Interplay Between pre-mRNA Splicing and microRNA Biogenesis

within the Supraspliceosome

Lily Agranat-Tamir[1], Noam Shomron[2], Joseph Sperling[3] and Ruth Sperling[1]

Supplementary Data

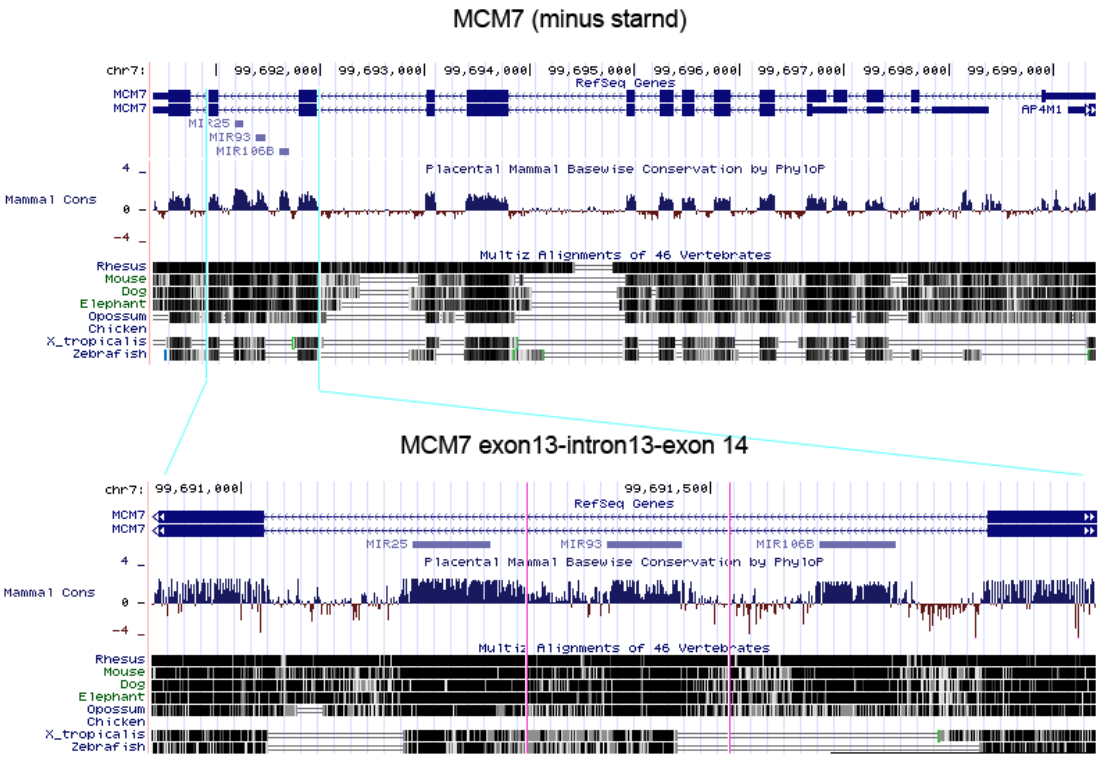

Figure S1. Conservation of the Sequences of the miR-106b-25 cluster (sequences taken from the UCSC genome browser).

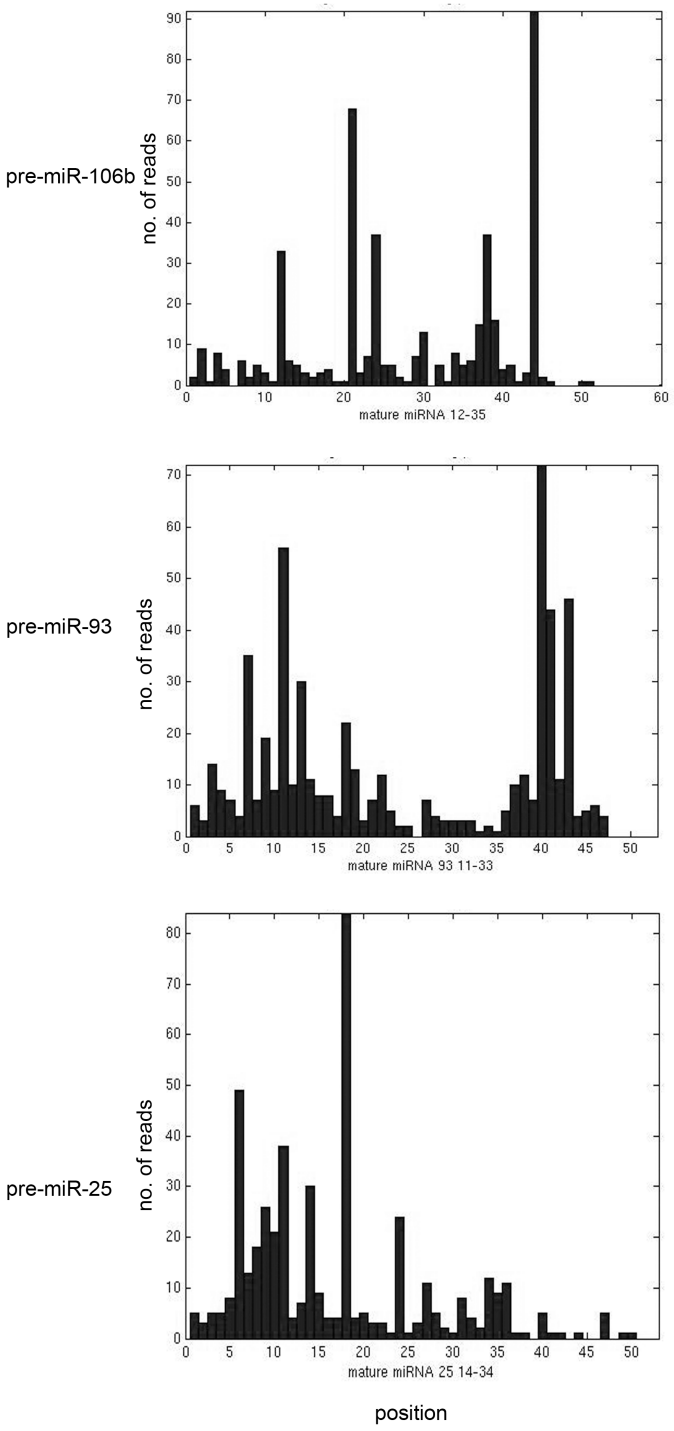

Figure S2. Read starts of pre-miRs 106b, 93 and 25. Results of deep sequencing of small RNA from supraspliceosome fractions.

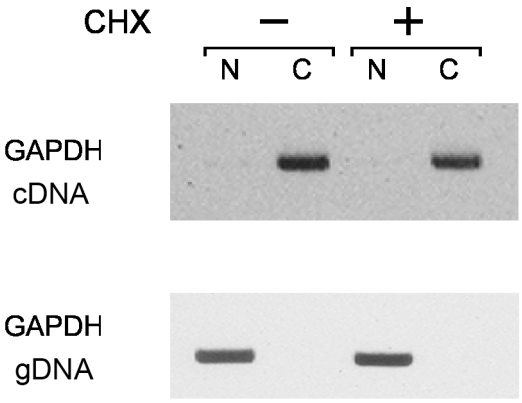

Figure S3. Fractionation into Nuclear and cytoplasmic fractions. Negative and positive controls for the fractionation depicted in Figure 4. GAPDH mRNA is found in the cytoplasmic fractions, while GAPDH DNA is found in the nuclear fractions. HeLa cells, either treated (+) or untreated (-) with 50 µg/ml cycloheximide (CHX) for 2 hours, were fractionated into nuclear and cytoplasmic fractions. RT-PCR analysis of GAPDH mRNA (upper panel); and PCR of GAPDH gDNA (lower panel).