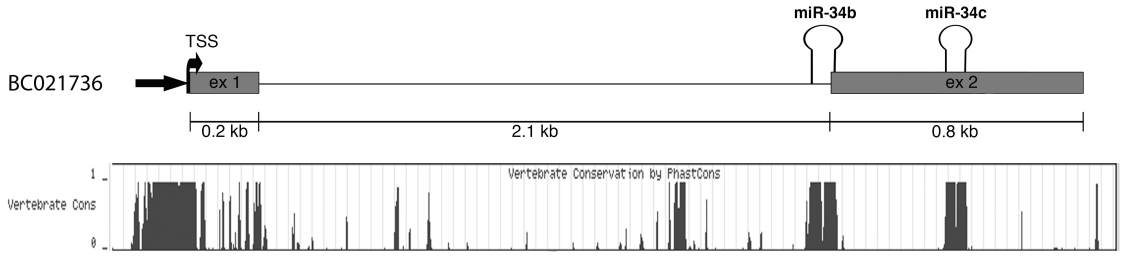
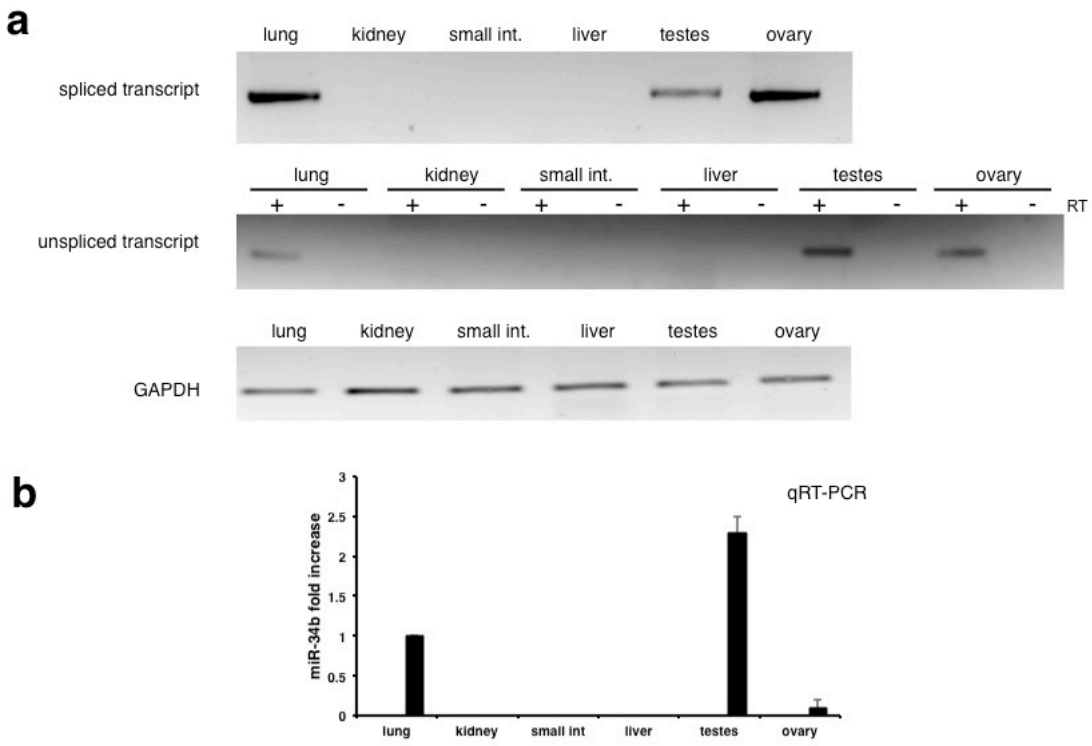
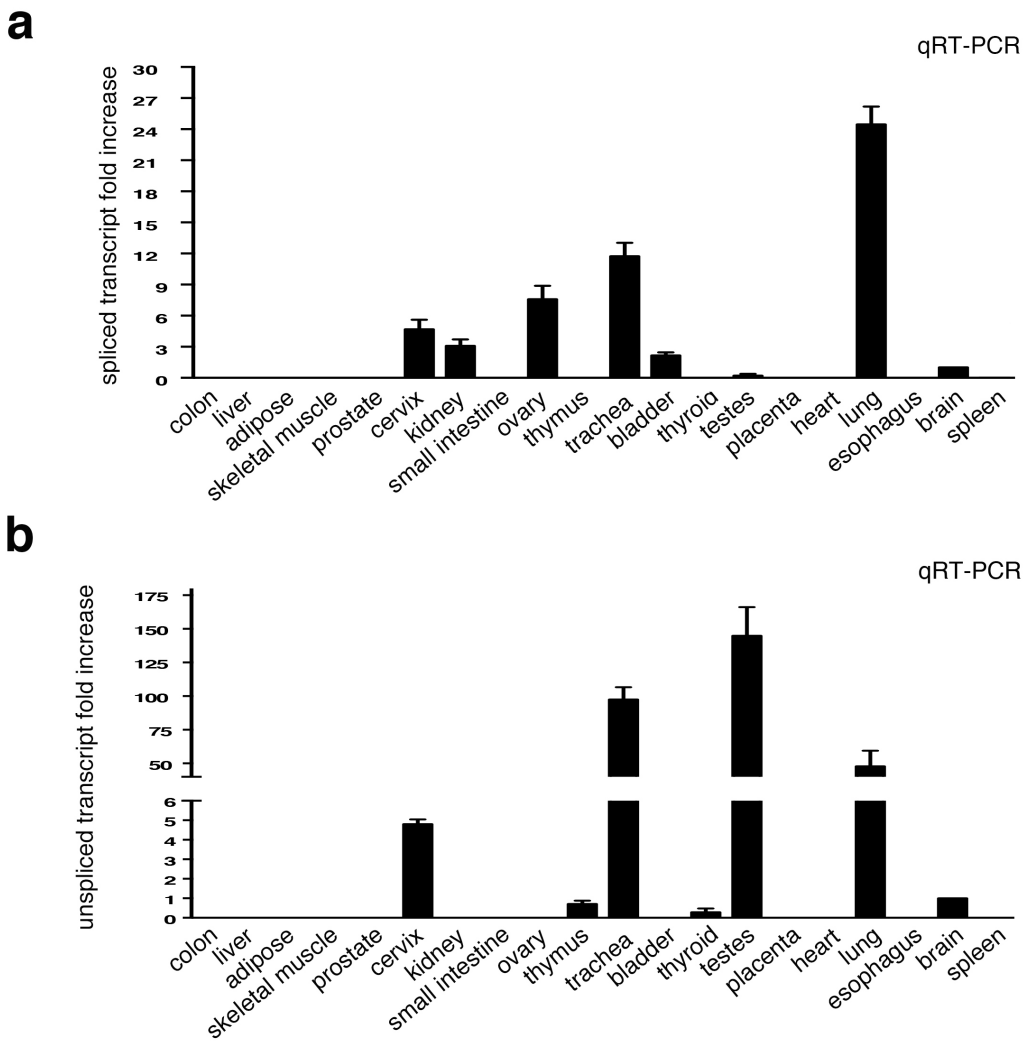


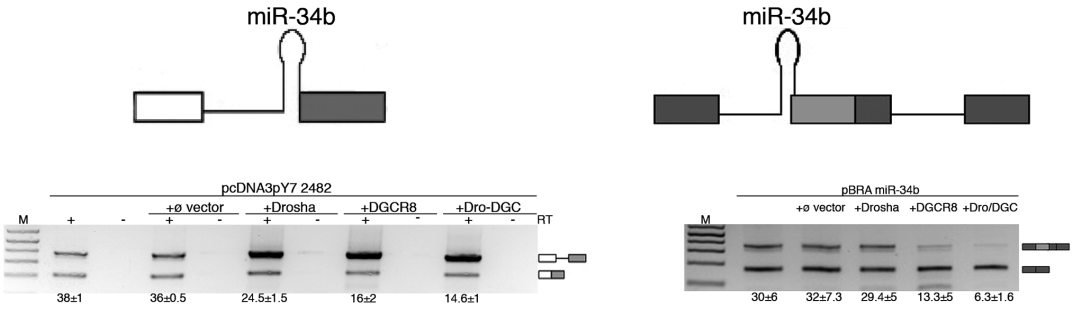
Supplementary Figure 1. Genomic locus and conservation of SO pri-miR-34b transcript. Schematic representation of pri-miR-34b transcript (BC021736) as shown in http://genome.uscs.edu/. The promoter (black arrow on the left) and the transcription start site (TSS) are indicated. The length (in kb) of the transcript is shown below the scheme. The bottom panel represents the conservation of the gene in vertebrates.



Supplementary Figure 2. SO pri-miR-34b spliced and unspliced transcript and mature mmu-miR-34b abundance in mouse tissues. a) Analysis of the spliced and unspliced transcripts in six mouse tissues. RT means reverse transcriptase. **b)** The histogram shows the quantitative PCR analysis of mmu-miR-34b, normalized for GAPDH. The values are expressed as fold increase compared to lung, set to 1.



Supplementary Figure 3. Quantitative analysis of spliced and unspliced miR-34b transcripts in human tissues. qRT-PCR analysis of the spliced **(a)** and unspliced **(b)** isoforms of miR-34b transcript in human tissues. Values are normalized for the GAPDH and are indicated as fold increase compared to brain, set to 1. No transcripts were detected in samples without reverse transcriptase. The corresponding RT-PCR profiles, loaded on agarose gels, are provided in Figure 2a.



Supplementary Fig. 4 Overexpression of Drosha and DGCR8 decreases splicing efficiency. RT-PCR analysis of pcDNA3pY7 2482 (left panel) and pBRA miR-34b (right panel) after co-transfection with an empty vector, Drosha or/and DGCR8 in HeLa cells. Band identity is shown on the right. The numbers below the panel indicate the percentage of splicing (for pcDNA3pY7 2482) and exon inclusion (for pBRA miR-34b) ± st.dev.