

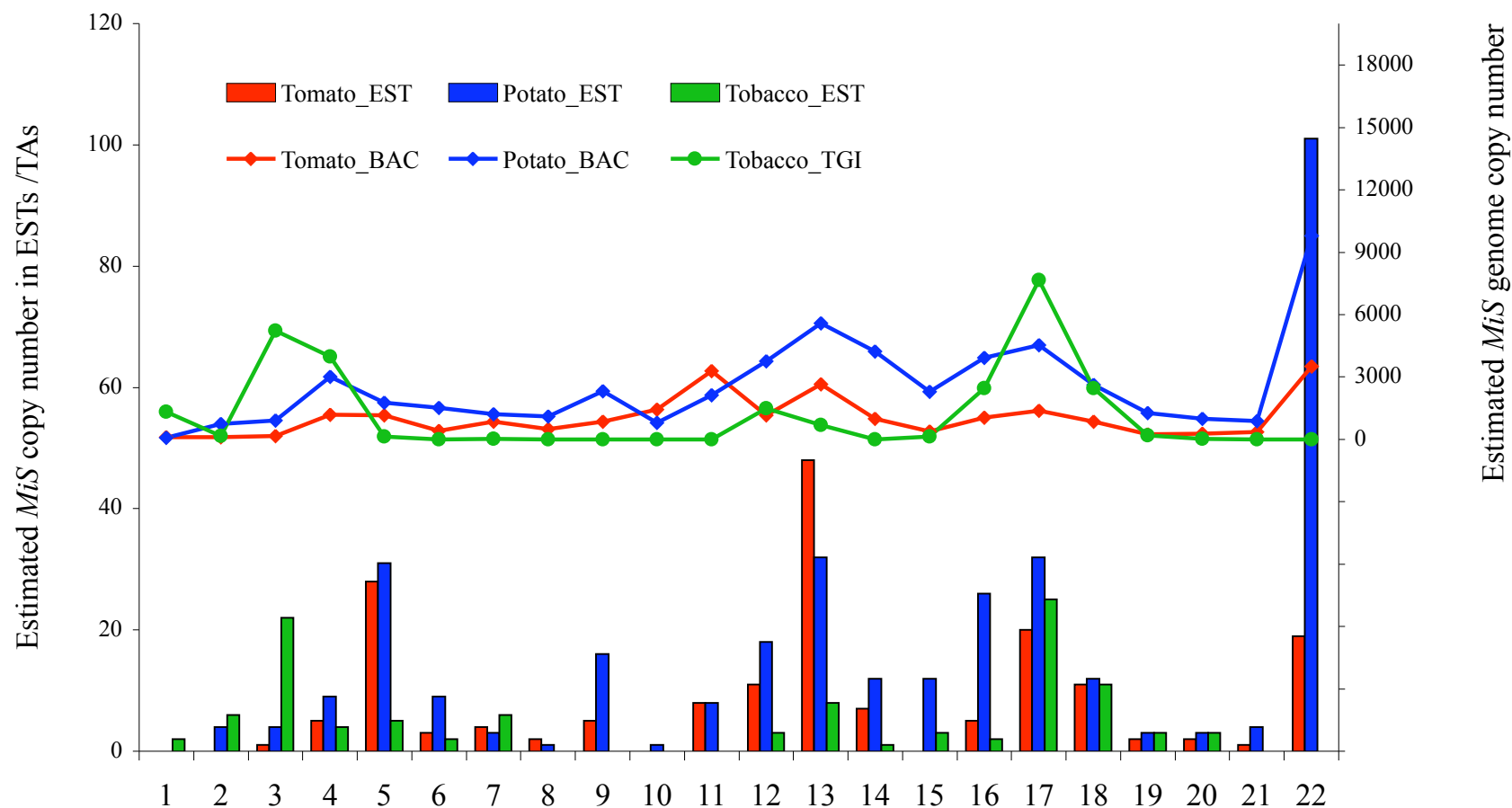


Figure S1. Comparison of estimated abundance MiS copy number in Solanaceae geneomes. MiS sequences. Upper lines chart the number of ESTs detected of each MiS family in tomato (red), potato (blue) and tobacco (green) databases. Filled bars represent the estimated copy number of each MITE family in genomic tomato (red), potato (blue) and tobacco (green) DNA. The number of MiS-ESTs/TAs are indicated in the leftward-Y axis and estimated copy numbers of MiS in genomic DNA are indicated in the rightward-Y-axis.