Figure S1: The Phylogenetic tree by RNApdist using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) for the four RNA classes (5S rRNA, miRNA, RNaseP arch and tRNA).

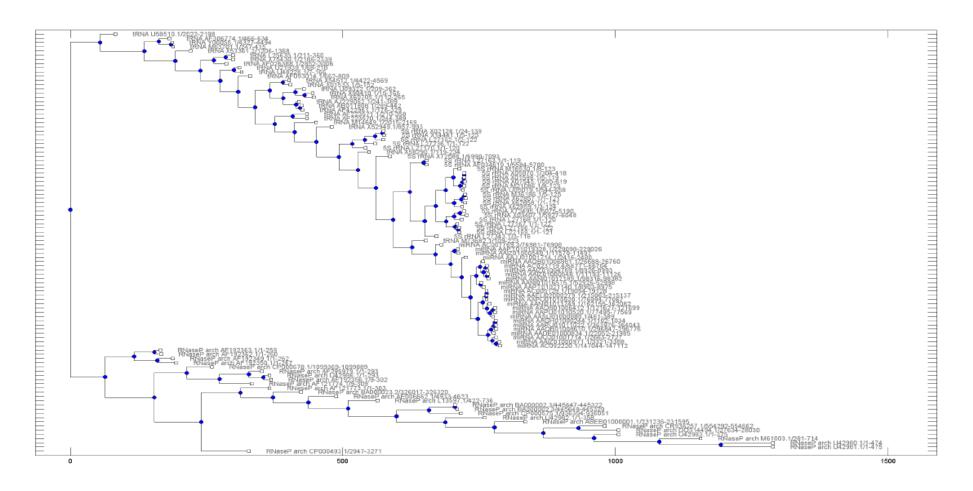
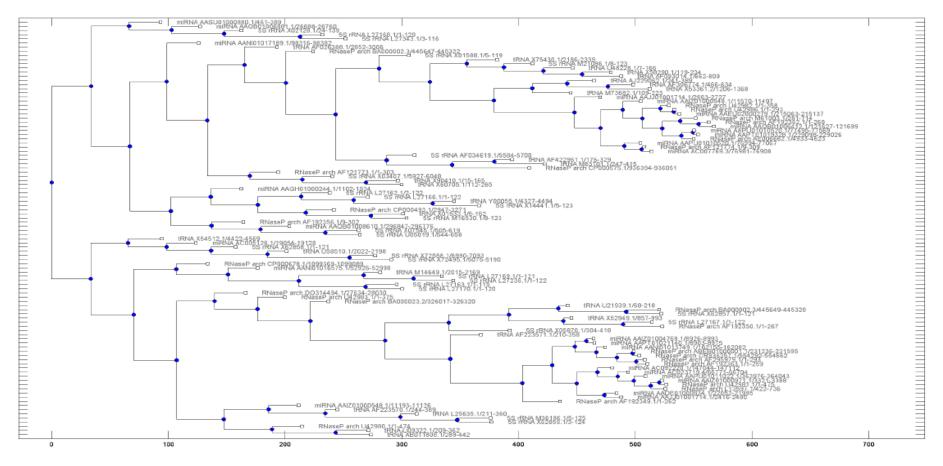


Figure S2: The Phylogenetic tree by RNAdistance using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) for the four RNA classes (5S rRNA, miRNA, RNaseP arch and tRNA).



RNApdist RNAmscTV-curve Wild type RNAdistance G21A G7C C41G 1 GGAU Wild type RNApdist RNAmscTV-curve RNAdistance G19A G19C G19C 2 Wild type RNApdist RNAmscTV-curve RNAdistance G43C C14A C6A 3 RNApdist Wild type RNAmscTV-curve RNAdistance C4A G35C C4A

Figure S3: Largest structure mutation for 21 RNA Ribosomal sequences using RNAmscTV-Curve, RNAdistance and RNApdist

