



Figure 3. (a) Phylogenetic network inferred by Treemix of the relationships among *Phellinus noxius* populations with eight migration edges that explain 99.8% variance in the model. The migration edges are numbered from 1 to 8 reflecting the order in which they were added to the model. **(b)** f index representing the fraction of the variance in the sample covariance matrix accounted for by the model covariance matrix as a function of the number of modelled migration events. For populations abbreviations see Table S1.