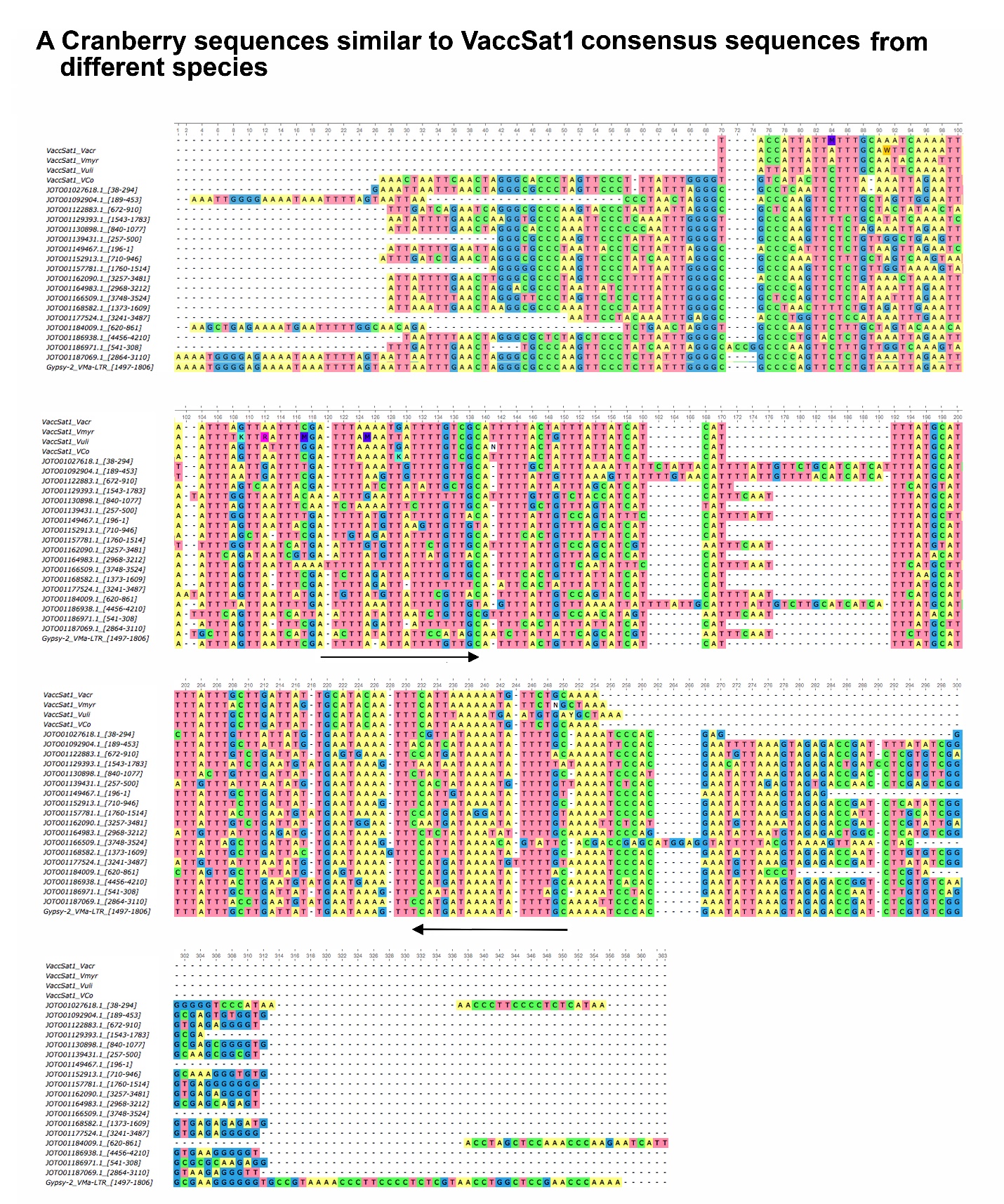
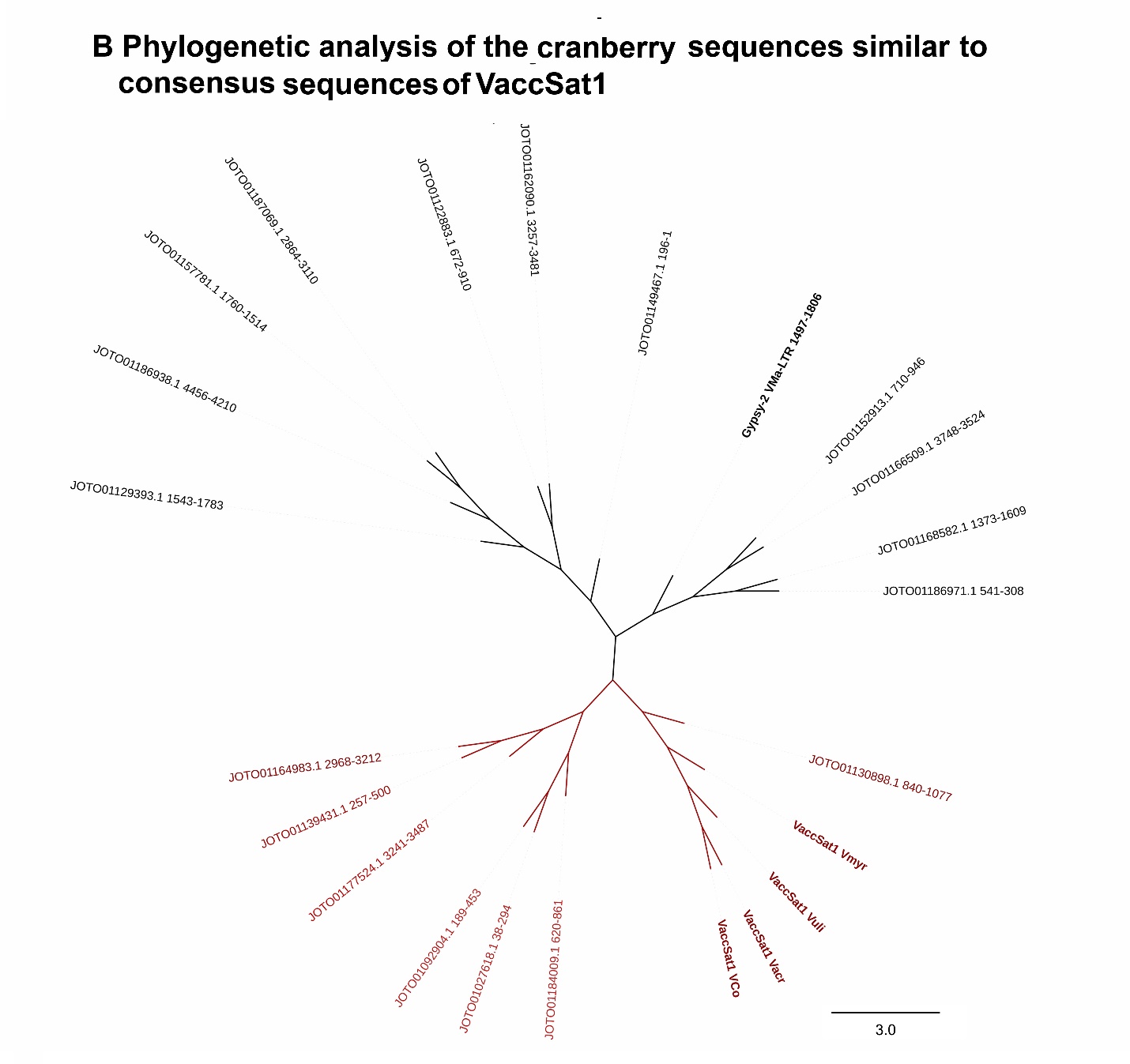
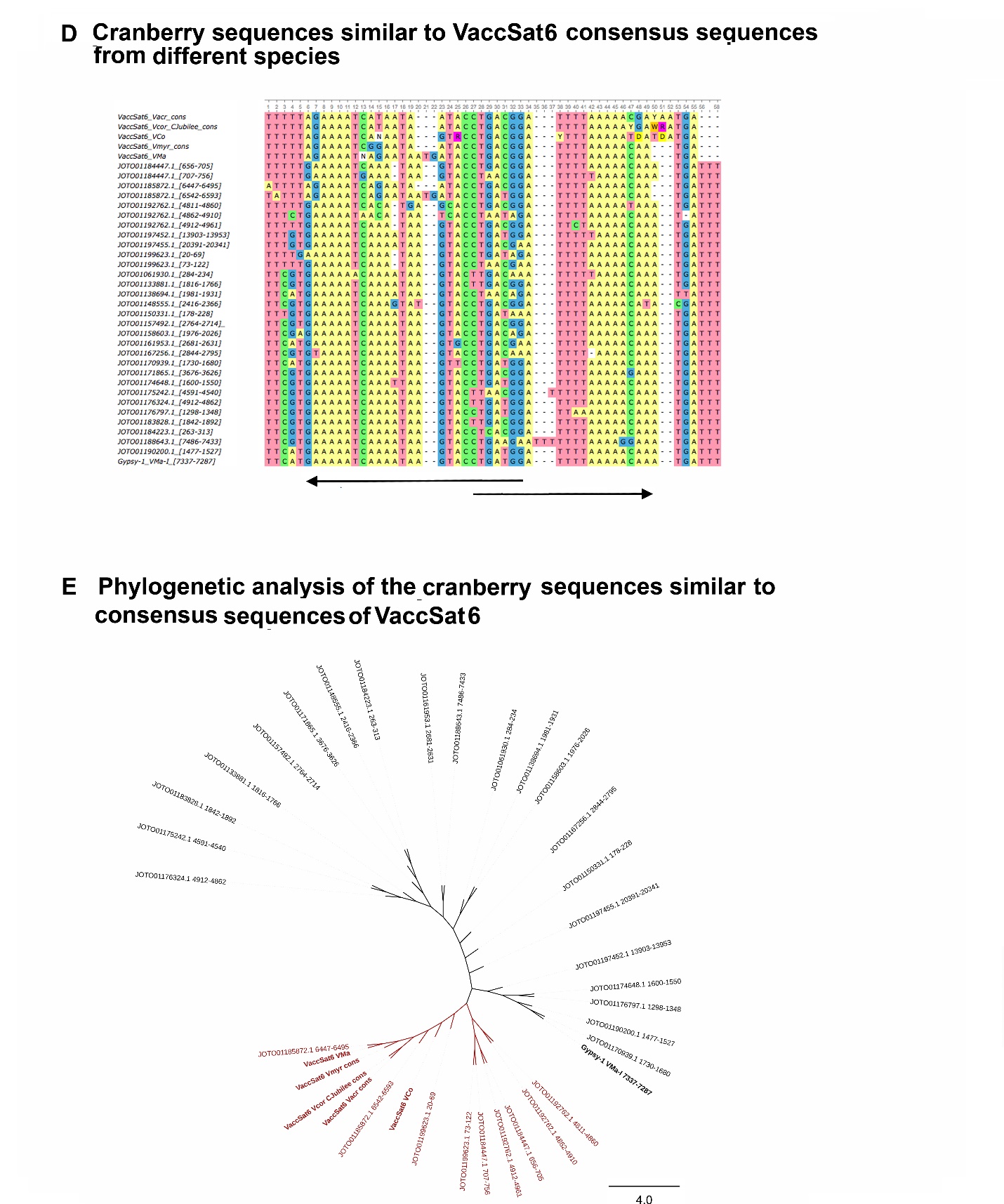
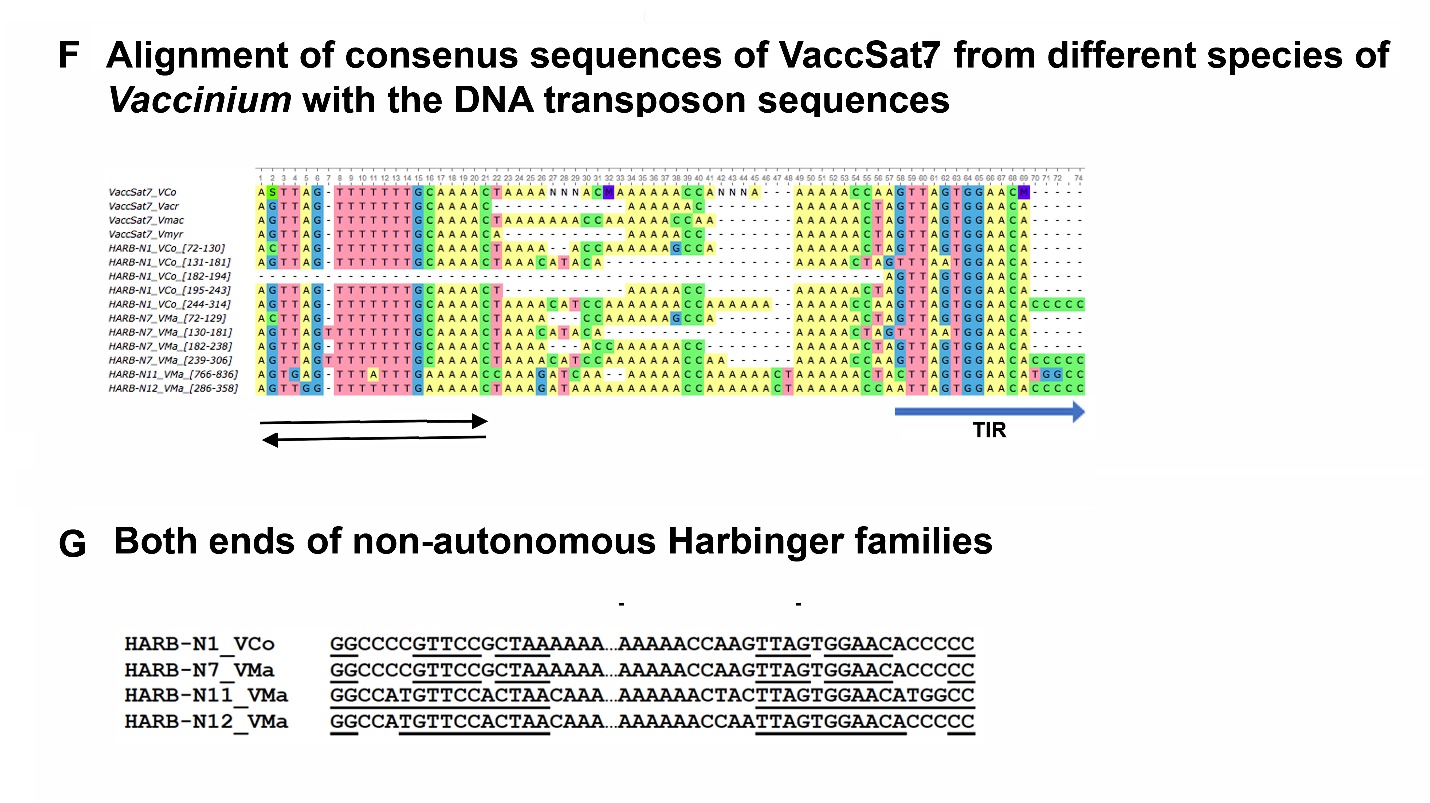
**Supplementary Figure S7: Similarities between satellite repeats and TEs**











**Supplementary Figure 7: Similarities between satellite repeats and TEs.** The consensus satellite repeats name are VA = *V. arctostaphylos*, VC = *V. corymbosum* cultivar ‘Jubilee’, VC-W8520 = *V. corymbosum* strain ‘W8520’, VM = *V. myrtillus* and VU = *V. uliginosum*, VMAC = *V. macrocarpon* cultivar ‘Ben Lear’.(A) Multiple sequence alignment of cranberry sequences similar to VaccSat1 with both 50-bp flanking sequences are aligned with the VaccSat1 consensus sequences from different *Vaccinium* species and a part of *Gypsy-2\_VMa-LTR*. The start positions of the repeat units were chosen to maximize the number of aligned nucleotides. (B) Dendrogram based on maximum Parsimony method from the consensus sequences of VaccSat1 and *Gypsy-2\_VMa-LTR* with the cranberry sequences showing the seperation of two sequence groups (one group with VaccSat1 and the other with *Gypsy-2\_VMa-LTR*). (C) Multiple sequence alignment of VaccSat3 consensus sequences with the different families of DNA transposon sequences from the *V. corymbosum* and *V. macrocarpon* (cranberry) genome showing the similarities among them. (D) Multiple sequence alignment of cranberry sequences along with a part of internal portion of *Gypsy* LTR retrotransposon with the consensus sequences of VaccSat6 satellite repeats from different *Vaccinium* species. (E) The Maximum Parsimony-based dendrogram groups the VaccSat6 consensus with an internal portion of the *Gypsy* LTR retrotransposon and other sequences of cranberry genome. (F) Multiple sequence alignment of consensus VaccSat7 sequences from different *Vaccinium* species along with the Harbinger DNA transposon of *V. corymbosum* and *V. macrocarpon* genome. The blue arrow indicates the partial terminal inverted repeat (TIR). (G) Multiple sequence alignment of the sequence regions flanking the Harbinger families with identity to VaccSat7. The 5’ and 3’TIR of the Harbinger families is shown by a black underscore. Multiple sequence alignment of each satellite repeat and TEs are marked with forward orientated black arrows for forward primer binding sites and reverse oriented back arrows for reverse primer binding to show the polymorphism in homogeneous primer binding regions.