Inventory of Supplemental Information:

1. Table S1 – Comprehensive list of examined rodent fossils. The Excel spread sheet contains the complete list of genera used in the study. These data were used to generate Figure 1A.

2. Supplemental Information PDF. The PDF contains the remaining Supplemental figures and tables, described in detail below:

Figure S1. Fossil record dynamic of molar phenotype changes at inter-Family levels. Fossil record revealed that the trends towards a taller crown were preserved within each examined family. Clades did not evolve hypselodonty until the Pliocene. This figure is related to Figure 1.

Figure S2. Markov model probability. The probability of being in state brachydont, mesodont, hypsodont, and hypselodont is P_{Brach}, P_{Meso}, P_{Hypso}, and P_{Hypsel}, respectively. The probability of transition from a lower molar crown height state to a higher molar crown height state is represented by *i* and the probability of transition from a higher molar crown height state to a lower molar crown height state is represented by *d*. This figure is related to Figures 3 and 4.

Figure S3. The observed (fossil record; broken lines) and expected (model; smooth lines) probabilities of the one, two, three, and six parameter changes through time. The x-axis shows the time bins based on NALMA. The blue represents the brachydont state, the red represents the hypsodont state, the green represents the hypsodont state and the purple represents the hypselodont state. This figure is related to Figure 3.

Table S2. Total number of genera and tooth morphology phenotype prevalence per million year bin. This table is related to Figure 1A.

Table S3. Model comparison for the AICc determined by the residual sum of squares (RSS) and the number of parameters (k). This table is related to Figure 3.

Table S4. NALMA and corresponding age ranges. This table is related to Figure 4.