Fig. 3.17. Alignment of the 5’UTR between the MBFV. The annotated features include the elements of the secondary structures that are depicted in Fig. 3.16B:

**Stem 0** – the boundaries of sequences for Stem 0 are specified by black lines and joined by bi-directed dotted oval arrows to show that they interact with each other to form a stem.

**Loop 1** - the boundaries of sequences for loop1 (emboldened blue and underlined) are specified by blue lines.

**CYCL** – 8-nucleotide sequence that comprises the circularization domain and as inverted repeat is presented in the 3’UTR.

**Circularization** – other sequences ie in addition to CYCL, that interact with the 3’UTR are depicted by the emboldened brown underlined letters.

**Initiation codon** is specified by arrows.

**Replicon** – the arrow shows the maximal deletion that was introduced into the Kunjin virus genome to produce a viable replicon (Khromykh and Westaway, 1997)

Positions of absolute conservation are highlighted in blue and transitions in green.