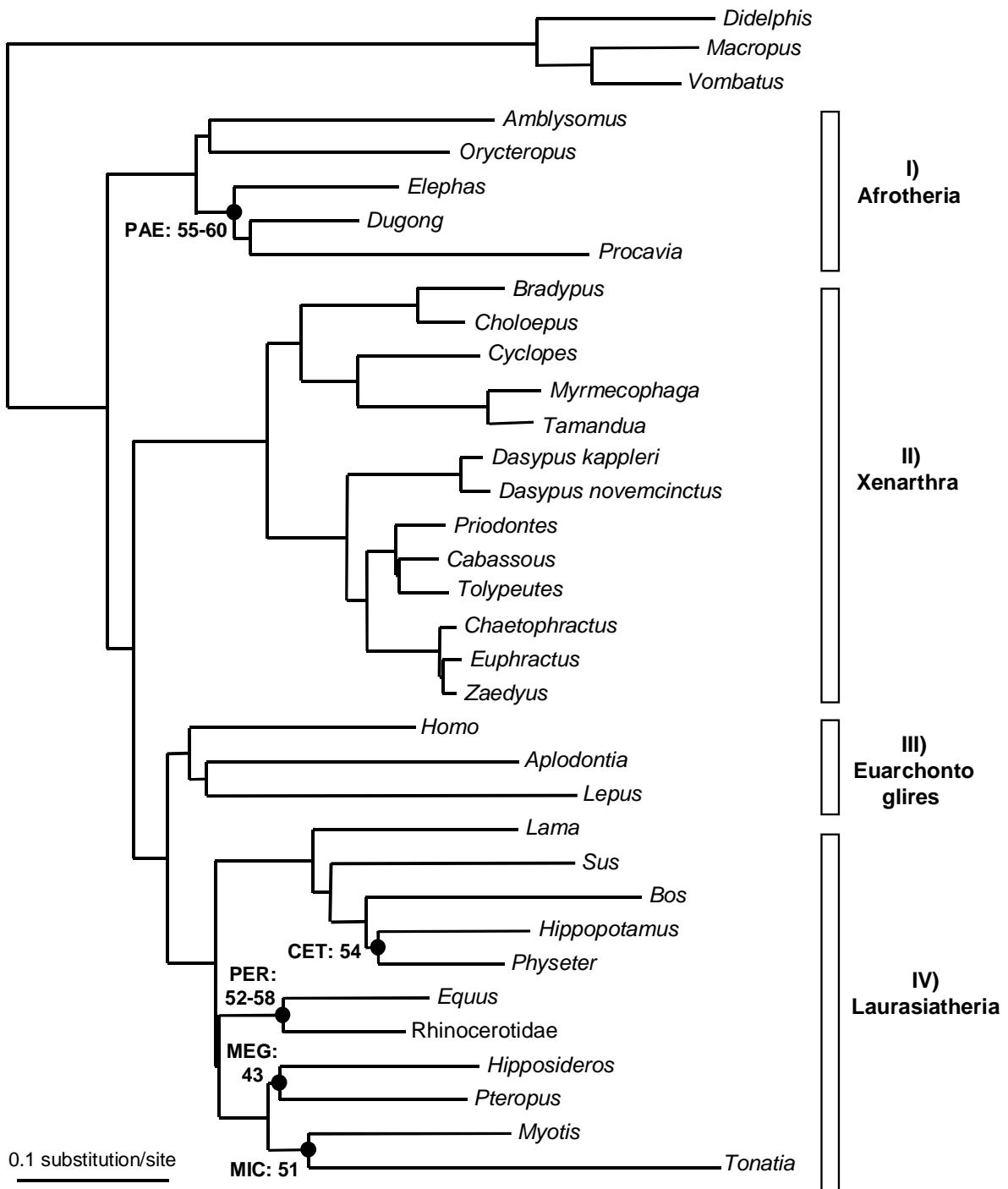


**Figure 1**



**Appendix 3:** Maximum likelihood estimated phylogram of the constrained Placental topology for the combined dataset (5130 sites) of the three nuclear genes ADRA2B, BRCA1 and VWF (Delsuc *et al.* 2002). The F84+ $\Gamma_8$  model of nucleotide sequence evolution was used as implemented in the program ESTBRANCHES. Model parameters were previously estimated by PAML (Yang 1997). The names of four major placental clades and the position and value of the five calibration points are indicated. PAE: Paenungulata; CET: Cetacea; PER: Perissodactyla; MEG: Megachiroptera; MIC: Microchiroptera.