



**Figure S1.** Unrooted Maximum-Likelihood phylogenetic tree of the terminal repeat sequence of mmr-b based on the substitution model TPM2u+F+I+G4. Terminal repeats identified in this study (Hap A – Hap H in bold in the tree) and available sequences for other species of the *B. plicatilis* species complex were used. Node values represent SH-aLRT support (%)/aBayes support/ultrafast bootstrap support (%). Nodes with an ultrafast bootstrap support lower than 50 % have been collapsed.