter	5,23E-05
23062	GGA2	-	3utr_1	4	2,75	3,02	Shorter	5,28E-05
6632	SNRPD1	+	3utr_1	2	1,06	1,13	Shorter	5,30E-05
126272	EID2B	-	3utr_1	2	1,87	1,99	Shorter	5,33E-05
7411	VBP1	+	3utr_1	2	1,66	1,54	Longer	5,35E-05
2549	GAB1	+	3utr_1	4	3,49	3,46	Longer	5,36E-05

153339	TMEM167A	-	3utr_1	4	3,27	3,50	Shorter	5,39E-05
2729	GCLC	-	3utr_1	5	2,61	2,82	Shorter	5,40E-05
200185	KRTCAP2	-	3utr_1	2	1,46	1,71	Shorter	5,45E-05
55593	OTUD5	-	3utr_1	3	2,00	1,88	Longer	5,71E-05
9456	HOMER1	-	3utr_1	3	2,04	1,84	Longer	5,88E-05
23087	TRIM35	-	3utr_1	5	3,57	2,63	Longer	5,94E-05
11059	WWP1	+	3utr_2	7	2,19	2,29	Shorter	6,03E-05
8076	MFAP5	-	3utr_1	3	2,60	2,40	Longer	6,14E-05
9748	SLK	+	3utr_1	4	3,63	3,50	Longer	6,29E-05
117177	RAB3IP	+	3utr_3	2	1,30	1,12	Longer	6,49E-05
210	ALAD	-	3utr_1	2	1,89	1,98	Shorter	6,59E-05
25949	SYF2	-	3utr_1	4	1,96	2,17	Shorter	6,71E-05
80012	PHC3	-	3utr_1	2	1,78	1,98	Shorter	6,76E-05
9057	SLC7A6	+	3utr_1	2	1,57	1,39	Longer	6,87E-05
56261	GPCPD1	-	3utr_1	3	1,73	2,08	Shorter	7,07E-05
84978	FRMD5	-	3utr_1	5	2,65	3,04	Shorter	7,22E-05
23607	CD2AP	+	3utr_1	3	1,82	1,75	Longer	7,65E-05
80760	ITIH5	-	3utr_1	4	2,70	2,43	Longer	7,67E-05
55101	ATP5SL	-	3utr_1	2	1,95	1,99	Shorter	7,67E-05
81619	TSPAN14	+	3utr_1	3	1,99	2,20	Shorter	8,12E-05
9409	PEX16	-	3utr_1	2	1,29	1,02	Longer	8,15E-05
8490	RGS5	-	3utr_2	6	5,19	5,06	Longer	8,30E-05
10658	CELF1	-	3utr_1	3	2,39	2,71	Shorter	8,42E-05
23310	NCAPD3	-	3utr_2	2	1,73	2,00	Shorter	8,63E-05
3911	LAMA5	-	3utr_2	2	1,94	1,80	Longer	8,92E-05
9213	XPR1	+	3utr_2	3	2,09	1,85	Longer	9,17E-05
9128	PRPF4	+	3utr_1	2	1,27	1,06	Longer	9,29E-05
23158	TBC1D9	-	3utr_1	2	1,85	1,95	Shorter	9,38E-05
8570	KHSRP	-	3utr_1	3	2,78	2,71	Longer	9,85E-05
9531	BAG3	+	3utr_1	3	2,79	2,88	Shorter	9,86E-05
5791	PTPRE	+	3utr_2	2	1,95	1,87	Longer	9,88E-05
1069	CETN2	-	3utr_1	3	1,99	2,03	Shorter	1,00E-04
25942	SIN3A	-	3utr_1	3	1,58	1,77	Shorter	1,01E-04
10611	PDLIM5	+	3utr_5	6	4,21	4,24	Shorter	1,01E-04
1741	DLG3	+	3utr_1	3	1,76	2,08	Shorter	1,02E-04
3667	IRS1	-	3utr_1	2	1,89	1,66	Longer	1,03E-04
79639	TMEM53	-	3utr_2	2	1,02	1,12	Shorter	1,04E-04
25962	KIAA1429	-	3utr_1	2	1,25	1,04	Longer	1,05E-04
55863	TMEM126B	+	3utr_2	2	1,24	1,49	Shorter	1,06E-04
221092	HNRNPUL2	-	3utr_1	3	1,68	1,56	Longer	1,07E-04
4862	NPAS2	+	3utr_1	4	3,36	3,12	Longer	1,08E-04
64769	MEAF6	-	3utr_1	2	1,81	1,86	Shorter	1,09E-04
9927	MFN2	+	3utr_1	2	2,00	2,00	Shorter	1,09E-04
5125	PCSK5	+	3utr_2	3	2,19	2,15	Longer	1,10E-04
7551	ZNF3	-	3utr_2	2	1,98	1,71	Longer	1,11E-04
4864	NPC1	-	3utr_1	2	1,06	1,00	Longer	1,11E-04
4071	TM4SF1	-	3utr_1	2	1,98	1,94	Longer	1,14E-04
115708	TRMT61A	+	3utr_1	2	1,98	1,83	Longer	1,15E-04
23479	ISCU	+	3utr_1	3	2,71	2,76	Shorter	1,15E-04
51582	AZIN1	-	3utr_1	5	3,65	3,87	Shorter	1,16E-04
3714	JAG2	-	3utr_1	4	2,94	2,96	Shorter	1,17E-04
8763	CD164	-	3utr_1	3	2,36	2,32	Longer	1,17E-04
221035	REEP3	+	3utr_1	4	3,85	3,88	Shorter	1,19E-04
262	AMD1	+	3utr_1	3	2,28	2,35	Shorter	1,32E-04
10079	ATP9A	-	3utr_1	2	1,96	2,00	Shorter	1,35E-04
406886	MIRLET7D	+	3utr-extend	2	1,38	1,54	Shorter	1,43E-04
3257	HPS1	-	3utr_1	2	1,02	1,07	Shorter	1,46E-04
159195	USP54	-	3utr_1	2	1,74	1,94	Shorter	1,47E-04
63931	MRPS14	-	3utr_2	3	2,12	2,42	Shorter	1,47E-04
89796	NAV1	+	3utr_2	2	1,84	1,92	Shorter	1,47E-04
2287	FKBP3	-	3utr_1	2	1,91	1,96	Shorter	1,53E-04
64089	SNX16	-	3utr_1	2	1,62	1,93	Shorter	1,53E-04
84284	NTPCR	+	3utr_2	2	1,70	1,36	Longer	1,57E-04
5775	PTPN4	+	3utr_1	3	2,17	1,78	Longer	1,63E-04
7701	ZNF142	-	3utr_1	2	1,91	1,59	Longer	1,66E-04
51776	ZAK	+	3utr_2	3	2,86	2,78	Longer	1,71E-04
134218	DNAJC21	+	3utr_1	5	3,30	3,29	Longer	1,73E-04
10197	PSME3	+	3utr_1	4	2,79	2,80	Shorter	1,75E-04
6160	RPL31	+	3utr_1	2	2,00	1,99	Longer	1,80E-04

6341	SCO1	-	3utr_1	2	1,99	1,97	Longer	1,84E-04
55845	BRK1	+	3utr_1	2	1,97	1,88	Longer	1,84E-04
64065	PERP	-	3utr_1	3	2,00	1,99	Longer	1,87E-04
57534	MIB1	+	3utr_1	2	1,82	1,65	Longer	1,88E-04
54552	GNL3L	+	3utr_1	3	2,61	2,37	Longer	1,92E-04
5361	PLXNA1	+	3utr_1	3	1,91	1,92	Shorter	1,93E-04
10969	EBNA1BP2	-	3utr_1	2	1,10	1,36	Shorter	2,00E-04
11176	BAZ2A	-	3utr_1	2	1,25	1,44	Shorter	2,00E-04
55219	TMEM57	+	3utr_1	2	1,01	1,15	Shorter	2,01E-04
476	ATP1A1	+	3utr_2	2	1,87	1,72	Longer	2,13E-04
7871	SLMAP	+	3utr_3	3	2,16	1,84	Longer	2,18E-04
6745	SSR1	-	3utr_2	5	3,09	3,01	Longer	2,18E-04
11031	RAB31	+	3utr_1	3	1,70	2,21	Shorter	2,20E-04
55278	QRSL1	+	3utr_2	2	1,83	1,47	Longer	2,23E-04
28988	DBNL	+	3utr_5	3	2,48	2,30	Longer	2,24E-04
493869	GPX8	+	3utr_1	2	1,81	1,98	Shorter	2,28E-04
23522	KAT6B	+	3utr_1	2	1,34	1,13	Longer	2,28E-04
427	ASAH1	-	3utr_7	2	1,81	1,85	Shorter	2,30E-04
116143	WDR92	-	3utr_2	3	2,05	2,14	Shorter	2,41E-04
65979	PHACTR4	+	3utr_2	2	1,84	1,98	Shorter	2,42E-04
8405	SPOP	-	3utr_1	3	1,81	1,97	Shorter	2,45E-04
2669	GEM	-	3utr_1	2	1,97	1,87	Longer	2,49E-04
2935	GSPT1	-	3utr_1	4	1,76	1,94	Shorter	2,50E-04
4189	DNAJB9	+	3utr_1	2	1,26	1,19	Longer	2,50E-04
55795	PCID2	-	3utr_1	2	1,93	1,97	Shorter	2,54E-04
387921	NHLRC3	+	3utr_1	2	1,59	1,22	Longer	2,55E-04
9351	SLC9A3R2	+	3utr_1	2	1,99	1,97	Longer	2,59E-04
57498	KIDINS220	-	3utr_2	2	1,01	1,00	Longer	2,60E-04
8721	EDF1	-	3utr_1	2	1,99	1,99	Longer	2,61E-04
858	CAV2	+	3utr_2	6	2,11	2,10	Longer	2,61E-04
51390	AIG1	+	3utr_4	3	2,15	2,13	Longer	2,65E-04
3146	HMGB1	-	3utr_1	4	3,42	3,40	Longer	2,68E-04
29115	SAP30BP	+	3utr_2	3	1,36	1,28	Longer	2,70E-04
283349	RASSF3	+	3utr_1	3	2,70	2,89	Shorter	2,72E-04
56940	DUSP22	+	3utr_1	2	1,96	1,91	Longer	2,77E-04
55861	DBNDD2	+	3utr_1	2	1,99	2,00	Shorter	2,85E-04
23309	SIN3B	+	3utr_1	2	1,38	1,74	Shorter	2,86E-04
9931	HELZ	-	3utr_1	4	2,49	2,89	Shorter	2,89E-04
196740	VSTM4	-	3utr_1	4	2,72	2,83	Shorter	2,92E-04
205564	SENP5	+	3utr_1	2	1,84	1,99	Shorter	2,95E-04
9204	ZMYM6	-	3utr_3	3	2,71	2,30	Longer	3,11E-04
5216	PFN1	-	3utr_1	2	2,00	1,99	Longer	3,13E-04
10949	HNRNPA0	-	3utr_1	3	1,06	1,03	Longer	3,18E-04
6778	STAT6	-	3utr_1	2	1,88	1,79	Longer	3,20E-04
84823	LMNB2	-	3utr_2	2	1,88	1,67	Longer	3,31E-04
10015	PDCD6IP	+	3utr_5	2	1,44	1,33	Longer	3,34E-04
9706	ULK2	-	3utr_1	5	3,17	2,84	Longer	3,36E-04
3842	TNPO1	+	3utr_3	5	3,07	3,26	Shorter	3,37E-04
90196	SYS1	+	3utr_1	2	1,09	1,03	Longer	3,40E-04
5090	PBX3	+	3utr_1	3	2,81	2,64	Longer	3,44E-04
84196	USP48	-	3utr_1	2	1,82	1,49	Longer	3,46E-04
26000	TBC1D10B	-	3utr_1	2	2,00	1,90	Longer	3,46E-04
64426	SUDS3	+	3utr_1	2	1,83	1,95	Shorter	3,48E-04
23410	SIRT3	-	3utr_1	4	2,04	2,33	Shorter	3,53E-04
92979	mrt-09	+	3utr_1	4	2,19	1,58	Longer	3,57E-04
9522	SCAMP1	+	3utr_1	3	2,24	1,70	Longer	3,59E-04
8824	CES2	+	3utr_1	3	2,75	2,81	Shorter	3,63E-04
84937	ZNRF1	+	3utr_2	3	1,98	1,58	Longer	3,68E-04
9140	ATG12	-	3utr_1	6	3,37	3,82	Shorter	3,69E-04
1857	DVL3	+	3utr_2	3	1,16	1,21	Shorter	3,69E-04
51592	TRIM33	-	3utr_1	3	2,85	2,77	Longer	3,85E-04
10980	COPS6	+	3utr_2	2	1,36	1,28	Longer	3,85E-04
4089	SMAD4	+	3utr_2	4	3,37	3,46	Shorter	3,94E-04
55892	MYNN	+	3utr_1	5	2,79	2,56	Longer	4,12E-04
5529	PPP2R5E	-	3utr_1	4	2,55	2,51	Longer	4,25E-04
8242	KDM5C	-	3utr_1	2	1,91	1,77	Longer	4,26E-04
9797	TATDN2	+	3utr_1	2	1,94	1,98	Shorter	4,34E-04
4087	SMAD2	-	3utr_1	8	4,24	4,56	Shorter	4,37E-04
27231	ITGB1BP3	+	3utr-extend	2	1,09	1,00	Longer	4,48E-04

56889	TM9SF3	-	3utr_1	4	2,02	1,98	Longer	4,49E-04
5143	PDE4C	-	3utr_1	3	2,31	2,27	Longer	4,60E-04
11168	PSIP1	-	3utr_2	2	1,09	1,43	Shorter	4,62E-04
55783	FTSJD1	-	3utr_1	2	1,27	1,00	Longer	4,66E-04
4641	MYO1C	-	3utr_1	2	1,95	1,98	Shorter	4,67E-04
23167	EFR3A	+	3utr_1	3	1,80	1,74	Longer	4,69E-04
6667	SP1	+	3utr_1	4	2,21	2,21	Longer	4,72E-04
11007	CCDC85B	+	3utr_1	2	2,00	1,99	Longer	4,85E-04
5707	PSMD1	+	3utr_2	2	1,25	1,16	Longer	4,90E-04
57381	RHOJ	+	3utr_1	3	1,85	1,93	Shorter	4,93E-04
5660	PSAP	-	3utr_1	3	2,99	2,99	Longer	4,94E-04
9875	URB1	-	3utr_1	4	2,30	1,99	Longer	5,00E-04
154007	SNRNP48	+	3utr_1	4	2,78	2,72	Longer	5,04E-04
8655	DYNLL1	+	3utr_1	2	1,99	1,98	Longer	5,12E-04
113419	TEX261	-	3utr_1	2	1,96	1,99	Shorter	5,13E-04
56986	DTWD1	+	3utr_2	2	1,16	1,49	Shorter	5,14E-04
8502	PKP4	+	3utr_6	4	2,74	2,73	Longer	5,16E-04
28977	MRPL42	+	3utr_1	4	1,71	2,07	Shorter	5,29E-04
3920	LAMP2	-	3utr_1	3	1,94	2,18	Shorter	5,30E-04
8881	CDC16	+	3utr_2	2	1,10	1,22	Shorter	5,33E-04
4924	NUCB1	+	3utr_3	2	1,98	2,00	Shorter	5,51E-04
84256	FLYWCH1	+	3utr_2	2	1,07	1,02	Longer	5,54E-04
5049	PAFAH1B2	+	3utr_1	5	2,58	2,78	Shorter	5,55E-04
23609	MKRN2	+	3utr_1	3	2,22	2,41	Shorter	5,65E-04
81555	YIPF5	-	3utr_1	2	1,82	1,61	Longer	5,69E-04
6836	SURF4	-	3utr_1	3	2,34	2,34	Longer	5,91E-04
23283	CSTF2T	-	3utr_1	2	1,73	1,55	Longer	5,98E-04
1306	COL15A1	+	3utr_1	7	6,08	6,25	Shorter	6,02E-04
4683	NBN	-	3utr_1	2	1,99	1,95	Longer	6,07E-04
5137	PDE1C	-	3utr_2	5	3,18	3,29	Shorter	6,14E-04
57213	SPRYD7	-	3utr_1	5	3,08	2,99	Longer	6,30E-04
7975	MAFK	+	3utr_1	3	2,93	2,97	Shorter	6,36E-04
2557	GABRA4	-	3utr_1	3	1,15	1,19	Shorter	6,51E-04
79699	ZYG11B	+	3utr_2	4	3,81	3,64	Longer	6,79E-04
57186	RALGAPA2	-	3utr_1	2	1,91	1,76	Longer	6,81E-04
708	C1QBP	-	3utr_1	2	2,00	1,99	Longer	6,93E-04
171425	CLYBL	+	3utr_3	2	1,94	1,80	Longer	7,26E-04
56983	POGLUT1	+	3utr_3	2	1,93	1,59	Longer	7,43E-04
23429	RYBP	-	3utr	3	2,20	1,97	Longer	7,47E-04
2787	GNG5	-	3utr_1	2	1,93	1,98	Shorter	7,49E-04
84950	PRPF38A	+	3utr_1	2	1,22	1,49	Shorter	7,82E-04
51377	UCHL5	-	3utr_1	5	3,30	3,15	Longer	7,83E-04
6920	TCEA3	-	3utr_1	2	1,25	1,15	Longer	7,92E-04
4700	NDUFA6	-	3utr_1	2	1,31	1,26	Longer	7,95E-04
2060	EPS15	-	3utr_1	3	1,70	1,87	Shorter	7,95E-04
54867	TMEM214	+	3utr_2	2	1,88	1,95	Shorter	7,96E-04
6944	VPS72	-	3utr_2	3	2,93	2,90	Longer	8,13E-04
1783	DYNC1LI2	-	3utr_1	2	1,99	1,96	Longer	8,23E-04
84896	ATAD1	-	3utr_1	5	2,81	2,75	Longer	8,37E-04
53373	TPCN1	+	3utr_2	2	1,83	1,73	Longer	8,57E-04
254428	SLC41A1	-	3utr_1	3	2,75	2,85	Shorter	8,62E-04
23384	SPECC1L	+	3utr_1	2	1,36	1,18	Longer	8,84E-04
128486	FITM2	-	3utr_1	4	3,88	3,93	Shorter	8,99E-04
8481	OFD1	+	3utr_3	2	1,11	1,34	Shorter	9,22E-04
4139	MARK1	+	3utr_2	2	1,30	1,10	Longer	9,28E-04
2274	FHL2	-	3utr_1	4	1,51	1,44	Longer	9,30E-04
2744	GLS	+	3utr_3	2	1,91	1,98	Shorter	9,34E-04
57146	TMEM159	+	3utr_1	2	1,72	1,91	Shorter	9,55E-04
51371	POMP	+	3utr_1	2	1,13	1,09	Longer	9,77E-04
3680	ITGA9	+	3utr_2	3	2,83	2,70	Longer	9,85E-04
26234	FBXL5	-	3utr_1	3	1,46	1,33	Longer	9,86E-04
55280	CWF19L1	-	3utr_1	2	1,91	1,72	Longer	9,87E-04

Suppl. Table III. : Transcripts with APA changes in DCM, sorted on the largest absolute difference of the cleavage site reads between control and DCM. The median of the reads per CS were calculated in control and DCM hearts and the absolute difference is shown in column G (AbsoluteMedianDifference). Only transcripts with more than 75 reads and less than 8 CSs were taken into account. The minimal distance between peaks was set to 30 nucleotides. The candidates selected for further analysis are marked green.

Bonferroni correction was applied to the total number of 3'UTRs analyzed

geneid	sym	N.3utr.Peaks	minReadsPerGeneRegion	median_fraction_DCM	median_fraction_CNTR	absoluteMedianDifference	p-val_Bonferroni corrected
10169	SERF2	3	77,36	0,284846439	0,693477391	0,4086	2,42E-08
10026	PIGK	3	76,91	0,562580645	0,217863894	0,3447	1,796E-30
5175	PECAM1	4	245,68	0,403644395	0,700828729	0,2972	8,6E-24
4026	LPP	6	128,27	0,523494557	0,819969743	0,2965	2,54E-17
64344	HIF3A	3	81,27	0,55240062	0,265681183	0,2867	2,34E-31
163	AP2B1	3	283,73	0,684755174	0,427106697	0,2576	7,4E-38
155435	RBM33	4	166,55	0,143976624	0,397574124	0,2536	2,58E-55
26994	RNF11	4	139,64	0,337182448	0,589961718	0,2528	1,472E-59
55075	UACA	4	164,18	0,814990512	0,564102564	0,2509	2,68E-24
7072	TIA1	6	124,91	0,173605329	0,423673997	0,2501	1,328E-09
7750	ZMYM2	6	130,82	0,287757437	0,536483669	0,2487	2,22E-35
57666	FBRSL1	5	262,27	0,772186331	0,528347085	0,2438	6,84E-31
55973	BCAP29	5	163,45	0,80756396	0,565060551	0,2425	9,28E-24
8886	DDX18	3	118,27	0,537037037	0,778805121	0,2418	1,574E-35
2632	GBE1	2	154,55	0,583458647	0,342965061	0,2405	3,94E-32
55852	TEX2	2	120,73	0,4825	0,243663595	0,2388	1,01E-13
55692	LUC7L	2	83,45	0,063148789	0,301173662	0,2380	5,52E-08
8467	SMARCA5	3	112,27	0,271418287	0,034509804	0,2369	3,14E-19
54708	MARCH5	4	92,27	0,757124352	0,524681529	0,2324	2,7E-24
5569	PKIA	7	294,82	0,485728885	0,254584682	0,2311	1,396E-58
7326	UBE2G1	4	137,00	0,576681181	0,348039216	0,2286	0,000023
10776	ARPP19	4	466,32	0,230741163	0,458245119	0,2275	1,196E-58
9217	VAPB	2	77,73	0,39918652	0,173774666	0,2254	0,000918
23291	FBXW11	4	93,45	0,503979891	0,280908326	0,2231	1,422E-08
220988	HNRNPA3	8	116,55	0,544348383	0,321404682	0,2229	1,546E-30
3184	HNRNPD	4	127,73	0,459135489	0,240116597	0,2190	0,000000054

23327	NEDD4L	7	91,64	0,297984224	0,514677104	0,2167	4,3E-43
9827	RGP1	5	88,18	0,854089219	0,637398374	0,2167	5,22E-38
27	ABL2	2	106,00	0,411973393	0,19949495	0,2125	6,66E-08
1827	RCAN1	3	235,95	0,63942059	0,851008065	0,2116	1,832E-35
23313	KIAA0930	3	182,18	0,55649114	0,766833811	0,2103	0,0000832
553115	PEF1	2	164,00	0,307824592	0,098058902	0,2098	1,062E-20
2926	GRSF1	6	166,73	0,45376974	0,244844125	0,2089	2,48E-19
125150	ZSWIM7	2	90,09	0,411461687	0,202634245	0,2088	3,94E-16
11231	SEC63	3	83,18	0,028450363	0,236745887	0,2083	0,00426
813	CALU	6	525,68	0,638798763	0,844086022	0,2053	1,012E-55
6648	SOD2	5	147,00	0,549315069	0,345971564	0,2033	0,00000198
51704	GPRC5B	2	124,36	0,793551276	0,590785908	0,2028	1,482E-15
57125	PLXDC1	2	79,55	0,929347826	0,726857143	0,2025	3,62E-39
92906	HNRPLL	6	84,27	0,689058524	0,49003148	0,1990	4,2E-63
51110	LACTB2	2	140,91	0,271031456	0,466067048	0,1950	8,06E-13
10494	STK25	3	87,68	0,421847247	0,227766798	0,1941	3,78E-11
8566	PDXK	5	120,27	0,262282691	0,455865273	0,1936	2,02E-14
55122	AKIRIN2	3	310,18	0,482914843	0,674969705	0,1921	4,68E-50
7111	TMOD1	3	397,55	0,519617733	0,711165644	0,1915	4,68E-23
23350	U2SURP	4	121,45	0,382110632	0,1910267	0,1911	3,18E-26
5833	PCYT2	5	88,36	0,44077135	0,250476872	0,1903	3,12E-18
84191	FAM96A	2	149,27	0,231699554	0,043255695	0,1884	4,32E-08
91607	SLFN11	2	89,82	0,755358463	0,941694169	0,1863	9,94E-14
2332	FMR1	3	87,09	0,381928869	0,568263045	0,1863	4,56E-10
29103	DNAJC15	3	144,82	0,552524666	0,368570415	0,1840	7,3E-14
7453	WARS	4	142,09	0,573097212	0,756042237	0,1829	1,036E-12
23548	TTC33	2	87,95	0,159851301	0,340941512	0,1811	1,496E-16
22948	CCT5	4	208,95	0,256419799	0,437459213	0,1810	0,00025
2909	ARHGAP35	3	161,27	0,226872247	0,0462102	0,1807	3,96E-20
5887	RAD23B	5	134,18	0,596586377	0,418041064	0,1785	0,000000608
51705	EMCN	6	94,64	0,336241079	0,510849233	0,1746	9,34E-16
148534	TMEM56	6	243,36	0,160296971	0,332808812	0,1725	9,98E-27
57129	MRPL47	3	131,27	0,477146814	0,648888889	0,1717	7,04E-23

5537	PPP6C	6	109,91	0,198362147	0,029364656	0,1690	7,6E-19
1462	VCAN	7	147,50	0,519876733	0,350969686	0,1689	3,44E-21
55207	ARL8B	3	158,09	0,364963504	0,196365857	0,1686	2,78E-15
286451	YIPF6	3	111,91	0,581640942	0,414748708	0,1669	0,00724
26225	ARL5A	6	80,45	0,7	0,536111111	0,1639	2,16E-12
29117	BRD7	2	189,32	0,485010968	0,321248499	0,1638	0,0348
1979	EIF4EBP2	6	283,86	0,539715217	0,701747001	0,1620	3,88E-33
5164	PDK2	2	129,55	0,051861568	0,213666497	0,1618	6,32E-22
5562	PRKAA1	5	89,00	0,281890661	0,440816327	0,1589	0,001034
4289	MKLN1	5	158,45	0,021198532	0,17982018	0,1586	4,56E-09
3021	H3F3B	5	244,09	0,119100706	0,277699494	0,1586	0,00000426
23091	ZC3H13	2	123,36	0,429160063	0,585344828	0,1562	0,00000312
140739	UBE2F	6	185,09	0,493403694	0,337388598	0,1560	7,88E-20
10075	HUWE1	2	165,09	0,749237251	0,594797869	0,1544	6,58E-24
90139	TSPAN18	4	262,09	0,086060209	0,239742087	0,1537	2,78E-16
9209	LRRFIP2	4	279,64	0,674576271	0,827827412	0,1533	0,0000011
5480	PPIC	3	251,64	0,496196606	0,647770923	0,1516	4,36E-09
3655	ITGA6	2	90,27	0,878540444	0,727474619	0,1511	0,000326
8125	ANP32A	3	192,64	0,506279973	0,355828221	0,1505	5,66E-30
7465	WEE1	6	131,36	0,319031142	0,172905053	0,1461	4,48E-38
55740	ENAH	7	152,50	0,773070018	0,627223511	0,1458	8,5E-15
10602	CDC42EP3	6	188,14	0,207779657	0,064901219	0,1429	2,26E-46
5052	PRDX1	2	692,82	0,575135397	0,433391447	0,1417	7,38E-22
79139	DERL1	4	182,68	0,597596154	0,457189015	0,1404	2,06E-11
10328	COX4NB	3	95,36	0,533215235	0,672865596	0,1397	3,02E-08
51028	VPS36	4	109,27	0,444259567	0,305201699	0,1391	0,000000238
23	ABCF1	3	145,95	0,337758489	0,199505515	0,1383	1,866E-20
91746	YTHDC1	3	100,18	0,803828696	0,667077248	0,1368	2,12E-08
50862	RNF141	4	86,73	0,34354689	0,4786467	0,1351	1,962E-09
51747	LUC7L3	4	141,18	0,182762836	0,049011858	0,1338	6,88E-18
4052	LTBP1	4	92,91	0,627524144	0,496026012	0,1315	0,000884
81858	SHARPIN	2	82,45	0,20754717	0,077596996	0,1300	0,001116
3192	HNRNPU	4	103,09	0,060433295	0,190322581	0,1299	5,78E-09

57148	RALGAPB	3	92,18	0,324909747	0,454635109	0,1297	1,578E-12
83987	CCDC8	4	106,73	0,052193404	0,181782946	0,1296	5,94E-29
56172	ANKH	5	227,55	0,650037046	0,522200438	0,1278	2,8E-73
23012	STK38L	5	81,09	0,245932416	0,118834081	0,1271	1,598E-17
23499	MACF1	3	249,45	0,194097469	0,320731406	0,1266	5,6E-17
83660	TLN2	3	132,73	0,680359937	0,806974389	0,1266	7,54E-10
79577	CDC73	6	76,82	0,298465037	0,172535211	0,1259	7,44E-17
51520	LARS	2	201,82	0,792384406	0,666666667	0,1257	1,518E-42
91612	CHURC1	4	146,00	0,797633873	0,923076923	0,1254	5,08E-101
54664	TMEM106B	4	82,82	0,016113744	0,140484429	0,1244	0,00000506
55669	MFN1	2	137,82	0,813880126	0,937994723	0,1241	8,66E-11
6711	SPTBN1	7	203,82	0,122192867	0,246231156	0,1240	1,442E-17
8239	USP9X	7	84,64	0,144300955	0,020287405	0,1240	1,974E-17
84188	FAR1	3	143,91	0,128835026	0,252323289	0,1235	2,04E-09
140885	SIRPA	2	133,91	0,823430115	0,702414113	0,1210	9,5E-35
5685	PSMA4	2	93,18	0,84375	0,725202429	0,1185	1,166E-08
81611	ANP32E	3	142,36	0,590855107	0,4728223	0,1180	1,698E-08
1508	CTSB	5	456,36	0,778023389	0,89531556	0,1173	1,844E-36
10135	NAMPT	2	126,18	0,160132068	0,276754604	0,1166	1,554E-31
6566	SLC16A1	4	167,14	0,315267528	0,199813476	0,1155	7,44E-24
1213	CLTC	6	140,36	0,706807569	0,591515475	0,1153	5,54E-10
400961	PAIP2B	4	173,82	0,965846493	0,851129004	0,1147	1,96E-16
51097	SCCPDH	4	125,27	0,121909295	0,235897436	0,1140	1,062E-15
126298	IRGQ	3	102,27	0,951660736	0,838229683	0,1134	5,12E-13
400	ARL1	5	195,23	0,656716418	0,543803844	0,1129	1,754E-13
7468	WHSC1	3	114,73	0,531506148	0,420497566	0,1110	1,35E-31
4833	NME4	3	154,73	0,311260623	0,421966938	0,1107	2,06E-11
367	AR	6	80,45	0,005649718	0,112073357	0,1064	0,000536
8560	DEGS1	2	96,55	0,038606403	0,144980065	0,1064	0,000000026
10891	PPARGC1A	4	458,55	0,860721601	0,966169154	0,1054	2,06E-47
817	CAMK2D	5	190,09	0,822174447	0,717799954	0,1044	4,56E-25
85476	GFM1	4	104,45	0,757818011	0,653683053	0,1041	0,0346
6304	SATB1	5	128,45	0,921130325	0,817191754	0,1039	0,0047

55837	EAPP	2	96,64	0,28762046	0,184443536	0,1032	3,3E-10
138050	HGSNAT	2	80,27	0,214257109	0,111205074	0,1031	0,000378
8473	OGT	4	405,00	0,213350034	0,110526675	0,1028	1,682E-28
1345	COX6C	4	348,82	0,848332736	0,951013853	0,1027	2,58E-51
81669	CCNL2	3	172,00	0,524525317	0,423433445	0,1011	2,74E-27
23604	DAPK2	2	142,18	0,635549872	0,735597592	0,1000	1,824E-12

Suppl. Table IV:
Statistics for the number of sequenced and mapped reads in the 3'-Seq

	N_total_reads	N_mapped_reads (%)	N_uniq_mapped_reads (%)
CON1	6542258	6202844 (94.8 %)	4441317 (67.8 %)
CON2	10725983	10202105 (95.1 %)	6873256 (64.0 %)
CON3	10606540	10022625 (94.4 %)	7224854 (68.1 %)
CON4	10967801	10214344 (93.1 %)	6714344 (61.2 %)
CON5	6747941	6268448 (92.8 %)	4597927 (68.1 %)
DCM1	12181401	11296229 (92.7 %)	7795030 (63.9 %)
DCM2	12523654	11594499 (92.5 %)	7933661 (63.3 %)
DCM3	12295070	11744319 (95.5 %)	7702999 (62.6 %)
DCM4	13252900	12491472 (94.2 %)	8513519 (64.2 %)
DCM5	11678096	10875334 (93.1 %)	8065902 (69.0 %)