Dengue Virus (DENV) is a positive-sense RNA flavivirus, oscillating between its human host and the *Aedes* mosquito vector. The World Health Organization lists DENV as a neglected tropical disease and a global health challenge. We sought to identify conserved RNA sequence and structural elements within the coding-region of the viral genome to determine their potential to regulate the viral life cycle within mammalian and mosquito cells. Whole-genome sequence alignments were generated using Clustal Omega with representative viral sequences from the three major serogroups within the Flavivirus family (DENV1-4, Japanese Encephalitis Virus [JEV] and Tick-Borne Encephalitis Virus [TBEV]). Based on sequence alignments, we searched for regions of homology above a 70% threshold, when compared to background sequences. Using RNAalifold, modified alignments from each serogroup were folded into predictive RNA secondary structures based on their conservation within the serogroup. With these bioinformatic approaches, we identified several conserved RNA elements within the DENV genome but to characterize whether candidates have regulatory function, we designed mutant constructs that would disrupt the predicted secondary structure or primary nucleotide sequence without altering the reading frame, amino acid R groups and adjacent secondary structures while taking into account codon usage bias in both cell lines. Introducing mutations into our candidate RNA elements will determine their impact on the viral life cycle in mammalian and mosquito cell lines. These studies are critical to our understanding of the DENV viral life cycle, which may lead to the identification of new antiviral targets to address this ongoing and neglected epidemic.