



Figure 3: Pairwise Fst/(1-Fst) heatmap of the Fst values between the 12 sampling sites of *Mesonauta festivus* in the Amazon basin. Fst values were estimated using the *stamppFst* function in *R* with 100 bootstraps and assuming 4 genetic clusters. Fst values represent the genetic differentiation between each pair of sites, a value of one meaning that the populations are completely differentiated and a value of zero meaning that they are identical. Sites were ordered according to their watershed of origin. For BAR, CAT, JAR, MAN, CEM, BRA, TEF, SOL and PIR (n = 20), for ANA (n = 19), and for JAC and NEG (n = 16).