Figure S4. evolving miRNAs in the rat mir-463 cluster. A) Divergence of miRNAs that are almost fully conserved in mouse. Some seed regions in these miRNAs have altered while the largest part of the miRNA sequences have been conserved. Grey planes highlight conserved sequence. hp: hairpin structure (matching brackets () indicate matching ribonucleotides in a hairpin, a dot is an unmatched ribonucleotide). pre: precursor DNA sequence. clo: cloned miRNA sequence from rat. B) The miRNAs from A reside within this testis-specifically expressed miRNA cluster. This cluster is highly conserved in mouse: all miRNAs that are emphasized with ‘M’ have been observed in mouse, in the identical order. ND: not detected. dM: miRNAs from A, diverged seed sequence in mouse. Coordinates and orientation are in the top right corner. The numbers between the blocks indicate the distance (bp) between each miRNA locus. The barplots above and under each block represent the miRNA-3’ and 5’ arm read frequency, respectively. The height reflects the normalized linear read frequency in arbitrary units. All tissues are shown, these miRNAs are substantially over-represented in testis.