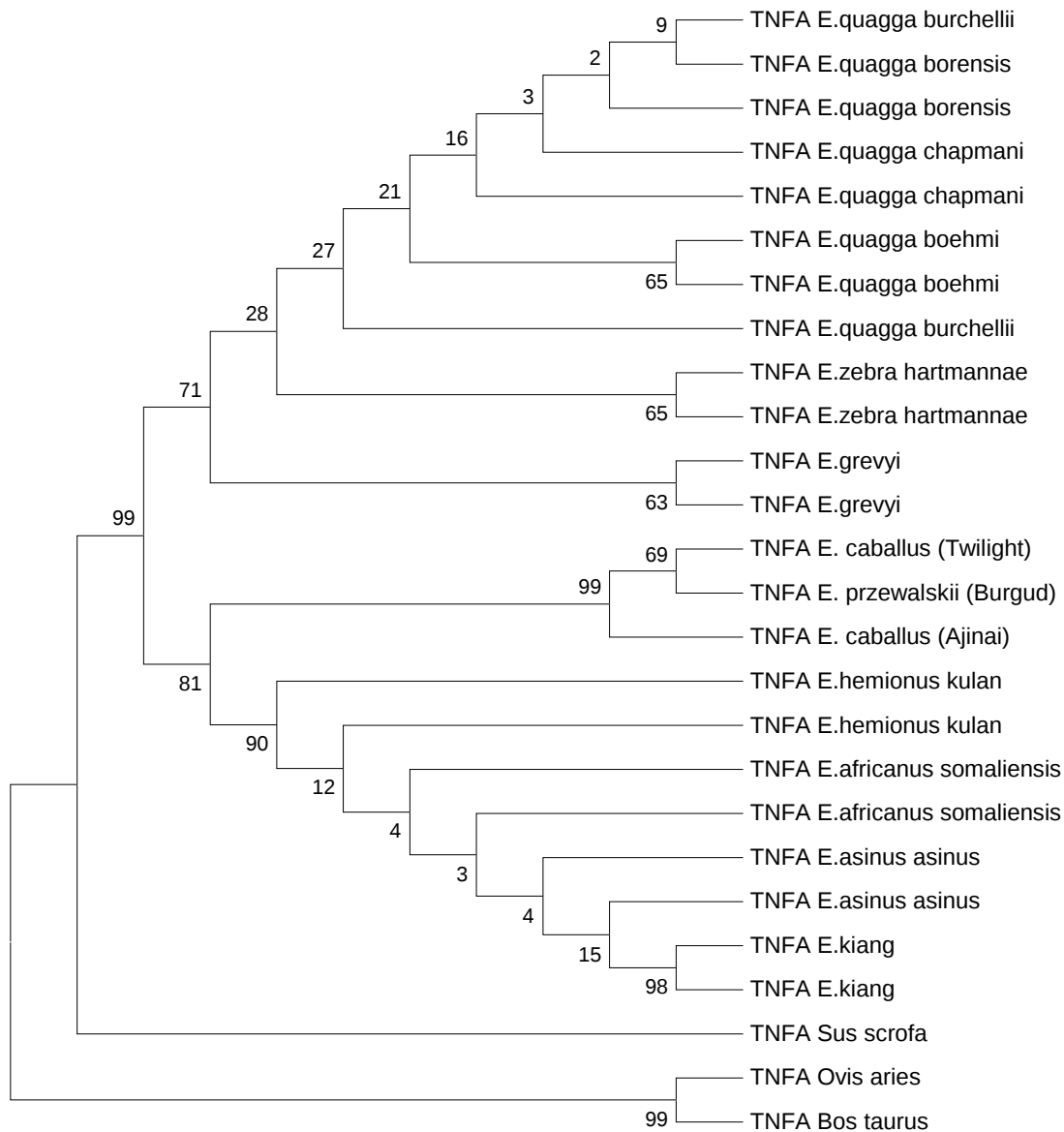




Additional file 6. Maximum likelihood phylogeny reconstruction of *TNFA* gene. The tree was inferred using the Hasegawa-Kishino-Yano model with discrete Gamma distribution and tested by 1000 Bootstrap replications. The tree is not drawn to scale, for better topology clarity.