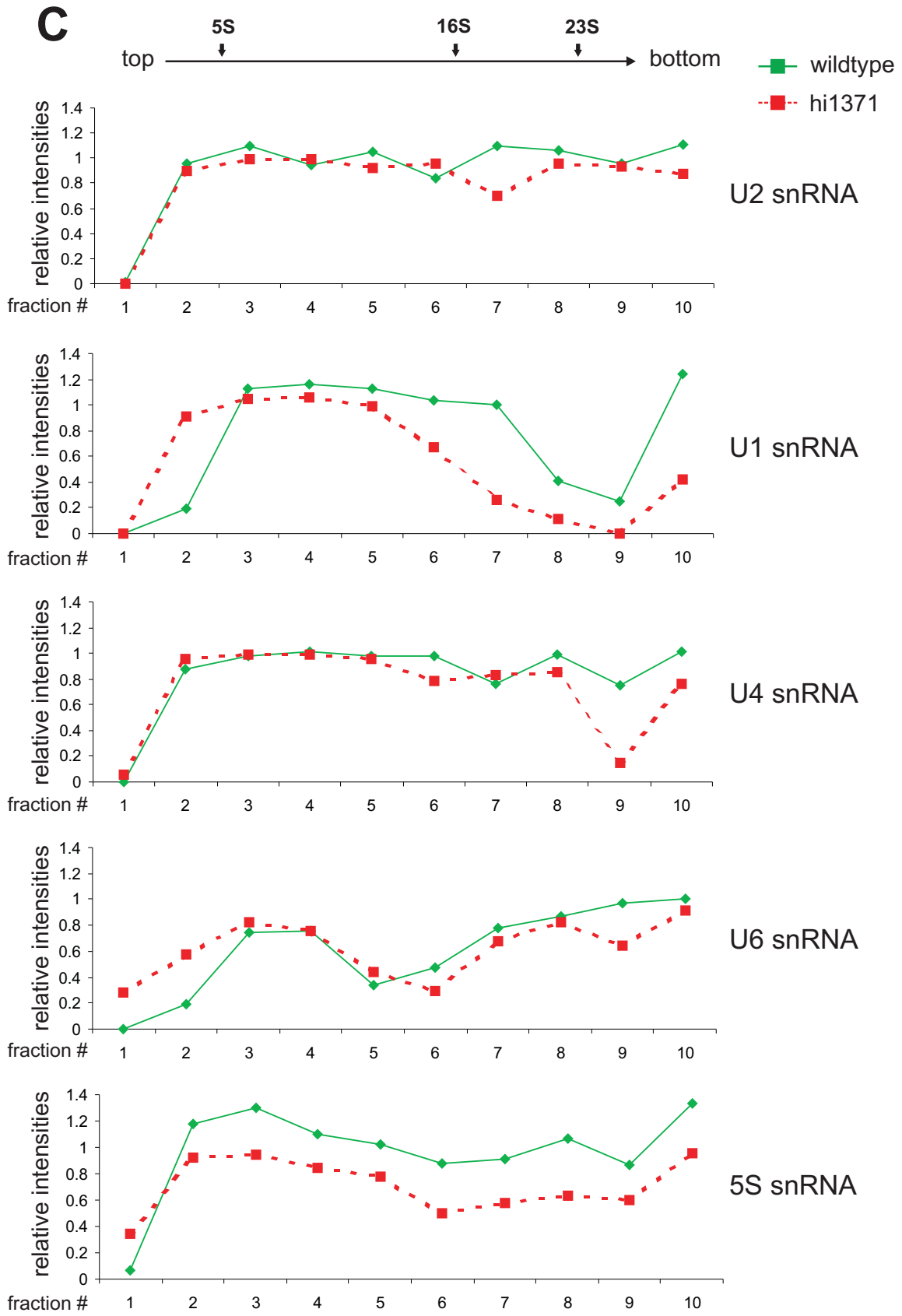


Supplementary Figure S1C

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Supplementary Figure S2

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Supplementary Figure S2.

Genomewide effects of U1C deficiency on alternative splicing in the zebrafish: RT-PCR validation.

(A-E) Alternative splicing of 72 target genes (as indicated above the lanes) was analyzed by RT-PCR, using total RNA from wildtype (wt) versus U1C knockout mutant (mut) embryos at 3 dpf and specific primer sets (indicated by arrows in the schematic of each panel). The numbers given below each reaction refer to the respective primer mixes (for sequences, see Supplementary Table S8). Labeled in green are genes that are also shown in Figure 4. *M*, DNA size markers in bp.

(A) Increased exon skipping of 36 target genes in the absence of U1C. Top and lower bands (except if specifically labeled) represent the exon inclusion and skipping products, respectively; arrows mark additional, unspecific RT-PCR products. Four genes, *sulf1*, *tpd52l2*, *sh3glb2* and *zgc:158450*, contain two adjacent exons that can be skipped individually: arrow heads indicate single-exon skipping products.

(B) U1C-dependent alternative 5' splice site usage of 25 target genes. The top and lower bands reflect usage of the proximal and distal 5' splice sites, respectively. Bands marked with arrow heads represent most likely intron retention products; unspecific RT-PCR products are labeled with arrows.

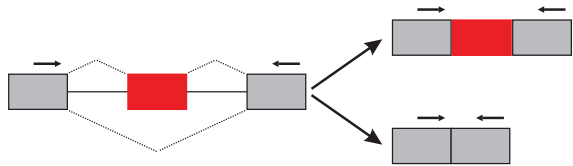
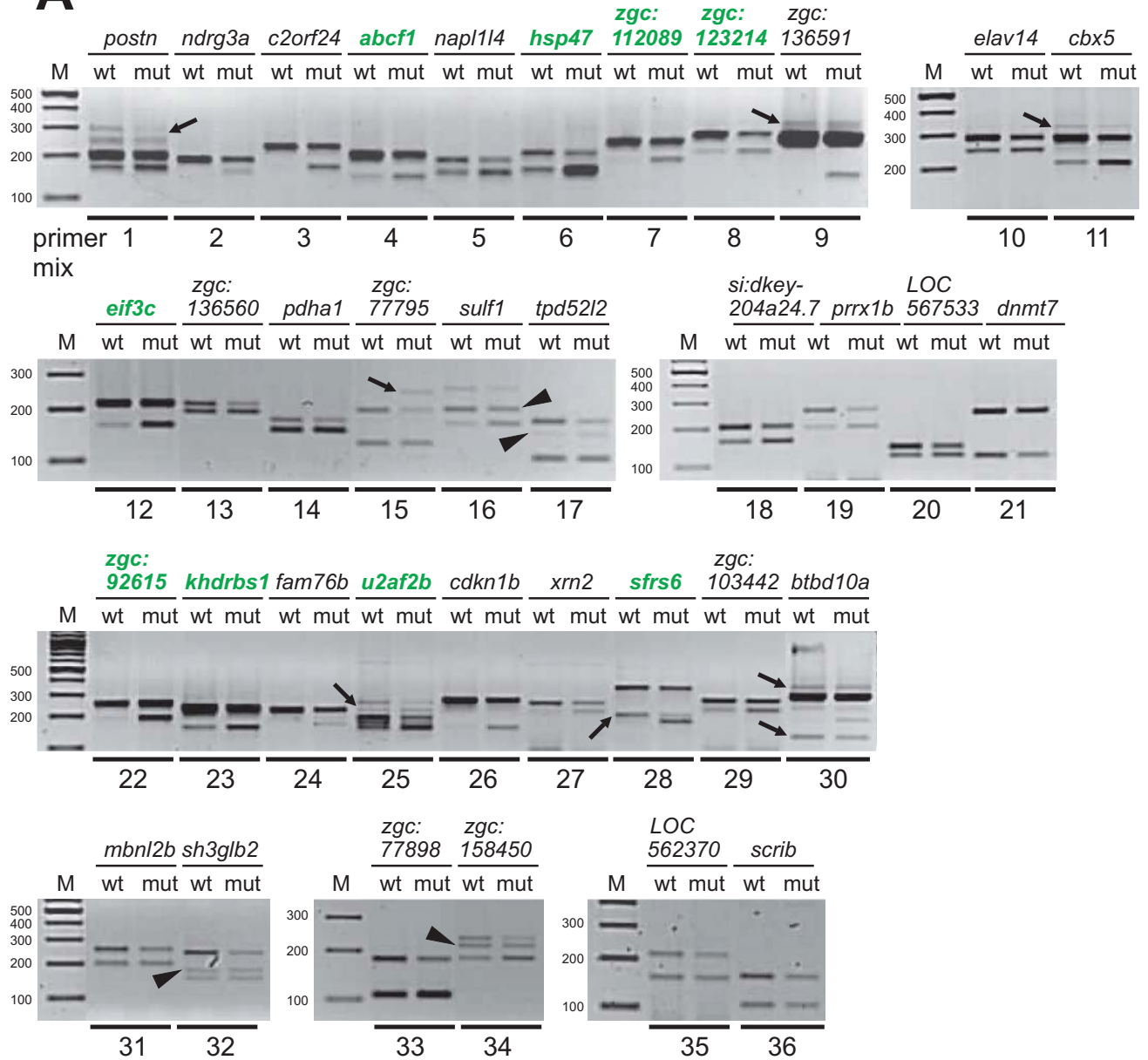
(C) U1C-dependent mutually exclusive exons in two genes (designated 4a and 4b for *eno1* and 8a and 9 for *pkm2a*).

(D) Increased intron retention in the absence of U1C, as validated for 9 target genes. To control for genomic DNA contamination, the same reactions were also done in the absence of reverse transcriptase (-RT panels); the arrows mark the intron retention products and the positions where the respective band would be expected in the -RT control reactions. The primer positions given in the schematic are representative for almost all reactions, except primer mixes 66, 73 and 75. For experimental reasons the reverse primers of those four reactions are located within the intron, and therefore only one intron-specific band is visible. One candidate which appeared to be negative after validation (showing no difference in the intron retention product between wildtype and mutant) was left out.

Supplementary Figure S2A

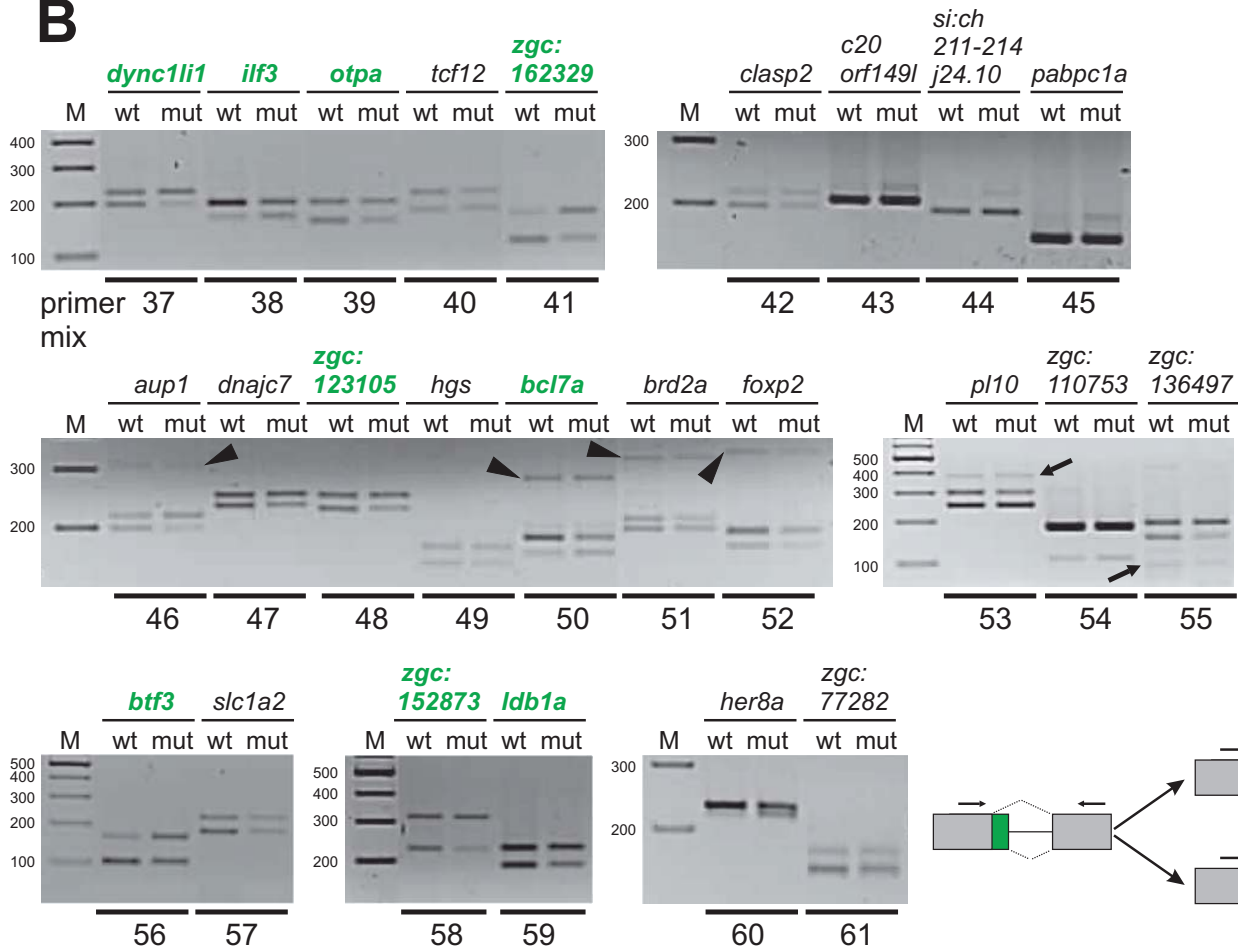
Rösel *et al.*

A

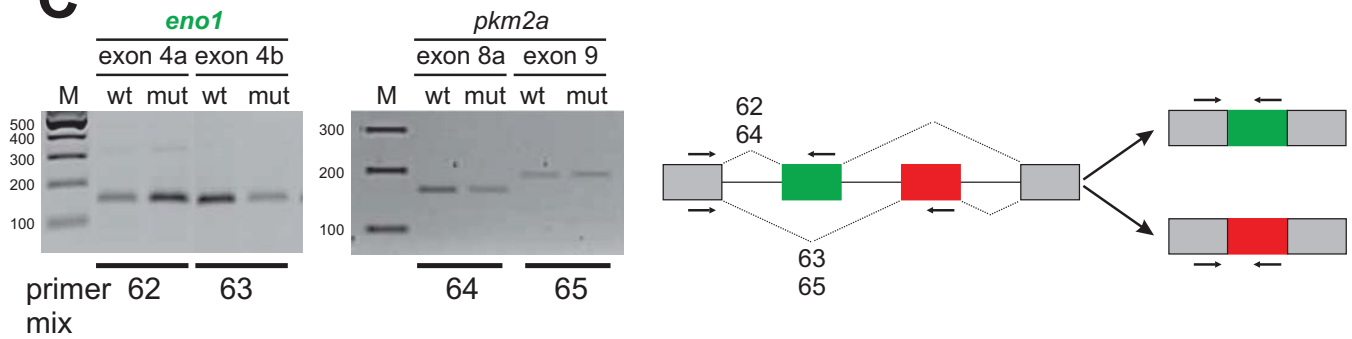


Supplementary Figure S2BC Rösel *et al.*

B

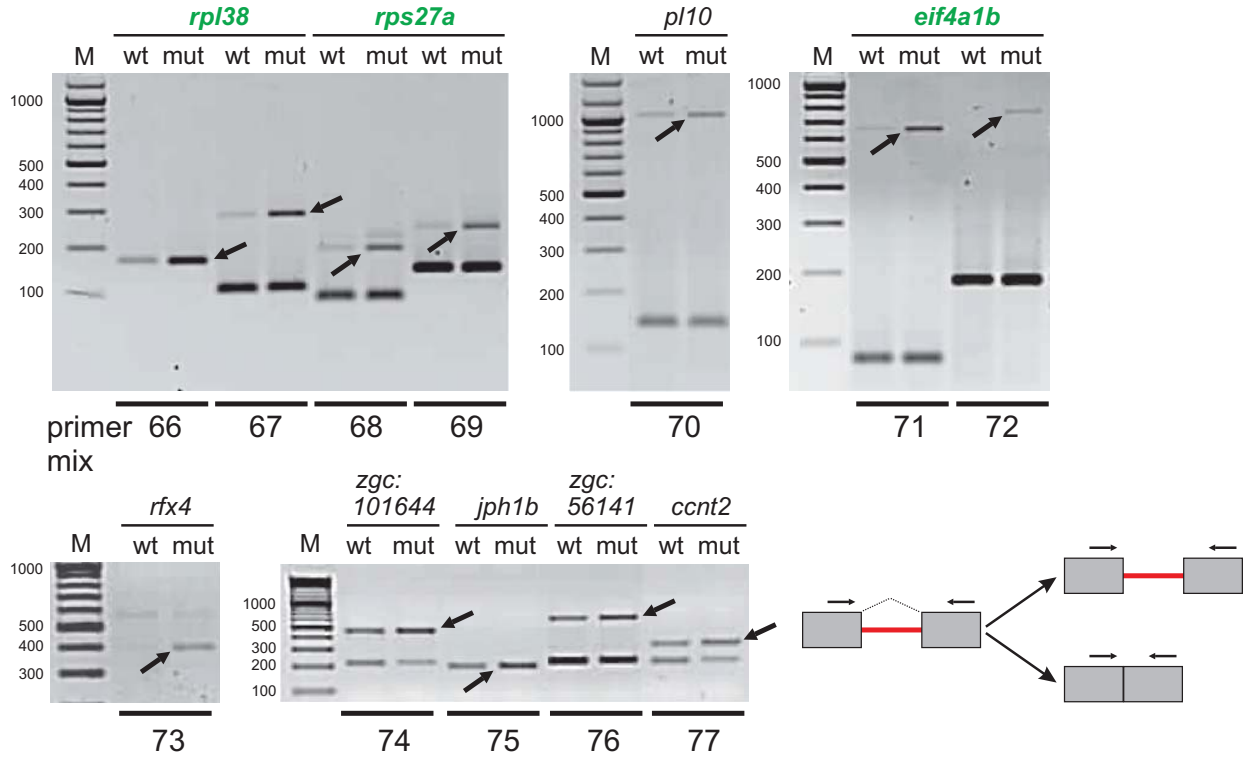


C

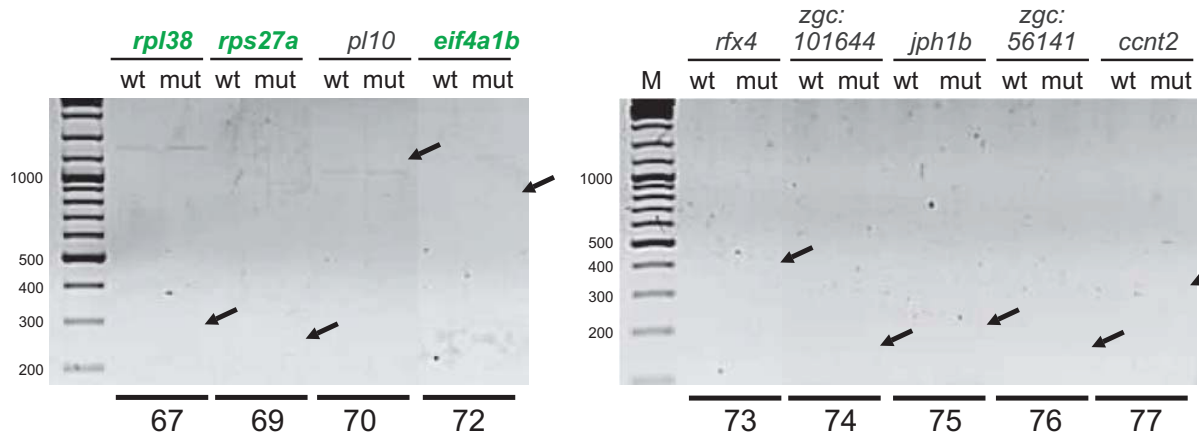


Supplementary Figure S2D Rösel *et al.*

D



- RT controls



Supplementary Figure S3 Rösel *et al.*

Supplementary Figure S3.

U1C knockdown in HeLa cells reproduces U1C-dependent alternative splicing changes in zebrafish and reveals functional role of associated U-rich elements (biological replicates).

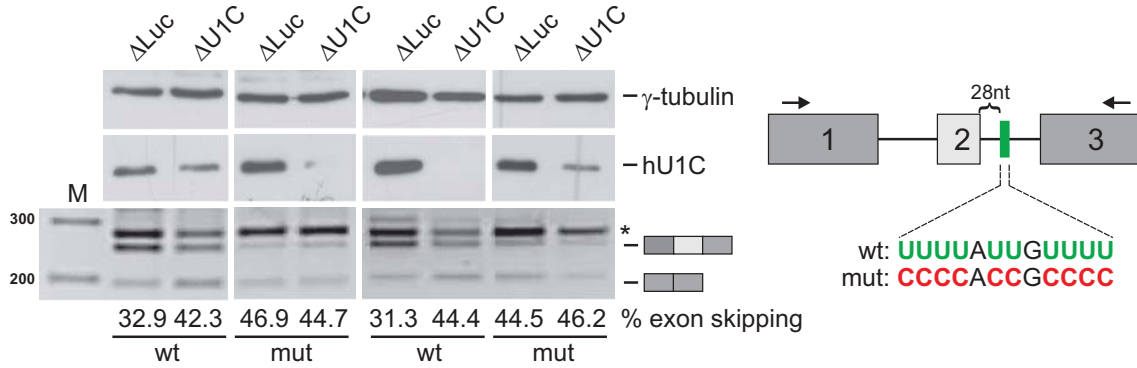
(A-B) Minigene constructs of four zebrafish target genes (*zgc:112089*, *c2orf24*, *zgc:162329*, and *ilf3*; as indicated above the panels) were transfected into HeLa cells after siRNA-mediated knockdown of U1C (Δ U1C) or luciferase (Δ Luc, as control). U1C knockdown efficiencies were assessed by Western blot analysis of whole cell lysates, detecting U1C and γ -tubulin (upper two panels). The splicing patterns were analyzed by RT-PCR on total RNA (lower panels), using specific primer sets (indicated by arrows in the schematics). The identities of the splicing products are depicted on the right of the gels. *M*, DNA size markers in bp.

(A) *In vivo* alternative splicing of two exon-skipping targets, *zgc:112089* (top), and *c2orf24* (bottom). For both genes the wildtype (wt) and a mutant construct (mut) were analyzed in replicates: two wt and mut replicates for *zgc:112089* and two wt and mut replicates for *c2orf24*. As shown in the schematics on the right (*zgc:112089*) and below (*c2orf24*), the U-rich elements (green boxes) located downstream of the 5' splice site of the middle exons were mutated to C-rich elements. Exon skipping ratios are given in % below each lane. The asterisk (*zgc:112089*) points to an unspecific PCR product.

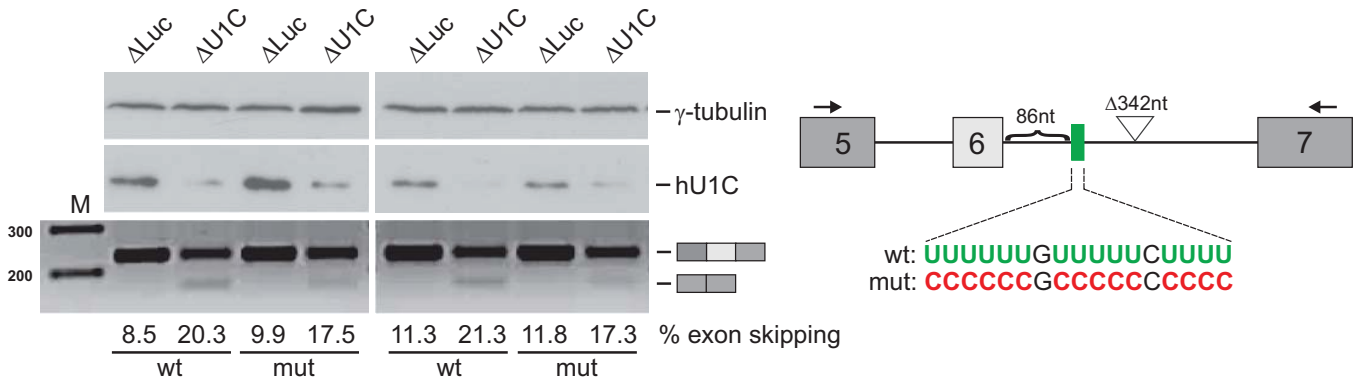
(B) *In vivo* splicing of two examples for alternative 5' splice site choice, *zgc:162329* (left) and *ilf3* (right); for *ilf3*, the wildtype (wt) and a mutant construct (mut) were analyzed. Shown are one wt replicate for *zgc:162329* and one wt and mut replicates for *ilf3*. In the mutant construct of *ilf3*, the U-stretch (green box in the schematic below) downstream of the proximal 5' splice site was substituted by a C-stretch. The use of the distal 5' splice site is quantitated in % below each lane.

Supplementary Figure S3 Rösel *et al.*

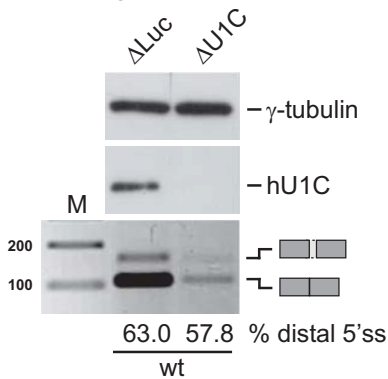
A *zgc:112089*



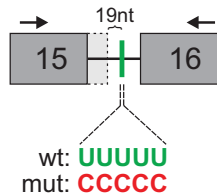
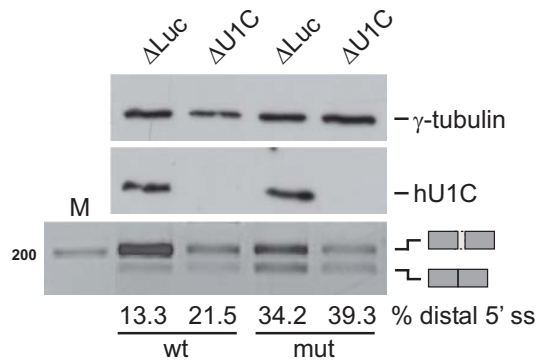
c2orf24



B *zgc:162329*



ilf3



Supplementary Figure S4 Rösel *et al.*

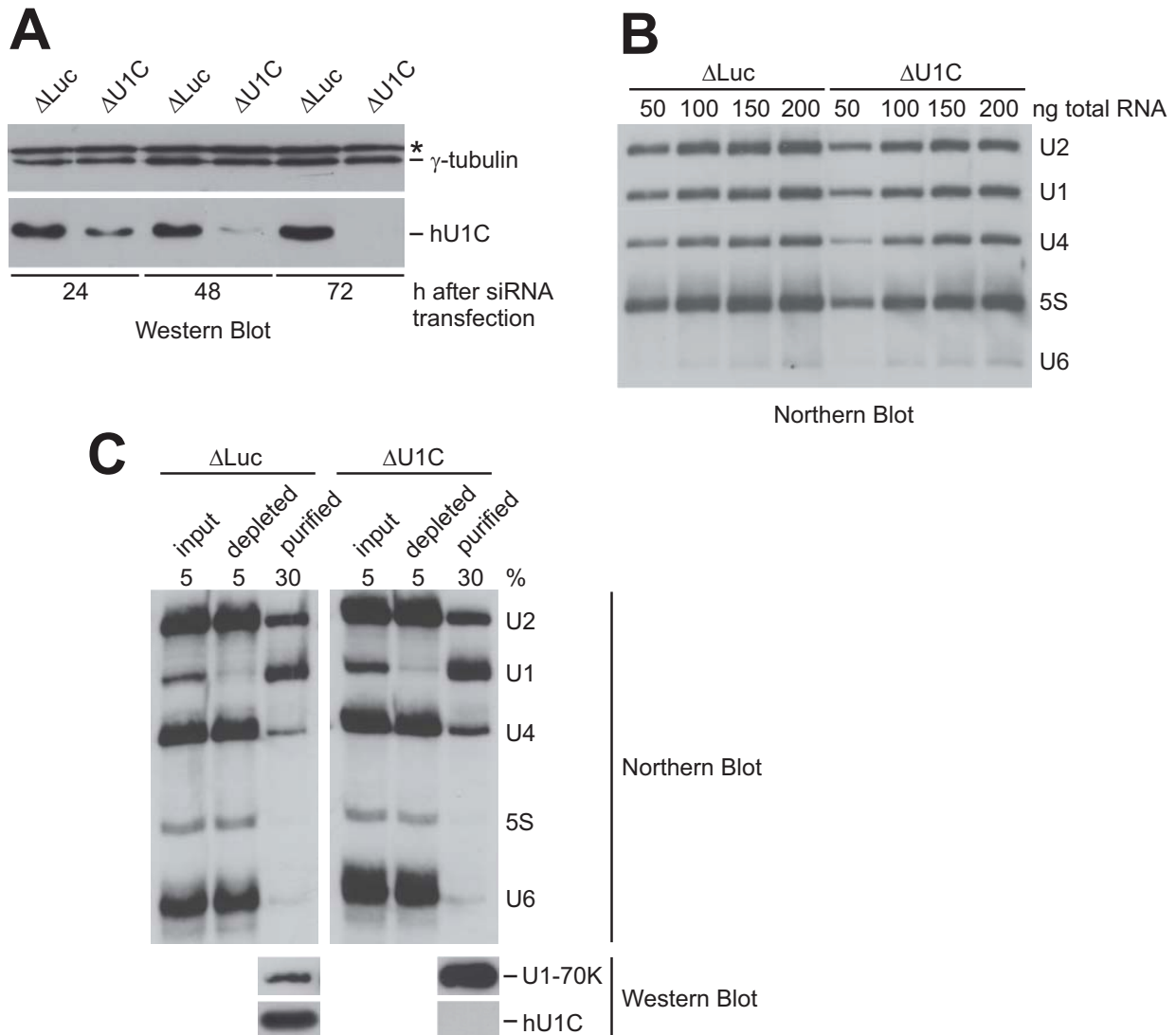
Supplementary Figure S4.

U1C knockdown in HeLa cells results in a U1C-deficient but stable U1 snRNP.

(A) Western blot of U1C knockdown in HeLa cells. 24, 48 and 72 h after siRNA transfection into HeLa cells, whole cell lysates were prepared from luciferase control (Δ Luc) and U1C knockdown (Δ U1C) cells, followed by SDS-PAGE and Western blot analysis for U1C and γ -tubulin. The asterisk marks an unspecific signal.

(B) Steady-state levels of the spliceosomal snRNAs. 50 ng to 200 ng of total RNA (as indicated above the lanes) from either control- (Δ Luc) or U1C-knockdown (Δ U1C) cells were analyzed by Northern blotting with probes specific for U1, U2, U4, U6, and, as a loading control, 5S rRNA (as marked on the right).

(C) Affinity purification of the U1 snRNP after U1C-knockdown. Whole-cell lysates from either control- (Δ Luc) or U1C-knockdown cells (Δ U1C) were used for affinity purification of the U1 snRNP, using a 2'-O-methyl-RNA antisense oligonucleotide. The total input lysate, the depleted lysate, and the affinity-selected material (lanes *input*, *depleted*, *purified*; portions tested are indicated in % above the lanes) were analyzed by Northern blotting for U1, U2, U4, and U6 snRNAs, and, as a loading control, for 5S rRNA (marked on the right). In addition, U1C and U1-70K were detected in the affinity-selected material by Western blot.



Supplementary Figure S5 Rösel *et al.*

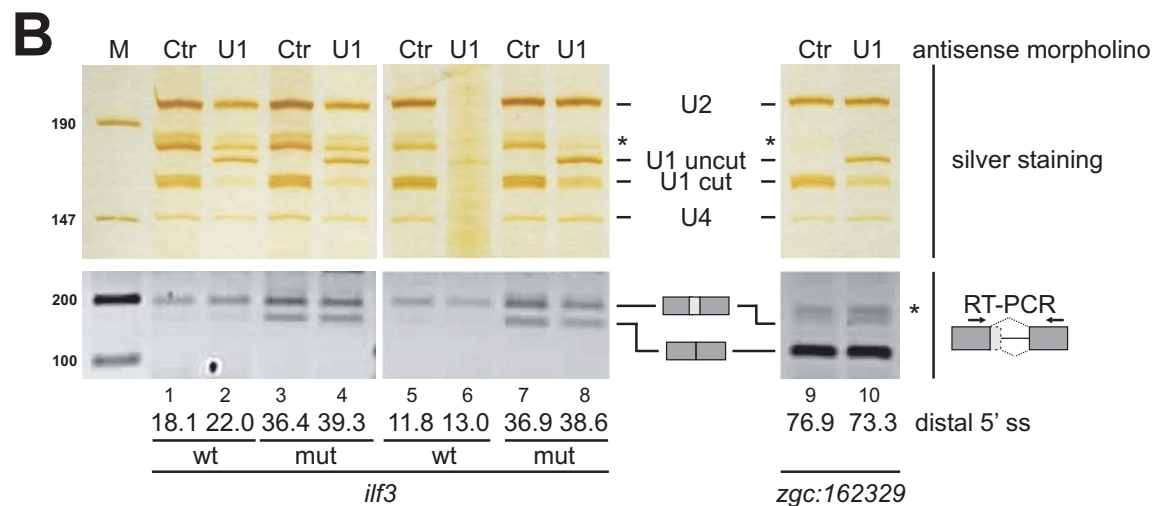
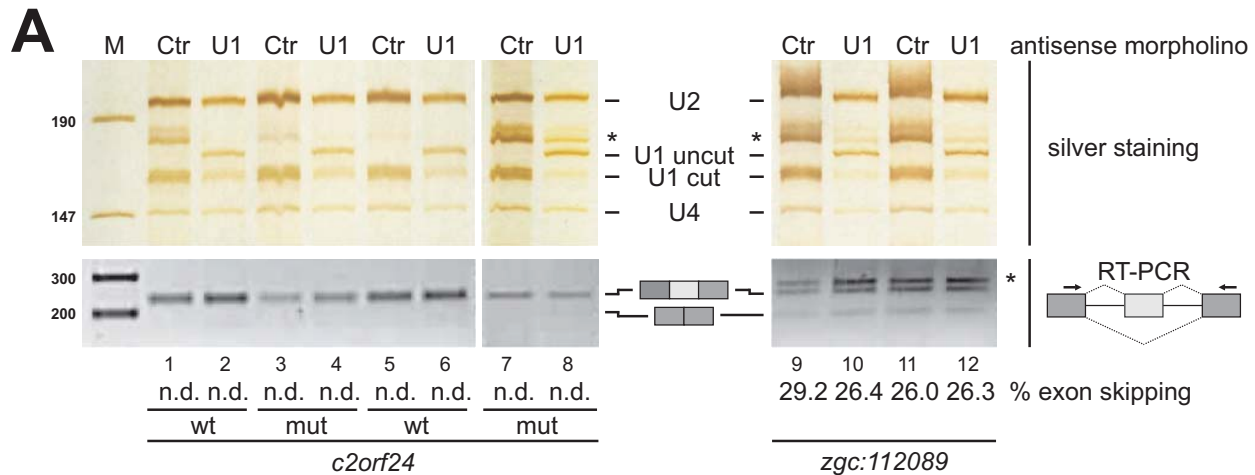
Supplementary Figure S5.

Morpholino-mediated knockdown of U1 snRNA in HeLa cells does not change the alternative splicing patterns of zebrafish-derived U1C target genes.

(A-B) Minigene constructs of four zebrafish target genes (*c2orf24*, *zgc:112089*, *ilf3*, and *zgc:162329*; as indicated below the panels) were transfected into HeLa cells after U1 snRNA knockdown; antisense morpholinos directed against the 5' end of the U1 snRNA (U1) or an unspecific control morpholino (Ctr) had been transfected 8 h before minigene transfection. The efficiency of morpholino blocking of the U1 snRNA was determined by Rnase H protection, using an antisense DNA oligomer binding to the 5' end of the U1 snRNA and silver staining (upper panels). Positions of the full-length U1 (uncut), U1 snRNA after Rnase H digestion (cut), U2, and U4 snRNAs are marked in the middle; the asterisk points to an unidentified band. Minigene splicing was analyzed by RT-PCR on total RNA, using specific primer sets (see panels and schematics on the right). RT-PCR reactions of two independent experiments for each minigene construct are shown, and the identities of the splicing products are depicted in the middle of the gels. *M*, DNA size markers in bp.

(A) *In vivo* alternative splicing of two exon-skipping targets, *c2orf24* (lanes 1-8), and *zgc:112089* (lanes 9-12). Exon skipping ratios for *c2orf24* could not be determined (n.d., skipped form not detectable) and for *zgc:112089* values are given in % below each lane. For *c2orf24*, the wildtype (wt, lanes 1/2 and 5/6) and a mutant construct were analyzed (mut, lanes 3/4 and 7/8; for details on the mutant construct, see **Supplementary Figure S3**). The asterisk points to an unspecific PCR product.

(B) *In vivo* splicing of two examples for alternative 5' splice site choice, *ilf3* (lanes 1-8), and *zgc:162329* (lanes 9/10). The use of the distal 5' splice site is quantitated in % below each lane. For *ilf3*, the wildtype (wt, lanes 1/2 and 5/6) and a mutant construct were analyzed (mut, lanes 3/4 and 7/8; for details on the mutant construct see **Supplementary Figure S3**); the asterisk marks an unspecific PCR product. In lane 6 (silver gel) the RNA was partially degraded during lysate preparation and/or RNase H treatment; however, the total RNA used for RT-PCR was isolated directly from the cells and therefore not affected by degradation.

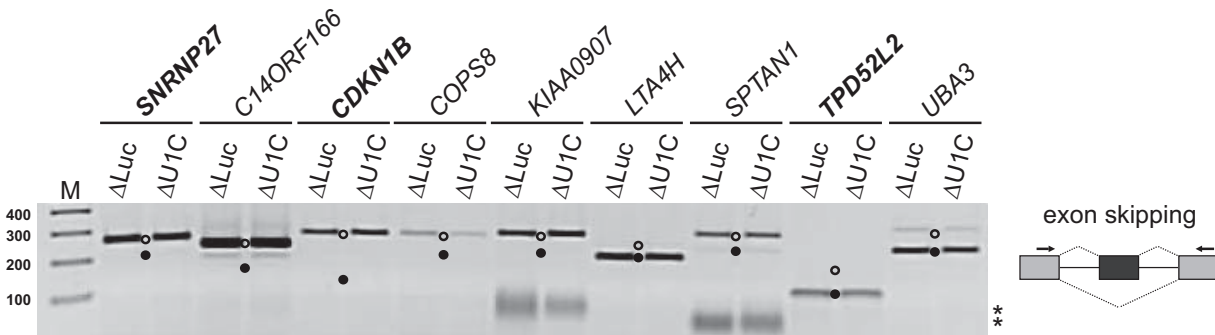


Supplementary Figure S6 Rösel *et al.*

Supplementary Figure S6.

Alternative splicing of human orthologs of zebrafish-derived U1C target genes is not U1C-regulated in HeLa cells.

The alternative splicing patterns of 9 human genes orthologous to zebrafish-derived U1C target genes (names above the lanes) were analyzed by RT-PCR, using total RNA from HeLa cells after siRNA-mediated knockdown of U1C (Δ U1C) or luciferase (Δ Luc, as control) and specific primer sets (arrows in the schematics on the right). The open circles mark the exon inclusion, the closed circles the exon skipping products; the asterisks point to primer dimers. Labeled in bold are three genes (*SNRNP27*, *CDKN1B*, and *TPD52L2*) that were also validated in the zebrafish system (cf. **Supplementary Figure S2A**, genes *zgc:92615*, *cdkn1b*, and *tpd51l2*, respectively). *M*, DNA size markers in bp.



SUPPLEMENTARY METHODS

This document is a companion to the paper:

Tanja Rösel, Lee-Hsueh Hung, Jan Medenbach, Katrin Donde, Stefan Starke, Vladimir Benes, Gunnar Rättsch, and Albrecht Bindereif

RNA-Seq analysis in mutant zebrafish reveals role of U1C protein in alternative splicing regulation

It describes the methods und results of the RNA-Seq data analysis.

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1. Annotation of refGene and its junction sequences

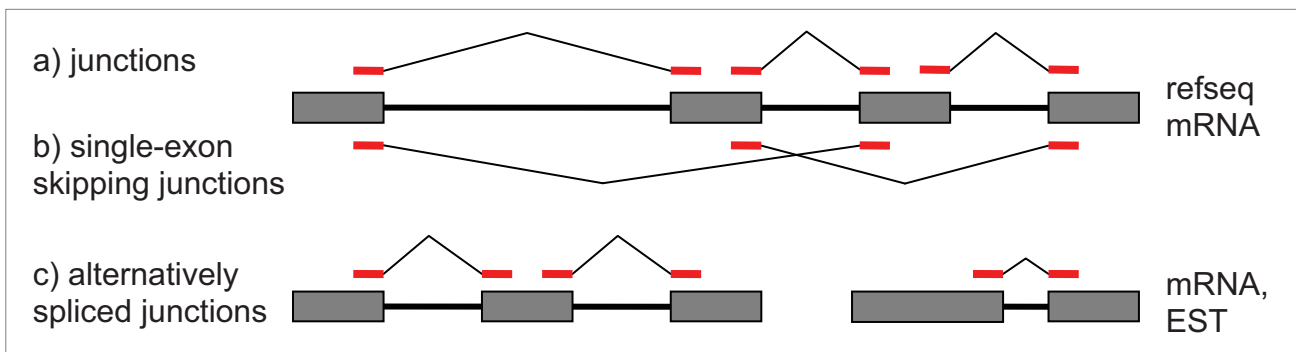
The Zv7 assembly of the Zebrafish genome (danRer5) was used for genomic sequence alignment. To analyze gene expression and alternative splicing changes in the U1C mutant zebrafish, we concentrated on the annotated genes with well-defined exon/intron structure, and built a zebrafish refGene junction database for further analysis. The following data were downloaded from the UCSC annotation database (<http://hgdownload.cse.ucsc.edu/goldenPath/danRer5/database/>): refGene, all_mran and all_est.

First, we selected unique (single-copy) refGenes in chromosomes 1-25. Junction sequences and annotation (upstream and downstream exon positions) were built by collecting

- refseq mRNA junctions,
- junctions skipping one refSeq mRNA exon,
- junctions alternatively spliced in all_mrna and all_est data,

In sum, our dataset covers 11,809 refGenes and 322,925 junctions (**Figure 1**).

Figure 1. Collection of junction sequence data



2. Sequence alignment and mapping

The number of total sequence reads (76 bp, single-end), which passed the standard parameter of Solexa's quality control from mutant (*-mut-* in the following text) and wildtype (*-wt-* in the following text) zebrafish samples were 31,821,414 (*mut*) and 35,497,176 (*wt*). These sequences were aligned to zebrafish genomic sequence (chromosomes 1-25) and refGene junction sequence (as described in section 1), using the program bwa (Burrows-Wheeler Alignment) version 0.4.6 (<http://bio-bwa.sourceforge.net/>, Li *et al.*, 2009). Standard parameters were selected, allowing 4 mismatches per 76-bp sequence.

From the genomic sequence alignment, reads were selected for further downstream analysis, based on the following criteria:

- Reads aligning uniquely to one chromosome position, but not over junction, and
- Reads aligning within the refGene region.

From the junction sequence alignment, reads aligning uniquely to junction sequence, but not genomic sequence, were selected for further downstream analysis.

In addition to the known junction sequence alignment, we also performed an unbiased alignment to look for novel junctions. For this we identified partial matches of each read to the genome of at least 35bp, using a modified version of GenomeMapper (Schneeberger *et al.*, 2009). For each such match we considered the genomic region of 10 kb each upstream and downstream of the match. We performed an intron-aware Smith-Waterman alignment of the read to this region, employing QPALMA (De Bona *et al.*, 2008), and reported alignments with at most six mismatches and two indels. We required the conventional splice site consensus dinucleotides (GT or GC for the 5', and AG for the 3' splice sites) for alignments over (predicted) intron junctions. Since the standard Solexa RNA-Seq protocol is not strand-sensitive, all reads were aligned to both strands and the best as well as suboptimal alignments were reported. In order to increase computational efficiency, we only selected junction sequences with an exact match of at least 12 bp on either side (Sonnenburg *et al.*, 2007). The strategy is capable of identifying intron junctions, if they are at least 12nt away from the read boundary, or if other evidence suggests to include the intronic region in the subsequence considered for the QPALMA alignment. The strategy described is implemented in the Palmapper software (Jean *et al.*, 2010) available at <http://ftp.tuebingen.mpg.de/fml/raetsch-lab/software/palmapper>).

Using the algorithm described we obtained alignments for 79.0% and 77.5% for all mutant and wildtype reads, respectively. On average, 28.2% of all alignments were spliced, i.e. spanned at least one predicted intron.

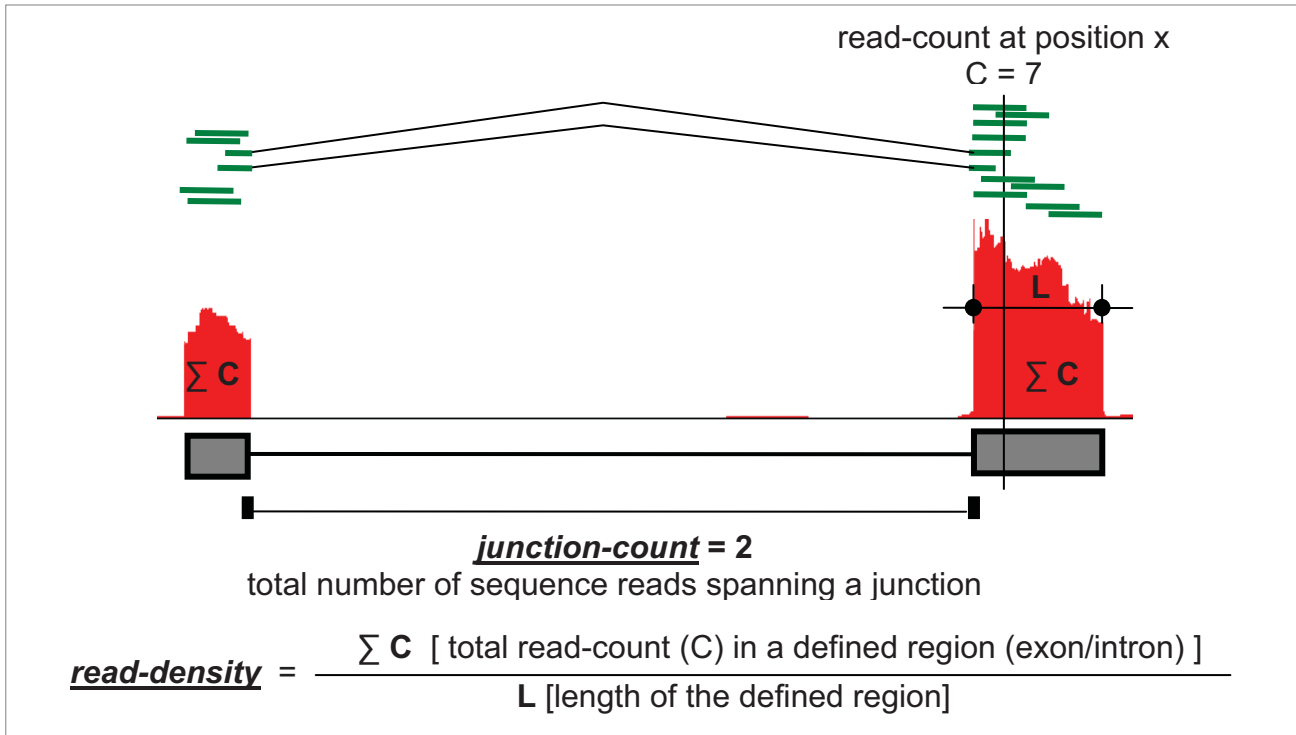
Uniquely mapped reads were defined as refGene transcript, ignoring antisense transcripts here. In sum, ~ 30 mil. reads (~ 45% of the total reads) aligned uniquely to the refGene genomic sequence or junction sequence, among them ~ 35 % spanned a junction. The table below summarizes the alignment results:

	total sequence reads	reads selected (in refGene)	selected / total reads	non-junction reads	junction reads	junction reads / selected reads
mut	31,821,414	14,411,654	45 %	9,309,611	5,102,043	35 %
wt	35,497,176	15,702,952	44 %	10,333,440	5,369,512	34 %

	junction reads recovered from unbiased alignment (novel junctions)	novel junction reads / total junction reads
mut	327,983	6.4 %
wt	211,513	4.0 %

All selected reads were mapped to each refGene genomic region, and
a) **read-density**
b) **junction-count**
were calculated for the downstream analysis (**Figure 2**).

Figure 2. Calculation of junction-count and read-density



3. Gene expression analysis

The transcripts of refseq mRNA from the refGenes were used to analyze and compare gene expression levels between mutant and wildtype zebrafish samples. Transcripts containing at least 1 read in either *mut* or *wt* were selected. First we calculated the **read-density** of these 11,651 transcripts by adding up all read-counts of refseq mRNA exons, and divided this value by the length of mRNA in nucleotides. The ratio of transcript **read-density** between *mut* and *wt* reflects the abundance of the mRNA (gene expression level). Transcripts with **read-density** lower than the 30 % quantile (3.9 in *mut*, 4.4 in *wt*) were defined as not significantly expressed and were removed from further downstream analysis. Here we assumed that ~ 70% of the annotated genes are expressed during the first 3 days of zebrafish embryonic development. The **read-density** in *wt* was normalized by the factor 0.92, which is the ratio of total selected reads between *mut* and *wt*.

The package edgeR (differential expression analysis of digital gene expression data) from Bioconductor (<http://www.bioconductor.org>) was used to determine the significance of gene up- and downregulation. We chose the Benjamini and Hochberg method (Benjamini and Hochberg, 1995) for controlling the false discovery rate (FDR) of hypothesis tests, which is a powerful method for correcting multiple comparisons. Among the 8,463 expressed genes (8,556 transcripts) analyzed, 437 genes (**Supplementary Table S1**) were upregulated, and 293 genes (**Supplementary Table S2**) were downregulated with adjusted-p values lower than 0.05.

4. Alternative splicing target detection

To detect alternative splicing events, we looked for the following 5 patterns (see sections 4.1 - 4.5) and collected the **read-density** and **junction-count** information around the alternatively spliced regions to determine whether a quantitative change of the alternative isoforms between **mut** and **wt** was significant.

To avoid the isoforms, which were at background expression levels or lacked the complete upstream or downstream exon/intron information, we set a minimal **junction-count** for the non-refseq (mRNA/est/novel) junctions of

a) 5 for **mut**,

b) 6 for **wt**.

This cut-off was based on the quantile distribution of **junction-count** of the 322,925 annotated junctions in **mut** and **wt** shown below.

	0 %	10 %	20 %	30 %	40 %	50 %	60 %	70 %	80 %	90 %	100 %
mut	0	0	0	0	0	1	1	1	5	18	28,349
wt	0	0	0	0	0	0	1	1	6	21	30,667

In addition to the minimal **junction-count**, we also set a minimal **read-density** of

a) 3.9 for **mut**,

b) 4.4 for **wt** (defined in section 3),

to determine whether a particular region (an exon or intron) is expressed or not.

The following subsections describe further details and criteria for target selection of the 5 alternative splicing modes, based on the following general rules and procedures:

a) The RNA-Seq protocol and the alignment procedure are biased, since random fragmentation and priming efficiency are sequence-dependent, as well as read selection of unique mapping with 76-bp read length. As shown in **Figure 5**, the read-count across each exon varies and the **read-density** of each exon within a gene differs. In order to detect significant changes of a particular exon or intron region, it therefore would be better to rely on the fold change of the **read-density** and **junction-count** in a limited region of the gene. The two exons flanking the alternative splicing event were selected to represent the constitutive region, providing the basis for comparison.

b) **Read-density** and **junction-count** information was collected in the constitutive and alternative exon region. The **wt** values were normalized with the **mut** to **wt** ratio of total reads in the corresponding refGene to correct for differences in total sequenced read number and transcription rate between **mut** and **wt**. In general, the read-count values in the first and last exon were relatively inconsistent. If the up-/downstream constitutive exon was the first or last exon and longer than 70 bp, only a 70-bp exonic region next to the splice site was used for calculating its read density, in order to reduce the degree of variation.

c) Basically, there are two sets of information, which contain the **read-density** and **junction-count** values, each of them indicating the quantity of one particular isoform. The fold change ($FC = \log_2 \text{mut/wt}$, used in the entire analysis) of each value indicates a relative increase ($FC > 0$) or decrease ($FC < 0$) of one particular splice form in **mut** vs. **wt**. Since the absolute values as well as the corresponding fold changes of the supporting information varied to a relatively high degree, we had to apply different parameters for target selection. In general, the higher the stringency of the selection criteria is, the lower the false positive and the higher the false negative rate will be.

The junction information is more reliable to predict whether an alternatively spliced isoform is expressed. We therefore started with the selection of significant junctions. From all junctions annotated in the 8,463 expressed genes (see section 3), we looked for refSeq junctions with at least one **junction-count** in **mut** or **wt**; and for non-refSeq junctions with a minimal **junction-count** as defined above. In sum, 84,885 junctions were selected. The package edgeR was used to calculate the fold change and p-value and to determine the significance of changes in each junction between **mut** and **wt** (**list_A**). The following sections describe the target selection of 5 different alternative splicing modes, which all start with the junction information in **list_A**.

4.1 Single-exon skipping

We started with the most frequent alternative splicing event, single-exon skipping. The shift of exon skipping vs. inclusion between **mut** and **wt** was detected by combining the **read-density** and **junction-count** values within a 3-exon context (**Figure 3**).

Based on significant **junction-count** of exon skipping and exon inclusion junctions we can predict that two isoforms exist that are experimentally detectable. Taking the junctions in **list_A**, we looked for a set of 3 junctions containing one exon skipping and two exon inclusion junctions with constitutive up-/downstream exons and one alternative exon. We calculated the **read-density** of constitutive exons (**RD-constit**) and alternative exon (**RD-alt**), the fold change of each exon, and the difference of fold change between **RD-alt** and **RD-constit** (which is the average of the two flanking constitutive exons). This yields the first exon inclusion information (**incl_1**). The fold change of **junction-count** from the two inclusion junctions give the second (**incl_2**) and third (**incl_3**) inclusion information. The skipping information is obtained from the fold change of **junction-count** in skipping junction (**skip**).

Ideally, a significant reciprocal effect between skipping and inclusion information indicates a quantitative shift of the two isoforms between **mut** and **wt**. As shown in **Figure 3**, increased values of skipping information (**skip**) and decreased values of inclusion information (**incl_1-3**) predict the increased exon skipping isoform in **mut**. On the other hand, decreased values of skipping information and increased values of inclusion information predict the increased exon inclusion isoform in **mut**.

Two controls for data filtering were applied to all 5 sections (4.1 – 4.5) with the following parameters:

Read-density-control: The **RD-constit** in both *mut* and *wt* is above the minimal **read-density**, and the difference of fold change between up- and downstream exons is not greater than 0.3. The **RD-alt** in *mut* or *wt* is above the minimal **read-density**. This control filtered out the very low (in background level) expressed isoforms and provided the evidence that the up-/downstream exons are constitutive.

Junction-ratio-control: The ratio of **junction-count** values between two groups (inclusion or skipping junctions) should be no less than 0.05. This control filtered out alternative isoforms that are expressed at very low levels, which may experimentally not be detectable.

We use *mut+* to illustrate an increase of the exon skipping isoform in *mut*, and *wt+* in *wt* in the single-/multiple-exon skipping analysis. Targets were selected according to one of the following criteria:

a) If the fold change of **junction-count** of skipping junction (**skip**) has a p-value less than 0.05, this strongly indicates a change of exon skipping form. Exon skipping targets were selected based on the following values of the skipping/inclusion information.

<i>mut+</i> :	skip > 0;	incl_1 < 0.2;	incl_2 < 0.2;	incl_3 < 0.2;
<i>wt+</i> :	skip < 0;	incl_1 > -0.2;	incl_2 > -0.2;	incl_3 > -0.2.

b) If there is not enough information provided from skipping junction (p-value of **skip** > 0.05), we relied on the information from the two inclusion junctions. If either **incl_2** or **incl_3** has a p-value less than 0.05 and the other has a p-value less than 0.2, exon skipping targets were selected based on the following values.

<i>mut+</i> :	skip > 0.5;	incl_1 < -0.5;	incl_2 < -0.5;	incl_3 < -0.5;
<i>wt+</i> :	skip < -0.5;	incl_1 > 0.5;	incl_2 > 0.5;	incl_3 > 0.5.

c) If none of the junctions indicates a significant change (p-value of all three > 0.05), we relied on the information from the fold change of **read-density** in alternative exon, and selected targets based on the following values.

<i>mut+</i> :	incl_1 < -1;	incl_2 < -0.2;	incl_3 < -0.2;	skip > 0.2;
<i>wt+</i> :	incl_1 > 1;	incl_2 > 0.2;	incl_3 > 0.2;	skip < -0.2.

Supplementary Table S3 lists 218 targets predicted with increased exon skipping in *mut* and 12 in *wt*. Among the 218 *mut+* targets, 31 were selected and positively validated by RT-PCR.

4.2 Multiple-exon skipping

To detect alternative splicing events involving multiple-exon skipping, the methods we applied were similar to single-exon skipping described in section 4.1. Taking the junctions in *list_A*, we looked for a set of junctions containing one exon skipping and more than two exon inclusion junctions with constitutive up-/downstream exons and multiple alternative exons (**Figure 4**). Only dataset containing two alternative exons were found that passed the two filtering controls. Here we have **incl_1** (a, b) values from two alternative exons, and **incl_2/3/4** from three intermediate junctions. Target selection followed the same criteria for single-exon skipping as described in section 4.1.

Supplementary Table S4 listed 9 targets predicted with increased multiple-exon skipping in *mut* and 1 in *wt*. Among the 9 *mut+* targets, 5 were selected and positively validated by RT-PCR.

4.3 Intron retention

To predict intron retention events, we relied on the **junction-count** and the **read-density** of target intron. Taking the junctions in *list_A*, we selected junctions spanning less than 2000-bp, which have no significant intermediate junction, and obtained the corresponding up-/downstream exons (**Figure 5**). Two parts of information are required, one indicating intron retention, which is the fold change of the intron **read-density (retained)**, the other indicating intron splicing, which is the fold change of the **junction-count (spliced)**.

Positive value of intron retained information and negative of spliced information indicate an increase of intron retention in *mut* (*mut+*). While negative value of intron retained information and positive of spliced information indicate an increase of intron retention in *wt* (*wt+*).

In addition to the two filtering controls, we applied a p-value control (< 0.1) for the fold change of **junction-count**. Targets were predicted by the following criteria:

<i>mut+</i> :	retained > 0.5;	spliced < 0;	retained – spliced > 0.7;
<i>wt+</i> :	retained < - 0.5;	spliced > 0;	retained – spliced < - 0.7.

Supplementary Table S5 listed 32 targets predicted with an increase of intron retention in *mut* and 12 targets in *wt*. Among the 32 *mut+* targets, 9 were positively validated (from 10 selected) by RT-PCR.

4.4 Alternative 5' and 3' splice sites

To predict alternative usage of 5' and 3' splice sites, we needed a pair of junctions with a specific up- (down-) stream position and different positions on the down- (up-) stream positions. Here we set the limits for the distance of the alternative 5' or 3' splice sites to a minimum of 10 bp and a maximum of 150 bp. Taking the junctions in *List_A*, we obtained 501 pairs of junctions and calculated the **read-density** and **junction-count**, similarly as described in section 4.1 (**Figure 6**).

The same principle applied for alternative 5' and 3' splice site target selection. Here the case of alternative 5' splice sites is illustrated in detail: Two pieces of information are required, one indicating the distal splice site usage, which is the fold change of the distal 5' splice site **junction-count (distal)**, the other indicating the usage of the proximal splice site, which contains the difference of fold change between **RD-alt** and **RD-constit (proximal_1)** and the fold change of the proximal 5'SS **junction-count (proximal_2)**. As shown in **Figure 6**, increased values of distal 5' splice site usage information and decreased values of proximal 5' splice site usage information predict the increase of shorter isoform with distal splice site in

mut. In analogy, decreased values of distal 5' splice site usage information and increased values of proximal 5' splice site usage information predict the increase of longer isoform with proximal splice site in *mut*.

We use *distal_mut+* to illustrate an increase of the distal 5' splice site usage in *mut*, and *proximal_mut+* of the proximal splice site. Targets were selected with the following parameters:

<i>distal_mut+</i> :	$\text{proximal_1} < -0.35;$	$\text{proximal_2} < 0;$	$\text{distal} > 0;$
	$(\text{distal} - \text{proximal_2}) > 0.75;$		
<i>proximal_mut+</i> :	$\text{proximal_1} > 0.35;$	$\text{proximal_2} > 0;$	$\text{distal} < 0;$
	$(\text{distal} - \text{proximal_2}) < -0.75.$		

Supplementary Table S6 lists 43 targets predicted to show a change in alternative 5' splice site usage between *mut* and *wt*; and 12 targets with alternative 3' splice sites. Among the 43 alternative 5' splice site targets, 25 were selected and positively validated by RT-PCR.

4.5 Mutually exclusive exons

To detect mutually exclusive exons, we needed two pairs of junctions, one indicating the inclusion of the upstream exon, the other the inclusion of the downstream exon, and both sharing the same up-/downstream constitutive exons. Datasets with this requirement were selected from junctions in *List_A*. Two groups of information were applied to predict targets as shown in **Figure 7**. One indicates the upstream exon inclusion, which contains the difference of fold change between *RD-alt* (upstream exon) and *RD-constit* (*up_1*) and the fold change of *junction-count* for the upstream exon inclusion (*up_2*, *up_3*). The other indicates the downstream exon inclusion, which contains the difference of fold change between *RD-alt* (downstream exon) and *RD-constit* (*down_1*) and the fold change of *junction-count* for the downstream exon inclusion (*down_2*, *down_3*).

In addition to the two filtering controls, p-value limits were further set here for the junctions flanking the two alternative exons. Targets were selected if either *up_2* or *up_3* had a p-value of less than 0.05, and either *down_2* or *down_3* had a p-value of less than 0.05. A reciprocal effect between the up-/downstream exon inclusion information provided the evidence of mutually exclusive exons.

- If all values of upstream exon inclusion information (*up_1*, *up_2*, *up_3*) were positive and downstream exon inclusion information (*down_1*, *down_2*, *down_3*) negative, we predicted an increased usage of the upstream alternative exon in *mut*.
- If all values of upstream exon inclusion information (*up_1*, *up_2*, *up_3*) were negative and downstream exon inclusion information (*down_1*, *down_2*, *down_3*) positive, we predicted an increased usage of the downstream alternative exon in *mut*.

Supplementary Table S7 lists three predicted targets, of which two were selected and positively validated with RT-PCR.

Figure 3. Single-exon skipping

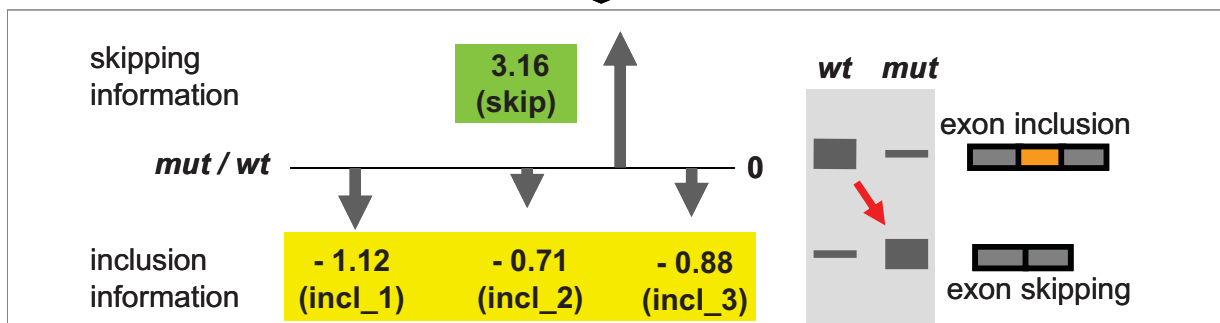
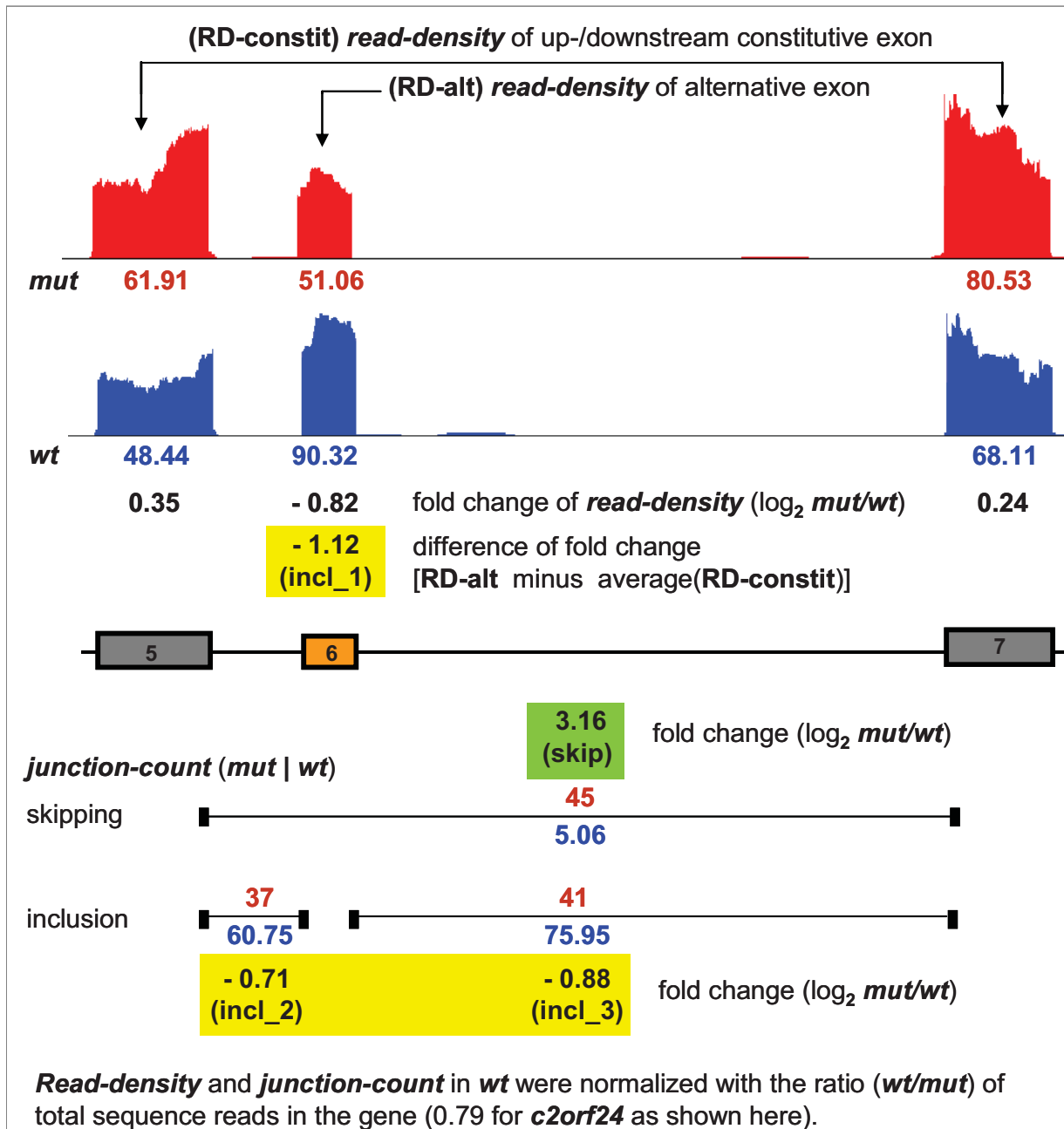


Figure 4. Multiple-exon skipping

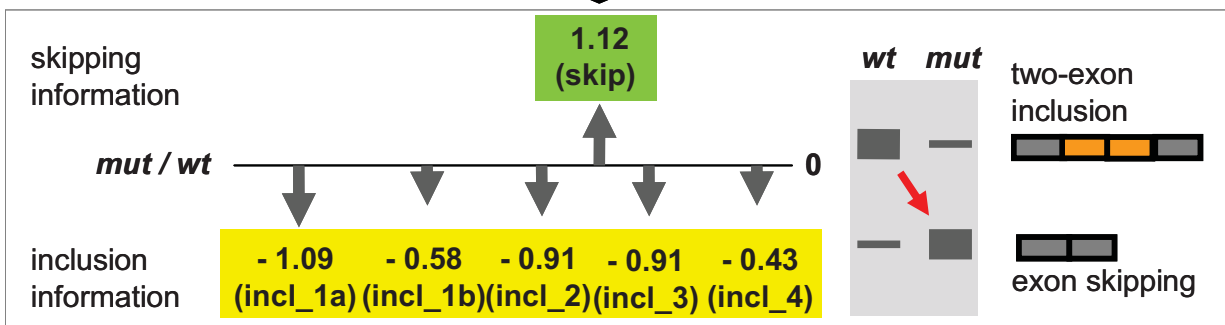
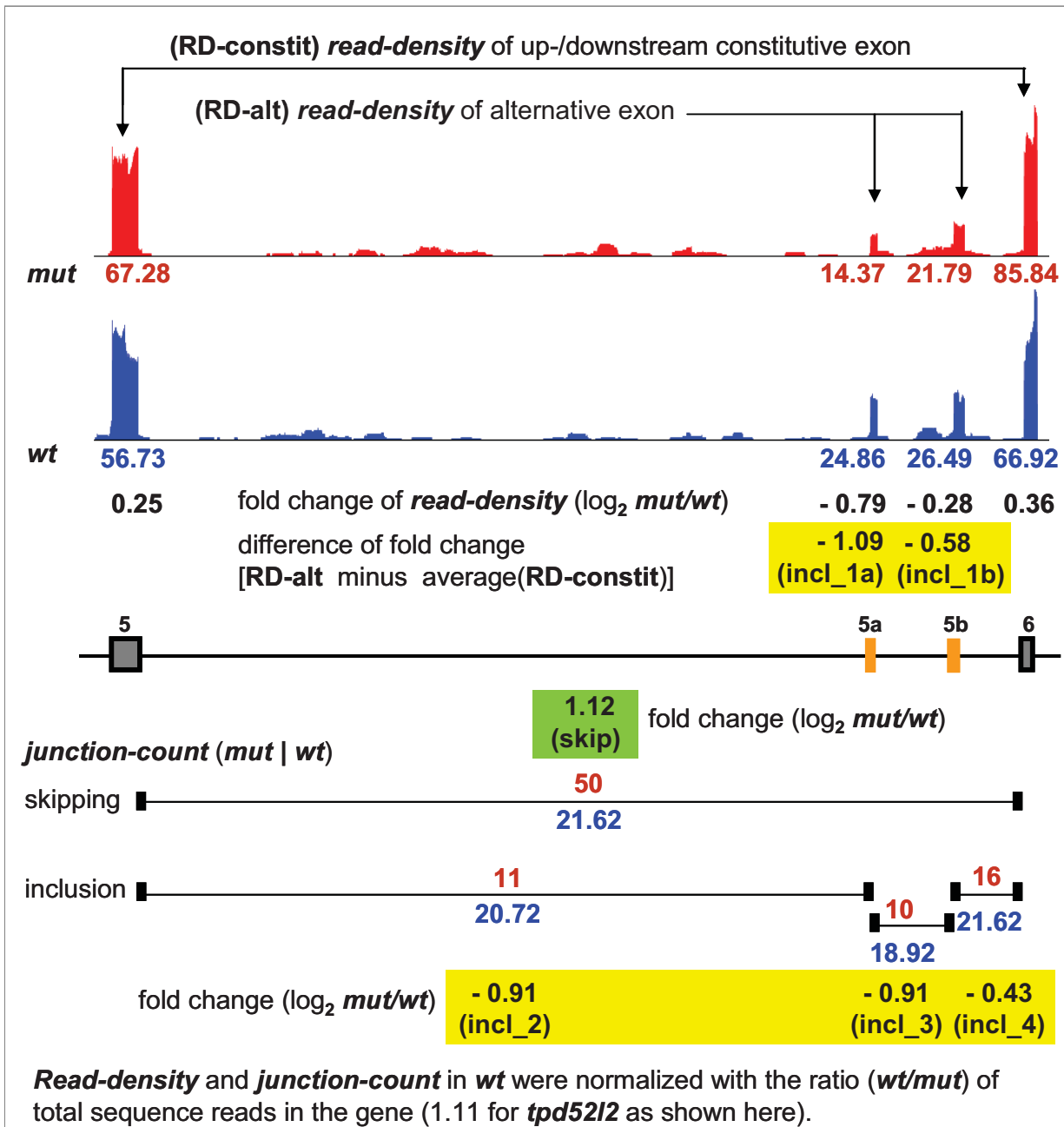


Figure 5. Intron retention

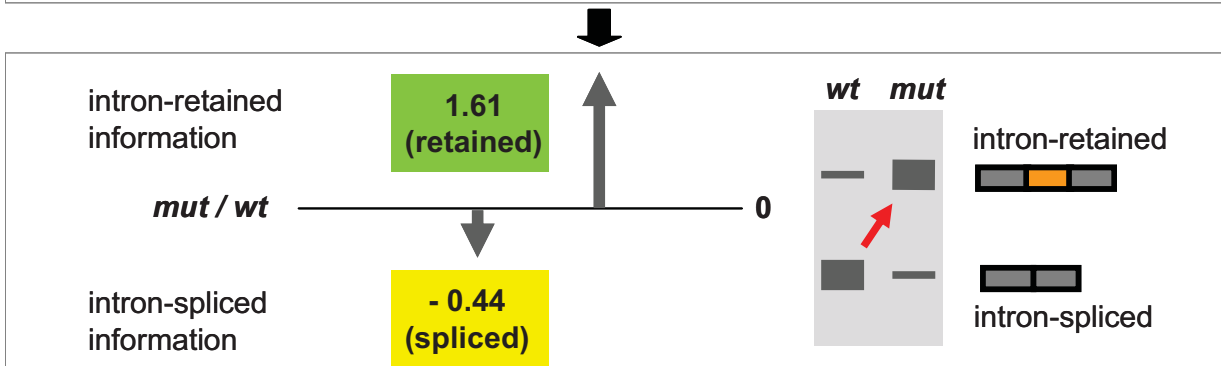
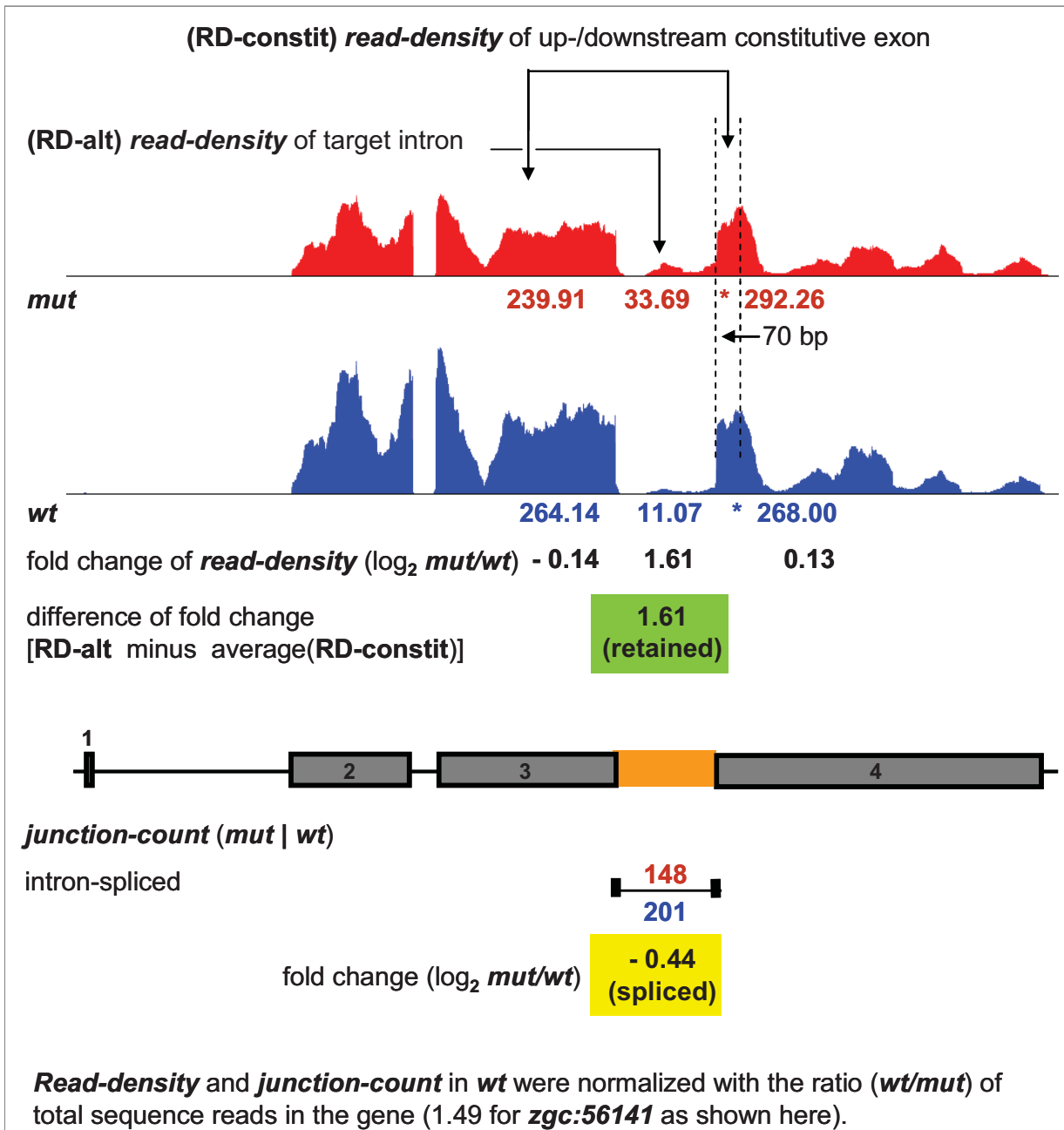


Figure 6. Alternative 5' and 3' splice sites

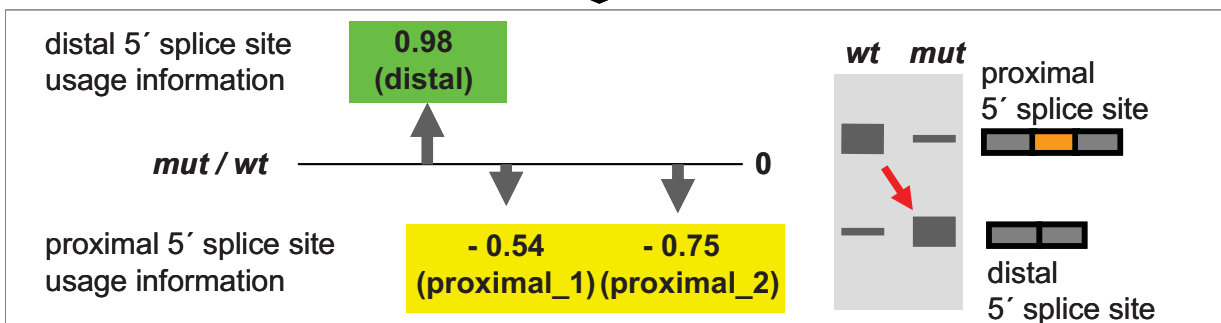
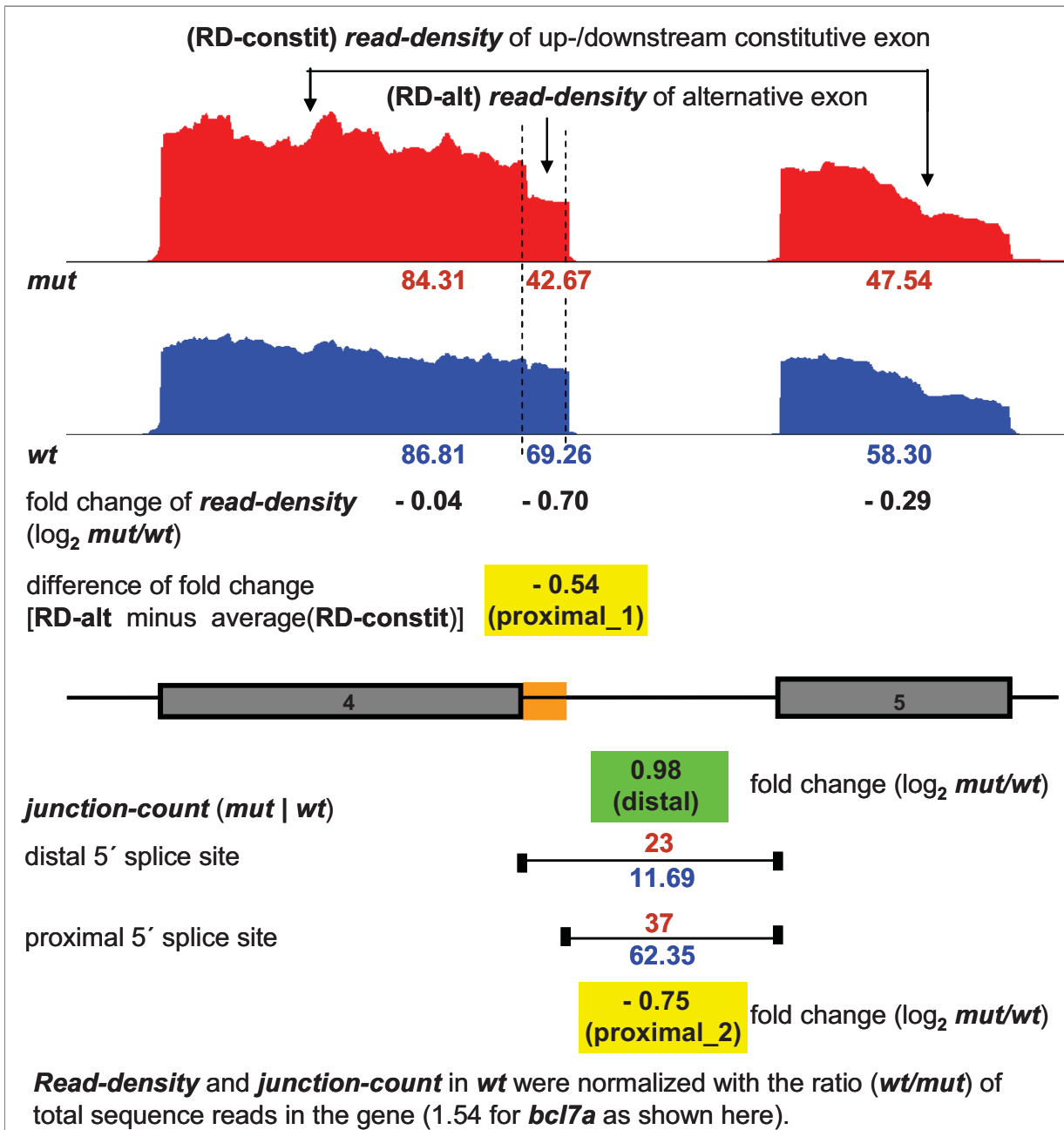
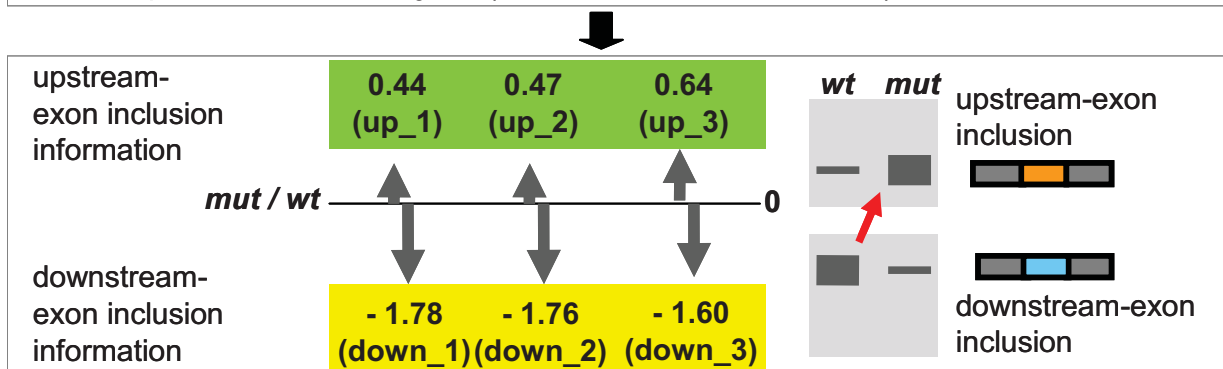
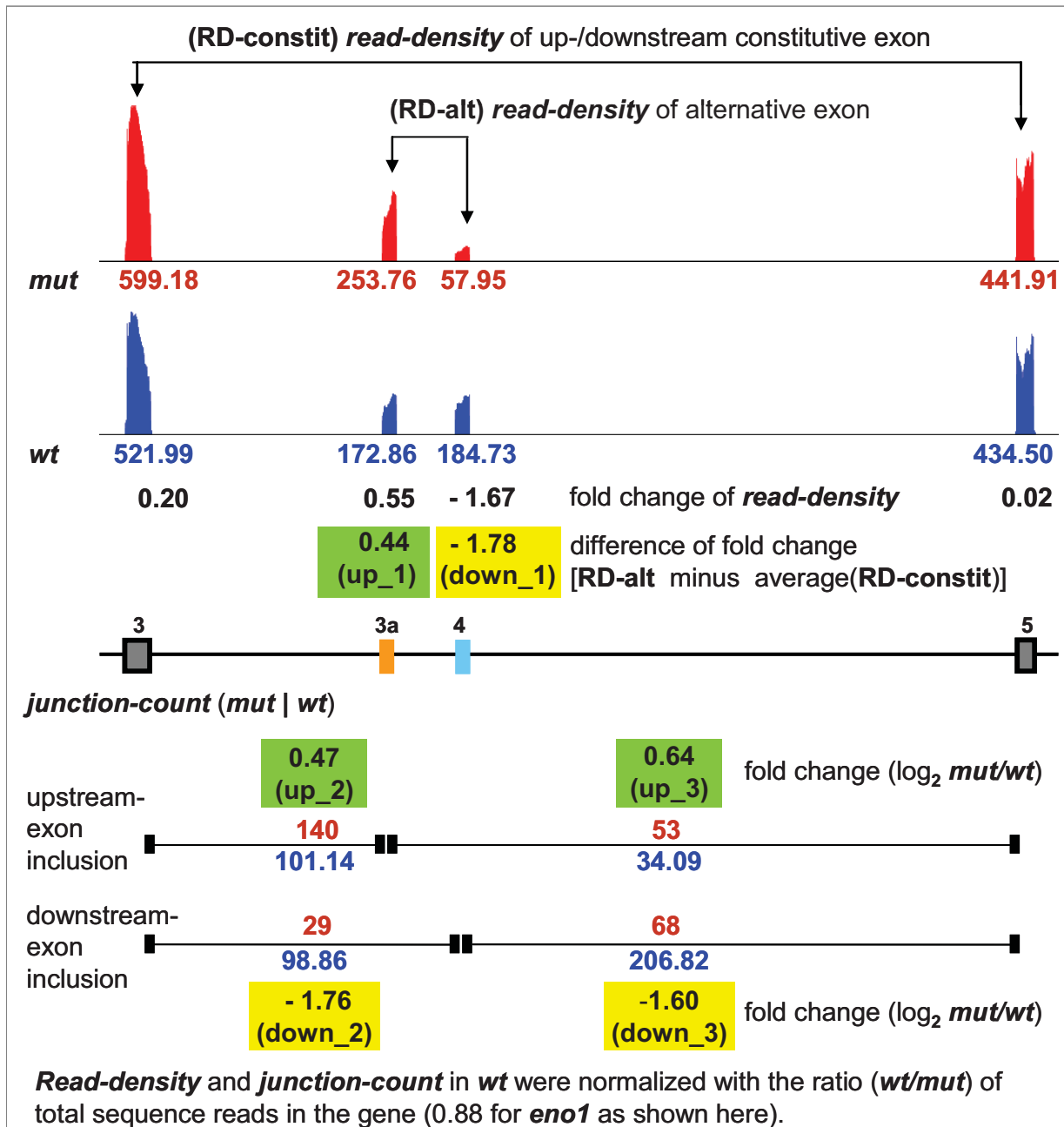


Figure 7. Mutually exclusive exon



5. Sequence motif analysis of single-exon skipping targets

To search for significant sequence features in the U1C-dependent alternative splicing targets, we concentrated on the 5' splice sites of the 218 predicted single-exon skipping targets. We selected the target exons and their corresponding upstream exons with a GU at 5' splice site positions +1/+2, and a downstream intron of at least 135 bp. As background control we used all exons except for the first and last ones of the expressed refSeq mRNAs, which have a GU at their 5' splice sites and a minimal intron length of 135 bp. Each of these three datasets

- **target-exon** (176),
- **upstream-exon** (176),
- **background-exon** (46,713),

was analyzed for these three sequence features:

- 1) **5' splice site** (11 nucleotides; positions -3 to +8),
- 2) **downstream-intron** (positions +7 to +100), and
- 3) **exon**.

First, we looked at the **5' splice site** quality, based on the HBond Score Concept (<http://www.uni-duesseldorf.de/rna/html/background.php>), which considers the 11-nt of the 5' splice site sequence for score calculation. Comparing the **target-exon** to the **upstream-exon**, no significant difference in score distribution was observed, neither could we detect any correlation between the two datasets (data not shown).

Second, we looked at the **downstream-intron** sequences: In all three datasets, T and A nucleotides represent ~ 65% of these sequences. However, there was a slight increase of T and a decrease of A nucleotides in the **target-exon** dataset. The table below summarizes the nucleotide distributions in each dataset.

dataset	A	C	G	T
downstream-intron of target-exon	27.83	18.31	16.28	37.58
downstream-intron of upstream-exon	28.61	18.25	17.91	35.23
downstream-intron of background-exon	30.69	17.76	16.56	34.99

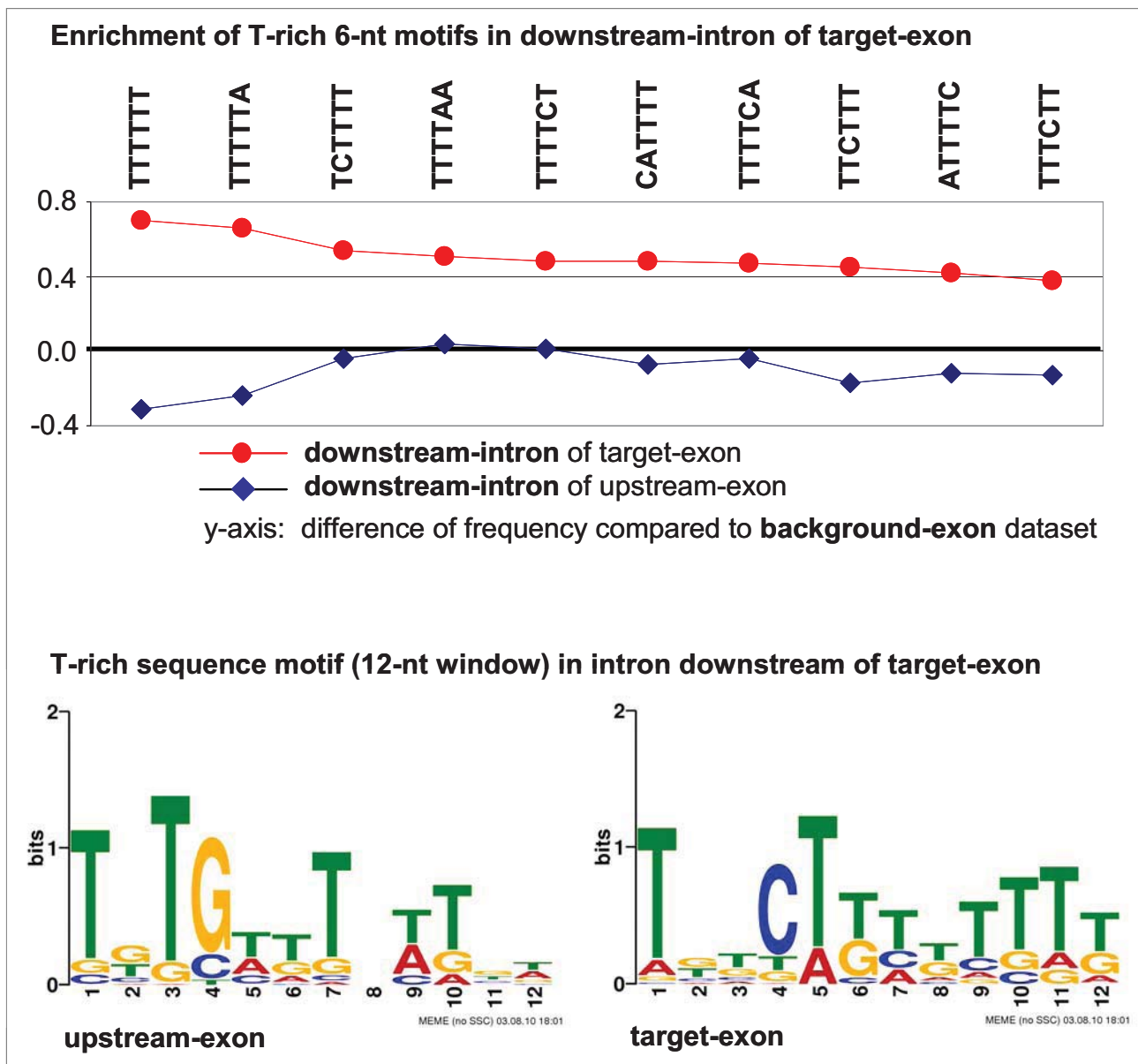
In addition, the frequency of 4-nt and 6-nt motifs in the **downstream-intron** sequences was calculated, as well as its differences between the three datasets. The most significant difference was that the T₄- and T₆ motifs occurred at a higher frequency in the **target-exon** dataset. **Figure 8** (upper panel) shows the ten most significant 6-nt motifs that occur at a higher frequency in target-exon versus upstream-exon and background-exon datasets (> 0.995 quantile). Furthermore, we applied the Motif-based sequence analysis tools MEME (http://meme.nbcr.net/meme4_4_0/intro.html, Baily *et al.*, 1994) to look for significant motifs in the **downstream intron** sequences of the **target-exon** and **upstream-exon**. Here we used the following parameters to search the high-score motifs in 12-nt windows:

- a) zero or one occurrence per sequence (zoops),
- b) 158 (90% of total 176) sites (nsites).

Based on the motif with the highest information content obtained (**Figure 8**, lower panel), we conclude that T-stretches are enriched in the introns downstream of **target-exons**.

Third, the same approach was applied to the **exon** sequences of the **target-exon** and **upstream-exon** datasets to search for high-score motifs in 6- or 8-nt windows. As a result, no significantly enriched motif was found (data not shown).

Figure 8. Sequence motif analysis of U1C dependent exon



6. References

- Bailey TL, Elkan C. 1994. Fitting a mixture model by expectation maximization to discover motifs in biopolymers. *Proc Int Conf Intell Syst Mol Biol.* **2**: 28-36.
- Benjamini Y, Hochberg Y. 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society: Series B*, **57**: 289–300.
- De Bona F, Ossowski S, Schneeberger K, Rättsch G. 2008. Optimal spliced alignments of short sequence reads. *Bioinformatics* **24**: i174-i180.
- Jean G, Kahles A, Sreedharan VT, De Bona F, Rättsch G. 2010. RNA-seq Read Alignments with PALMapper. *Current Protocols in Bioinformatics*, in press.
- Li H and Durbin R. 2009. Fast and accurate short read alignment with Burrows-Wheeler Transform. *Bioinformatics* **25**: 1754-60.
- Schneeberger K, Hagmann J, Ossowski S, Warthmann N, Gesing S, Kohlbacher O, Weigel D. 2009. Simultaneous alignment of short reads against multiple genomes. *Genome Biol.* **10**: R98.
- Sonnenburg S, Schweikert G, Philips P, Behr J, Rättsch G. 2007. Accurate splice site prediction using support vector machines. *BMC Bioinformatics* **8(Suppl 10)**: S7.

Supplementary Table S1. List of down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
rho	NM_131084	-5.44	3.83E-127	6.56E-124
zgc:165530	NM_001098730	-1.13	6.27E-098	7.66E-095
fabp7a	NM_131605	-1.78	8.93E-084	7.64E-081
zgc:136930	NM_001039819	-2.61	5.49E-080	4.27E-077
opn1sw1	NM_131319	-8.01	1.43E-079	1.02E-076
ckb	NM_173222	-1.52	5.31E-078	3.50E-075
opn1lw2	NM_001002443	-6.76	5.37E-070	3.28E-067
si:dkeyp-113d7.4	NM_001114342	-0.78	2.83E-060	1.43E-057
zgc:112134	NM_001017738	-0.92	8.87E-060	4.22E-057
tubb5	NM_198818	-1.75	1.60E-058	7.19E-056
zgc:92692	NM_001002408	-0.84	3.00E-053	1.28E-050
zgc:110021	NM_001024427	-0.85	8.37E-045	3.11E-042
crygn2	NM_001003428	-0.97	1.34E-043	4.79E-041
h3f3c	NM_200003	-1.19	2.40E-043	8.23E-041
arr3l	NM_001002405	-4.83	4.24E-043	1.40E-040
zgc:123194	NM_001037410	-0.84	2.63E-042	8.35E-040
cryba4	NM_001018125	-0.83	3.98E-039	1.17E-036
hmgb3a	NM_001122836	-1.22	4.70E-039	1.34E-036
cirbp	NM_001040321	-0.82	9.27E-037	2.33E-034
cryba1b	NM_001002586	-0.66	1.00E-033	2.32E-031
zgc:86723	NM_001002142	-1.15	1.61E-031	3.44E-029
ppial	NM_199957	-0.81	3.71E-031	7.74E-029
tmsb	NM_205581	-1.92	5.01E-031	1.02E-028
zgc:171793	NM_001109858	-2.54	1.34E-030	2.60E-028
MGC171407	NM_001105126	-1.36	2.23E-030	4.25E-028
krt5	NM_131156	-0.65	4.32E-029	8.04E-027
opn1mw1	NM_131253	-9.23	4.04E-028	7.35E-026
zgc:171773	NM_001100437	-0.67	4.39E-028	7.82E-026
zgc:56085	NM_199816	-4.82	9.24E-027	1.55E-024
ptma	NM_194376	-1.01	1.60E-026	2.63E-024
opn1sw2	NM_131192	-5.96	3.06E-026	4.94E-024
cryba2b	NM_001002584	-0.71	2.63E-025	4.02E-023
rs1	NM_001003438	-4.02	3.38E-025	5.08E-023
neurod	NM_130978	-2.34	4.56E-024	6.62E-022
mdkb	NM_131716	-1.48	4.40E-023	6.07E-021
zgc:165618	NM_001099251	-1.19	6.42E-023	8.72E-021
slc1a2	NM_199979	-1.39	7.02E-023	9.39E-021
crx	NM_152940	-2.55	1.27E-022	1.67E-020
calm2b	NM_214736	-0.74	4.93E-021	5.94E-019
zgc:158409	NM_001080033	-1.06	6.85E-021	8.14E-019
zgc:92355	NM_001007311	-1.91	7.59E-021	8.90E-019
zgc:136220	NM_001033722	-3.39	2.41E-020	2.79E-018
zgc:92724	NM_001002582	-1.27	1.61E-019	1.76E-017
gfap	NM_131373	-1.79	5.29E-019	5.52E-017
h3f3a	NM_212996	-0.69	8.45E-019	8.71E-017
gnb3	NM_213202	-6.81	1.82E-018	1.85E-016
gpm6aa	NM_213200	-1.24	2.97E-018	2.95E-016
zgc:85717	NM_213223	-0.74	7.72E-018	7.51E-016
rbp4	NM_130920	-0.85	1.05E-017	1.01E-015

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
col1a2	NM_182968	-0.86	1.22E-017	1.16E-015
gnat2	NM_131869	-5.25	1.59E-017	1.50E-015
rcv1	NM_199964	-4.38	2.64E-017	2.43E-015
crygmx	NM_001013262	-1.14	3.67E-017	3.34E-015
marcks	NM_001015060	-1.02	4.90E-017	4.41E-015
rpl5a	NM_199756	-0.48	1.32E-016	1.18E-014
zgc:165347	NM_001099243	-0.90	5.25E-016	4.49E-014
hmgb2	NM_001004674	-0.62	9.74E-016	8.17E-014
elavl3	NM_131449	-1.05	1.37E-015	1.14E-013
anp32e	NM_213277	-1.28	2.55E-015	2.06E-013
snap25b	NM_131434	-1.72	3.60E-015	2.85E-013
tyrp1b	NM_001002749	-1.09	1.19E-014	9.18E-013
dpysl2	NM_001020517	-1.54	1.22E-014	9.34E-013
zgc:86896	NM_001002100	-1.40	1.49E-014	1.13E-012
zgc:77366	NM_212645	-1.21	1.86E-014	1.39E-012
cryba2a	NM_001002049	-0.56	3.36E-014	2.50E-012
tubb2c	NM_198809	-0.48	4.64E-014	3.39E-012
zgc:175106	NM_001111190	-1.96	9.21E-014	6.62E-012
zgc:56418	NM_201101	-0.50	1.32E-013	9.33E-012
atp1a3a	NM_131684	-1.17	2.24E-013	1.56E-011
zgc:114180	NM_001030248	-3.94	4.85E-013	3.30E-011
rps12	NM_200046	-0.28	8.96E-013	6.04E-011
calb2	NM_200711	-1.82	2.05E-012	1.34E-010
sox4a	NM_213122	-1.12	2.50E-012	1.62E-010
eef1g	NM_173263	-0.39	2.73E-012	1.74E-010
stmn2	NM_001024222	-1.23	2.77E-012	1.76E-010
zgc:153208	NM_001045853	-1.73	2.91E-012	1.83E-010
zgc:173645	NM_001102644	-1.04	3.10E-012	1.93E-010
khdrbs1	NM_130925	-0.54	3.17E-012	1.97E-010
vsx1	NM_131333	-2.09	3.24E-012	1.99E-010
cd99l2	NM_194369	-1.08	1.21E-011	7.12E-010
zgc:109988	NM_001020546	-2.53	1.39E-011	8.11E-010
zgc:103639	NM_001004668	-0.30	1.45E-011	8.38E-010
elovl4	NM_199972	-4.15	3.08E-011	1.72E-009
zgc:171791	NM_001100442	-1.23	3.40E-011	1.89E-009
hnrnpa0	NM_214706	-0.62	5.06E-011	2.78E-009
ywhah	NM_213164	-0.99	6.12E-011	3.34E-009
zgc:101846	NM_001005967	-0.70	6.64E-011	3.60E-009
eef2l	NM_200458	-0.25	7.93E-011	4.24E-009
zgc:158829	NM_001080602	-1.48	7.89E-011	4.24E-009
dpysl3	NM_001020512	-1.43	1.12E-010	5.89E-009
vamp2	NM_200005	-1.24	1.52E-010	7.99E-009
matn1	NM_001099740	-1.75	2.26E-010	1.18E-008
gng3	NM_131841	-1.13	2.91E-010	1.49E-008
zgc:171792	NM_001102394	-1.48	3.03E-010	1.54E-008
fabp11b	NM_001020558	-1.90	3.80E-010	1.91E-008
hapln1a	NM_001007790	-1.25	4.25E-010	2.10E-008
kera	NM_001025548	-1.94	6.68E-010	3.26E-008
gpm6ab	NM_214687	-1.12	6.73E-010	3.27E-008

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
zgc:92241	NM_001003422	-1.00	1.04E-009	4.96E-008
zgc:103663	NM_001007362	-1.49	1.30E-009	6.13E-008
col1a3	NM_201478	-0.58	1.75E-009	8.07E-008
cfl1	NM_213639	-0.74	2.41E-009	1.11E-007
neurod4	NM_170762	-1.70	2.44E-009	1.11E-007
gngt1	NM_199967	-3.51	3.02E-009	1.37E-007
actc1	NM_214784	-0.16	3.62E-009	1.63E-007
pbx3b	NM_001098243	-1.24	3.88E-009	1.74E-007
snrpc	NM_173251	-2.37	4.47E-009	1.96E-007
tnrc4	NM_131494	-1.34	6.48E-009	2.79E-007
lim2.4	NM_001002407	-0.89	6.83E-009	2.92E-007
isl1	NM_130962	-1.63	7.12E-009	3.03E-007
hnrpa1	NM_200104	-0.69	8.62E-009	3.63E-007
zgc:85677	NM_213168	-0.32	1.01E-008	4.22E-007
tuba2	NM_213030	-1.12	1.01E-008	4.23E-007
mab2111	NM_152974	-1.33	1.34E-008	5.52E-007
zgc:55429	NM_201099	-0.78	1.50E-008	6.12E-007
gapdhs	NM_213094	-0.45	1.54E-008	6.21E-007
zgc:109965	NM_001033747	-3.12	1.71E-008	6.82E-007
zgc:63849	NM_199642	-1.00	1.92E-008	7.65E-007
zgc:153426	NM_001076715	-1.18	2.09E-008	8.27E-007
sparc	NM_001001942	-0.49	2.19E-008	8.65E-007
atp1b2a	NM_131669	-0.85	2.33E-008	9.13E-007
zgc:73153	NM_200828	-1.84	2.71E-008	1.06E-006
stxbp1	NM_001025182	-0.87	2.76E-008	1.07E-006
otx5	NM_181331	-1.83	2.92E-008	1.13E-006
zgc:162825	NM_001089526	-1.22	2.95E-008	1.14E-006
rps24	NM_001012316	-0.23	2.99E-008	1.15E-006
gap43	NM_131341	-0.87	3.00E-008	1.15E-006
sag	NM_001033749	-3.73	3.61E-008	1.36E-006
tcf7l2	NM_131259	-1.28	3.83E-008	1.44E-006
tfap2a	NM_176859	-1.23	4.87E-008	1.82E-006
meis2.2	NM_131896	-0.91	5.54E-008	2.05E-006
tnw	NM_131036	-0.98	5.82E-008	2.13E-006
atp1a1b	NM_131690	-1.39	7.57E-008	2.74E-006
zgc:92890	NM_001002469	-1.28	7.83E-008	2.83E-006
otx2	NM_131251	-1.59	8.31E-008	2.97E-006
col1a1	NM_199214	-0.39	9.85E-008	3.48E-006
mb	NM_200586	-1.64	1.05E-007	3.70E-006
fam49a	NM_001003606	-1.77	1.14E-007	3.97E-006
a2bp1	NM_001005596	-1.18	1.15E-007	3.99E-006
si:rp71-10d23.3	NM_001089376	-2.66	1.21E-007	4.20E-006
pax6a	NM_131304	-1.60	1.43E-007	4.86E-006
gdi1	NM_001020608	-1.09	1.63E-007	5.50E-006
zgc:109984	NM_001029963	-1.40	2.04E-007	6.80E-006
zgc:110292	NM_001017599	-0.69	2.24E-007	7.46E-006
tfap2b	NM_001017847	-1.85	2.27E-007	7.52E-006
gnb3l	NM_001002437	-2.41	2.37E-007	7.82E-006
prox1	NM_131405	-1.93	2.55E-007	8.40E-006

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
mfap2	NM_001039357	-1.22	2.67E-007	8.71E-006
mip2	NM_001020520	-1.16	2.68E-007	8.72E-006
rplp2l	NM_001100436	-0.19	3.72E-007	1.19E-005
rtn1a	NM_001029967	-0.89	3.82E-007	1.21E-005
elavl4	NM_131453	-0.84	3.93E-007	1.24E-005
pou4f2	NM_212807	-1.90	4.09E-007	1.29E-005
zgc:194937	NM_001130624	-1.13	4.37E-007	1.37E-005
syt1	NM_001002463	-1.26	4.40E-007	1.38E-005
syncrip	NM_214696	-0.71	5.79E-007	1.79E-005
lmo3	NM_001020739	-1.56	6.40E-007	1.97E-005
crabp1a	NM_182858	-1.87	6.54E-007	2.01E-005
LOC795575	NM_001123311	-1.93	6.92E-007	2.11E-005
zgc:111964	NM_001030133	-2.69	7.84E-007	2.38E-005
h2afvl	NM_001043323	-0.33	9.67E-007	2.89E-005
atoh2b	NM_131817	-1.93	1.11E-006	3.30E-005
lim2.3	NM_001002587	-1.41	1.37E-006	4.05E-005
ndrg4	NM_001045173	-1.28	1.44E-006	4.22E-005
zgc:73075	NM_200825	-3.72	1.62E-006	4.73E-005
zgc:110025	NM_001020557	-4.03	1.62E-006	4.73E-005
rlbp1a	NM_200705	-2.51	1.64E-006	4.75E-005
gnao1	NM_200787	-0.99	1.75E-006	5.05E-005
zgc:86661	NM_001002059	-1.69	1.77E-006	5.11E-005
bhlhb5	NM_200955	-1.92	1.88E-006	5.40E-005
sfpq	NM_213278	-0.73	2.13E-006	6.06E-005
sox11b	NM_131337	-0.88	2.32E-006	6.59E-005
rps4x	NM_001005589	-0.17	2.76E-006	7.77E-005
crmp1	NM_001020725	-1.87	2.82E-006	7.92E-005
rpepa	NM_200751	-1.53	2.88E-006	8.05E-005
fez1	NM_213396	-1.00	2.95E-006	8.23E-005
guk1	NM_200724	-5.21	2.98E-006	8.25E-005
syntaxin1b	NM_131523	-0.79	2.97E-006	8.25E-005
cugbp2	NM_194401	-1.08	3.10E-006	8.54E-005
zgc:153593	NM_001076582	-2.41	3.12E-006	8.56E-005
zgc:109973	NM_001020540	-0.75	3.71E-006	0.000101
si:dkey-76p14.4	NM_001030278	-1.68	4.19E-006	0.000113
zgc:114051	NM_001025502	-0.76	4.20E-006	0.000113
rrm2	NM_131450	-0.92	4.33E-006	0.000117
zgc:86878	NM_001004601	-0.81	4.71E-006	0.000125
klf11a	NM_001044941	-2.37	5.30E-006	0.000141
cry2a	NM_131791	-0.99	5.37E-006	0.000142
nr2f1a	NM_131180	-1.10	5.60E-006	0.000147
islr2	NM_001013523	-0.87	5.66E-006	0.000149
zgc:123215	NM_001037424	-0.36	5.71E-006	0.000149
zgc:158291	NM_001080058	-1.73	6.46E-006	0.000167
defbl1	NM_001081553	-1.33	6.57E-006	0.000170
lhx9	NM_001017710	-1.39	6.90E-006	0.000177
zgc:113456	NM_001030072	-1.21	6.97E-006	0.000179
hdac1	NM_173236	-0.56	7.02E-006	0.000179
mab21l2	NM_152975	-0.88	7.16E-006	0.000182

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
zgc:73310	NM_200785	-5.45	7.63E-006	0.000193
dpysl5a	NM_001018149	-1.28	8.00E-006	0.000202
nsf	NM_001044328	-1.05	8.29E-006	0.000208
zgc:92631	NM_001002695	-0.94	8.46E-006	0.000212
silvb	NM_001033918	-1.17	9.80E-006	0.000243
ctbp2	NM_131715	-1.42	1.01E-005	0.000249
rbp2a	NM_153004	-1.81	1.01E-005	0.000249
rpl34	NM_201122	-0.18	1.01E-005	0.000249
barhl2	NM_205740	-1.84	1.11E-005	0.000270
krt15	NM_213523	-1.06	1.18E-005	0.000287
zgc:101859	NM_001005965	-2.60	1.29E-005	0.000311
mpp6	NM_001044777	-1.60	1.30E-005	0.000312
zgc:153632	NM_001076560	-0.71	1.38E-005	0.000329
calb2l	NM_200718	-1.21	1.39E-005	0.000330
pde6g	NM_212799	-1.89	1.40E-005	0.000332
dmbx1a	NM_152977	-2.03	1.47E-005	0.000346
zgc:77708	NM_205554	-0.84	1.47E-005	0.000346
sept5b	NM_001003782	-1.55	1.48E-005	0.000348
zgc:153686	NM_001077804	-0.35	1.51E-005	0.000354
rorb	NM_001082856	-1.74	1.57E-005	0.000366
tmem59l	NM_213337	-1.05	1.61E-005	0.000375
si:ch211-237l4.2	NM_001025511	-1.46	1.69E-005	0.000393
calm3b	NM_199570	-0.44	1.77E-005	0.000409
id2a	NM_201291	-0.79	1.81E-005	0.000415
rps19	NM_200750	-0.19	1.87E-005	0.000426
rps15a	NM_212762	-0.19	1.95E-005	0.000443
mbd3b	NM_212580	-1.20	1.96E-005	0.000444
si:ch211-51m24.3	NM_001044858	-0.96	2.05E-005	0.000462
zgc:158449	NM_001082838	-0.89	2.05E-005	0.000462
arl3l1	NM_200693	-4.70	2.10E-005	0.000470
zgc:158677	NM_001082995	-4.52	2.10E-005	0.000470
si:dkeyp-114f9.4	NM_001044892	-1.88	2.25E-005	0.000502
zgc:85741	NM_001002166	-1.00	2.36E-005	0.000525
rds2	NM_131566	-5.58	3.05E-005	0.000675
pvalb6	NM_205573	-1.78	3.31E-005	0.000725
rorab	NM_201067	-1.76	3.31E-005	0.000725
pax6b	NM_131641	-1.52	3.38E-005	0.000737
zgc:158363	NM_001079973	-0.62	3.91E-005	0.000844
si:dkey-98n4.1	NM_001045191	-1.06	3.94E-005	0.000849
rds4	NM_131567	-4.53	4.01E-005	0.000861
dynl12	NM_213024	-0.46	4.05E-005	0.000869
mip1	NM_001003534	-1.41	4.08E-005	0.000872
prdm8b	NM_001105105	-2.17	4.23E-005	0.000902
anp32a	NM_199986	-0.58	4.27E-005	0.000908
col4a5	NM_001123230	-0.86	4.97E-005	0.001043
smarcb1b	NM_131448	-1.20	5.49E-005	0.001147
zgc:92783	NM_001002549	-1.25	5.53E-005	0.001152
sfrs3b	NM_201323	-0.55	6.52E-005	0.001347
atp1b2b	NM_131838	-2.37	6.62E-005	0.001365

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
pvalb5	NM_207167	-1.07	6.74E-005	0.001386
bcl11a	NM_001040391	-1.36	7.40E-005	0.001514
zgc:103625	NM_001004669	-3.79	7.63E-005	0.001558
nat11	NM_001017632	-1.30	7.66E-005	0.001559
nr2f2	NM_131183	-0.91	7.95E-005	0.001607
meis1	NM_131893	-0.67	8.31E-005	0.001673
rbm4.1	NM_199705	-1.09	8.72E-005	0.001751
snap25a	NM_131435	-0.67	8.78E-005	0.001755
lmo1	NM_173219	-1.51	8.77E-005	0.001755
gpm6bb	NM_001013334	-1.15	9.31E-005	0.001843
sumo3	NM_213124	-0.55	0.000103	0.002023
stm	NM_198817	-1.07	0.000104	0.002050
ywhabl	NM_199562	-0.38	0.000110	0.002153
sparcl	NM_001130605	-2.24	0.000113	0.002204
zgc:158340	NM_001079657	-3.59	0.000121	0.002318
nme2l	NM_199970	-3.72	0.000121	0.002318
gnat1	NM_131868	-3.40	0.000121	0.002318
clstn1	NM_001077784	-0.68	0.000126	0.002411
zgc:171758	NM_001109860	-0.63	0.000127	0.002411
rrm1	NM_131455	-0.94	0.000136	0.002565
zgc:73358	NM_213045	-0.50	0.000143	0.002690
si:ch211-221n23.1	NM_001082952	-1.39	0.000149	0.002792
unc119.2	NM_001040394	-1.84	0.000156	0.002903
otpa	NM_001128703	-0.69	0.000161	0.002978
zgc:153948	NM_001077276	-1.90	0.000170	0.003128
fabp11a	NM_001004682	-0.59	0.000171	0.003128
zgc:101840	NM_001005968	-1.68	0.000175	0.003202
calm1a	NM_213351	-0.46	0.000179	0.003254
zgc:173495	NM_001103134	-2.41	0.000180	0.003270
zgc:77785	NM_205678	-1.18	0.000183	0.003320
top2a	NM_001003834	-1.27	0.000187	0.003379
zgc:92905	NM_001005923	-1.05	0.000189	0.003417
glula	NM_181559	-0.95	0.000202	0.003635
esrrg	NM_212954	-1.40	0.000208	0.003726
chn1	NM_213000	-1.35	0.000208	0.003726
ewsr1b	NM_212630	-0.60	0.000211	0.003785
MGC163045	NM_001098755	-3.42	0.000221	0.003952
zgc:165430	NM_001099239	-0.95	0.000242	0.004281
st13	NM_199769	-1.02	0.000244	0.004303
jmjd3	NM_001030178	-1.07	0.000247	0.004333
camk2d2	NM_001002542	-1.00	0.000258	0.004519
sox4b	NM_200901	-0.89	0.000261	0.004565
zgc:153440	NM_001076658	-0.76	0.000269	0.004689
cfi2l	NM_213641	-0.28	0.000272	0.004717
carm1	NM_001003645	-1.05	0.000272	0.004717
grk7a	NM_001031841	-4.45	0.000275	0.004738
si:ch211-233a1.5	NM_001077300	-4.28	0.000275	0.004738
pde6c	NM_200871	-4.09	0.000275	0.004738
dnl2l	NM_001030000	-1.38	0.000303	0.005209

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
rcor2	NM_205638	-1.47	0.000307	0.005263
zgc:110069	NM_001025301	-0.65	0.000313	0.005341
mcm2	NM_173257	-1.25	0.000317	0.005376
zeb2a	NM_001114551	-1.20	0.000317	0.005376
tal2	NM_201339	-1.64	0.000346	0.005782
tuba8l3	NM_001003558	-1.51	0.000355	0.005914
zgc:136569	NM_001045287	-1.52	0.000355	0.005914
cbx1b	NM_001002090	-1.45	0.000394	0.006521
atf7ip	NM_001077603	-0.69	0.000405	0.006682
hes6	NM_194400	-1.11	0.000438	0.007206
appb	NM_152886	-0.64	0.000453	0.007432
cpsf6	NM_001017993	-0.78	0.000472	0.007708
ckmt1	NM_198801	-0.80	0.000472	0.007708
atp6v1al	NM_201135	-0.72	0.000481	0.007825
zgc:165461	NM_001100139	-2.53	0.000488	0.007912
epd	NM_131005	-2.87	0.000488	0.007912
rtn1b	NM_001029948	-0.69	0.000499	0.008062
lhx1a	NM_131216	-0.93	0.000499	0.008062
slc25a3l	NM_200715	-4.93	0.000519	0.008344
hnrnpa0l	NM_001114881	-0.40	0.000531	0.008526
gpm6ba	NM_203427	-1.46	0.000535	0.008531
slc32a1	NM_001080701	-1.18	0.000535	0.008531
atp6v1ba	NM_182878	-0.76	0.000548	0.008705
ilf3	NM_212599	-0.61	0.000577	0.009138
zgc:110045	NM_001039984	-1.67	0.000606	0.009515
sox14	NM_001037680	-1.65	0.000606	0.009515
zgc:110344	NM_001020585	-1.71	0.000606	0.009515
zic1	NM_130933	-1.14	0.000610	0.009545
lmo4l	NM_212689	-1.07	0.000610	0.009545
tuba8l4	NM_200185	-0.32	0.000624	0.009737
stmn1a	NM_001040375	-0.91	0.000631	0.009838
pou47	NM_131160	-1.26	0.000636	0.009897
vamp1	NM_213398	-0.91	0.000685	0.010592
sox2	NM_213118	-1.00	0.000684	0.010592
LOC794865	NM_001082905	-0.81	0.000692	0.010644
hnrnpu	NM_001033595	-0.57	0.000690	0.010644
cbx5	NM_001080184	-0.56	0.000718	0.011035
nfia	NM_001079962	-1.93	0.000753	0.011462
ndufa4	NM_213025	-0.80	0.000760	0.011522
zgc:110141	NM_001017856	-1.21	0.000767	0.011591
sox19a	NM_130908	-1.22	0.000767	0.011591
zgc:92164	NM_001004554	-0.70	0.000794	0.011946
ss18	NM_199744	-0.76	0.000794	0.011946
cct5	NM_212613	-0.46	0.000801	0.012029
rab3c	NM_001002530	-1.57	0.000824	0.012327
foxp2	NM_001030082	-1.05	0.000846	0.012640
elavl1	NM_131452	-0.72	0.000860	0.012815
zgc:154044	NM_001076776	-1.02	0.000874	0.012978
zgc:114196	NM_001025546	-2.10	0.000912	0.013480

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
prkcbp1l	NM_199641	-0.94	0.000923	0.013595
ldb1a	NM_131316	-0.72	0.000953	0.013985
zgc:92712	NM_001002395	-4.49	0.000977	0.014283
pdc2	NM_001025464	-4.34	0.000977	0.014283
sncgb	NM_001020652	-0.51	0.001006	0.014658
zgc:92278	NM_001002610	-0.75	0.001016	0.014783
zgc:158335	NM_001083844	-0.47	0.001084	0.015719
zgc:110126	NM_001017569	-0.99	0.001109	0.015942
pou50	NM_131161	-0.98	0.001109	0.015942
syn2a	NM_001002597	-0.95	0.001109	0.015942
lim2.1	NM_001020556	-1.05	0.001111	0.015948
zgc:136952	NM_001040043	-0.13	0.001118	0.016023
marcks1l	NM_213133	-0.41	0.001177	0.016845
Tnni2	NM_205742	-0.20	0.001184	0.016912
zgc:109966	NM_001020731	-1.48	0.001195	0.017014
sept3	NM_001024418	-1.13	0.001220	0.017287
calm2a	NM_199996	-0.50	0.001273	0.018003
zgc:158869	NM_001080673	-1.16	0.001294	0.018261
smarce1	NM_201298	-0.49	0.001295	0.018261
zgc:165520	NM_001099425	-2.92	0.001312	0.018316
rybpa	NM_201317	-1.19	0.001307	0.018316
hug	NM_130909	-0.85	0.001304	0.018316
zgc:56141	NM_213317	-0.47	0.001352	0.018807
zgc:92039	NM_001003486	-0.86	0.001429	0.019787
ndrg1l	NM_200692	-1.54	0.001450	0.020049
sept8b	NM_001083566	-2.42	0.001490	0.020458
sox3	NM_001001811	-0.97	0.001517	0.020694
zgc:109949	NM_001020730	-2.27	0.001544	0.021001
sypb	NM_001002501	-1.35	0.001547	0.021012
atp6v1d	NM_200960	-0.75	0.001647	0.022190
zgc:85948	NM_213235	-0.58	0.001645	0.022190
msi1	NM_001013516	-1.14	0.001820	0.024261
cadm1a	NM_001113551	-1.17	0.001820	0.024261
zgc:110549	NM_001017566	-1.24	0.001842	0.024391
zgc:162551	NM_213637	-1.29	0.001842	0.024391
zgc:63523	NM_200601	-1.08	0.001931	0.025385
ncam1	NM_131202	-0.75	0.001943	0.025491
zgc:152760	NM_001076577	-4.84	0.001953	0.025591
zgc:110158	NM_001020567	-0.89	0.002033	0.026437
cnot6	NM_212660	-0.88	0.002033	0.026437
zgc:73355	NM_200803	-1.72	0.002102	0.027255
zgc:112198	NM_001017708	-1.13	0.002118	0.027376
lhx5	NM_131218	-1.11	0.002118	0.027376
zgc:110552	NM_001017565	-0.65	0.002166	0.027910
arnt2	NM_131674	-0.83	0.002243	0.028768
rpl35a	NM_001002487	-0.12	0.002240	0.028768
zgc:153988	NM_001077376	-0.76	0.002313	0.029583
zgc:136337	NM_001042753	-2.70	0.002350	0.030008
zgc:162402	NM_001082939	-0.67	0.002400	0.030604

Down-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
zgc:110551	NM_001020598	-0.82	0.002418	0.030781
tuba8l	NM_212772	-0.38	0.002526	0.031925
rpl13a	NM_212784	-0.15	0.002547	0.032102
zgc:110622	NM_001020751	-1.08	0.002548	0.032102
rbpms2	NM_200259	-1.34	0.002602	0.032550
LOC555593	NM_001128332	-1.30	0.002602	0.032550
zgc:136878	NM_001040248	-2.04	0.002599	0.032550
vat1	NM_001007051	-0.68	0.002673	0.033241
fyna	NM_001007286	-1.17	0.002670	0.033241
lef1	NM_131426	-1.22	0.002667	0.033241
zgc:123242	NM_001037387	-1.18	0.002670	0.033241
zgc:100994	NM_001003607	-1.03	0.002799	0.034708
eno2	NM_001003848	-0.76	0.002829	0.034977
sf1	NM_212653	-0.66	0.002844	0.035115
zgc:77449	NM_212899	-0.79	0.002888	0.035608
zgc:171702	NM_001103192	-0.52	0.003005	0.036936
irx1a	NM_207184	-1.07	0.003065	0.037628
rpl19	NM_213208	-0.12	0.003073	0.037664
lgals1l1	NM_001005958	-0.83	0.003183	0.038908
ing4	NM_001020468	-0.71	0.003259	0.039669
capn3	NM_001004571	-0.60	0.003255	0.039669
sox5	NM_001033585	-0.99	0.003353	0.040754
tfa	NM_001015057	-0.68	0.003538	0.042756
zgc:92761	NM_001002562	-0.96	0.003596	0.043278
ctcf	NM_001001844	-0.72	0.003625	0.043497
zgc:165647	NM_001100152	-1.37	0.003658	0.043832
tnni2a.4	NM_001009901	-0.12	0.003679	0.044027
ube2e3	NM_200921	-0.51	0.003687	0.044063
ascl1b	NM_131231	-1.84	0.003719	0.044319
gnb5	NM_200746	-1.69	0.003719	0.044319
lhx4	NM_001122973	-1.26	0.003802	0.045073
acbd7	NM_001128768	-1.13	0.003794	0.045073
zic2a	NM_131558	-1.24	0.003838	0.045359
zgc:153588	NM_001077290	-1.61	0.003933	0.046353
mta2	NM_214695	-0.74	0.004031	0.047342
h2afx	NM_201073	-0.96	0.004039	0.047342
zgc:112335	NM_001024422	-0.99	0.004039	0.047342
zgc:65861	NM_199552	-0.31	0.004066	0.047531
ctbp1	NM_131714	-0.54	0.004165	0.048471
mag	NM_001007062	-2.83	0.004181	0.048471
zgc:77155	NM_205673	-0.53	0.004177	0.048471
wu:fq40g12	NM_212571	-0.93	0.004165	0.048471
si:dkey-260n20.1	NM_001044899	-1.37	0.004324	0.049927
isl2b	NM_130964	-1.34	0.004324	0.049927
si:dkey-52k20.12	NM_001128716	-1.98	0.004344	0.049950
si:dkey-46a12.1	NM_001100065	-0.99	0.004335	0.049950

Supplementary Table S2. List of up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
wu:cegs655	NM_001007029	1.02	0	0
tpma	NM_131105	0.56	1.83E-175	7.85E-172
krt4	NM_131509	0.45	1.32E-151	3.78E-148
desm	NM_130963	2.44	6.67E-136	1.43E-132
mylz2	NM_131188	0.51	6.46E-127	9.21E-124
bhmt	NM_001012480	1.14	4.20E-090	4.49E-087
gapdh	NM_001115114	0.90	2.11E-085	2.00E-082
apoeb	NM_131098	1.83	1.24E-066	7.05E-064
cyt1	NM_131107	0.79	1.53E-063	8.16E-061
fn1b	NM_001013261	3.76	2.27E-048	9.23E-046
zgc:92061	NM_001002383	1.78	4.48E-045	1.74E-042
actc1l	NM_001001409	0.73	3.37E-040	1.03E-037
krt18	NM_178437	1.48	9.70E-039	2.68E-036
ctsl1a	NM_212584	1.40	4.58E-037	1.22E-034
actn3	NM_131522	0.81	5.38E-037	1.40E-034
c20orf149l	NM_200008	0.90	5.90E-035	1.40E-032
pvalb2	NM_131516	0.23	6.86E-033	1.54E-030
hspb9	NM_001114705	3.53	7.82E-033	1.72E-030
mdm2	NM_131364	2.91	5.39E-031	1.07E-028
zgc:63663	NM_200614	1.73	1.86E-027	3.25E-025
cyt1l	NM_001082882	0.48	5.61E-027	9.60E-025
apoa1	NM_131128	0.47	1.14E-025	1.81E-023
eno3	NM_214723	0.79	2.02E-025	3.15E-023
pgk1	NM_213387	1.13	3.84E-024	5.66E-022
smyhc1	NM_001020507	0.99	1.31E-023	1.87E-021
tp53	NM_131327	2.04	1.88E-023	2.63E-021
rplp0	NM_131580	0.31	1.48E-022	1.92E-020
zgc:193613	NM_001130586	0.58	2.21E-022	2.82E-020
junbl	NM_212750	2.65	2.30E-022	2.85E-020
fos	NM_205569	2.85	2.28E-022	2.85E-020
krt8	NM_200080	0.77	1.66E-021	2.03E-019
zgc:110152	NM_001017853	4.70	3.80E-020	4.34E-018
igfbp1	NM_173283	3.49	4.86E-020	5.47E-018
zgc:91930	NM_001003993	0.45	7.59E-020	8.44E-018
zgc:77231	NM_200000	0.30	1.88E-019	2.04E-017
gstp1	NM_131734	0.90	3.11E-019	3.33E-017
hspa8	NM_001110403	0.29	3.54E-019	3.74E-017
ccng1	NM_199481	0.86	2.96E-018	2.95E-016
zgc:110679	NM_001017871	0.56	4.56E-018	4.49E-016
anxa2a	NM_181761	1.44	2.51E-017	2.34E-015
myhz2	NM_152982	0.66	1.65E-016	1.45E-014
timp2b	NM_213296	3.90	2.80E-016	2.45E-014
ldb3b	NM_199858	0.83	3.29E-016	2.84E-014
cebpd	NM_131887	1.84	7.36E-016	6.23E-014
tdh	NM_213245	1.45	2.05E-015	1.69E-013
myhz1	NM_001115089	0.40	2.36E-015	1.92E-013
hsp47	NM_131204	1.40	3.58E-015	2.85E-013
jph2	NM_001089364	1.34	4.03E-015	3.17E-013
hbbe2	NM_212846	1.02	6.42E-015	4.99E-013

Up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
ckmb	NM_001105683	0.19	4.11E-014	3.03E-012
hspb11	NM_001099427	2.98	7.71E-014	5.59E-012
rps29	NM_212953	0.28	9.63E-014	6.87E-012
socs3a	NM_199950	3.72	1.38E-013	9.69E-012
mmp9	NM_213123	4.23	2.26E-013	1.56E-011
zgc:92903	NM_001002461	2.03	2.77E-013	1.89E-011
cebpb	NM_131884	2.40	9.95E-013	6.65E-011
ckma	NM_130932	0.20	1.05E-012	6.95E-011
gamt	NM_001105595	0.57	1.68E-012	1.11E-010
aldoab	NM_213215	0.41	2.67E-012	1.72E-010
si:ch211-158m24.7	NM_001130666	0.37	6.35E-012	3.88E-010
psat1	NM_200895	1.49	7.26E-012	4.41E-010
eef2k	NM_001002740	1.50	9.51E-012	5.73E-010
zgc:66286	NM_200516	0.57	9.76E-012	5.84E-010
chac1	NM_001110126	1.04	1.09E-011	6.45E-010
sdc4l	NM_001048149	1.14	2.00E-011	1.15E-009
socs3b	NM_213304	2.59	2.05E-011	1.17E-009
mvp	NM_201325	1.56	2.11E-011	1.20E-009
glulb	NM_182866	0.91	2.27E-011	1.28E-009
hhatla	NM_200887	0.81	5.06E-011	2.78E-009
zgc:77243	NM_205544	0.70	8.93E-011	4.75E-009
si:ch211-203b8.5	NM_001089363	1.35	2.38E-010	1.23E-008
zgc:162132	NM_001089577	4.01	2.46E-010	1.27E-008
jun	NM_199987	1.27	3.35E-010	1.70E-008
fabp1b	NM_001024651	1.14	4.18E-010	2.09E-008
cd63	NM_199543	1.09	4.25E-010	2.10E-008
mmp2	NM_198067	1.29	5.43E-010	2.67E-008
ccn1	NM_199740	1.39	6.90E-010	3.34E-008
acta1	NM_131591	0.08	7.32E-010	3.52E-008
ctsba	NM_213336	1.41	8.02E-010	3.83E-008
pygma	NM_001020628	0.95	1.30E-009	6.13E-008
s100a10b	NM_213003	0.77	1.33E-009	6.21E-008
zgc:56682	NM_201004	0.95	1.54E-009	7.18E-008
pkm2b	NM_001003488	0.51	2.43E-009	1.11E-007
vdac2	NM_199585	0.44	4.10E-009	1.83E-007
odc1	NM_131801	1.28	4.33E-009	1.92E-007
zgc:110064	NM_001020565	0.96	4.38E-009	1.93E-007
zgc:100868	NM_001003526	1.99	5.15E-009	2.25E-007
slc1a4	NM_001002513	1.61	5.61E-009	2.44E-007
kbtbd10	NM_198979	1.19	6.49E-009	2.79E-007
phlda3	NM_001002455	2.35	7.56E-009	3.20E-007
ptgds	NM_213634	1.13	1.03E-008	4.29E-007
rplp1	NM_200029	0.18	1.23E-008	5.07E-007
junb	NM_213556	1.98	1.35E-008	5.52E-007
kars	NM_001002386	0.84	1.53E-008	6.20E-007
ssb	NM_199547	1.36	1.65E-008	6.64E-007
LOC795785	NM_001115060	3.12	3.11E-008	1.18E-006
klhl31	NM_001003727	1.04	3.37E-008	1.28E-006
rplp2	NM_212743	0.30	5.48E-008	2.04E-006

Up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
tnni2b.1	NM_001017587	1.14	5.58E-008	2.06E-006
glud1b	NM_199545	0.99	5.82E-008	2.13E-006
rtn4a	NM_001079912	0.71	7.34E-008	2.67E-006
tpm4	NM_213158	1.03	8.09E-008	2.91E-006
c13orf22l	NM_001003880	1.64	9.37E-008	3.34E-006
atp5g	NM_131761	0.37	9.74E-008	3.46E-006
gadd45a1	NM_200576	2.84	1.01E-007	3.55E-006
LOC556921	NM_001099983	3.64	1.31E-007	4.51E-006
pdia4	NM_199779	1.15	1.32E-007	4.55E-006
zgc:154065	NM_001076564	2.59	1.38E-007	4.74E-006
zgc:56493	NM_200023	0.57	1.51E-007	5.13E-006
fth1	NM_131585	0.37	1.67E-007	5.63E-006
snrpf1	NM_001003881	0.78	1.68E-007	5.63E-006
zgc:86810	NM_001002119	0.55	2.67E-007	8.71E-006
lox12a	NM_001099244	2.19	2.78E-007	9.00E-006
rrad	NM_199798	2.67	3.62E-007	1.17E-005
psap	NM_131883	0.71	3.80E-007	1.21E-005
zgc:100919	NM_001002748	1.21	4.51E-007	1.41E-005
il6st	NM_001113504	2.16	4.57E-007	1.42E-005
prpf31	NM_200504	1.63	5.35E-007	1.66E-005
cav3	NM_205738	0.83	6.58E-007	2.01E-005
hspe1	NM_131526	0.69	8.13E-007	2.46E-005
pgam2	NM_201024	0.53	8.27E-007	2.49E-005
LOC560626	NM_001123257	1.06	8.33E-007	2.50E-005
cpn1	NM_212770	1.18	1.05E-006	3.14E-005
rps26l	NM_200742	0.22	1.23E-006	3.65E-005
rpl10	NM_200027	0.19	1.44E-006	4.22E-005
ssr3	NM_200053	0.63	2.02E-006	5.79E-005
zgc:73367	NM_213034	0.18	2.43E-006	6.88E-005
lamc1	NM_173277	0.95	2.62E-006	7.40E-005
zgc:64137	NM_199645	0.88	3.03E-006	8.38E-005
zgc:154020	NM_001077607	2.10	3.31E-006	9.05E-005
cdh1	NM_131820	1.20	4.15E-006	0.000113
zgc:136871	NM_001040379	3.13	4.65E-006	0.000125
zgc:192851	NM_001134411	1.14	4.70E-006	0.000125
zgc:162968	NM_001083553	1.14	5.60E-006	0.000147
zgc:171710	NM_001110121	0.22	5.92E-006	0.000154
vcp	NM_201481	0.51	6.46E-006	0.000167
zgc:91870	NM_001002190	0.99	6.79E-006	0.000175
zgc:100799	NM_001002732	1.35	7.37E-006	0.000187
snrpd3	NM_001002081	1.08	8.29E-006	0.000208
fkbp5	NM_213149	2.35	8.96E-006	0.000224
zgc:110459	NM_001020596	1.50	9.81E-006	0.000243
tob1b	NM_212974	1.04	1.02E-005	0.000251
slc25a4	NM_214702	0.33	1.27E-005	0.000308
dusp6	NM_194380	1.12	1.31E-005	0.000315
sart1	NM_001002673	0.96	1.34E-005	0.000321
smyd2b	NM_001030223	1.01	1.75E-005	0.000404
EIF2S2	NM_212675	0.46	1.81E-005	0.000415

Up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
pdip5	NM_197933	0.78	1.81E-005	0.000415
lgals1l2	NM_212894	1.28	1.89E-005	0.000431
zgc:73197	NM_200058	0.73	2.29E-005	0.000510
hif1a1	NM_200405	0.73	2.71E-005	0.000600
rtn2a	NM_001029965	0.68	3.17E-005	0.000699
rhoub	NM_001017784	1.63	3.33E-005	0.000728
atf3	NM_200964	2.65	3.40E-005	0.000739
thns12	NM_001037566	3.40	3.59E-005	0.000779
stat3	NM_131479	1.61	3.76E-005	0.000815
prpf3	NM_205748	1.31	4.32E-005	0.000917
rpl36a	NM_173262	0.18	4.61E-005	0.000975
rps2	NM_213279	0.13	4.76E-005	0.001005
zgc:92615	NM_001002703	0.98	4.80E-005	0.001011
cyp24a1l	NM_001089458	3.02	4.92E-005	0.001035
phb	NM_201297	0.63	5.42E-005	0.001133
tnfaip6	NM_001040243	2.46	5.95E-005	0.001235
btf3	NM_001076558	0.29	6.06E-005	0.001255
psmb7	NM_001045564	0.47	7.16E-005	0.001468
ruvbl1	NM_173835	0.94	7.67E-005	0.001559
mknk2b	NM_194402	1.23	7.85E-005	0.001592
zgc:92066	NM_001002378	0.49	8.20E-005	0.001655
si:ch211-122l24.4	NM_001130655	3.10	8.80E-005	0.001755
ldha	NM_131246	0.48	8.95E-005	0.001781
smyd1b	NM_001039636	1.02	9.21E-005	0.001828
ybx1	NM_131620	0.20	9.92E-005	0.001960
hsp90a.1	NM_131328	0.83	0.000109	0.002132
zgc:158347	NM_001082998	2.13	0.000112	0.002192
zgc:158664	NM_001080198	0.63	0.000114	0.002212
hsp90b1	NM_198210	0.48	0.000115	0.002233
zgc:162730	NM_001089404	0.94	0.000118	0.002276
ahcy	NM_199218	0.43	0.000118	0.002282
arg2	NM_199611	3.08	0.000121	0.002318
fbl	NM_213002	0.66	0.000127	0.002421
zgc:110304	NM_001017593	0.49	0.000136	0.002565
zgc:91999	NM_001003498	0.83	0.000142	0.002670
wu:fj23a05	NM_001100074	1.75	0.000142	0.002670
gpd1b	NM_199706	0.95	0.000146	0.002739
bzw1b	NM_213092	0.97	0.000150	0.002804
bag3	NM_001003533	1.76	0.000156	0.002903
c20orf45	NM_199734	0.81	0.000169	0.003117
fstl1b	NM_001039621	0.69	0.000171	0.003128
sf3a2	NM_201043	0.69	0.000171	0.003128
zgc:110330	NM_001017801	0.47	0.000176	0.003207
zgc:77517	NM_200568	0.77	0.000227	0.004041
lsm6	NM_001002077	0.66	0.000228	0.004055
hig1	NM_200100	1.53	0.000234	0.004162
fga	NM_001002039	1.35	0.000244	0.004303
tpm3	NM_201492	0.48	0.000245	0.004312
myl9l	NM_214699	0.36	0.000286	0.004923

Up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
si:ch211-214j24.10	NM_001025503	1.01	0.000310	0.005298
adsl	NM_199899	0.65	0.000313	0.005341
pdlim1	NM_001017870	1.16	0.000317	0.005376
zgc:123218	NM_001037117	2.27	0.000325	0.005483
zgc:172278	NM_001113337	2.32	0.000325	0.005483
itgb1b	NM_001034987	0.91	0.000333	0.005608
ldb3	NM_201505	0.52	0.000335	0.005634
zgc:194470	NM_001128765	0.55	0.000345	0.005782
zgc:175091	NM_001111226	1.68	0.000346	0.005782
eftud2	NM_200508	0.91	0.000368	0.006117
dtng	NM_199709	0.83	0.000372	0.006170
tpi1b	NM_153668	0.39	0.000423	0.006980
stom	NM_131758	0.92	0.000477	0.007777
si:dkey-204i11.1	NM_001109739	3.29	0.000519	0.008344
gch2	NM_131667	0.60	0.000533	0.008531
zgc:123068	NM_001007132	2.08	0.000535	0.008531
si:dkey-25f3.3	NM_001044875	2.06	0.000546	0.008685
myhc4	NM_001020485	0.60	0.000594	0.009390
zgc:171630	NM_001110374	0.97	0.000606	0.009515
mcl1a	NM_131599	0.84	0.000640	0.009935
cfl2	NM_205700	0.81	0.000692	0.010644
atp5a1	NM_001077355	0.20	0.000723	0.011086
yars	NM_201316	1.02	0.000728	0.011136
atp1b1a	NM_131668	0.63	0.000732	0.011181
zgc:92215	NM_001004586	0.66	0.000736	0.011232
zgc:113334	NM_001013320	0.92	0.000756	0.011487
zgc:92586	NM_001005932	0.77	0.000794	0.011946
casq2	NM_001002682	0.57	0.000810	0.012135
tnnt3b	NM_181653	0.10	0.000868	0.012912
kiaa0947l	NM_001034965	1.93	0.000878	0.013018
zgc:152876	NM_001077742	1.16	0.000901	0.013337
unc45b	NM_153673	1.20	0.000914	0.013489
si:dkey-199i1.2	NM_001102673	1.61	0.000941	0.013829
anxa1a	NM_181758	0.46	0.000982	0.014339
jak1	NM_131073	1.16	0.001080	0.015681
eno1	NM_212722	0.30	0.001091	0.015769
ctnnb2	NM_001001889	0.76	0.001091	0.015769
lmna	NM_152971	1.70	0.001193	0.017014
psma4	NM_214697	0.47	0.001217	0.017287
tnnt1	NM_181499	1.12	0.001220	0.017287
zgc:112426	NM_001017793	1.20	0.001307	0.018316
slc16a9a	NM_200410	3.13	0.001312	0.018316
vegfaa	NM_131408	2.58	0.001312	0.018316
atp5o	NM_001003843	0.26	0.001350	0.018805
tuba8l2	NM_200691	0.46	0.001372	0.019052
zgc:76871	NM_213103	0.90	0.001382	0.019159
selt2	NM_001098487	0.66	0.001482	0.020451
si:ch211-138a11.1	NM_001114559	2.54	0.001490	0.020458
zgc:86706	NM_001002068	0.27	0.001506	0.020654

Up-regulated genes

gene_id	refSeq_mRNA	fc(log ₂ <i>mut/wt</i>)	p-value	FDR
prpf39	NM_001004520	0.58	0.001513	0.020682
cd81	NM_131518	0.35	0.001512	0.020682
gadd45bl	NM_001012386	2.25	0.001544	0.021001
mat1a	NM_199871	1.18	0.001550	0.021021
si:dkey-42i9.6	NM_001044870	0.83	0.001565	0.021183
cox7c	NM_199995	0.28	0.001628	0.022010
zgc:174888	NM_001113584	1.59	0.001658	0.022284
rtn2b	NM_001029959	0.96	0.001659	0.022284
itm2bl	NM_212976	0.85	0.001709	0.022925
asns	NM_201163	1.31	0.001769	0.023689
psmb1	NM_001003889	0.47	0.001801	0.024080
lifrb	NM_001113732	3.57	0.001831	0.024365
wdr82	NM_001009897	1.34	0.001842	0.024391
cmlc1	NM_131692	1.29	0.001868	0.024704
uqcrb	NM_001024442	0.32	0.001882	0.024853
eif4ebp2	NM_212803	0.49	0.001890	0.024913
zgc:103420	NM_001006043	1.08	0.001931	0.025385
zgc:77429	NM_213262	0.42	0.001967	0.025692
kny	NM_131860	0.95	0.001993	0.025992
zp3a.2	NM_001030120	1.85	0.002102	0.027255
ppib	NM_213019	0.25	0.002141	0.027627
zgc:136833	NM_001039982	1.50	0.002221	0.028581
pgm1	NM_201025	0.58	0.002247	0.028777
hyou1	NM_212703	0.84	0.002447	0.031061
rapsn	NM_178305	1.09	0.002444	0.031061
cacna1s	NM_214726	1.02	0.002479	0.031428
zgc:194249	NM_001130591	0.55	0.002498	0.031621
casp8	NM_131510	2.51	0.002577	0.032423
clu	NM_200802	1.34	0.002602	0.032550
zgc:110617	NM_001020612	0.78	0.002829	0.034977
zgc:154116	NM_001077259	1.02	0.002985	0.036752
cox17	NM_001004652	0.54	0.003118	0.038168
cnn3a	NM_199753	0.73	0.003259	0.039669
pck1	NM_214751	2.87	0.003418	0.041422
il4r	NM_001013282	3.39	0.003418	0.041422
crtap	NM_001001406	0.83	0.003505	0.042413
si:ch211-219i10.1	NM_001030062	1.06	0.003545	0.042778
zgc:136474	NM_001045308	0.47	0.003565	0.042966
rps21	NM_201191	0.12	0.003605	0.043315
spint1a	NM_213152	0.94	0.003747	0.044583
zgc:92239	NM_001008579	0.56	0.003803	0.045073
zgc:76966	NM_212869	0.99	0.003836	0.045359
ob	NM_001128576	33.71	0.003906	0.046099
cd9l	NM_213428	0.70	0.004031	0.047342
zgc:171577	NM_001110124	1.05	0.004065	0.047531
zgc:161979	NM_001045488	0.52	0.004171	0.048471
adam8a	NM_200637	2.38	0.004181	0.048471
zgc:158334	NM_001080619	2.28	0.004344	0.049950

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Supplementary Table S3. List of single-exon skipping targets

Targets selected and positively validated by RT-PCR are in red/bold under gene_id

gene_id	AS	skip	incl_1	incl_2	incl_3	alt.exon / refSeq	chr	position_alt.exon
abcc4	mut+	30,06	-0,09	-0,62	0,17	exon-10 / NM_001007038	6	3107159..3107248
abcf1	mut+	30,73	-0,11	-0,10	-0,38	exon-26 / NM_213186	19	28525516..28525588
abcf1	mut+	2,40	-0,49	-0,36	-0,40	exon-7 / NM_213186	19	28513572..28513631
acvr1	mut+	3,33	-0,68	-0,46	0,03	exon-2 / NM_131345	2	51261750..51261825
ada	mut+	27,73	-0,59	-1,08	-1,19	exon-2 / NM_001002646	23	24408995..24409056
adcyap1b	mut+	0,54	-0,98	-1,22	-1,00	exon-4 / NM_214715	2	25739121..25739225
adcyap1r1	mut+	0,65	-1,29	-0,38	-2,60	exon-5 / NM_001013444	9	1203982..1204065
adipor1a	mut+	30,06	-0,33	-0,15	-0,36	exon-2 / NM_001002467	11	22020035..22020111
alcam	mut+	0,40	-0,88	-1,09	-1,10	exon-13 / NM_131000	10	23337197..23337223
atp1b2a	mut+	0,57	-1,93	-3,28	-1,84	exon-5a / NM_131669	23	40615220..40615243
atp2b2	mut+	2,82	-1,32	-1,25	-1,19	exon-5 / NM_001123238	11	37966719..37966751
bin2	mut+	27,73	-1,09	-0,82	-0,55	exon-2 / NM_001007421	23	32512260..32512409
birc5a	mut+	3,08	-0,57	-0,13	-0,12	exon-3 / NM_194397	12	31698782..31698899
btbd10a	mut+	29,32	-0,54	-0,85	-1,08	exon-8 / NM_001110459	25	8451431..8451541
c15orf15	mut+	30,06	-0,27	-0,14	-0,25	exon-4 / NM_212993	25	4257138..4257201
c2orf24	mut+	3,16	-1,11	-0,71	-0,88	exon-6 / NM_199928	1	2783637..2783698
capn1a	mut+	27,73	-1,05	-1,02	-0,82	exon-16 / NM_200445	13	44699758..44699815
cbx5	mut+	2,02	-0,39	-0,70	-0,34	exon-2 / NM_001080184	23	33952424..33952498
cd99l2	mut+	1,35	-0,60	-0,26	-0,09	exon-4a / NM_194369	7	16870106..16870213
cdc123	mut+	27,73	-1,24	-1,08	-1,55	exon-10 / NM_200721	4	5744118..5744146
cdc14b	mut+	30,54	-0,82	-0,62	-0,77	exon-13 / NM_200179	8	55892736..55892783
cdkn1b	mut+	3,82	-0,42	-0,40	-0,58	exon-2 / NM_212792	25	1508423..1508539
cdkrap3	mut+	29,73	-1,21	-1,33	-1,55	exon-2 / NM_001002105	12	23568532..23568577
ck2a1	mut+	3,24	-0,33	-0,05	-0,30	exon-14 / NM_131252	16	28090258..28090347
cops8	mut+	31,90	-0,67	-0,38	-0,81	exon-2 / NM_200229	9	17245234..17245304
cox17	mut+	32,32	-0,28	0,03	-0,18	exon-3 / NM_001004652	9	14585490..14585604
crb2	mut+	30,32	-0,24	-1,88	-0,30	exon-11 / NM_001045299	21	39079464..39079580
ctnnb1	mut+	0,26	-1,04	-1,09	-1,14	exon-8a / NM_131059	16	2098381..2098407
dap1a	mut+	30,32	-0,20	-0,08	-0,28	exon-3 / NM_131572	24	20664956..20664998
dap3	mut+	2,39	-0,71	-0,96	-0,33	exon-8 / NM_001098737	16	10749259..10749339
dcun1d4	mut+	30,54	-0,49	-0,90	-0,64	exon-3 / NM_001032366	20	24976797..24976836

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ddef2a	mut+	27,73	-1,67	-2,22	-1,12	exon-2 / NM_001045207	17	25024077..25024149
dmd	mut+	0,67	-1,29	-1,14	-1,56	exon-11 / NM_131785	4	8566149..8566214
dnmt7	mut+	1,28	-1,09	-0,99	-0,40	exon-7a / NM_001020476	8	21790527..21790658
dpcc	mut+	31,32	-1,29	-1,76	-1,17	exon-5 / NM_001045377	1	29433383..29433485
drg2	mut+	2,93	-0,53	-0,62	-0,72	exon-4 / NM_212638	3	37969136..37969225
eef2k	mut+	0,26	-1,35	-1,15	-1,35	exon-2a / NM_001002740	12	8750617..8750673
ef3c	mut+	2,19	-0,47	-0,85	-0,64	exon-21a / NM_213463	12	1890233..1890283
elavl1	mut+	1,48	-0,53	-0,14	-0,12	exon-3 / NM_131452	2	35670371..35670474
elavl4	mut+	0,24	-0,63	-0,61	-0,79	exon-7 / NM_131453	8	48143998..48144036
ewsr1b	mut+	1,37	-0,27	-0,26	-0,25	exon-8 / NM_212630	5	14418955..14418992
fam3c	mut+	30,54	-0,54	-0,66	-0,55	exon-4 / NM_212725	4	20849573..20849599
fam76b	mut+	30,06	-0,42	-0,92	-0,89	exon-3 / NM_199932	5	13135384..13135438
fkbp7	mut+	30,54	-0,10	-0,42	-0,30	exon-2 / NM_001004506	9	36686956..36687107
fstl1a	mut+	30,32	-0,53	-0,08	-0,16	exon-5 / NM_001017860	1	44419858..44419890
gamt	mut+	4,31	-0,02	-0,24	-0,17	exon-4 / NM_001105595	11	5186293..5186360
gna12	mut+	27,73	-0,93	-1,62	-1,20	exon-3 / NM_001013277	3	39510295..39510345
golim4a	mut+	30,32	-0,99	-0,17	-0,81	exon-3 / NM_001098192	18	48020971..48021024
gtpbp1	mut+	1,24	-0,65	-0,98	-0,36	exon-11a / NM_213475	3	31228716..31228754
gtpbp1	mut+	2,23	-0,64	-0,30	-0,60	exon-2 / NM_213475	3	31216404..31216515
hccs	mut+	2,70	-0,34	-0,11	-0,25	exon-6 / NM_201451	24	29860026..29860112
hnrpd1	mut+	0,68	-0,43	-2,32	-0,16	exon-8 / NM_213392	10	2425148..2425251
hsf1	mut+	1,69	-1,81	-1,21	-1,53	exon-10 / NM_131600	19	701012..701089
hsp47	mut+	0,95	-2,69	-2,53	-2,01	exon-2 / NM_131204	15	30438117..30438164
ikbkg	mut+	2,13	-1,67	-1,26	-1,52	exon-6a / NM_001014344	23	16442075..16442122
im:7153495	mut+	0,83	-1,31	-1,49	-1,20	exon-9 / NM_001100007	2	15088168..15088227
im:7159661	mut+	3,38	-0,67	-0,78	0,14	exon-10 / NM_001079980	1	27162557..27162637
imp4	mut+	30,32	-0,69	-0,73	-0,06	exon-8 / NM_001002719	5	18696756..18696829
isoc2	mut+	0,67	-1,16	-1,14	-0,87	exon-5 / NM_001079953	16	9535207..9535277
kars	mut+	0,46	-1,77	-2,63	-1,12	exon-2 / NM_001002386	7	66853175..66853305
khdrbs1	mut+	1,67	-0,47	-0,54	-0,46	exon-7 / NM_130925	13	40660102..40660175
LOC100005403	mut+	31,64	-0,51	-0,06	-0,31	exon-2 / NM_001128812	19	29267471..29267515
LOC562370	mut+	1,16	-0,62	-0,89	-0,45	exon-9a / NM_001105588	2	27099181..27099237
LOC564395	mut+	1,43	-0,31	-0,95	-0,53	exon-2 / NM_001045051	18	14522715..14522771
LOC565206	mut+	30,06	-0,29	-0,49	-0,02	exon-27 / NM_001128537	8	1871472..1871535
LOC567533	mut+	0,43	-1,42	-1,62	-1,38	exon-5a / NM_001089415	5	3462254..3462274

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LOC794796	mut+	28,73	-0,50	-2,09	-1,06	exon-17 / NM_001111217	21	12804105..12804170
lta4h	mut+	31,06	-0,74	-0,45	-0,59	exon-9 / NM_213286	4	5964124..5964147
mak16	mut+	31,19	-1,15	-1,71	-0,92	exon-2 / NM_173239	8	41716621..41716670
mapk10	mut+	0,43	-1,76	-29,53	-28,72	exon-2 / NM_001037701	21	36784297..36784343
mark3	mut+	30,06	-0,23	-0,28	-0,83	exon-3 / NM_199885	13	16955915..16955968
matn3b	mut+	1,73	-0,70	-0,73	-0,11	exon-4 / NM_001012385	13	32111943..32112074
mbnl2b	mut+	0,48	-1,27	-1,56	-1,31	exon-4a / NM_001099998	1	754211..754264
mcam	mut+	0,85	-1,64	-0,73	-2,05	exon-13a / NM_001012367	15	22870195..22870233
mdm2	mut+	32,90	-0,65	-0,31	-0,58	exon-2 / NM_131364	4	27591518..27591592
mef2b	mut+	1,21	-1,66	-1,75	-0,66	exon-5 / NM_001098247	22	21064946..21065019
mibp2	mut+	1,41	-0,30	-0,05	-0,13	exon-3 / NM_198877	18	2960618..2960666
myo6a	mut+	27,73	-1,92	-1,31	-1,50	exon-6 / NM_001004111	20	515517..515572
nadl1.1	mut+	27,73	-0,42	-1,58	-0,63	exon-26 / NM_131383	23	604518..604649
nap1l1	mut+	4,74	-0,20	-0,30	-0,31	exon-2 / NM_201318	4	2464582..2464623
nap1l1	mut+	0,22	-1,40	-1,42	-1,35	exon-14a / NM_201318	4	2484007..2484038
nap1l4	mut+	0,74	-0,86	-0,56	-0,94	exon-14 / NM_001089347	25	19772224..19772256
ndrg1	mut+	2,40	-0,62	-0,69	-0,77	exon-13 / NM_213348	19	32479463..32479514
ndrg3a	mut+	4,43	-1,14	-1,46	-1,06	exon-3 / NM_199517	11	22328854..22328886
neo1	mut+	0,42	-1,02	-1,28	-0,67	exon-21 / NM_173218	7	58707722..58707754
nf2	mut+	30,06	-1,00	-1,12	-0,98	exon-8 / NM_212951	21	16143773..16143848
nmd3	mut+	30,32	-0,08	-0,53	-0,03	exon-2 / NM_001013569	15	3169547..3169592
nr1d2b	mut+	2,54	-0,42	0,19	-0,24	exon-3 / NM_131065	19	9114539..9114627
nupl1	mut+	29,73	-0,71	-1,02	-0,83	exon-10 / NM_213229	24	23603879..23603961
oxsr1a	mut+	30,06	-0,47	-0,60	-1,04	exon-15 / NM_001098747	2	19264092..19264144
pccb	mut+	30,32	-0,07	-0,10	-0,42	exon-2 / NM_212925	2	20572363..20572482
pdha1	mut+	0,47	-0,60	-0,64	-0,44	exon-1a / NM_213393	5	13586552..13586572
phactr4	mut+	27,73	-0,91	-1,04	-1,64	exon-3 / NM_200670	16	40775575..40775619
phf5a	mut+	30,73	-0,45	-0,60	-0,44	exon-2 / NM_173266	12	18431321..18431344
pitpna	mut+	31,73	-0,80	-0,73	-0,24	exon-2 / NM_200935	15	26029577..26029607
pmp22a	mut+	1,06	-1,74	0,11	-1,47	exon-2 / NM_201311	3	60429272..60429365
postn	mut+	0,74	-0,60	-0,94	-0,87	exon-20 / NM_203421	15	25155128..25155163
ppme1	mut+	3,74	-0,26	-0,63	0,07	exon-11 / NM_199937	21	16565804..16565848
prelid1	mut+	3,57	-0,45	0,08	-0,54	exon-4 / NM_200366	14	11955759..11955872
prmt5	mut+	31,06	-0,40	-0,43	0,14	exon-11 / NM_001007183	2	34440563..34440685
prrx1b	mut+	2,08	-1,26	-1,22	-0,85	exon-3a / NM_200050	20	32743157..32743218

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ptk2.1	mut+	0,27	-1,08	-1,47	-1,76	exon-14a / NM_131796	16	27451133..27451150
ptpn4	mut+	27,73	-1,05	-0,89	-0,61	exon-5 / NM_001007200	9	22886479..22886523
ptpra	mut+	1,73	-1,53	-1,76	-1,67	exon-5 / NM_131888	21	8028898..8028909
puf60b	mut+	3,77	-0,40	-0,49	-0,07	exon-6 / NM_001002121	7	37033465..37033557
puf60b	mut+	3,77	-0,36	-0,04	-0,37	exon-2 / NM_001002121	7	37028237..37028316
rac1	mut+	31,82	-0,28	0,18	-0,28	exon-2 / NM_199771	12	8819999..8820070
rae1	mut+	30,06	-0,38	-0,20	0,03	exon-5 / NM_200998	6	47171780..47171866
rbm39a	mut+	2,32	-0,53	-0,26	-0,57	exon-5 / NM_001012304	11	21558010..21558075
rgs7	mut+	2,03	-2,28	-1,54	-1,65	exon-17 / NM_001002541	17	18405553..18405592
rhbdl3	mut+	3,74	-2,21	-29,37	-2,00	exon-8 / NM_001017556	6	42804401..42804461
rnd2	mut+	29,32	-0,45	-1,43	-1,14	exon-4 / NM_001045364	3	16890421..16890555
rpl71	mut+	30,54	-0,40	-0,27	0,12	exon-5 / NM_199590	20	30585643..30585752
rtn4b	mut+	2,33	-0,24	-0,02	-0,76	exon-3 / NM_001040335	13	51543573..51543617
sb:cb363	mut+	1,89	-1,53	-2,28	-1,78	exon-2 / NM_001122654	11	42312772..42312822
scrib	mut+	0,71	-0,60	-0,67	-1,68	exon-27a / NM_001007175	7	37131010..37131066
sec11a	mut+	30,06	-0,30	-0,27	-0,25	exon-5 / NM_001002521	18	46242428..46242485
sec22bb	mut+	0,55	-2,14	-2,23	-2,23	exon-1a / NM_201302	8	17271560..17271571
sec63	mut+	32,06	-0,92	-0,98	-0,27	exon-19 / NM_001002588	20	34768136..34768240
selt1b	mut+	30,06	-0,31	0,09	-0,68	exon-2 / NM_178292	18	38161770..38161880
sep15	mut+	4,44	-0,33	-0,39	-0,28	exon-4 / NM_178294	2	17930529..17930578
sept3	mut+	3,51	-0,93	-0,58	0,14	exon-5 / NM_001024418	1	39932524..39932661
serhl	mut+	30,54	-0,42	-0,34	-0,82	exon-4 / NM_199615	1	39970263..39970376
sesn3	mut+	30,32	-0,54	-0,23	-0,57	exon-2 / NM_213519	15	31772882..31772938
setdb1b	mut+	30,32	-0,10	-0,25	-0,18	exon-21 / NM_001077277	16	18716819..18716907
sfrs3a	mut+	30,73	-0,30	-0,61	-0,61	exon-2 / NM_001002053	6	27938227..27938261
sfrs6	mut+	4,73	-0,46	-0,24	0,19	exon-2 / NM_001008732	11	393010..393896
sgce	mut+	27,73	-0,55	-1,07	-0,66	exon-4 / NM_001002594	19	37749736..37749808
sgce	mut+	1,37	-3,46	-2,66	-30,97	exon-10a / NM_001002594	19	37731018..37731055
sh3gl2	mut+	30,06	-0,24	-0,14	-0,63	exon-2 / NM_201116	1	25027359..25027427
si:ch211-114c12.2	mut+	30,54	-0,72	-1,08	-0,08	exon-2 / NM_001002300	5	13673101..13673162
si:ch211-181h6.2	mut+	27,73	-1,27	-1,79	-0,71	exon-4 / NM_001029960	20	29333447..29333516
si:ch211-22i13.2	mut+	30,90	-0,32	-0,39	-0,37	exon-5 / NM_001020779	20	15421857..15421946
si:ch211-276g21.1	mut+	30,73	-0,17	-0,35	-0,58	exon-7 / NM_001098742	14	37506030..37506080
si:ch73-18j6.1	mut+	30,06	-0,70	-0,24	0,10	exon-2 / NM_001099986	20	14490188..14490245
si:dkey-110c1.7	mut+	1,42	-1,43	-0,70	-1,28	exon-34 / NM_001045165	22	20221619..20221648

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si:dkey-204a24.7	mut+	0,84	-1,41	-1,29	-1,85	exon-6a / NM_001083066	19	5453771..5453815
si:dkey-42i9.6	mut+	31,19	-0,21	-0,15	-0,13	exon-3 / NM_001044870	22	8172798..8172925
si:xx-bac7cse.2	mut+	30,54	-0,21	-0,24	-0,64	exon-5 / NM_001089348	10	6342538..6342633
slit2	mut+	30,32	-0,12	-0,38	-0,35	exon-22 / NM_131735	1	20703370..20703441
smarcb1b	mut+	1,50	-0,68	-0,89	-0,88	exon-8 / NM_131448	21	7847138..7847149
spna2	mut+	0,43	-0,53	-0,69	-0,65	exon-36 / NM_001098488	21	5224240..5224254
spna2	mut+	1,05	-0,94	-1,44	-0,66	exon-22 / NM_001098488	21	5212162..5212221
srp14	mut+	30,54	-0,15	-0,36	-0,33	exon-4 / NM_001033741	17	3322844..3322876
stm	mut+	2,61	-0,61	-0,59	-0,54	exon-20 / NM_198817	19	769580..769621
supt5h	mut+	3,97	-0,25	-0,13	-0,28	exon-29 / NM_131673	15	18027919..18028014
tardbp1	mut+	0,39	-0,57	-2,07	-0,82	exon-6a / NM_198364	23	25345338..25345609
tbx1	mut+	2,50	-0,66	-0,68	-0,08	exon-6 / NM_183339	7	23098926..23099026
thyn1	mut+	2,54	-1,16	-1,55	-30,78	exon-5 / NM_200657	15	16655154..16655249
tmem48	mut+	30,06	-0,70	-1,20	-0,82	exon-14 / NM_199943	2	22231586..22231636
tnfsf10l	mut+	29,73	-0,46	-1,67	-1,37	exon-4 / NM_131843	7	13541005..13541097
tomm34	mut+	27,73	-0,57	-0,95	-1,23	exon-3 / NM_199638	6	53320674..53320773
u2af2b	mut+	0,83	-0,43	-0,51	-0,91	exon-4 / NM_205689	19	7990248..7990283
uba3	mut+	30,73	-0,87	-0,75	-0,86	exon-12 / NM_213467	11	14571466..14571519
ubl3	mut+	27,73	-0,33	-1,06	-0,79	exon-3 / NM_212856	14	27828508..27828616
usp14	mut+	30,06	-0,06	-0,83	-0,21	exon-3 / NM_199973	18	39381503..39381535
usp9	mut+	0,81	-0,54	-0,61	-0,61	exon-43a / NM_001077449	9	27282328..27282435
wu:fe11e12	mut+	30,06	-0,41	-1,64	-1,11	exon-16 / NM_001024951	6	1323629..1323718
xrn2	mut+	30,32	-1,09	-0,68	-1,15	exon-30 / NM_001001944	20	48224884..48224923
zgc:100909	mut+	1,42	-1,09	-1,43	-1,75	exon-2 / NM_001003752	11	4963407..4963465
zgc:101555	mut+	31,73	-0,34	-0,38	-0,28	exon-4 / NM_001006000	18	12256360..12256458
zgc:101896	mut+	3,24	-0,99	-0,77	-0,60	exon-2 / NM_001007373	4	24124558..24124680
zgc:103421	mut+	29,73	-0,63	-0,72	-0,68	exon-9 / NM_001006042	1	10136324..10136377
zgc:103433	mut+	3,68	-0,53	-0,54	-0,23	exon-2 / NM_001006038	14	51529002..51529049
zgc:103442	mut+	1,49	-0,17	-0,27	-0,21	exon-10 / NM_001083855	8	16076834..16076881
zgc:103670	mut+	31,06	-0,71	-0,99	-0,41	exon-2 / NM_001004664	8	9546986..9547080
zgc:110113	mut+	3,87	-1,01	-0,90	-1,17	exon-5 / NM_001017574	9	3514022..3514099
zgc:110158	mut+	30,06	-0,34	-0,08	-0,10	exon-8 / NM_001020567	2	51196762..51196797
zgc:110179	mut+	29,73	-2,05	-2,67	-2,21	exon-2 / NM_001017840	7	50570174..50570230
zgc:110289	mut+	30,54	-1,08	-0,42	-0,06	exon-4 / NM_001017600	22	34727089..34727172
zgc:110796	mut+	27,73	-0,09	-0,78	-0,53	exon-2 / NM_001013333	13	47961333..47961373

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zgc:112064	<i>mut+</i>	29,73	-1,20	-0,99	-2,05	exon-7 / NM_001017651	15	21361866..21361895
zgc:112089	<i>mut+</i>	3,94	-0,57	0,11	-0,54	exon-2 / NM_001020761	9	15174736..15174795
zgc:112178	<i>mut+</i>	0,41	-2,75	-30,15	-30,56	exon-8a / NM_001017718	12	18627465..18627491
zgc:113056	<i>mut+</i>	0,68	-2,12	-28,47	-1,73	exon-2 / NM_001014355	12	30769566..30769661
zgc:113369	<i>mut+</i>	31,43	-0,13	-0,90	0,14	exon-4 / NM_001030064	13	49952736..49952790
zgc:114185	<i>mut+</i>	31,43	-0,80	-1,00	-0,48	exon-2 / NM_001025178	5	61899363..61899416
zgc:123178	<i>mut+</i>	3,15	-0,39	-0,43	-0,39	exon-3 / NM_001079946	15	9631543..9631609
zgc:123214	<i>mut+</i>	0,37	-0,58	-0,52	-0,82	exon-2 / NM_001039990	16	6309633..6309694
zgc:123246	<i>mut+</i>	1,34	-0,63	-1,15	-2,98	exon-5 / NM_001037694	1	55889735..55889767
zgc:136503	<i>mut+</i>	30,06	-0,93	-0,65	-1,61	exon-3 / NM_001045293	24	16329583..16329685
zgc:136560	<i>mut+</i>	1,01	-0,72	-0,55	-0,78	exon-3a / NM_001045297	6	9002422..9002439
zgc:136591	<i>mut+</i>	4,59	-0,36	-0,61	0,15	exon-3 / NM_001045335	24	25141618..25141739
zgc:136875	<i>mut+</i>	30,06	-0,52	-0,36	-0,32	exon-11 / NM_001040249	10	28925858..28925937
zgc:152902	<i>mut+</i>	30,06	-0,82	-0,26	-0,37	exon-5 / NM_001079951	25	12806814..12806882
zgc:153153	<i>mut+</i>	27,73	-1,27	-2,43	-2,07	exon-11 / NM_001077166	21	11116786..11116819
zgc:153867	<i>mut+</i>	0,28	-0,44	-0,77	-1,29	exon-5a / NM_213638	23	26322537..26322579
zgc:153966	<i>mut+</i>	30,32	-0,44	-0,56	-0,44	exon-2 / NM_001045846	16	50156701..50156769
zgc:153999	<i>mut+</i>	27,73	-0,53	-0,99	-1,82	exon-20 / NM_001077343	9	40562042..40562111
zgc:154027	<i>mut+</i>	1,06	-0,43	-0,30	-0,10	exon-1a / NM_001076724	7	63219090..63219122
zgc:158274	<i>mut+</i>	0,43	-1,80	-1,89	-2,74	exon-6 / NM_001082993	11	44221357..44221401
zgc:158363	<i>mut+</i>	2,50	-0,17	-0,23	-0,19	exon-8 / NM_001079973	15	1247289..1247323
zgc:158673	<i>mut+</i>	0,35	-1,94	-30,85	-1,66	exon-13 / NM_001080598	14	39658268..39658366
zgc:162329	<i>mut+</i>	27,73	-0,15	-1,21	-0,78	exon-3 / NM_001110479	25	28315649..28315835
zgc:162623	<i>mut+</i>	27,73	-1,19	-30,35	-2,51	exon-2 / NM_001089548	23	18679620..18679686
zgc:171542	<i>mut+</i>	3,46	-0,83	-0,79	-0,71	exon-5 / NM_001123057	9	41295083..41295187
zgc:171549	<i>mut+</i>	30,90	-0,31	-0,20	-0,29	exon-3 / NM_001127470	7	46011536..46011587
zgc:193686	<i>mut+</i>	27,73	-0,43	-1,49	-1,14	exon-3 / NM_001130587	1	21998304..21998342
zgc:194210	<i>mut+</i>	28,73	-1,64	-0,66	-0,66	exon-3 / NM_001130609	16	28082417..28082449
zgc:55327	<i>mut+</i>	31,43	-0,60	0,04	-0,40	exon-10 / NM_200946	20	55050486..55050566
zgc:55343	<i>mut+</i>	27,73	-1,63	-1,62	-1,18	exon-9 / NM_200252	4	42102734..42102872
zgc:56576	<i>mut+</i>	4,11	-0,74	-1,05	-1,47	exon-7 / NM_200270	17	14173561..14173609
zgc:63783	<i>mut+</i>	30,32	-0,34	-0,78	-0,92	exon-9 / NM_213451	2	4486090..4486179
zgc:63812	<i>mut+</i>	27,73	-1,54	-0,92	-2,20	exon-2 / NM_201109	15	29093283..29093323
zgc:66472	<i>mut+</i>	30,90	-0,20	-0,32	-1,27	exon-2 / NM_199812	1	42919374..42919425
zgc:73369	<i>mut+</i>	2,53	-0,43	-0,18	-0,22	exon-4 / NM_200807	24	13469389..13469448

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zgc:77407	<i>mut+</i>	27,73	-0,71	-0,88	-0,64	exon-23 / NM_213266	3	50356402..50356453
zgc:77898	<i>mut+</i>	0,73	-1,58	-1,14	-1,34	exon-1a / NM_213246	8	8615974..8616046
zgc:86751	<i>mut+</i>	32,26	-0,39	-0,20	-0,30	exon-6 / NM_001002137	23	1501232..1501256
zgc:86902	<i>mut+</i>	4,65	-0,46	-0,54	-0,23	exon-3 / NM_001002677	9	9590261..9590332
zgc:91802	<i>mut+</i>	0,27	-2,35	-2,64	-3,64	exon-4a / NM_001005584	23	32852506..32852529
zgc:92169	<i>mut+</i>	31,06	-0,33	-0,33	-0,17	exon-4 / NM_001004553	1	48822891..48822950
zgc:92317	<i>mut+</i>	28,73	-1,53	-1,16	-1,09	exon-4 / NM_001005587	5	27739648..27739701
zgc:92575	<i>mut+</i>	0,82	-1,60	-0,96	-1,96	exon-1a / NM_001007327	1	43524117..43524201
zgc:92615	<i>mut+</i>	33,46	-0,82	-0,83	-1,10	exon-5 / NM_001002703	5	6099613..6099677
zgc:92715	<i>mut+</i>	30,90	-0,82	-1,26	-1,41	exon-2 / NM_001002590	11	43465549..43465604
zgc:92723	<i>mut+</i>	0,61	-1,15	-0,71	-0,52	exon-4 / NM_001002583	9	17102308..17102357
zgc:92726	<i>mut+</i>	30,90	-0,24	0,02	-0,33	exon-2 / NM_001003427	25	32407324..32407368
tbc1d23	<i>wt+</i>	-2,69	0,25	0,34	-0,09	exon-14a / NM_200487	6	20290331..20290375
trpm7	<i>wt+</i>	-31,20	1,17	0,89	0,02	exon-19a / NM_001030061	18	43585466..43585513
zgc:194486	<i>wt+</i>	-1,92	0,40	0,08	0,14	exon-3 / NM_001089421	12	25283014..25283046
vcl	<i>wt+</i>	-1,04	0,41	1,65	0,42	exon-19 / NM_001128681	13	23881076..23881267
zgc:92380	<i>wt+</i>	-1,45	0,89	0,76	0,66	exon-6a / NM_001003480	9	41149915..41149949
rab11fip4a	<i>wt+</i>	-26,44	0,15	1,22	0,66	exon-11 / NM_001002533	3	33800226..33800307
wdr82	<i>wt+</i>	-2,47	0,22	1,00	0,91	exon-4a / NM_199551	6	28345398..28345412
amt2	<i>wt+</i>	-1,12	2,33	2,52	1,20	exon-4 / NM_131674	7	5907511..5907555
zgc:154102	<i>wt+</i>	-1,02	1,13	1,31	1,29	exon-2a / NM_001076615	2	16995887..16995919
fras1	<i>wt+</i>	-0,82	1,70	1,99	1,73	exon-33 / NM_001130840	5	29390584..29390616
zgc:91853	<i>wt+</i>	-0,29	2,30	2,90	2,42	exon-6a / NM_001002196	16	32644888..32644902
add1	<i>wt+</i>	-0,45	2,90	30,06	2,51	exon-12a / NM_001079958	21	134765..134782

Legend

gene_id	gene symbol (zV7/danRer5 annotation database)
AS	alternative splicing mode:
	<i>mut+</i> : increased exon-skipping in mut
	<i>wt+</i> : increased exon-skipping in wt
<i>skip</i>	value of exon-skipping information
<i>incl 1/2/3</i>	value of exon-inclusion information
alt.exon / refSeq	alternative exon number / refSeq mRNA
chr	chromosome name (zV7/danRer5)
position_alt.exon	chromosome position of alternative exon (0-based)

S4_sk2E

Supplementary Table S4. List of multiple-exon skipping targets

Targets selected and positively validated by RT-PCR are in red/bold under gene_id

gene_id	AS	skip	incl_1a	incl_1b	incl_2	incl_3	incl_4	alt.exon / refSeq	chr	position_alt.exon
cmn	mut+	1,68	-0,23	0,08	-0,64	-0,04	-0,08	exon-33a,b / NM_131014	12	16550715..16550762;16550525..16550600
tpd5212	mut+	1,21	-1,09	-0,58	-0,91	-0,91	-0,43	exon-5a,b / NM_199582	23	15234117..15234143;15233779..15233820
si:dkey-235d18.4	mut+	0,37	-0,62	-0,83	-0,56	-1,05	-0,61	exon-1a,b / NM_00103014	20	51896051..51896094;51899955..51900794
tnnt3b	mut+	0,85	-0,22	-0,55	-0,22	-0,83	-0,70	exon-4a,b / NM_00111041	7	39263550..39263567;39263275..39263291
elavl1	mut+	0,35	-1,63	-0,94	-30,57	-29,68	-0,78	exon-1a,b / NM_131452	2	35668187..35668199;35668341..35668400
sh3glb2	mut+	1,34	-0,68	-0,63	-1,17	-0,38	-0,89	exon-5a,b / NM_201119	5	23437479..23437541;23434269..23434291
sulf1	mut+	0,99	-1,04	-2,29	-0,88	-2,79	-1,01	exon-18a,b / NM_00100384	24	12115708..12115741;12117716..12117768
zgc:77795	mut+	0,20	-1,48	-1,10	-2,66	-2,58	-1,13	exon-5a,b / NM_212731	8	21631078..21631101;21631607..21631651
zgc:158450	mut+	0,46	-0,87	-1,31	-0,98	-2,10	-1,21	exon-5a,b / NM_00108020	2	12535736..12535768;12536740..12536761
rbm39b	wt+	-0,62	3,11	1,33	2,05	30,9	1,51	exon-3a,b / NM_00101437	8	35306253..35306328;35304476..35304621

Legend

gene_id	gene symbol (zV7/danRer5 annotation database)
AS	alternative splicing mode:
	mut+ : increased exon-skipping in mut
	wt+ : increased exon-skipping in wt
skip	value of exon-skipping information
incl_1a/1b/2/3/4	value of exon-inclusion information
alt.exon / refSeq	alternative exon number / refSeq mRNA
chr	chromosome name (zV7/danRer5)
position_alt.exon	chromosome position of alternative exon (0-based)

S5_intronR

Supplementary Table S5. List of intron-retention targets

Targets selected and positively validated by RT-PCR are in red/bold under gene_id (in blue: target that was not positively validated)

gene_id	AS	retained	spliced	target_intron / refseq	chr	position_target_intron
a2bp1	mut+	2,53	-0,92	intron-4 / NM_001005596	3	25621946..25622827
blcap	mut+	0,79	-2,88	intron-2 / NM_131493	6	52858533..52858541
brd2a	mut+	1,54	-1,81	intron-12 / NM_131200	19	4851942..4851953
c2cd2l	mut+	3,83	-1,54	intron-6 / NM_001077383	5	22331266..22331452
ccnf	mut+	0,62	-1,46	intron-14 / NM_207048	3	3947355..3947437
ccnt2	mut+	0,57	-1,18	intron-9 / NM_199828	9	16584736..16584830
cry2a	mut+	1,54	-0,73	intron-7 / NM_131791	8	19015937..19016881
eif4a1b	mut+	1,88	-0,20	intron-1 / NM_201510	5	13761737..13762342
hes6	mut+	3,02	-1,48	intron-2 / NM_194400	2	43100252..43100353
jph1b	mut+	0,77	-1,79	intron-5 / NM_001044348	2	24724858..24726540
mdm2	mut+	2,53	-0,58	intron-2 / NM_131364	4	27590062..27591517
mdm2	mut+	3,88	-0,77	intron-8 / NM_131364	4	27586080..27586189
ndufa4	mut+	2,71	-0,63	intron-2 / NM_213025	12	8100236..8100304
oclnb	mut+	1,18	-30,16	intron-3 / NM_001008618	5	19333887..19333907
papolg	mut+	0,56	-1,63	intron-15 / NM_200621	13	23246601..23246671
pl10	mut+	2,43	-0,58	intron-1 / NM_130941	6	59005302..59006145
ptcd3	mut+	3,24	-0,61	intron-16 / NM_001037372	14	12053643..12053731
rfx4	mut+	3,62	-1,33	intron-4 / NM_205712	18	18942435..18943234
rpl38	mut+	1,68	-0,44	intron-1 / NM_001002486	12	35914090..35914270
slc25a22	mut+	0,60	-0,89	intron-10 / NM_213408	6	35867519..35867527
ubxn1	mut+	8,16	-0,46	intron-2 / NM_212607	14	51213220..51213292
zgc:101644	mut+	1,14	-1,58	intron-1 / NM_001008643	9	17725809..17726036
zgc:110796	mut+	4,15	-0,78	intron-1 / NM_001013333	13	47961374..47961871
zgc:114129	mut+	0,97	-0,91	intron-9 / NM_001030102	17	10434724..10434815
zgc:136497	mut+	1,84	-0,97	intron-1 / NM_001040322	13	5707372..5707480
zgc:158284	mut+	0,87	-2,50	intron-1 / NM_001123045	14	53926535..53926547
zgc:158316	mut+	2,12	-1,00	intron-6 / NM_001080074	9	37220..37477
zgc:158803	mut+	0,52	-0,66	intron-11 / NM_001089547	1	51678799..51678808
zgc:56141	mut+	1,61	-0,44	intron-3 / NM_213317	7	13413366..13413729
zgc:63783	mut+	2,37	-0,74	intron-7 / NM_213451	2	4485435..4485734
zgc:66168(rps27a)	mut+	0,74	-0,35	intron-1 / NM_200502	6	4856580..4856681

S5_intronR

zgc:77517	mut+	1,08	-0,48	intron-6 / NM_200568	6	26340887..26340963
arrdc3	wt+	-2,18	1,06	intron-2 / NM_001080029	5	47559842..47559934
dnmt7	wt+	-0,54	3,88	intron-24 / NM_001020476	8	21805099..21805149
fga	wt+	-0,97	1,34	intron-5 / NM_001002039	1	6720269..6720488
sardh	wt+	-1,16	1,60	intron-16 / NM_201128	10	7499655..7500180
sfrs1	wt+	-0,84	0,60	intron-2 / NM_200593	21	31401902..31402226
sfrs18	wt+	-0,95	1,14	intron-11 / NM_001083837	16	39017464..39017760
sfrs2	wt+	-0,90	0,62	intron-2 / NM_213382	12	29337713..29338943
trspap1	wt+	-1,22	0,75	intron-3 / NM_001029966	2	19874145..19874586
zgc:113564	wt+	-1,15	1,15	intron-3 / NM_001013315	5	20944901..20946580
zgc:113564	wt+	-0,59	0,71	intron-7 / NM_001013315	5	20948368..20948627
zgc:65779	wt+	-1,39	2,17	intron-8 / NM_214750	5	68371673..68371688
zgc:91951	wt+	-0,58	1,42	intron-5 / NM_001007764	1	22969322..22969341

Legend

gene_id	gene symbol (zV7/danRer5 annotation database)
AS	alternative splicing mode:
	mut+ : increased intron-retention in mut
	wt+ : increased intron-retention in wt
retained	value of intron-retained information
spliced	value of intron-spliced information
target_intron / refSeq	target intron number / refSeq mRNA
chr	chromosome name (zV7/danRer5)
position_target_intron	chromosome position of target intron (0-based)

S6_altSS

Supplementary Table S6. List of targets with alternative 5' or 3' splice sites

Targets selected and positively validated by RT-PCR are in red/bold under gene_id

gene_id	AS	distal	proximal_1	proximal_2	target_exon / refsec	chr	position_distal_5'(3)SS	position_proximal_5'(3)SS
bcl7a	5'SS / distal_mut+	0,98	-0,53	-0,75	exon-4 / NM_212560	5	38526324(0)	38526306(+18)
brd2a	5'SS / distal_mut+	0,38	-0,88	-0,53	exon-3 / NM_131200	19	4846305(-12)	4846317(0)
her8a	5'SS / distal_mut+	0,62	-1,12	-1,59	exon-3 / NM_199624	7	17415059(-12)	17415047(0)
ilif3	5'SS / distal_mut+	1,08	-0,47	-0,71	exon-15 / NM_212595	3	4738803(-30)	4738833(0)
isoc1	5'SS / distal_mut+	2,76	-0,94	-0,40	exon-1 / NM_001079981	10	6497149(-77)	6497072(0)
pl10	5'SS / distal_mut+	0,51	-0,71	-1,09	exon-4 / NM_130941	6	59009792(0)	59009840(+48)
popdc2	5'SS / distal_mut+	1,87	-0,71	-0,45	exon-3 / NM_001114450	9	14576647(0)	14576504(+143)
pou2f1b	5'SS / distal_mut+	0,94	-1,50	-1,97	exon-12 / NM_001089325	9	28420890(0)	28420902(+12)
tcf12	5'SS / distal_mut+	0,71	-0,65	-0,72	exon-6 / NM_214816	7	49306883(-39)	49306922(0)
zgc:101828	5'SS / distal_mut+	2,02	-0,48	-0,65	exon-1 / NM_001005971	2	51090266(-38)	51090304(0)
zgc:110753	5'SS / distal_mut+	0,61	-0,60	-0,53	exon-1 / NM_001013293	19	38301871(-78)	38301793(0)
aup1	5'SS / proximal_mut+	-2,09	1,25	1,65	exon-8 / NM_199690	14	1714087(0)	1714105(+18)
btf3	5'SS / proximal_mut+	-0,39	1,55	1,27	exon-1 / NM_001076555	5	25494886(-63)	25494949(0)
c20orf1491	5'SS / proximal_mut+	-0,10	1,97	3,89	exon-1 / NM_200008	23	15228392(0)	15228381(+11)
cbx3a	5'SS / proximal_mut+	-0,95	0,47	0,14	exon-1 / NM_001045402	19	46027166(0)	46027046(+120)
clasp2	5'SS / proximal_mut+	-0,57	1,21	1,36	exon-29 / NM_207072	19	39681558(0)	39681576(+18)
dnajc7	5'SS / proximal_mut+	-0,93	0,66	0,53	exon-13 / NM_213290	3	14913135(0)	14913117(+18)
dync1li1	5'SS / proximal_mut+	-1,31	0,96	1,01	exon-11 / NM_001102428	19	9845344(-30)	9845314(0)
foxp2	5'SS / proximal_mut+	-0,96	0,74	1,09	exon-18 / NM_001030082	4	40364906(-18)	40364924(0)
hgs	5'SS / proximal_mut+	-0,59	0,92	0,75	exon-9 / NM_199868	3	57924489(0)	57924507(+18)
htt	5'SS / proximal_mut+	-1,00	1,38	0,36	exon-63 / NM_131018	1	39236344(-18)	39236326(0)
ldb1a	5'SS / proximal_mut+	-1,08	0,78	0,64	exon-1 / NM_131316	13	20333670(0)	20333631(+39)
magi1	5'SS / proximal_mut+	-1,31	1,74	1,44	exon-9 / NM_001007063	11	16802963(0)	16802945(+18)
nrf1	5'SS / proximal_mut+	-0,16	0,77	1,30	exon-9 / NM_131680	4	15539005(0)	15538975(+30)
otpa	5'SS / proximal_mut+	-0,33	0,91	0,88	exon-1 / NM_001128703	24	28613482(-39)	28613521(0)
pabpc1a	5'SS / proximal_mut+	-0,09	1,08	1,45	exon-15 / NM_001031676	16	48346182(-21)	48346161(0)
si:ch211-13c6.3	5'SS / proximal_mut+	-0,92	0,70	0,74	exon-2 / NM_001045167	19	38858843(-15)	38858858(0)
si:ch211-214j24.10	5'SS / proximal_mut+	-0,47	2,43	31,32	exon-1 / NM_001025503	4	3952109(0)	3952133(+24)
slc1a2	5'SS / proximal_mut+	-0,16	0,48	0,59	exon-8 / NM_199978	25	29371187(-46)	29371233(0)
slc4a4	5'SS / proximal_mut+	-0,53	0,76	1,05	exon-6 / NM_001034984	5	34439349(-27)	34439376(0)
stau2	5'SS / proximal_mut+	-0,05	1,54	2,49	exon-14 / NM_200925	24	16565402(0)	16565420(+18)
stk25	5'SS / proximal_mut+	-0,01	1,14	2,05	exon-7 / NM_213308	2	18171355(0)	18171337(+18)
yars	5'SS / proximal_mut+	-0,21	0,56	1,82	exon-1 / NM_201316	19	28047810(0)	28047798(+12)
ywhae1	5'SS / proximal_mut+	-0,13	1,38	3,86	exon-1 / NM_212605	15	21443887(0)	21443870(+17)
zgc:112066	5'SS / proximal_mut+	-2,97	2,53	1,68	exon-3 / NM_001017649	10	20236356(0)	20236332(+24)
zgc:112221	5'SS / proximal_mut+	-0,96	1,47	1,68	exon-5 / NM_001020763	5	19459983(-21)	19460004(0)
zgc:123105	5'SS / proximal_mut+	-0,96	0,70	0,79	exon-8 / NM_001039994	21	25176145(-21)	25176124(0)
zgc:136497	5'SS / proximal_mut+	-3,22	1,15	0,48	exon-4 / NM_001040322	13	5709589(-39)	5709628(0)
zgc:152873	5'SS / proximal_mut+	-1,05	1,18	0,80	exon-7 / NM_001077560	15	20836676(-89)	20836765(0)

S6_altSS

zgc:158161	5'SS / proximal_mut+	-0.62	1.68	1.39	exon-29 / NM_001004526	17	856242(0)	856287(+45)
zgc:162329	5'SS / proximal_mut+	-0.64	1.69	2.17	exon-1 / NM_001110478	25	28324403(-49)	28324354(0)
zgc:77282	5'SS / proximal_mut+	-0.41	0.90	1.38	exon-1 / NM_205698	15	5088592(-18)	5088574(0)
zgc:92567	5'SS / proximal_mut+	-0.78	1.39	1.76	exon-6 / NM_001002731	8	23452347(-18)	23452329(0)
im:7162273	3'SS / distal_mut+	0.53	-1.16	-30.98	exon 8/NM_001079966	1	29608935(0)	29609081(-146)
mdm4	3'SS / distal_mut+	0.09	-0.74	-1.02	exon 9/NM_212732	11	18724249(0)	18724234(-15)
si:ch211-255/12.2	3'SS / distal_mut+	1.03	-0.57	-2.01	exon 5/NM_001113218	18	41517071(+10)	41517081(0)
ssb	3'SS / distal_mut+	0.12	-4.49	-4.57	exon 2/NM_199547	6	1487587(+16)	1487603(0)
zgc:109973	3'SS / distal_mut+	0.36	-1.29	-1.19	exon 2/NM_001020540	10	38442953(0)	38442926(-27)
zgc:55671	3'SS / distal_mut+	0.06	-0.90	-1.19	exon 9/NM_212588	7	55484246(+39)	55484207(0)
hspg2	3'SS / proximal_mut+	-0.17	0.82	0.99	exon 11/NM_001127467	23	28072195(+27)	28072168(0)
pax2a	3'SS / proximal_mut+	-0.79	1.35	0.75	exon 5/NM_131184	13	29261023(0)	29261074(-51)
rhogc	3'SS / proximal_mut+	-2.50	0.88	0.24	exon 2/NM_199692	5	31770009(+15)	31769994(0)
sf1	3'SS / proximal_mut+	-0.96	0.58	0.79	exon 11/NM_212653	7	13438924(0)	13438846(-78)
ucp2	3'SS / proximal_mut+	-0.64	0.89	2.89	exon 4/NM_131176	10	34191429(0)	34191318(-111)
zgc:112214	3'SS / proximal_mut+	-0.20	0.61	0.81	exon 18/NM_001020666	24	6875862(0)	6875775(-87)

Legend

gene_id	gene symbol (zV7/danRer5 annotation database)
AS	alternative splicing mode:
	5'SS / distal_mut+ : increased distal 5' splice site usage <i>immut</i>
	5'SS / proximal_mut+ : increased proximal 5' splice site usage <i>immut</i>
	3'SS / distal_mut+ : increased distal 3' splice site usage <i>immut</i>
	3'SS / proximal_mut+ : increased proximal 3' splice site usage <i>immut</i>
distal	value of distal 5' splice site usage information
proximal_1/2	value of proximal 5' splice site usage information
target_exon / refSeq	target exon (with alt 5'/3' splice site) number / refSeq mRNA
chr	chromosome name (zV7/danRer5)
position_distal_5'(3')SS	chromosome position of 5' (3') splice site (relative to splice site of refSeq mRNA target exon)
position_proximal_5'(3')SS	chromosome position of 5' (3') splice site (relative to splice site of refSeq mRNA target exon)

S7_mutuallyExcl

Supplementary Table S7. List of targets with mutually exclusive exons

Targets selected and positively validated by RT-PCR are in red/bold under gene_id

gene_id	<i>up_1</i>	<i>up_2</i>	<i>up_3</i>	<i>down_1</i>	<i>down_2</i>	<i>down_3</i>	chr	position_upstream_exon	position_downstream_exon	refSeq
eno1	0.44	0.47	0.64	-1.78	-1.76	-1.60	23	21063020..21063078 (Exon 3a, mut+)	21063316..21063374 (Exon 4, wt+)	NM_212722
cpne3l	-0.53	-0.79	-0.97	0.20	0.38	0.58	11	23621096..23621191 (Exon 8, wt+)	23621279..23621377 (Exon 8a, mut+)	NM_199699
pkm2a	-0.97	-0.31	-0.55	0.20	1.12	1.56	18	343962..344128 (Exon 8a, wt+)	341896..342062 (Exon 9, mut+)	NM_199333

Legend

gene_id	gene symbol (zV7/danRer5 annotation database)
<i>up_1/2/3</i>	value of upstream exon inclusion information
<i>down_1/2/3</i>	value of downstream exon inclusion information
chr	chromosome name (zV7/danRer5)
position_upstream exon / position_downstream exon	chromosome position of target exon; (exon number in RefSeq mRNA; increased inclusion in mut [mut+] or wt [wt+]).
refSeq	refSeq mRNA

Supplementary Table S8.**List of primers used for cloning, genotyping, qRT-PCR, cRNA detection, and validation RT-PCRs.**

The primer name provides information on the target gene as well as on the location (“E” for exon and “I” for intron) and direction (forward or reverse). The numbers of the primer mixes refer to Figure S2.

application	name	sequence 5' → 3'
cloning of ZFU1C expression construct	ZFU1C 3'end KpnI fwd	CTAGTCGGTACCTTATTATCGATCAGGACGCACCA TACC
	ZFU1C 5'end BsmBI rev	ACTTACCGTCTCCCATGCCGAAGTTTTATTGCGATT ACTGTGAC
qRT-PCR analysis of ZFU1C mRNA levels	ZFU1C qPCR fwd	CGGATCCCTGCTACCTCATCC
	ZFU1C qPCR rev	GACCTGGTCCTCCAGGCATC
	ZF b-actin E1 fwd	GATCTTCACTCCCCTTGTTCA
	ZF b-actin E2 rev	ATGTCTGGGTCGTCCAACAA
genotyping of zebrafish embryos	msl4 fwd	GCTAGCTTGCCAAACCTACAGGT
	hi1371 wt positive fwd	CTACGGCACTTCTGTTATTTAAACACG
	hi1371 rev	CTCACCGAATCATGTGTCAGGTATG
	wnt5a fwd	CAGTTCTCACGTCTGCTACTTGCA
	wnt5a rev	ACTTCCGGCGTGTGGAGAATTC
cRNA detection	ZFU1C cmRNA fwd	TGCCAGCCGTTAGACCTGGTATG
	ZFU1C endo. mRNA spec. rev	CGCACATCACACACAAACCCATTAC
	ZFU1C inj. cRNA spec. rev	TCACTCAAGCGGAACGAGGTTTCC
cloning of minigene constructs	ZFc2orf24 mini E5 fwd	ACGTACGGTACCGAGGAGGAGGTTTTCAA
	ZFc2orf24 mini iF rev	GTTGCAAAAACAAGTAAATACTCATGAGGATG
	ZFc2orf24 mini iF fwd	CTTGTTTTGCAACCAGTGTGATTTGTGTTAG
	ZF c2orf24 mini E7 rev	CTAGTCCTCGAGGGTAAAGTGCTGGTATATAG
	ZFc2orf24 U-rich A mini iF rev	CTTTGGGGGGGGGGGGCGGGGGGGGGTATGCCGTG ACCCC
	ZFc2orf24 U-rich A mini iF fwd	GTCACGGCATAACCCCCCGCCCCCCCCCAAA AGATCAAGG
	ZFzgc112089 mini E1 fwd	ACGTACGGTACCGTGTAGTTTACTCAGAG
	ZFzgc112089 mini E2 rev	CTAGTCCTCGAGCTTCATGAGCCCCAAAC
	ZFzgc112089 mini iB C-rich rev	GGTTGGGGGCGGTGGGGCTATATTTGCAGTTTACC
	ZFzgc112089 mini iB C-rich fwd	TATAGCCCCACCGCCCCCAACCCACTAAACGTAAT AAC
	ZFilf3 mini E15 fwd	ACGTACGGTACCGTTGAGATCGATGGACA
	ZFilf3 mini E16 rev	CTAGTCCTCGAGCTTGGTTAAATCCTCCA
	ZFilf3 mini C-rich iO rev	CAGTGGGGGCGAGCAGGAATGGGGCCTAC
	ZFilf3 mini C-rich iO fwd	GCTGCCCCACTGTCGTTGGCCTAAATATTC
	ZFzgc162329 mini E1 fwd	ACGTACGAATTCGCAGAAACGAGTCCC
	ZFzgc162329 mini iA rev	TAAAGTATCAGTGCTCTTCTTAAGTGTTC AACAGG
	ZFzgc162329 mini iA fwd	AGCACTGATACTTAGTACGGGATTATTATCGC
	ZFzgc162329 mini E2 rev	CTACTGTCTAGACGGGTCGGGTCCTTG

primer mix		
1	ZFpostn E19 fwd	CGGTGAGGACTCTGAGGGAATC
	ZFpostn E21 rev	CCTAATAGGCTCTGGATCATTGTGC
2	ZFndrg3a E2 fwd	GCAGACCAACACAAAGATGGATGAG
	ZFndrg3a E4 rev	GGTCAAAATGACGGGACGGTTGC
3	ZFc2orf24 E5 fwd	TCAACGATGAATGGGGTACTGCGG
	ZFc2orf24 E7 rev	GGGCTTCCCTCCAATTGAGGTTTC
4	ZFabcf1 E6 fwd	TGGCAATATATTTGCTGCACTGAGCC
	ZFabcf1 E8 rev	GCACCTTCATCTTGCTCGTCCTC
5	ZFnap1l4 E13 fwd	GAAGAGGAGGAGGGTGATTTTGACC
	ZFnap1la E15 rev	GTTGCGAGTCCACGAGGAAATTAGG
6	ZFhsp47 E1 fwd	GAAAACATCCAAACAGCTGTCCAAG
	ZFhsp47 E3 rev	CCAGATTGGCGCTGGTGTCTGC
7	ZFzgc112089 E1 fwd	GGCAGCAGCATCAAACAGTCGTG
	ZFzgc112089 E3 rev	CCAGTATGGCCGTCTCATCGTG
8	ZFzgc123214 E1 fwd	ACGCTTGGTGCCCACTATTCCG
	ZFzgc123214 E3 rev	GAAGCTGGGCTTGGCTTTGGATG
9	ZFzgc136591 E2 fwd	CTGGACTGCACTCACCTGTGG
	ZFzgc136591 E4 rev	GAAGTAGCGCAGCTCATAGCTTTCC
10	ZFelavl4 E6 fwd	GCCATCAAGGGTCTGAATGGACAG
	ZFelavl4 E8 rev	ACCAGCCTGTTCTGTGTGACC
11	ZFcbx5 E1 fwd	GTGCAAGGAAAAAGCCGCCGCC
	ZFcbx5 E3 rev	GTA CTCTTCCTCATCTGAGGAAGCAG
12	ZFeifc3 E21 fwd	CCAACAGAAGCAAGGCTACCAGAG
	ZFeifc3 E22 rev	GAGGAAGCTGCAGTCTGGTCCTG
13	ZFzgc136560 E3 fwd	CGAGAGATTGGCATCCTCACCAC
	ZFzgc136560 E4 rev	GGCTGCTGTGTGTGGAGTTGTTC
14	ZFpdha1 E1 fwd	GCTAGCTGGGCTGGTTCTGTGAG
	ZFpdha1 E2 rev	GTCCTGGCAGATACCACAATCCTG
15	ZFzgc77795 E5 fwd	GACTCTCTCTCAGGCCGGTCAG
	ZFzgc77795 E6 rev	CATGTTCTCCACCTTGTCTCAAACG
16	ZFsulf1 E18 fwd	CAGACCCAGAAGCTCAGATGCAG
	ZFsulf1 E19 rev	CAGTCATCCAGAACGGGACTGTAG
17	ZFtdp52l2 E5 fwd	CAGGCTGGACAGAAGACCTCAG
	ZFtdp52l2 E6 rev	TGTCCTCAAATGACTTGAAGGTTGGAG
18	ZFsi:dkey-204a24.7 E6 fwd	GTGGAGCTGGAAGGCGAGGAG
	ZFsi:dkey-204a24.7 E7 rev	TCCATCTTCAGGTTCCAGATTGCCTG
19	ZFprrx1b E3 fwd	GCTGGCCAGTAAGAACGCTTCAC
	ZFprrx1b E4 rev	ATTCATTCCCTGGGTGGAAGTGGTG
20	ZFLOC567533 E5 fwd	GTCATGCCAGTGATGGACGCAAG
	ZFLOC567533 E6 rev	CATGGACATCTGCACCGTACTGC
21	ZFdnmt E7 fwd	AAGTGAACCTGAAGAACGATGGAGCC
	ZFdnmt E8 rev	GTCTGGGACTCGGTGTGGAATTTG
22	ZFzgc92615 E4 fwd	GGGCTTTGGATCCTTCGAGACG
	ZFzgc92615 E6 rev	CAGATGGGGAAAACCTGATGGAGCAC
23	ZFkhdrbs1 E6 fwd	GGAGCAGCATCCCCTCAAGG
	ZFkhdrbs1 E8 rev	TCGTA ACTCTCTGTGCCTCTCC
24	ZFfam76b E2 fwd	GAATGTCCGATTGCGCATCCCATAG
	ZFfam76b E4 rev	GGTTTGTGGAGGGCCGTA CTTC

25	ZFu2af2b E3fwd	GCAGTCGAGAACCGAAGAGAAGG
	ZFu2af2b E5 rev	CAAAGCCTGGAGGAGGGACATC
26	ZFcdkn1b E1 fwd	CGTGGATGTTAACGGGAATCACGAC
	ZFcdkn1b E3 rev	AAATCAGCCACCAGGCACTGAGG
27	ZFxr2 E29 fwd	CACCATGTGGGCAGAAGTGATGG
	ZFxr2 E31 rev	GAAGAGCCCTGGTTCTGCATGG
28	ZFsfrs6 E1 fwd	GGGTGTACATCGGCAAGCTGAG
	ZFsfrs6 E3 rev	ACGATCAGCCGGTACTCTGTGC
29	ZFzgc103442 E9 fwd	CCTGCTGGCCATGATCAACTCAG
	ZFzgc103442 E11 rev	GCTTTCCTGGGTGCAATCCTTCC
30	ZFbtbd10a E7 fwd	CCAGTGCTCAGAGCGGAGAGAG
	ZFbtbd10a E9 rev	GATAAAGGGCCGCTGGACGTAG
31	ZFmbnl2b E4 fwd	CACCTGCAGGCCAAGATCAAAGC
	ZFmbnl2b E5 rev	CTGGCCAAAGCCTGTTGGTAGTG
32	ZFsh3glb2 E5 fwd	TTGAGAACCGACGTCTTGACCTGG
	ZFsh3glb2 E6 rev	CTCCAGCAGGAGGCGAGTCAC
33	ZFzgc77898 E1 fwd	AAACCCGTCAGGAACATCGACACG
	ZFzgc77898 E2 rev	CGTATCCTTTGCTGAAGATGTCTTTGGC
34	ZFzgc158450 E5 fwd	ACACTGCACCACAACCCAGACAG
	ZFzgc158450 E6 rev	ATGGGATGGCCCTGAGAGTTAGC
35	ZFLOC562370 E9 fwd	AGTACCTGCGAGTGGGCAAAGC
	ZFLOC562370 E10 rev	CCAAGAATAGAGGCTCCTGCTACCG
36	ZFscrib E27 fwd	GAAATGGTAAGAGAGACGTCCAGTG
	ZFscribE28 rev	GGCAGAGCCGCCAGTGTCTTATAG
37	ZFdync1li1 E11 fwd	TCCCACAGGCTCACCAAGGAC
	ZFdync1li1 E12 rev	CCTGGTGTGTTGCTCCCTCCTC
38	ZFilf3 E15 fwd	CCTGGCGGCTCTGGAGAAACTG
	ZFilf3 E16 rev	TCCTCCACCGTTGTTGAATCCCC
39	ZFotpa E1 fwd	CATGCCGACCTGCTGGATGCTC
	ZFotpa E2 rev	CCTTCCACCGCATCGGAGACC
40	ZFtcf12 E6 fwd	TTCTCCTGACCACACCAGCAGTAG
	ZFtcf12 E7 rev	TGGAGGGAGTTCTCGTAGCTTGG
41	ZFzgc162329 E1 fwd	TGGCACCATAACTTCGGCTTGAGG
	ZFzgc162329 E2 rev	GTCGGGTCCCTGGCTGGAAATATG
42	ZFclasp2 E29 fwd	CGCAGCCAGGAGGACATGACAG
	ZFclasp2 E30 rev	GAGGAGGAGCCGAAGGAGGAG
43	ZFc20orf149l E1 fwd	CGGACGTGGAAGGTCTTATCCATC
	ZFc20orf149l E2 rev	GTCGTGAGTGGCAACAAGAGAACC
44	ZFsich211-214j24.10 E1 fwd	TGCGCGACACTCTCACGTACAC
	ZFsich211-214j24.10 E2 rev	GACGGTTGCGGATCTGTGGTTC
45	ZFpabpc1a E15 fwd	TCAGTGCCAGTCTCTGCTGTGC
	ZFpabpc1a E16 rev	GCCTCTCAACCTGGCAGAGATTTG
46	ZFaup1E8 fwd	CTCAACGCAGATCACCAAAGCAGAC
	ZFaup1E9 rev	GGACGTCTGGCAGCACTTCTTTC
47	ZFdnajc7 E13 fwd	TGATGCCAACAACATCTTCAAAGCATTC
	ZFdnajc7 E14 rev	TGGCACAGATGCAGGTCCAACCTG
48	ZFzgc123105 E8 fwd	GTCAGGGCTCCACCGCTTCTC
	ZFzgc123105 E9 rev	GGGTGGCCTGGGCCTTCATTAC
49	ZFhgs E9 fwd	CCAGCACTGGGCCATCGGAAC

	ZFhgs E10 rev	TTCTCCTCGGCCTCACTCTGGG
50	ZFbcl7 E4 fwd	TGGCCGCTTCTCAGAATGACAGC
	ZFbcl7 E5 rev	CTGGGCCGATTTGGAAGAGTCTA
51	ZFbrd2a E8 fwd	GGCGGTGACTCCTCCTCTTCC
	ZFbrd2a E9 rev	GATGATGGGCGTGGAGGACAGC
52	ZFfoxp2 E18 fwd	CGCAGTGCGACACAACCTCAGC
	ZFfoxp2 E19 rev	CTGTAAGCTGGCGTTAAGAGCTGCC
53	ZFpl10 E4 fwd	GGGATAACGGACGCAGCAATGG
	ZFpl10 E5 rev	GACCCGCGGTCATTGAAGAACG
54	ZFzgc110753 E1 fwd	GTCTGAAACAAACATGGAGGAGACAG
	ZFzgc110753 E2 rev	CGAGGAAAGAGCCAAGTGTCTGG
55	ZFzgc136497 E4 fwd	TCTGCAGATGGGTCAGTGTGGGC
	ZFzgc136497 E5 rev	GCTCGCTCTCCTCCCTCTTCC
56	ZFbtf3 E1 fwd	TCTCGCTTCCATCTTGCTCTCCG
	ZFbtf3 E2 rev	CAATGCGGACTTGTGCCTGCAAC
57	ZFslc1a2 E8 fwd	CTCGTACGGCGCAGGTATCGTC
	ZFslc1a2 E9 rev	ATCTCCGCAGTCGAGCCGTTGG
58	ZFzgc152873 E7 fwd	CTGAAGACTCGGAGGCCACCAC
	ZFzgc152873 E8 rev	GGGTTGAAGCGAATGTGCAAGGAG
50	ZFldb1a E1 fwd	CTGCTTTCCGCACAGCACGATGG
	ZFldb1a E2 rev	CACTACCGTTGGGAGGCTCCTTTG
60	ZFher8a E3 fwd	CTGGAGATCACAGTTCAGCACATGG
	ZFher8a E4 rev	GGGTTCGGTGCTGATGTGAGG
61	ZFzgc77282 E1 fwd	CGAGACTCCAGAGAAGACTTCGAC
	ZFzgc77282 E2 rev	CCATCTCTGAAGCGTCCCATGC
62	ZFeno1 E3 fwd	AGAGCTGCAGTGCCCAGTGGTG
	ZFeno1 E4a rev	GCAGGGGCCAAGAACTCATTAC
63	ZFeno1 E3 fwd	AGAGCTGCAGTGCCCAGTGGTG
	ZFeno1 E4b rev	CCAGACCAGGTGCAATTGTTTTATTGATA
64	ZFpkm2a E8 fwd	GCAGTGATGTGGCCAATGCAGTTC
	ZF pkm2a E8a rev	GTCCTCAAACACCTGCCGATGAAAC
65	ZFpkm2a E8 fwd	GCAGTGATGTGGCCAATGCAGTTC
	ZF pkm2a E9 rev	GTCACGGGTGAGAACAGAGGAG
66	ZFrpl38 E4 fwd	AGGCTGAGAAGCTCAAGCAGTCC
	ZFrpl38 iD rev	CTGAAAAACCAAAATGCTGGACACAAATG
67	ZFrpl38 E4 fwd	AGGCTGAGAAGCTCAAGCAGTCC
	ZFrpl38 E5 rev	CCAACATTTGTACAAGAGACATCTACTTC
68	ZFrps27a E1 fwd	TCGGTTTCCGCCATCTAAGAGCTG
	ZFrps27a E2 rev	CGAGGGTGATGGTTTTACCCGTGAG
69	ZFrps27a E1 fwd	TCGGTTTCCGCCATCTAAGAGCTG
	ZFrps27a E3 rev	TCCTTGTCTTGAATCTTTGCCTTGAC
70	ZFpl10 E1 fwd	AGGAACCCGTCTATCCGCGACAC
	ZFpl10 E2 rev	CATCAGCGGAGCTCAAGTCTAGGG
71	ZFeif4a1b E1 fwd	GTGATAATGTCGGCAGATTATGAAGGG
	ZFeif4a1b E2 rev	CAATGACTCCATCTGGCTCCATGC
72	ZFeif4a1b E1 fwd	GTGATAATGTCGGCAGATTATGAAGGG
	ZFeif4a1b E3 rev	TTTGCTGGATGGCAGAGGGCTTC
73	ZFrfox4 E4 fwd	TACGAGATCGCAGAGGGTGTGTG
	ZFrfox4 iE rev	GGGAGCGGGATAAGGGTGTGCG

74	ZFzgc101644 E1 fwd	CTCACACACGGCTGTGGTATTGC
	ZFzgc101644 E2 rev	CCGCTCTTATCCGCCACTCTAC
75	ZFjph1b E5 fwd	CCTCACTTGACGGAACATTAACCTCAG
	ZFjph1b iE rev	TGAGCTCACTGAAGGGTCGAAACAG
76	ZFzgc56141 E3 fwd	GCACCCGCAGGAAATGGTACTC
	ZFzgc56141 E4 rev	GGAGACGACGACGACGATCTTG
77	ZFcct2 E9 fwd	CACAACCTGGTCCGTTGCTGATGG
	ZFcct2 E10 rev	TTCTCAGGGCCATGACTCTCCAC
control ZFrpl38	ZFrpl38 E4 fwd	AGGCTGAGAAGCTCAAGCAGTCC
	ZFrpl38 E5 rev	CCAACATTTGTACAAGAGACATCTACTTC
control ZFrps27a	ZFrps27a E5 fwd	TCCACACTTCATCTGGTGCTGAG
	ZFrps27a E6 rev	AGACGGTGGATCTTGCCATTCTC
control ZFeif4a1b	ZFeif4a1b E7 fwd	CCCTTGAGGGTATCCGTCAGTTC
	ZFeif4a1b E8 rev	GAAGTCCCTGGCATGCATCTTTTCTG