



Figure 3: Pairwise $F_{ST}/(1-F_{ST})$ heatmap of the F_{ST} values between the 12 sampling sites of *Mesonauta festivus* in the Amazon basin. F_{ST} values were estimated using the *stamppFst* function in *R* with 100 bootstraps and assuming 4 genetic clusters. F_{ST} 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 ($n = 16$).