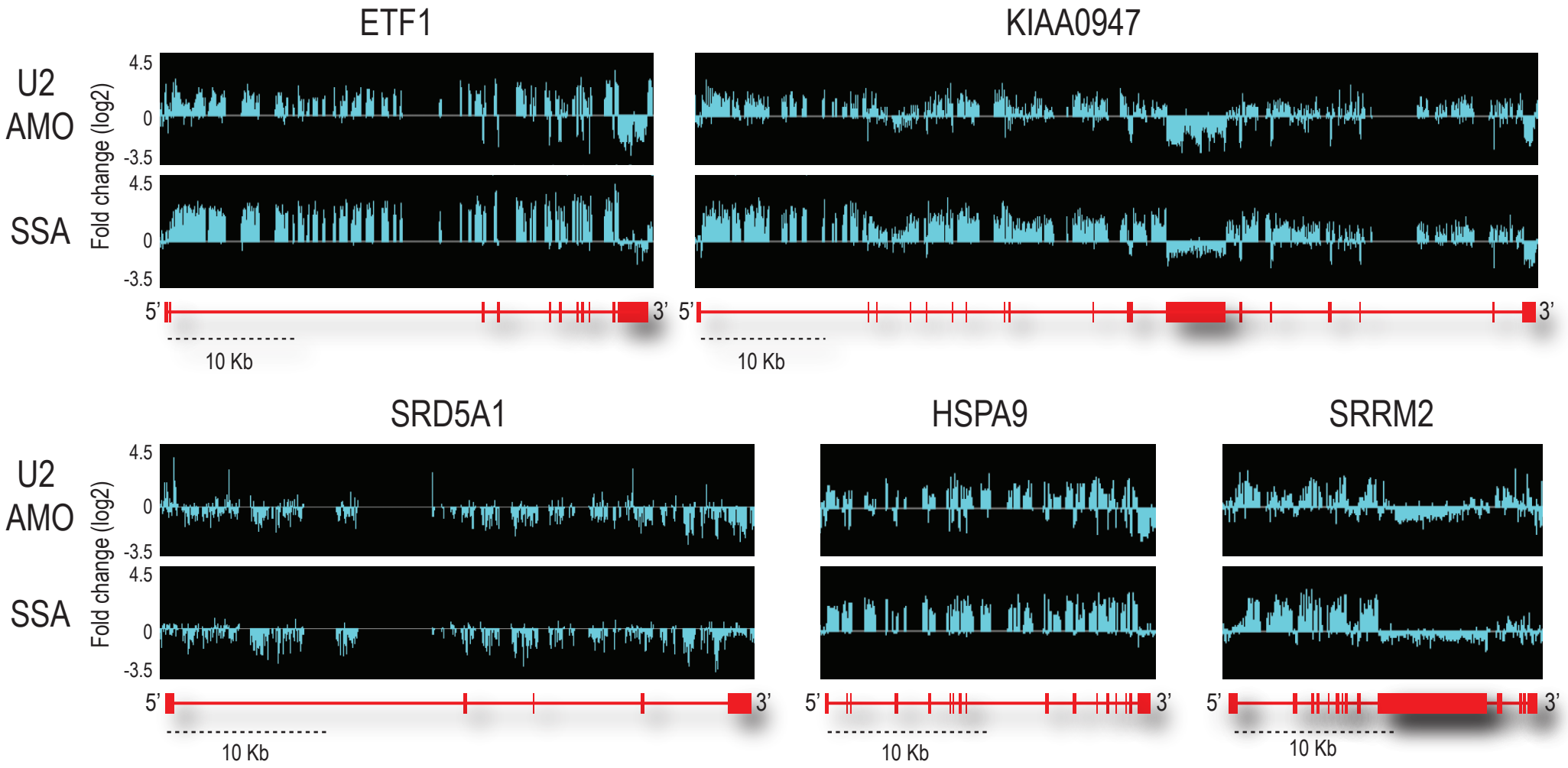
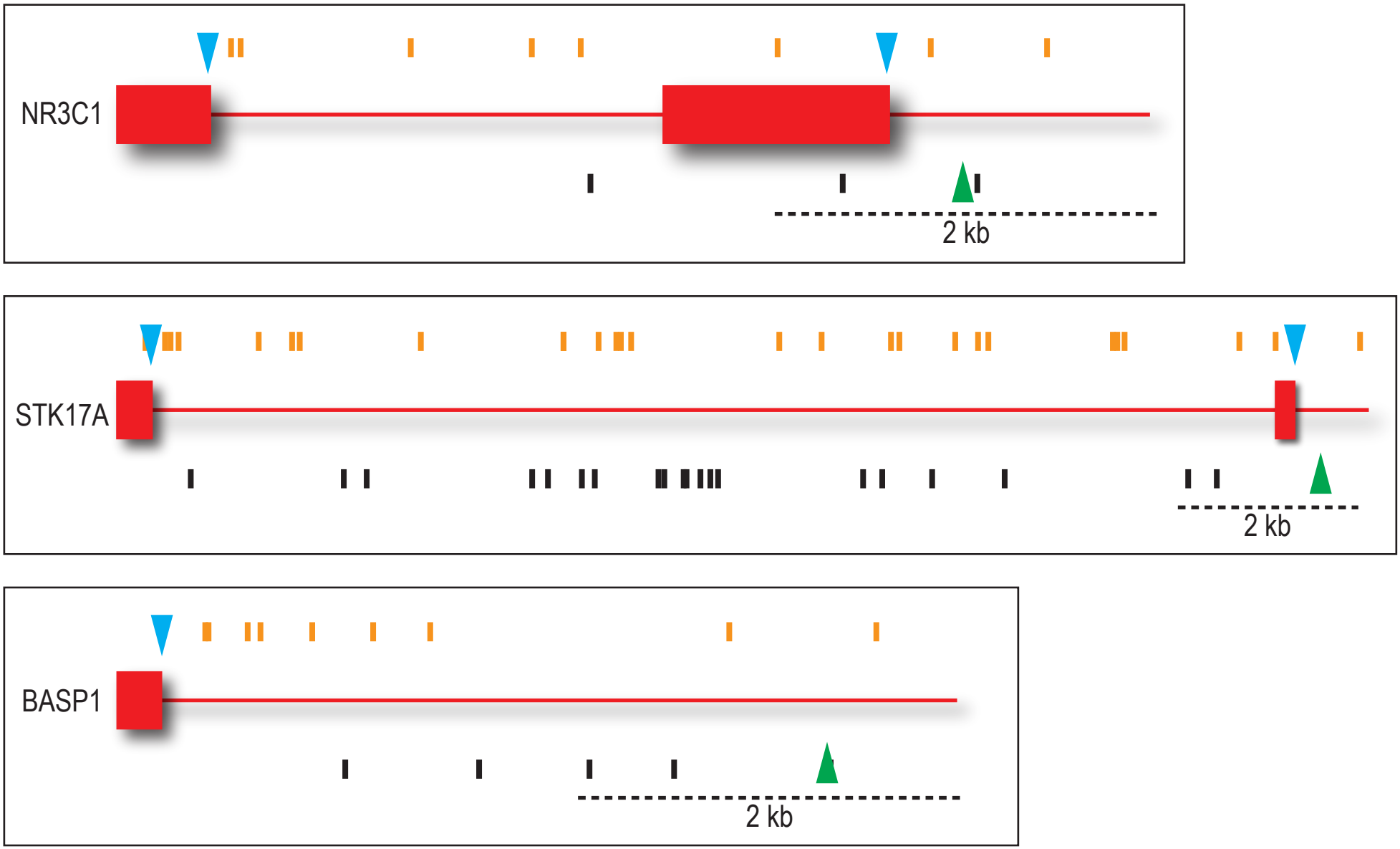


Supplementary Figure 1. Genomic tiling arrays identify unspliced pre-mRNAs with U2 AMO and spliceostatin A (SSA) treatment. RNA samples prepared from control, U2 AMOs-transfected cells (25 μM, 8 hrs) or SSA (100 ng/ml, 8 hrs)-treated cells were analyzed using genomic tiling array of human chromosomes 5, 7 and 16. Fold-changes of signal intensities of U2 AMO-transfected and SSA-treated cells compared to control cells are shown above the corresponding structure of each gene. Gene structures are depicted in red with lines indicating introns and boxes indicating exons.



Supplementary Figure 2. Predicted 5' ss and polyadenylation signals on three genes.

5' ss and polyadenylation signals were predicted using ESEfinder 3.0 (http://rulai.cshl.edu/cgi-bin/tools/ESE3/esefinder.cgi?process=home) and polyadq (http://rulai.cshl.org/tools/polyadq/polyadq_form.html) with default setting. Only high confidence 5' splice sites are depicted with orange lines above the gene structures. Gene structures are depicted in red with horizontal lines indicating introns and boxes indicating exons. Cyan arrow heads: canonical 5' splice sites; black lines: predicted polyadenylation signals; green arrow heads: polyadenylation signals used in U1 AMO-treated cells.

Supplementary text

We designed antisense morpholino oligo (AMO) for U1 snRNA that covers the first 25 nucleotides of U1 snRNA to inhibit binding between the 5' end of U1 snRNA and 5' splice site. AMOs of this length to U2, U12 and U6atac have been shown to interfere with the base pairing interaction between the snRNAs and pre-mRNAs and inhibit splicing of several test introns. The control AMO used in this paper consists of a 25 nt scrambled sequence.