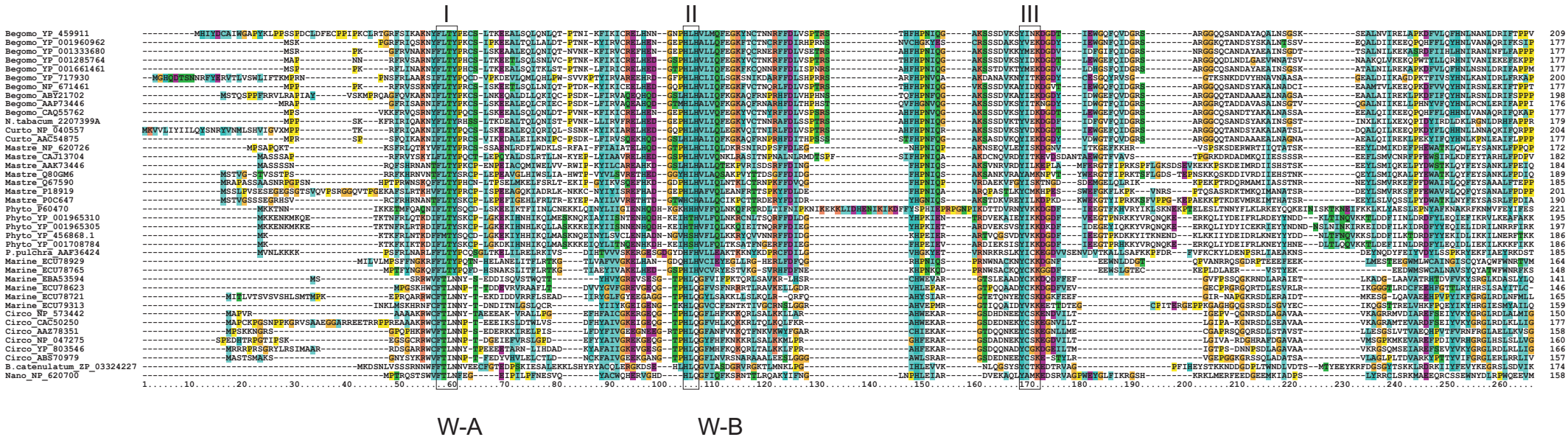

Figure S1. Multiple sequence alignment of 40 RCR Rep proteins. The five motifs conserved in geminiviral Reps are boxed. W-A, Walker A motif; W-B, Walker B motif. The alignment was constructed using CLUSTALW [1] and then edited manually.

Reference:

1. Thompson JD, Higgins DG, Gibson TJ: **CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice**. *Nucleic Acids Res*. 1994 **22**:4673–4680.