**Supplementary Material**

Supplementary Table S1. GenBank Accession Numbers of the genes used in this study.

Supplementary Table S2. Missing species in our phylogenetic and diversification analyses.

Supplementary Table S3. Genes used in this study.

Supplementary Table S4. Gene partition scheme selected using PartitionFinder within Bayesian information criterion for phylogenetic analyses.

Supplementary Table S5. Fossils used for the PyRate analysis.

Supplementary Table S6. Musteloids and mean body length and mean body mass used in this study.

Supplementary Table S7. Bootstrap support, posterior probabilities, and estimated divergence times of each node. Node numbers correspond to those shown in Figure 1 and Figure 2.

Supplementary Figure S1. **Musteloid supertree using the MRP (matrix representation with parsimony) matrix implemented in Clann**.

Supplementary Figure S2. **Time-calibrated phylogenetic tree (“pruned-after”) of Musteloidea**. Mean divergence times estimated using a relaxed molecular clock model on the complete 46 gene dataset with 74 fossil priors. Blue bars across nodes indicate 95% confidence intervals around the mean divergence time estimates. Posterior estimates of mean and 95% HPD of divergence times are presented in Supplementary Table S7. Nodes are numbered (1–74, same as Figure 1). Outgroup taxa were pruned from the tree, and geological time scale is shown below the tree.

Supplementary Figure S3. **Lineage diversification rates through time using the pruned-after MCC tree**. (**a)** Phylorate plot of lineage diversification based on the “pruned-before” MCC phylogeny. Colors at each point in time along the branches of the phylorate plot denote instantaneous rate of diversification. Warmer colors (red) indicate faster rates and cooler colors (blue) indicate slower rates. Below the phylorate plot is the global deep-sea oxygen isotope records (modified from (Zachos et al. 2008)). These records indicate a rapid decrease in global temperatures following the Eocene-Oligocene Transition and the Mid-Miocene Climate Transition (Zachos et al. 2008), giving rise to more open vegetation habitats such as grasslands and woodlands (Singh 1988; Prothero and Berggren 2014; Leopold et al. 2014). However, the lack of rate shifts suggests that there are no significant increases in diversification rates after these climate events. **(b–d).** Diversification-through-time plots depicting family-specific net diversification trajectories computed from the joint posterior density of macroevolutionary rate parameters in BAMM. The black lines denote the background diversification rate (the rate of all musteloids minus the rate of each respective family). Shading intensity of the colored lines indicate the 5% through 95% Bayesian credible regions on the distribution of rates at any point in time for Mustelidae (b), Procyonidae (c), and Mephitidae (d). The black lines denote the mean background diversification rate-through-time (the rate of all musteloids minus the rate of each respective family), and the grayscale shading illustrates the 95% credible interval of the distribution of background rates through time.

Supplementary Figure S4. **Phylorate plot of phenotypic (body length) evolution rates through time using the “pruned-after” MCC tree**. **(a)** Phylorate plot of the mean phenotypic evolutionary rate of body length across all shift configurations based the MCC phylogeny. **(b–d)** Phylorate plots of 4 distinct shift configurations with the highest posterior probability. Rate shifts, shown as red circles with sizes proportional to the marginal probability of the shift, demonstrate significant increase in evolutionary rate. 3 distinct shift configurations account for the majority of the posterior probability of the data but result in conflicting rate configurations. The most frequent shift configuration (*f = 0.35*) signifies no rate shift (b) whereas the second most frequent shift configuration (*f = 0.33*) indicates an increase in evolutionary rate at the node leading to the divergence of Ictonychinae, Mustelinae, and Lutrinae (c). Conversely, the third most frequent shift configuration (*f = 0.16*) reveals a rate shift at the root of Mustelidae (d).

Supplementary Figure S5. **Phylorate plot of phenotypic evolution rates through time based on body mass.**