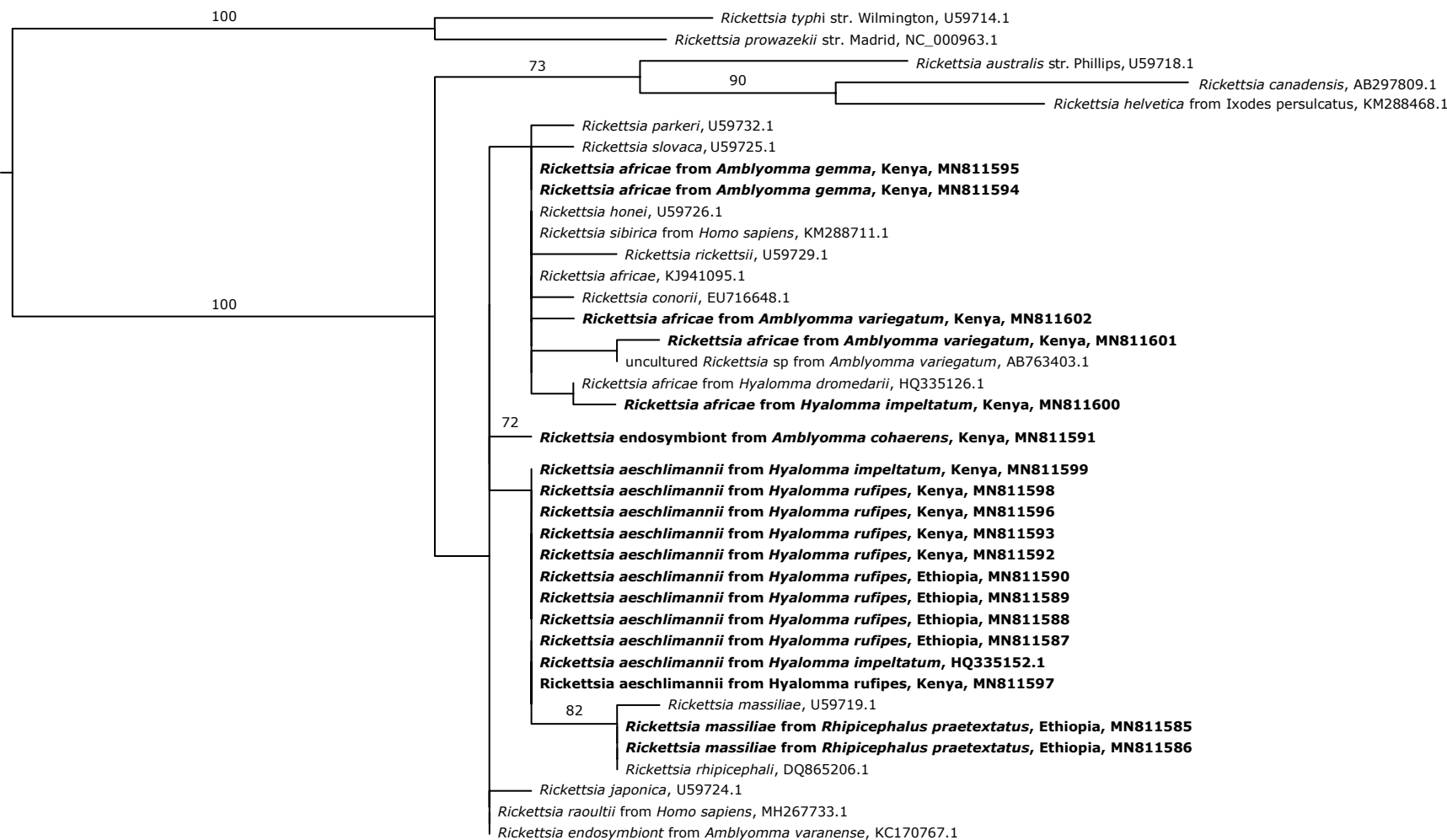


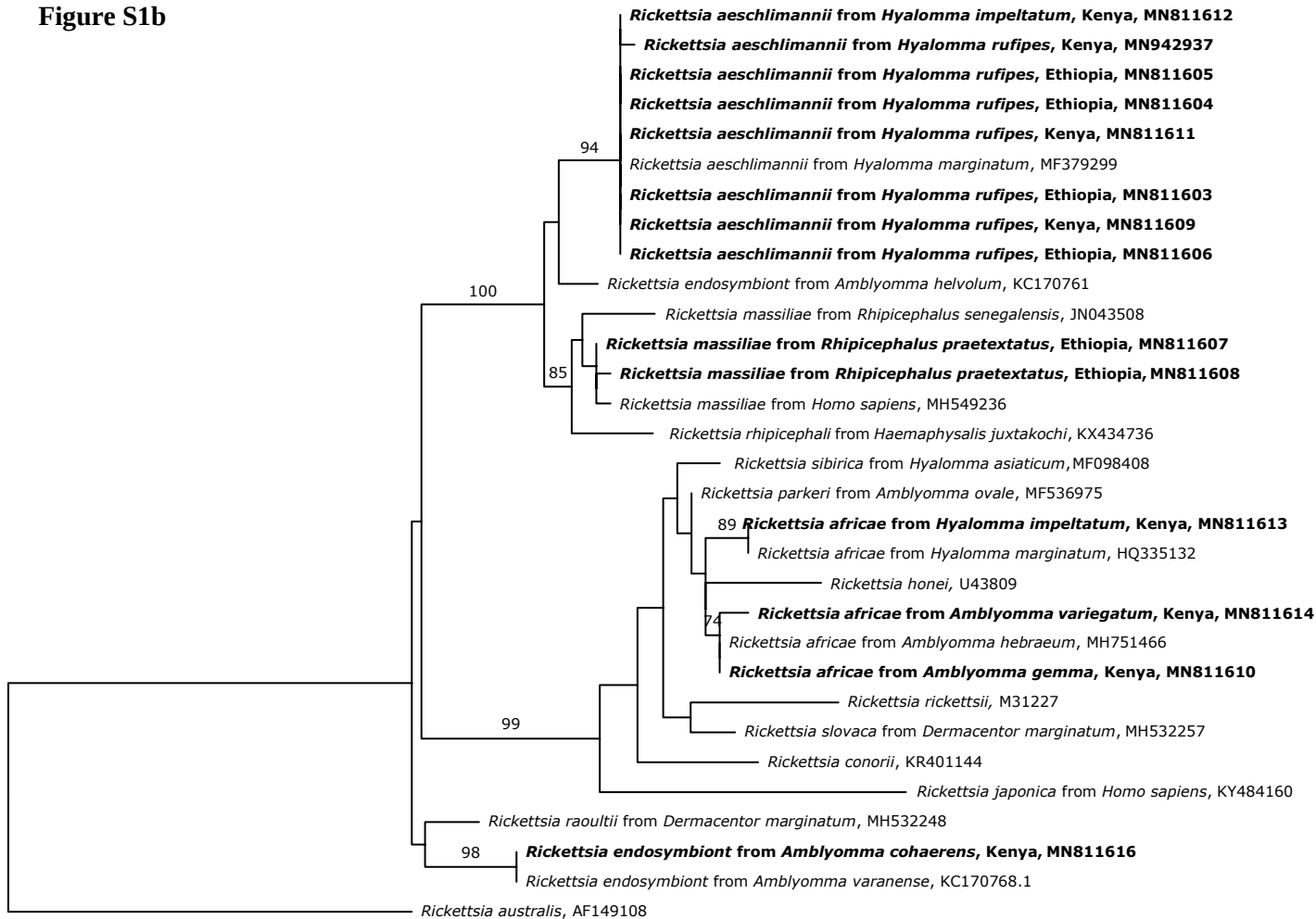
Additional file 2: Figures S1-S7. Maximum likelihood phylogenetic trees of organisms found in association with African ticks: *Rickettsia gltA* gene (**S1a**), *Rickettsia ompA* gene (**S1b**), *Rickettsia ompB* gene (**S1c**), *Anaplasmataceae* SSU rRNA gene (**S2**), piroplasmid SSU rRNA gene (**S3**), *Borrelia* ITS (**S4**), *Coxiella* SSU rRNA gene (**S5**), *Francisella rpoB* gene (**S6**), "Ca. Midichloria" SSU rRNA gene (**S7**). Newly obtained sequences are shown in bold. Numbers on branches indicate bootstrap support (values below 70% are not shown). Scale bars stand for estimated proportional sequences divergence.

Figure S1a



0.02

Figure S1b



0.02

Figure S1c

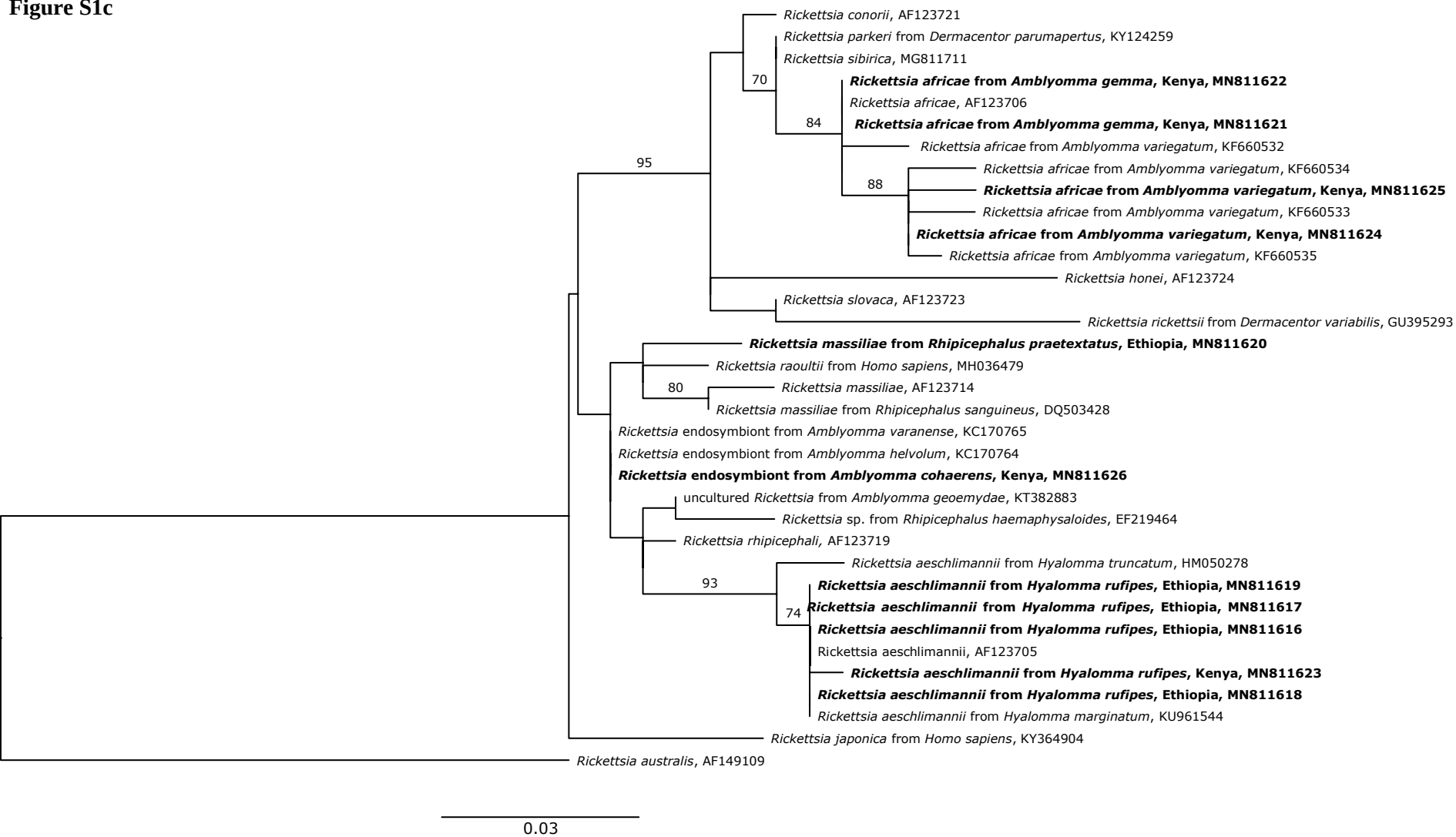
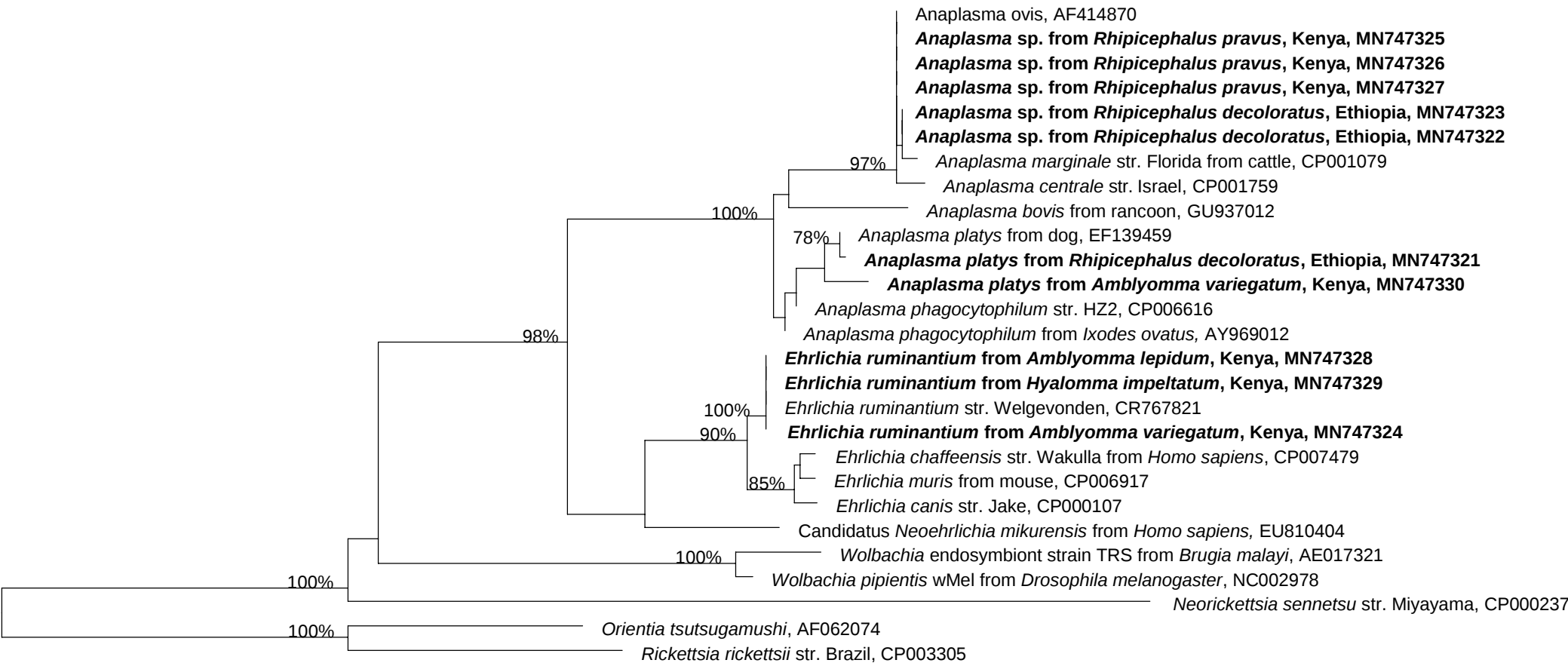


Figure S2



0.10

Figure S3

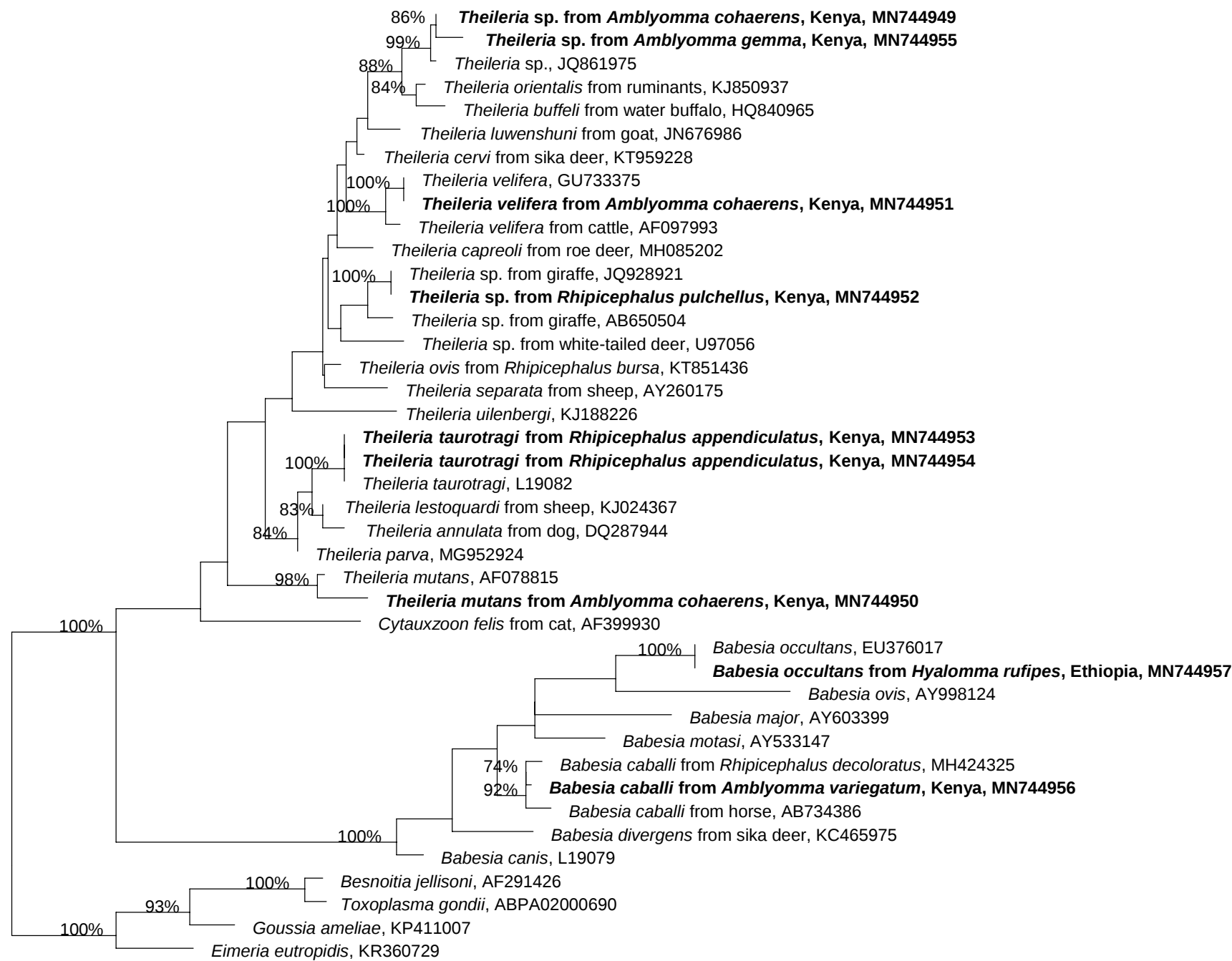


Figure S4

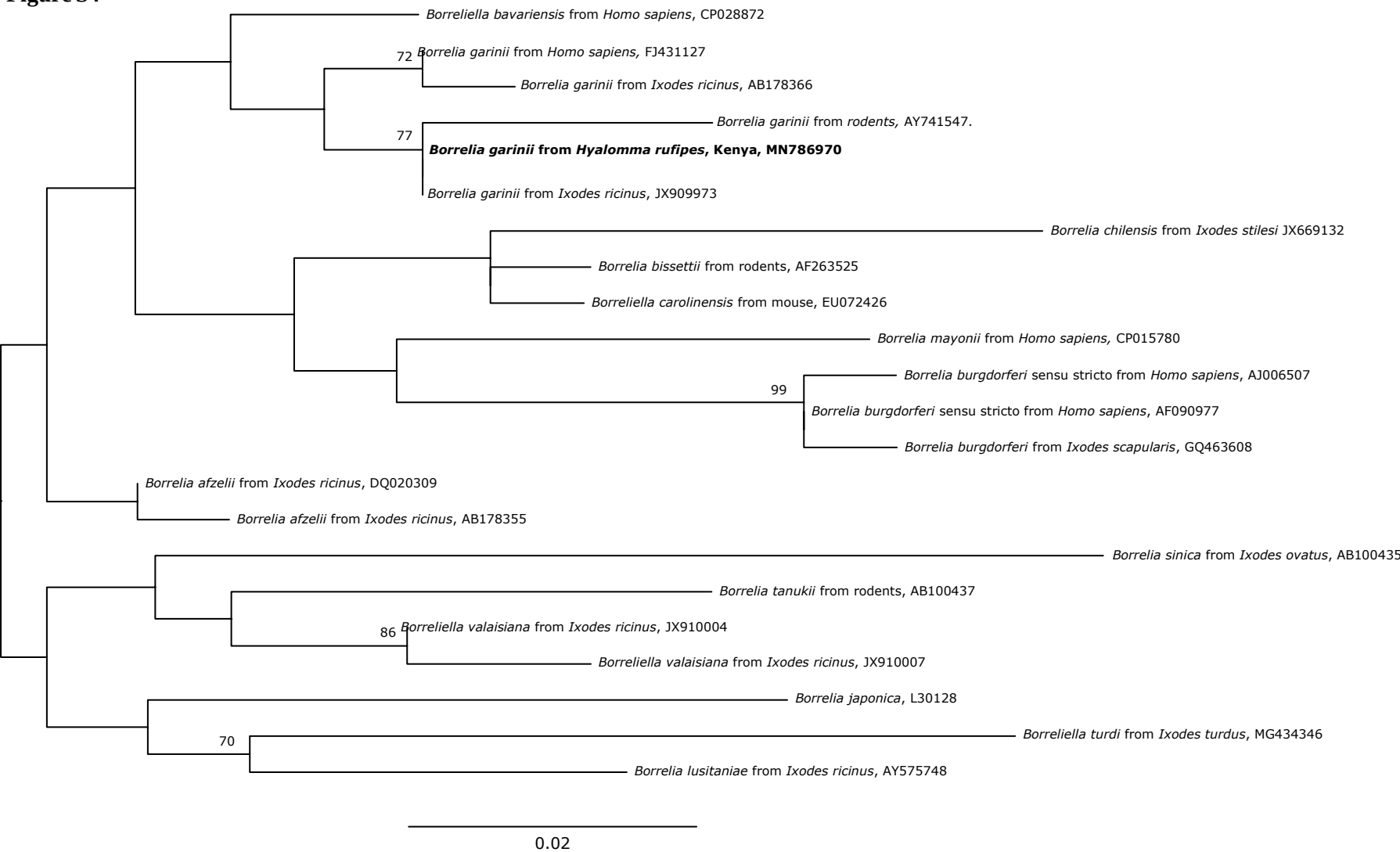


Figure S5

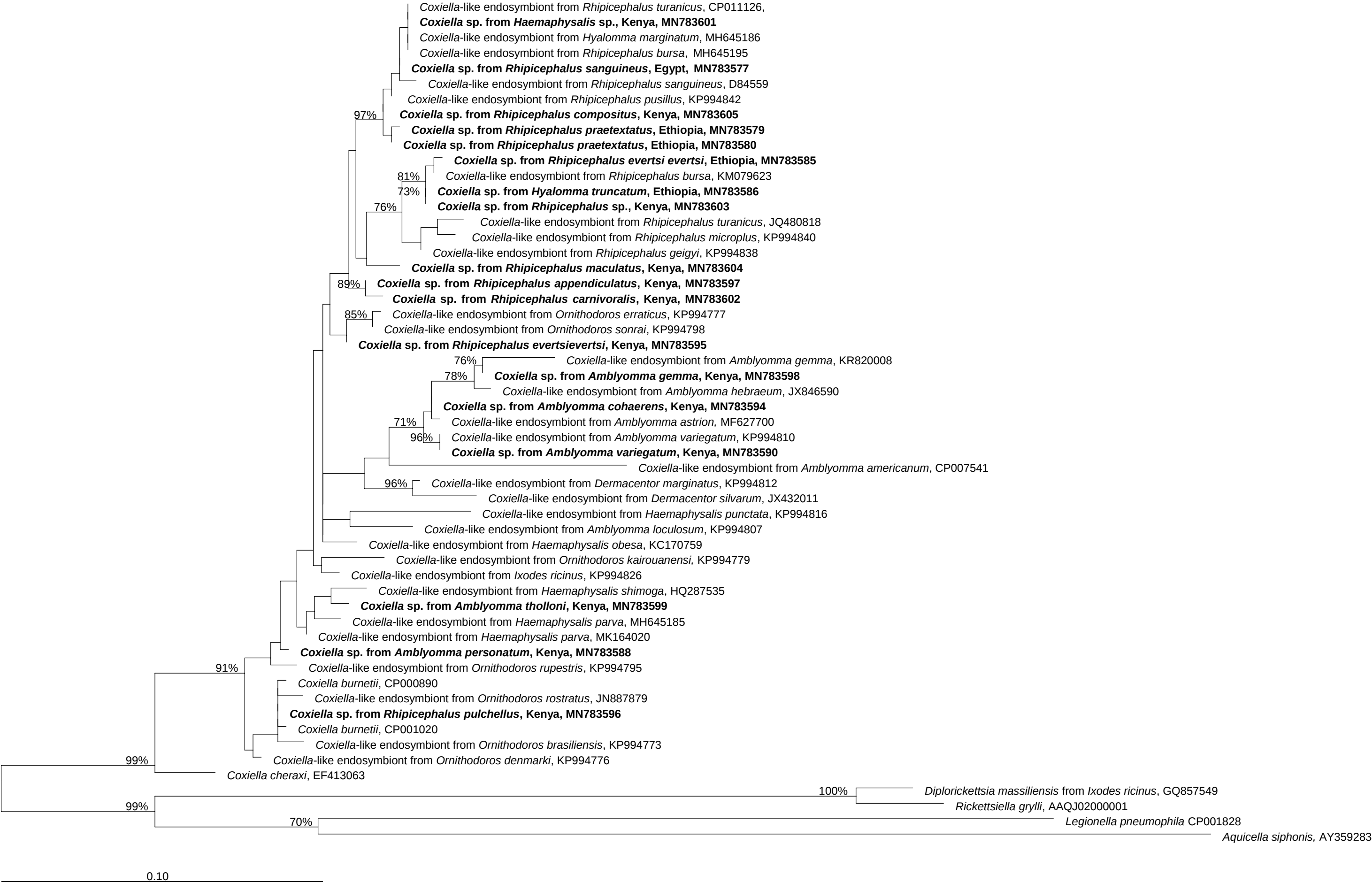


Figure S6

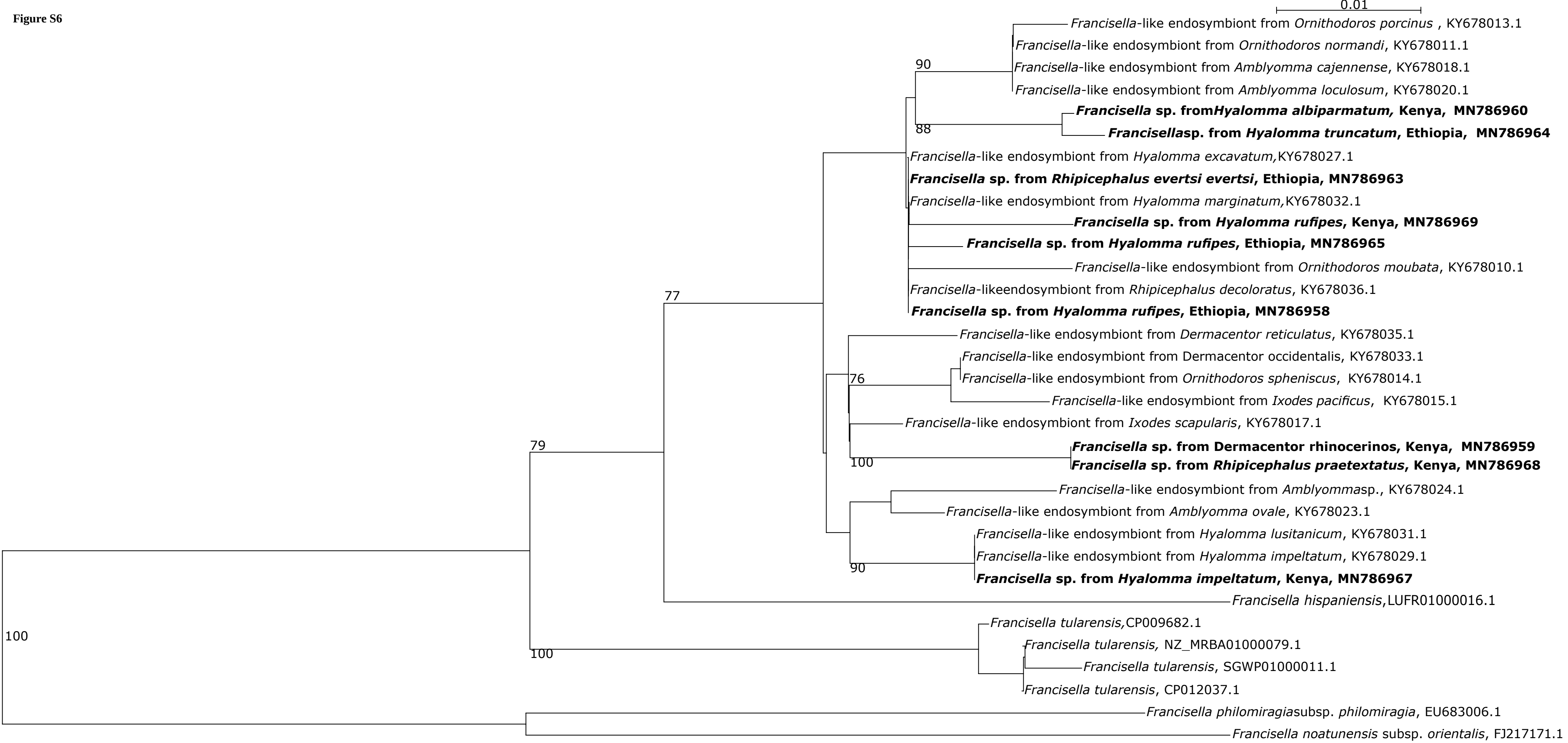


Figure S7

