



Fig. S3. Relationships of triploid *S. bicolor* in clade III. a) RAxML phylogeny based on 16,463 concatenated RAD loci and 97,576 SNPs, respectively. *S. reticulata* was used as outgroup to root the tree. Bootstrap support values below and QS support values above branches. Triploid *S. bicolor* is highlighted in a blue box b) Genetic structure analyses based on 16,104 unlinked SNPs for most likely K=4. c) Splitsgraph of the NeighbourNet analysis of clade III, bootstrap values given at branches.