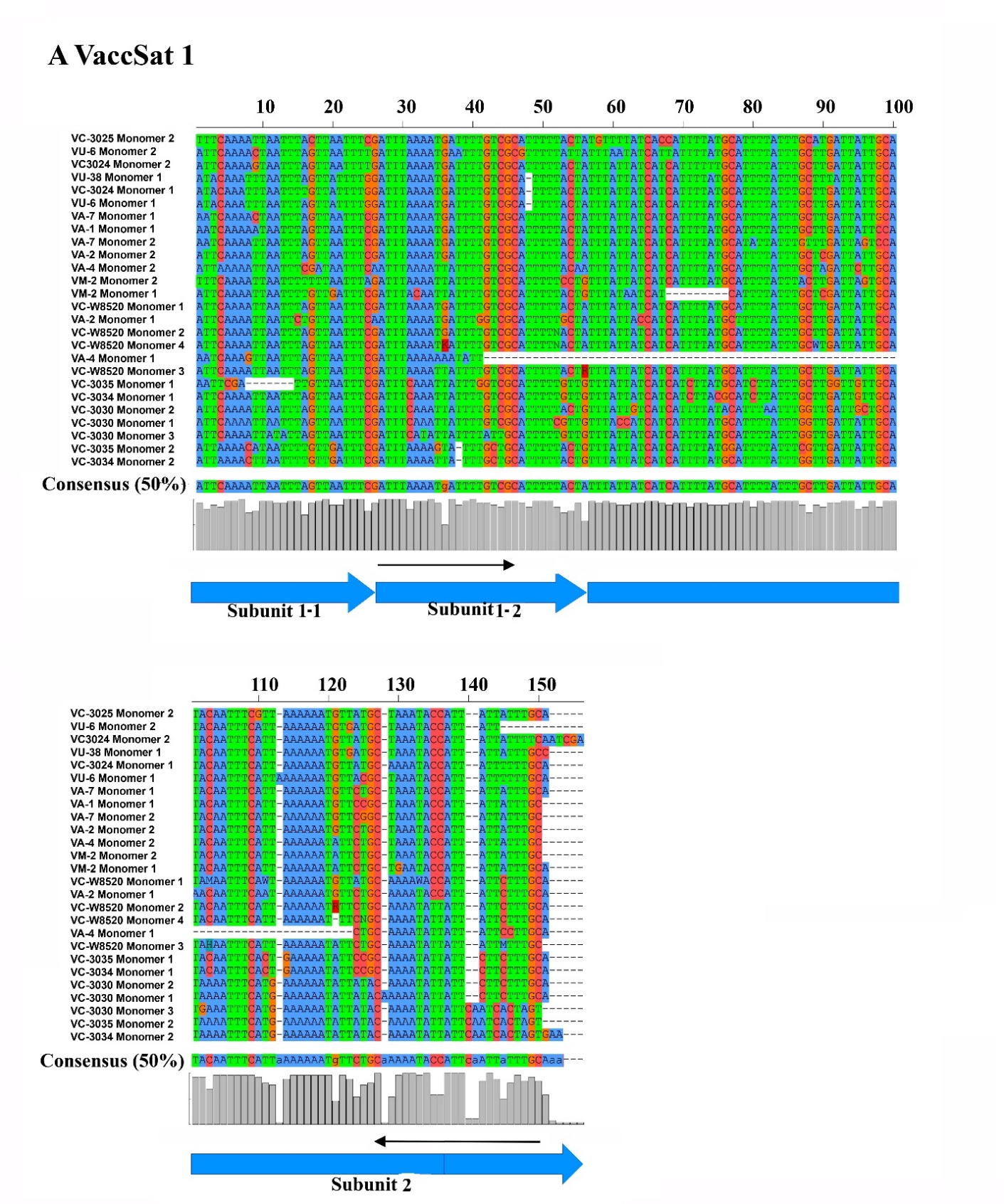
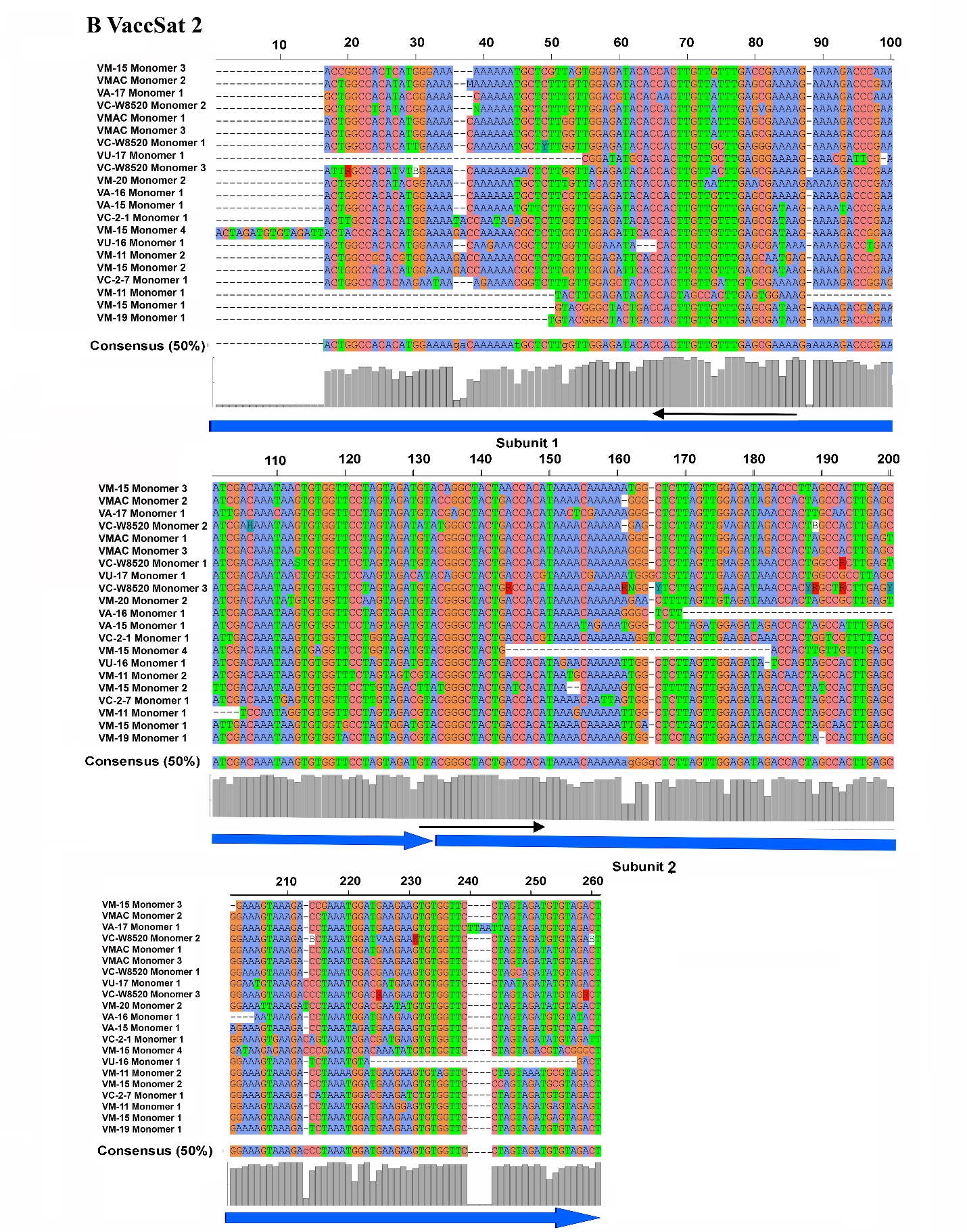
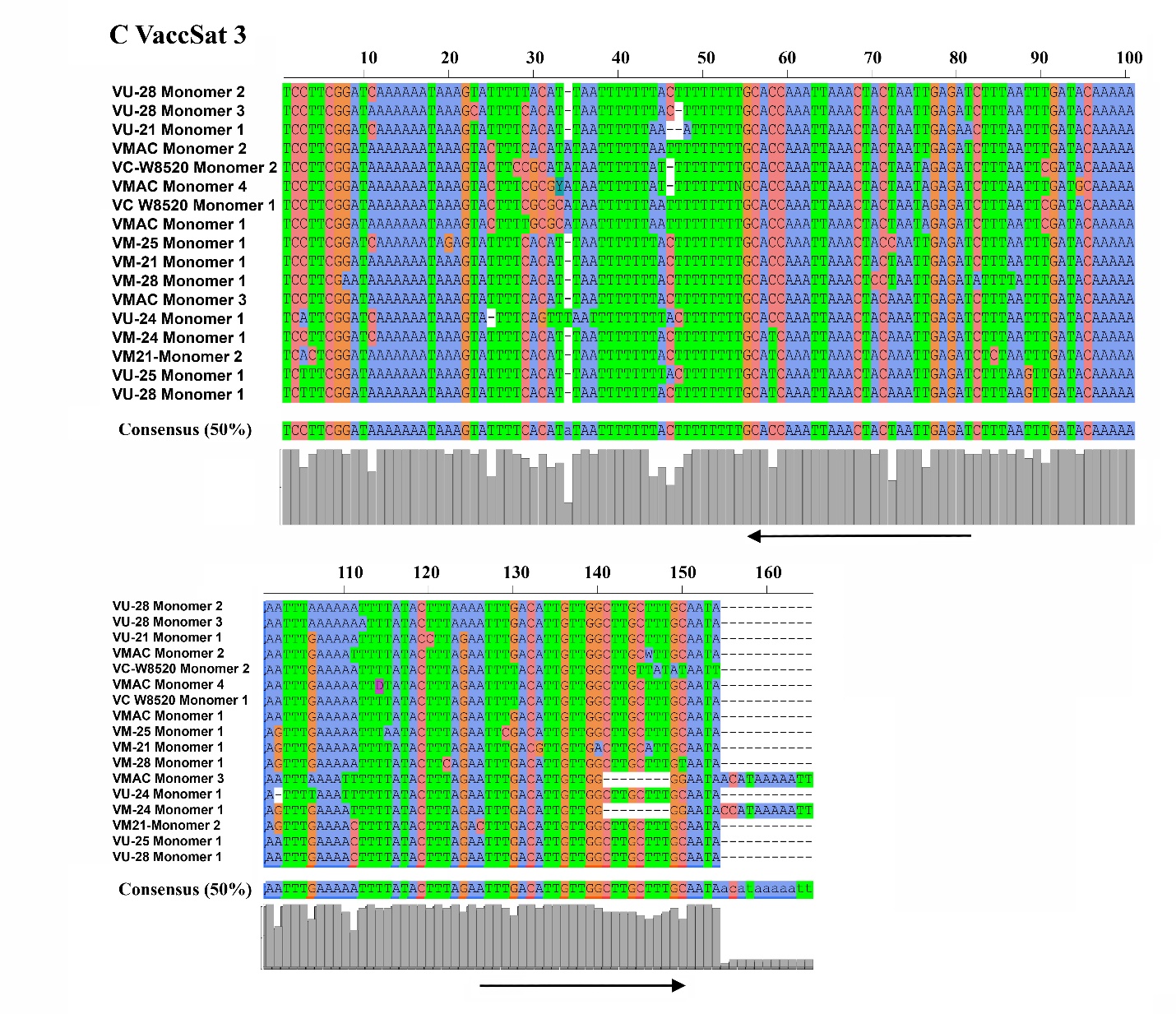
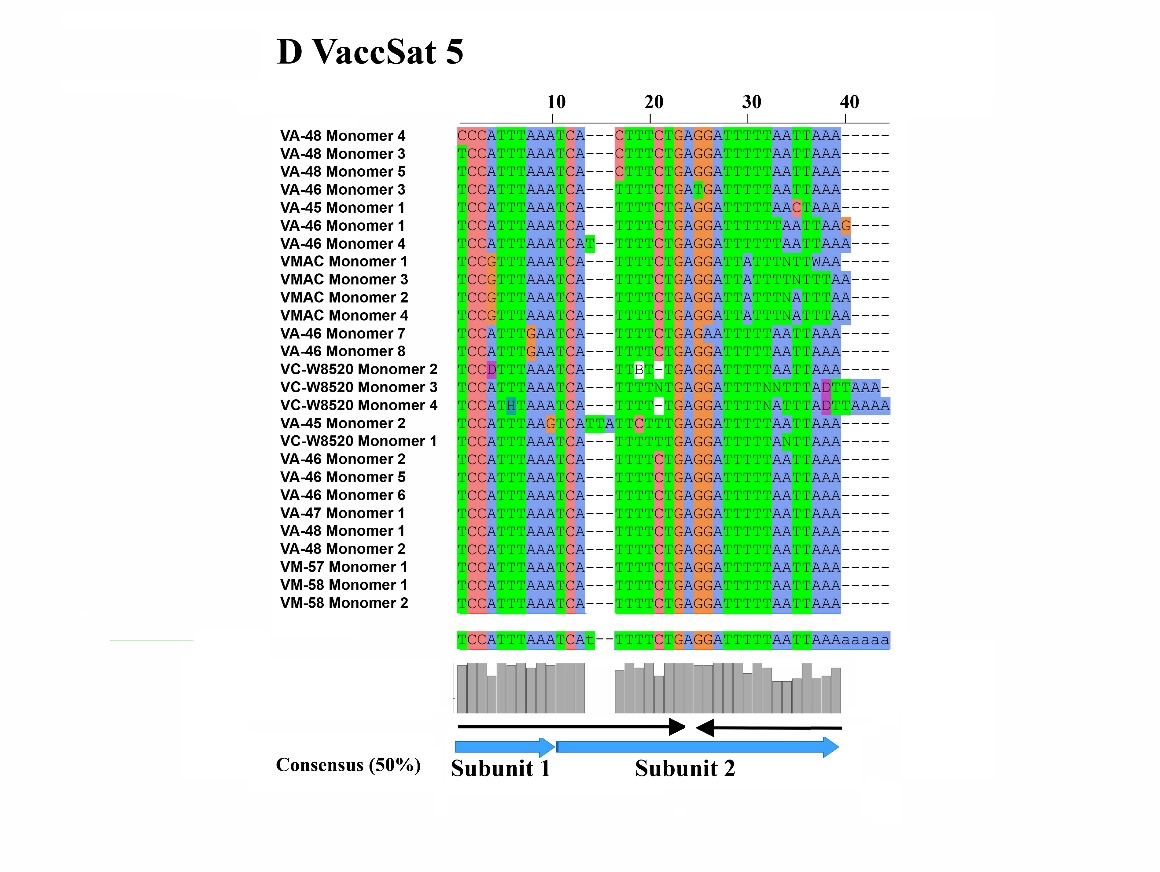
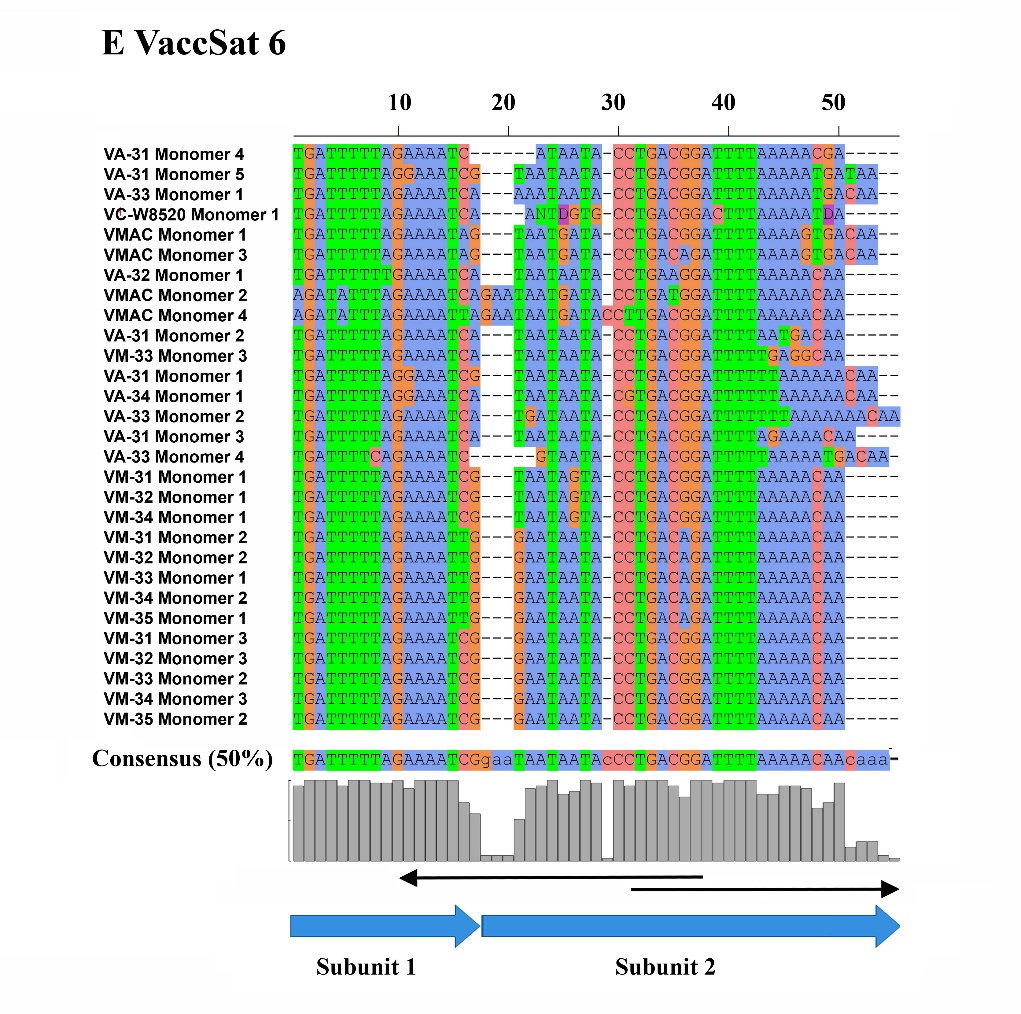
Supplementary Figure S4: Multiple sequence alignment of full-length monomer sequences from different *Vaccinium* species of six satellite repeats

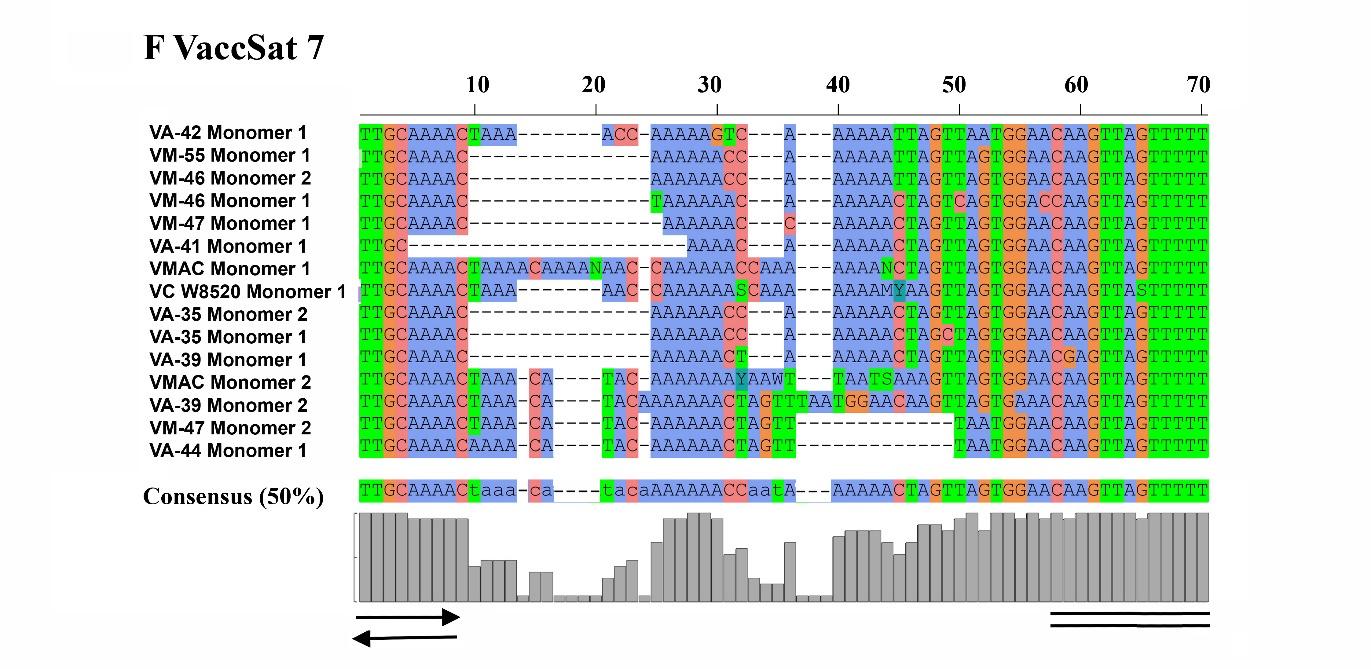












**Figure 4. Multiple sequence alignment of full-length monomers of *Vaccinium* satellite from different *Vaccinium* species.** (A-C) VaccSat 1-3, (D) VaccSat 5, (E) VaccSat 6 and (F) VaccSat 7. VA = *V. arctostaphylos*, VC = *V. corymbosum* cultivar ‘Jubilee’, VC-W8520 = *V. corymbosum* strain ‘W8520’ (reference sequence), VM = *V. myrtillus* and VU = *V. uliginosum,* VMAC = *V. macrocarpon* cultivar ‘Ben Lear’ (reference sequence). Four nucleotide bases are colored with four different colors (A blue, T green, C red and G orange). Gaps in the multiple sequence alignment were denoted as dashes (-). Consensus sequences with at least 50% conservation are shown below each alignment. Satellite subunit structures were shown below with thick blue arrows for *Vaccinium* satellites VaccSat1, VaccSat2, VaccSat5 and VaccSat6. For each satellite repeat forward primer binding sites are marked with forward orientated black arrows and reverse primer binding sites are shown with reverse oriented black arrows and shown the polymorphism in the primer binding site.