



Figure S2: Conservation profiles of *C. elegans* miRNAs. Conservation profiles were calculated by determining the nucleotide conservation between *C. elegans* miRNA hairpins and their orthologous sequences in *C. briggsae* A), *C. remanei* B) and *P. pacificus* C). The cumulative nucleotide conservation rate was determined by aligning the conservation profiles on the start of the mature miRNAs. miRNAs were separated into two groups according to whether they originated from the 5' or the 3' arm of the miRNA hairpin (left and right). Dark red bars indicate the position of the canonical 22 nt miRNA.