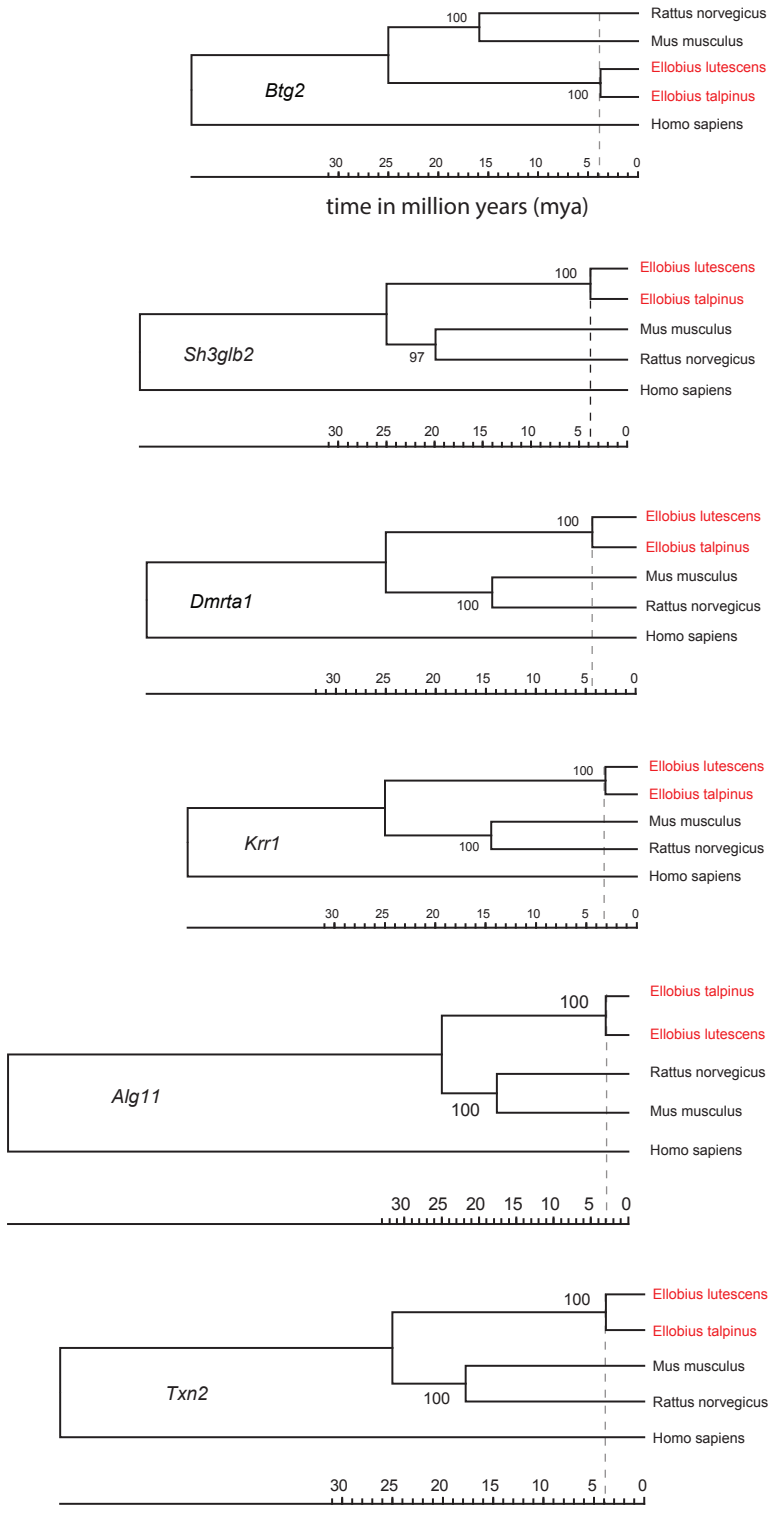

Supplemental Figure S1: Evolutionary divergence of *E. lutescens* and *E. talpinus*

Dendrograms were composed for the gene sequences as indicated, representing orthologs in *H. sapiens*, *M. musculus*, *R. norvegicus* *E. lutescens* and *E. talpinus*. Bootstrap values are shown on two nodes for each gene. To estimate the divergence time of Ellobius species, we first defined a calibration point, for which we aimed at the best estimate of the divergence time of the placental families Muridae (which includes mouse and rat) and Cricetidae (which includes *Ellobius*). From analysis of a molecular supermatrix, Meredith et al. (2011) arrived at a divergence time of these two families around the Oligocene/Miocene boundary, 23 Mya. Using a similar approach focused on rodents, Fabre et al. (2012) proposed a divergence time towards the end of the Oligocene. Using fossil calibration points, Wu et al.(2012) calculated a mean divergence time for Muridae and Cricetidae of 23.4 Mya. Based on the above, we set the calibration point, the divergence time between Muridae and Cricetidae, at 25 Mya. For several DNA sequences, this resulted in an estimated divergence time between mouse and rat around 20-15 Mya, and between *E. lutescens* and *E. talpinus* around 4-3 Mya. The divergence between mouse and rat has been dated at maximally 12.2 Mya (Wu et al. 2012), and we therefore consider 4-3 Mya as a maximum estimate of the divergence time between *E. lutescens* and *E. talpinus*. For *Xist*, sequence information was available also for *E. fuscocapillus*, in addition to that for *E. lutescens* and *E. talpinus*. The composed phylogenetic tree, using the 25 Mya calibration point, shows that *E. lutescens* and *E. fuscocapillus* shared a common ancestor less than 1 Mya (Figure 1).

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