

Fig. S1. The complete Bayesian tree of *Microtus* species as inferred from the *cytb* data on 229 specimens in MrBayes. The designations are as in Fig. 2.

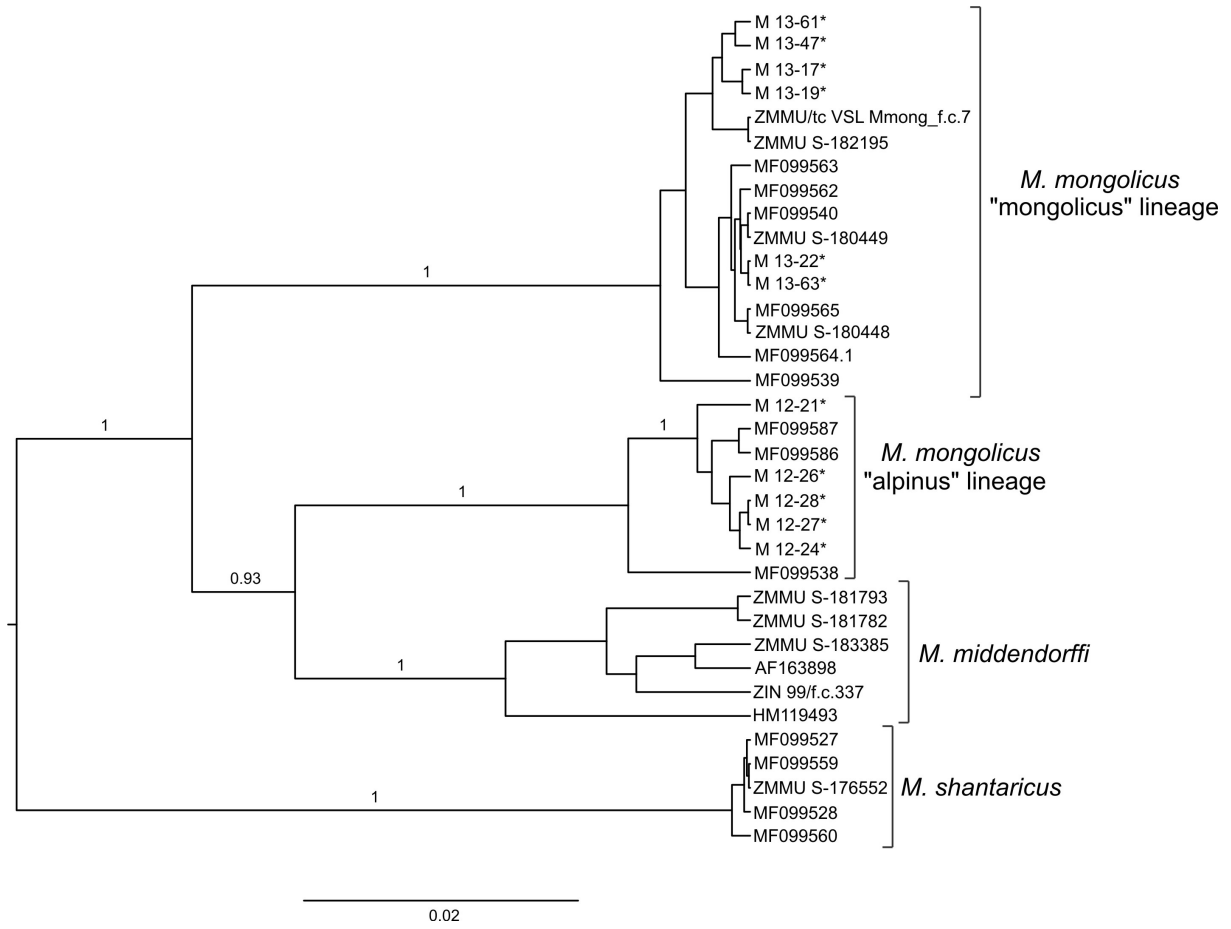


Fig. S2. The fragment of the Bayesian ultrametric tree illustrating the relationships among the haplogroups of *M. maximowiczii* including short sequences not shown in Fig. 2.

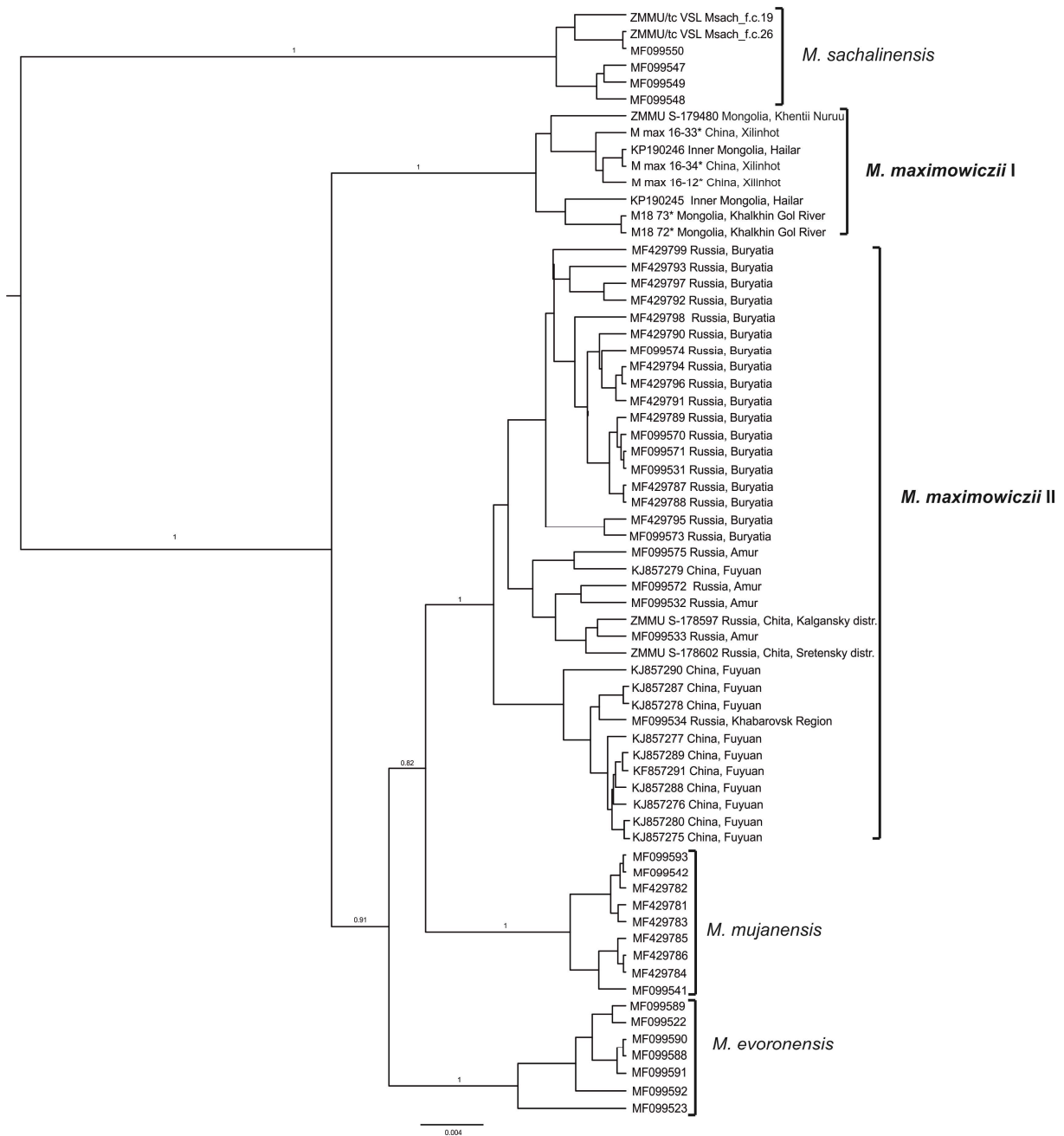


Fig. S3. The fragment of the Bayesian ultrametric tree illustrating the relationships among the haplogroups of *Microtus mongolicus* including short sequences not shown in Fig. 2.

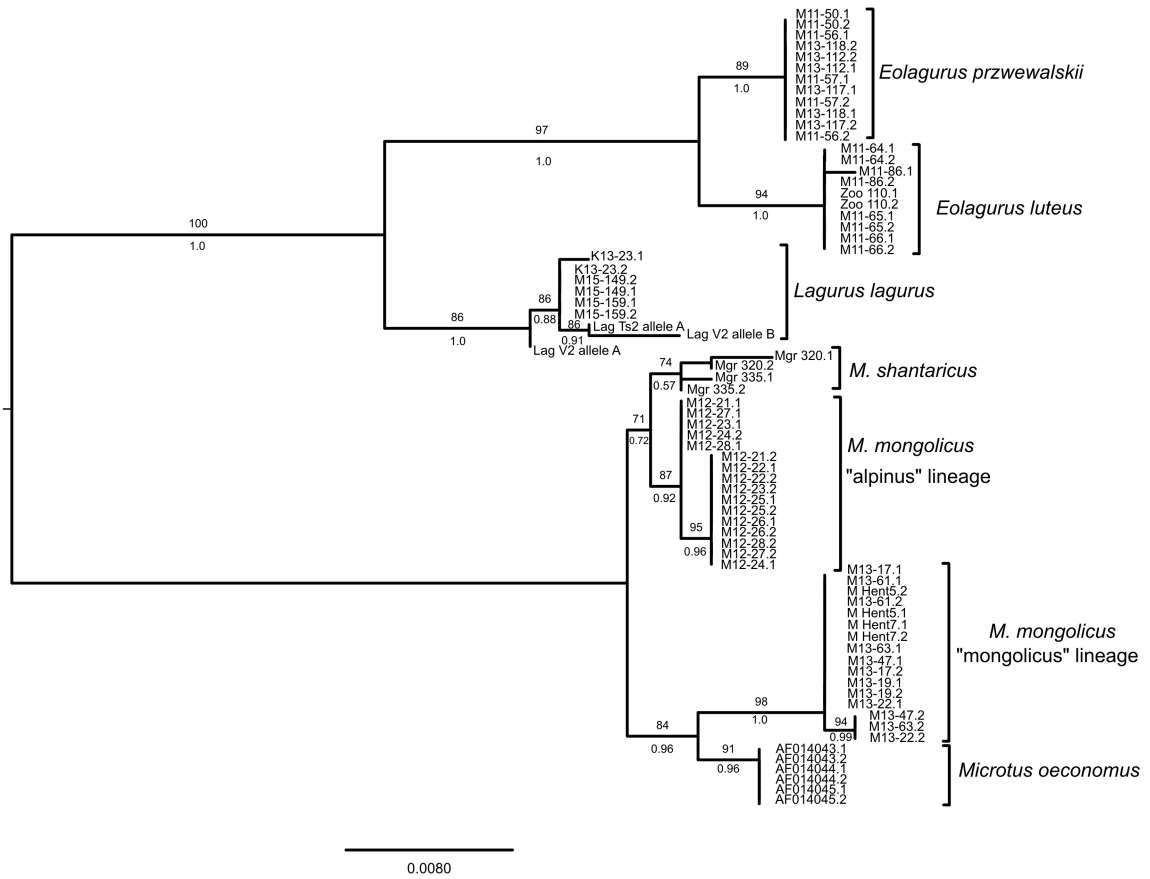


Fig. S4. The ML tree illustrating the relationships among the sequences of *P53* in the examined species of *Microtus* and Lagurini. Numbers above and below branches correspond to ML fast bootstrap support (> 50 %) and Bayesian posterior probabilities (MrBayes), correspondingly.

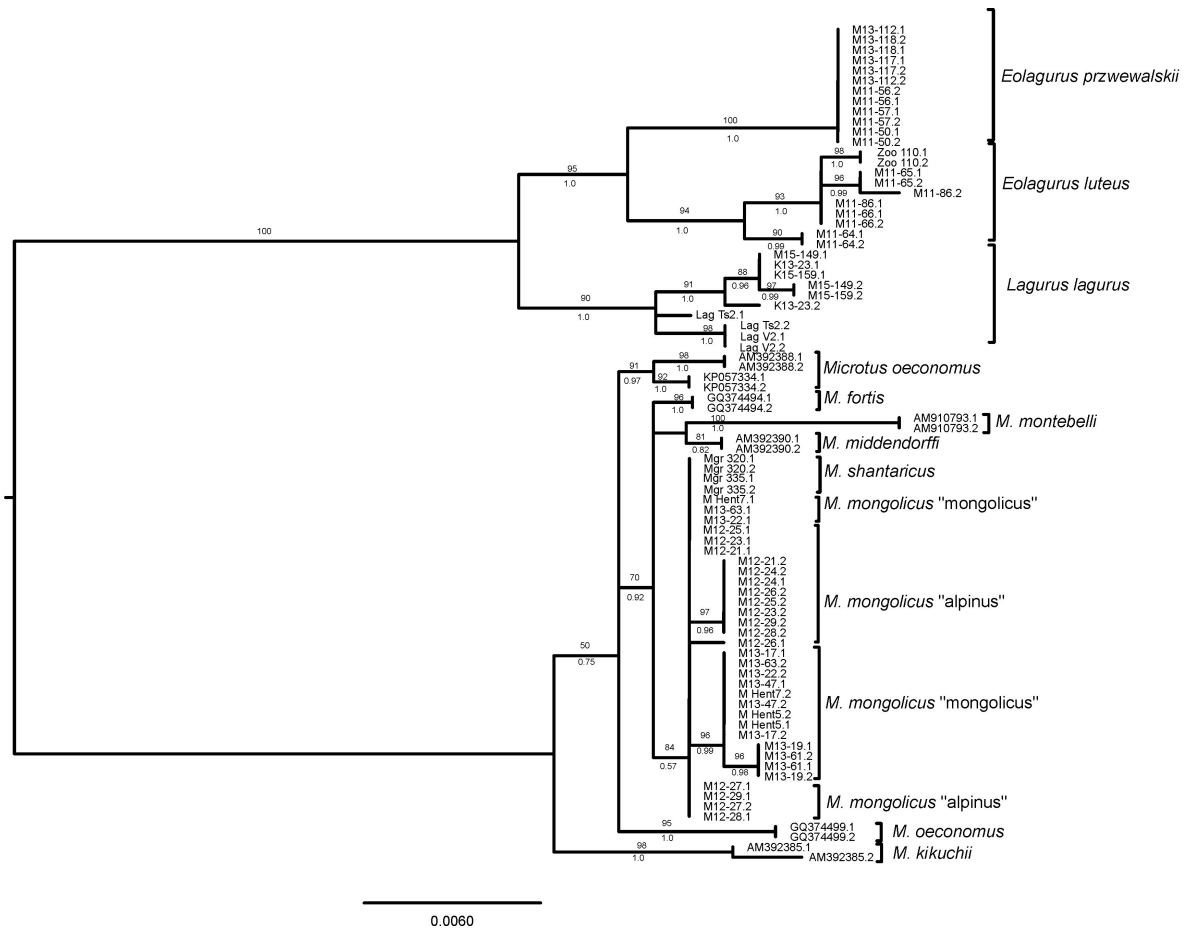


Fig. S5. The ML tree illustrating the relationships among the sequences of *GHR* in *Microtus* and Lagurini. Designations are as in Fig. S4.

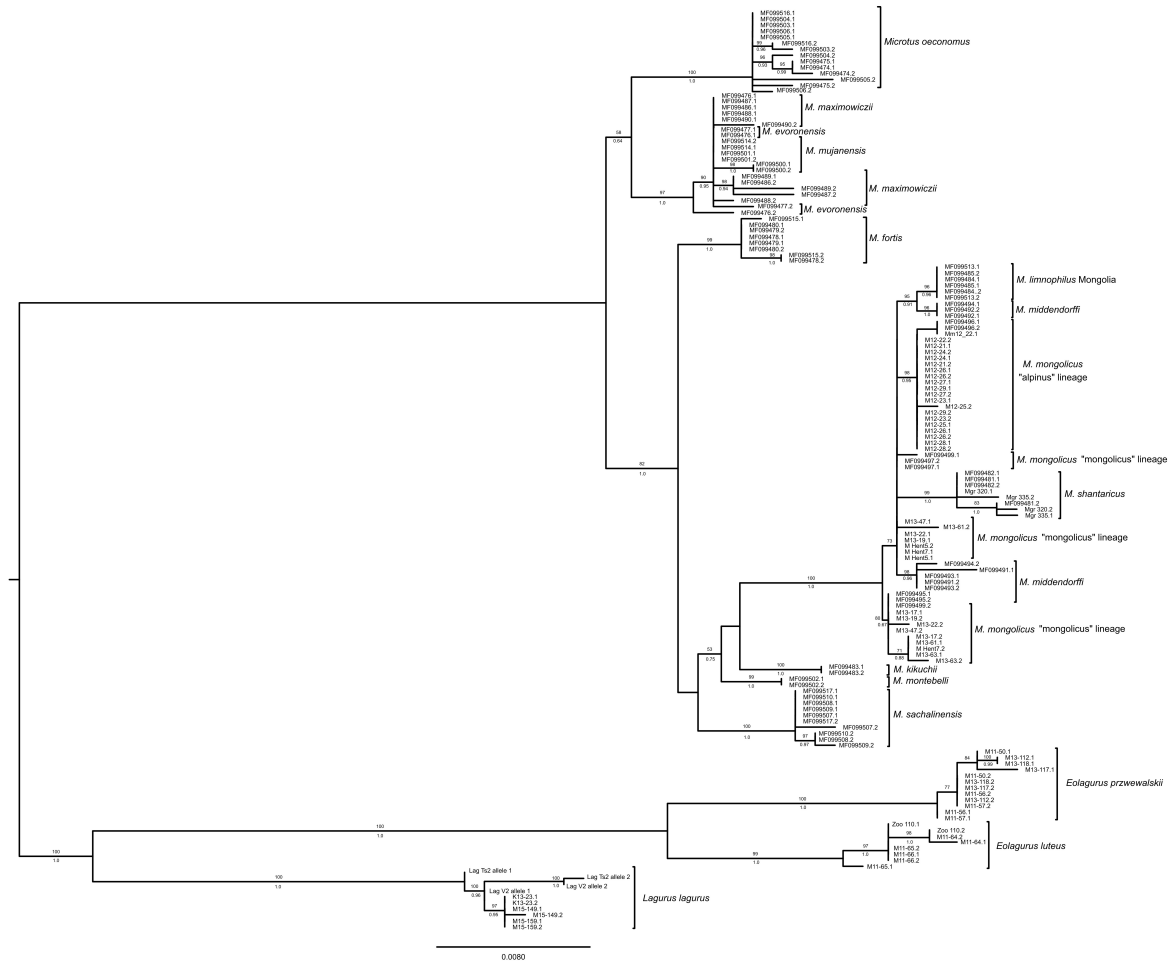


Fig. S6. The ML tree illustrating the relationships among the sequences of *BRCA1* in *Microtus* and Lagurini. Designations are as in Fig. S4.

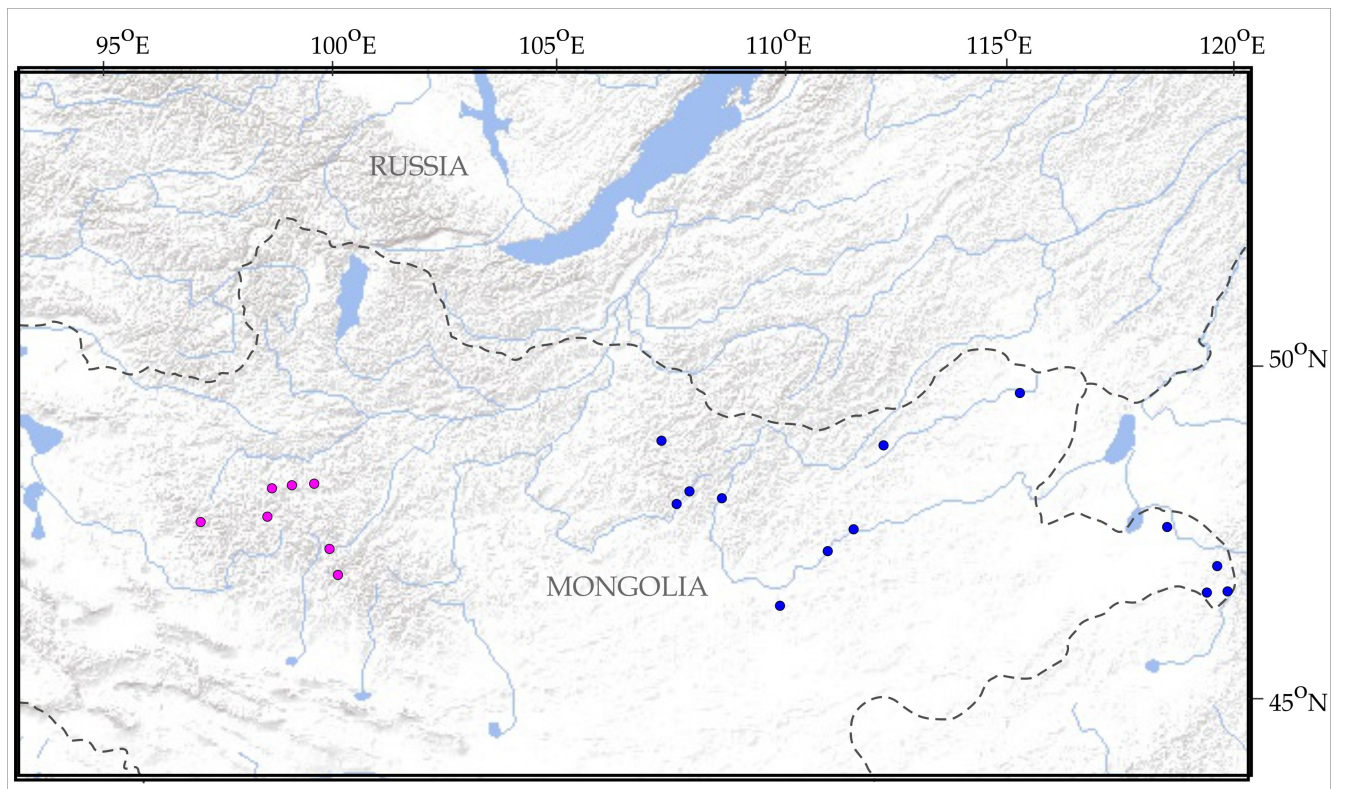


Fig. S7. Distribution of *M. mongolicus* s.l. in central and eastern Mongolia based on the specimens stored in the collection of the Zoological Museum of Moscow State University. Blue and magenta points denote localities for *M. mongolicus* s.str. (eastern lineage) and *M. alpinus* (western lineage).