**Read Me File**

The sequence file contains all sequences that remained after quality control and that were used in this manuscript to cluster MOTUs. Each sequence name starts with a species abbreviation (Paur = *P. auritus*, Mbec = *M. bechsteinii* and Mnat = *M. nattereri*) followed by an underscore and a field ID (all sequences with the same field ID belong to the same individual) followed by a second underscore and a sequence ID.