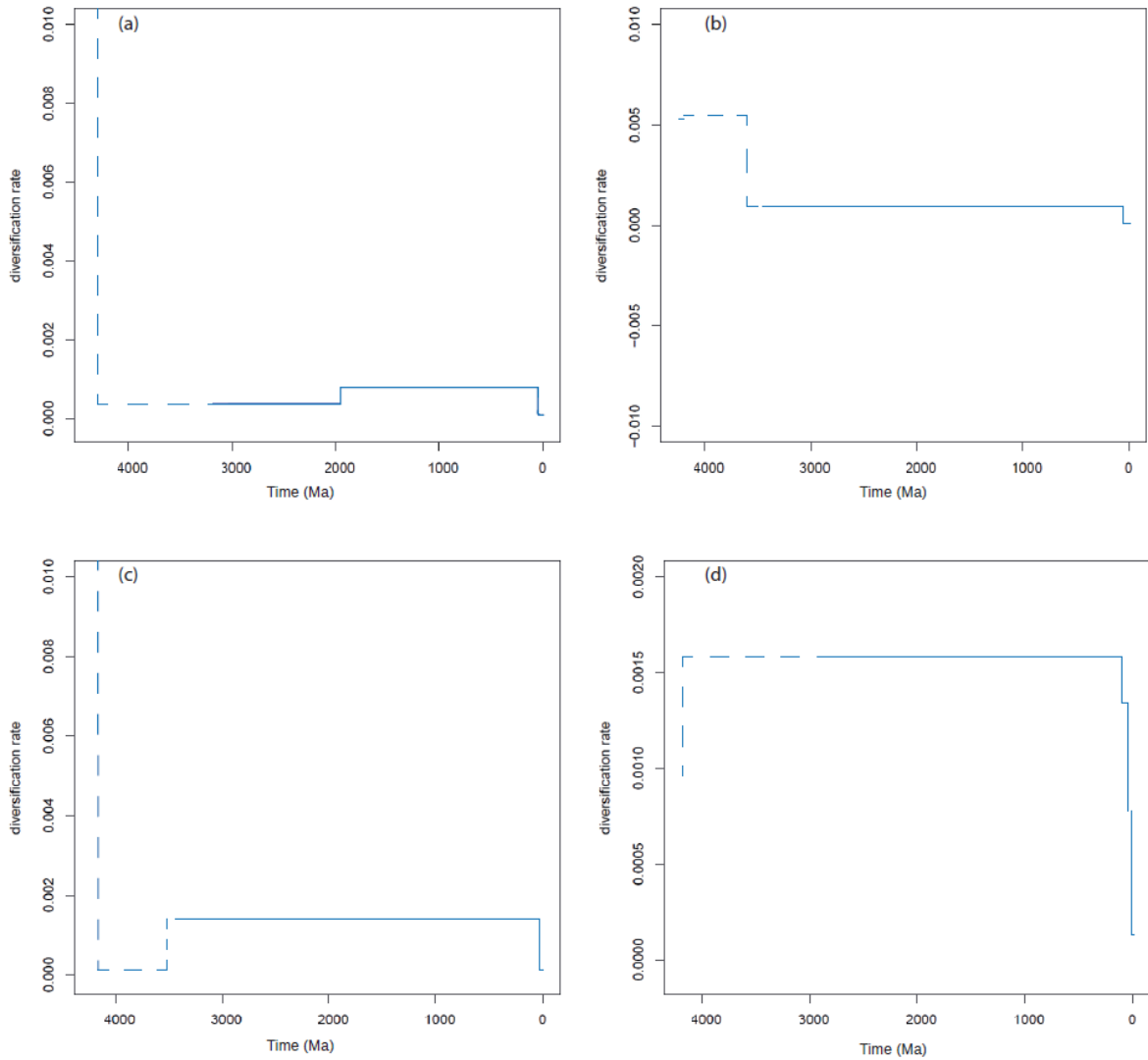
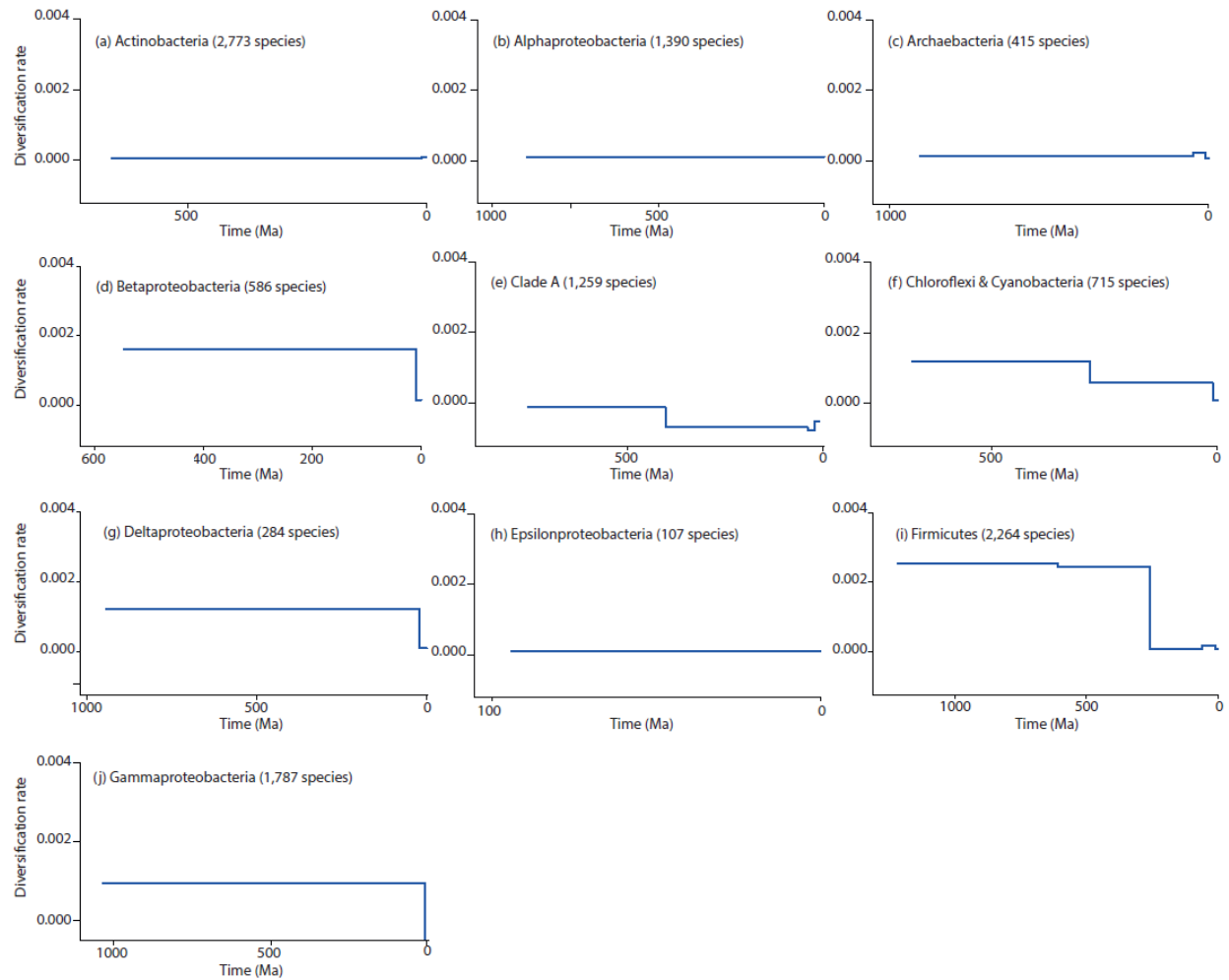


**Figure S2.** Regression through the origin between our estimates (x-axis) and those of Sheridan et al. (2003) ( $p$ -value  $< 2.2e-16$ ;  $r^2=0.95$ ; slope=0.95). In grey are represented the non calibrated nodes during our timing process of the species-level prokaryote timetree (regression by origin:  $p$ -value=1.297e-06;  $r^2=0.91$ ; slope=1.11).



**Figure S3.** Net diversification rate plot (TreePar analyses) of the species level prokaryote timetrees built under the topology B (a; Lang et al. 2013) and C (b; Rinke et al. 2013), of the PTT when using a high estimate of described species (500,000 OTUs) (c) and of the bacteria timetree (d). Tree sections with less than 30 nodes involved are represented by dashed lines.



**Figure S4.** Net diversification rate plot (TreePar analyses) of subclades of the prokaryote timetree (topology A). Only tree sections with 30 or more nodes are represented. Rate changes at or near time zero are considered an artifact.