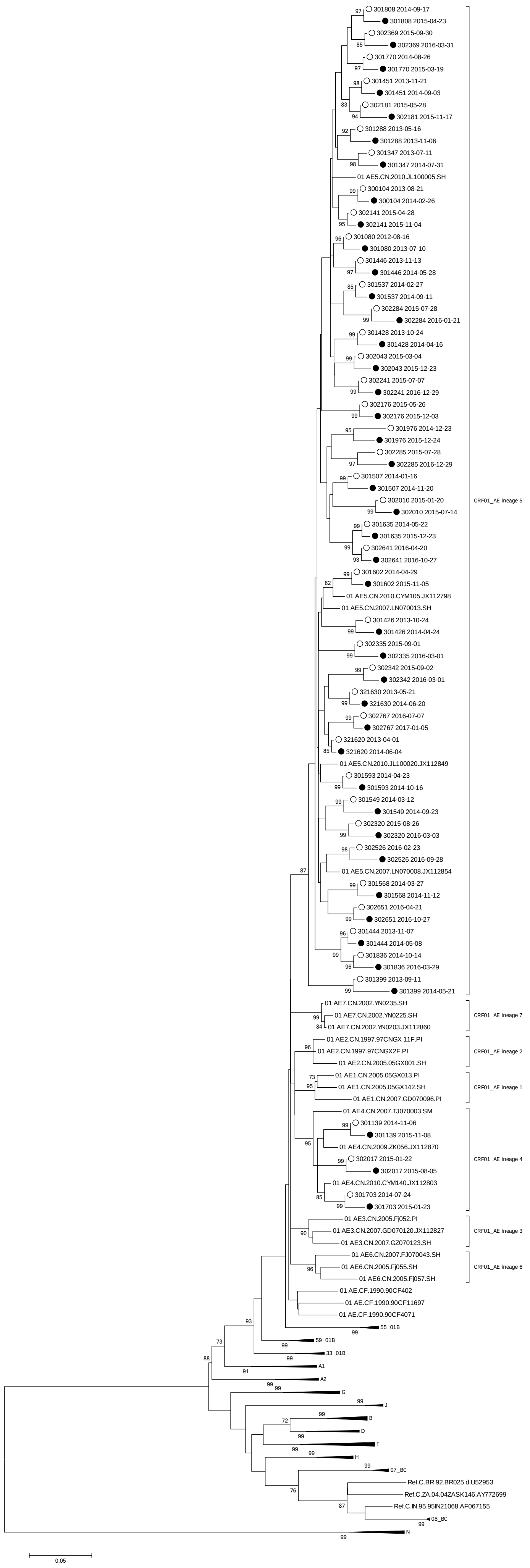

Figure S3. Phylogenetic analysis of the 42 TF CRF01_AE-infected patients.

The *pol* sequences of 42 CRF01_AE-infected patients at baseline and TF time point were analyzed by the Maximum likelihood method in Mega v7.0. The nucleotide substitution model was GTR+G+I. The bootstrap values of the 1000 replicates were labeled on the major branches. Bootstrap values <70 were hidden. The sequences at baseline were represented by hollow circles and the sequences at TF time point were represented by solid circles.