



Fig. S4. Maximum likelihood NR phylogeny with fast-evolving sites removed. We used PAML software to identify sites in the top two octiles of the gamma-distribution of among site rate variation on the ML tree, excluded the resulting 113 sites from the alignment, and repeated the phylogenetic analysis using PhyML. For sites excluded, see table S3. Branch labels show approximate likelihood ratio statistics. Sequence names are colored as in Fig. S2.