



**Supplementary Fig. 1.** The nucleotide diversity index (Pi), the average number of nt differences per site, was calculated along the genome using a sliding window of 100 nt moved by steps of 25 nt after alignment of RNA1 (A), RNA2 (B), and RNA3 (C) of three complete beet soil-borne virus (BSBV) sequences. Genomic organization of BSBV RNA1, RNA2, and RNA3 are shown below the graphs.