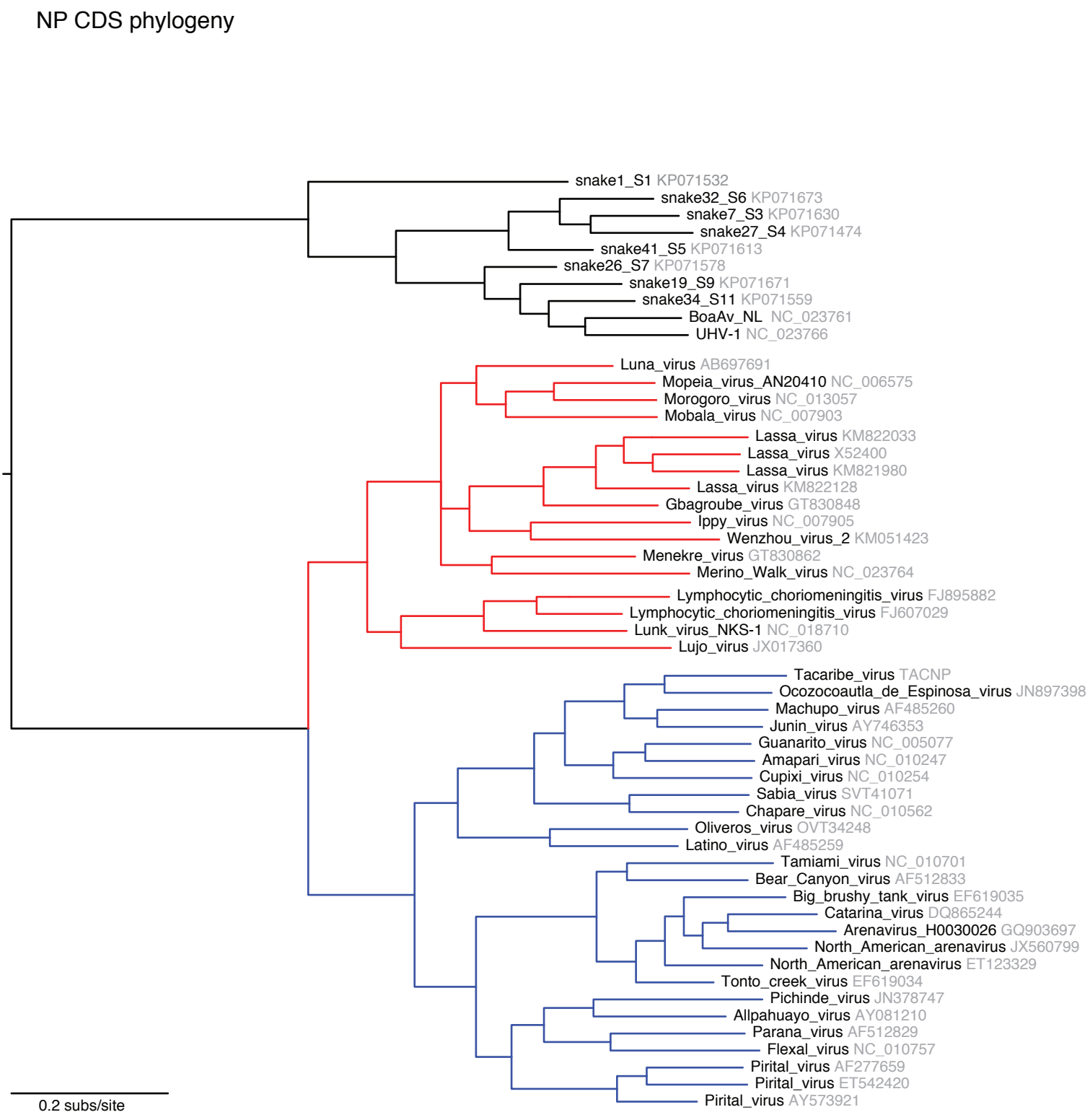

S3 Fig: **Phylogeny of representative snake and mammalian arenavirus S segments**. Representative snake and mammalian arenavirus sequences were collected and used to create a multiple sequence alignment of the NP CDS, which were used to create a Bayesian phylogeny. Red lines indicate Old World mammalian arenaviruses and blue lines New World viruses. Sequences accession numbers are indicated.