



Figure 1 Phylogenetic analysis of the MuKVs based on the nucleotide sequences of partial 3D regions. The tree is generated by maximum-likelihood method based on Kimura 2-parameter model (Gamma distributed and partial deletion) with 1000 bootstrap replicates, and the statistics values $>70\%$ are displayed above the tree branches. YY101 (MW292457) and each of various lateral blank triangles indicate the MuKVs identified in the present study. The strains YY12 (MW292465), YY91 (MW292464), YY93 (MW292463), YY95 (MW292461), YY96 (MW292460), YY98 (MW292459), YY100 (MW292458), YY101, YY103 (MW292456), YY104 (MW292455), YY106 (MW292453), YY108 (MW292451), YN21 (MW292469), YN25 (accession no.MW292468), YN45 (MW292467) and YN52 (MW292466) were isolated from *Rattus norvegicus*. The strains YY94 (MW292462), YY105 (MW292454), YY107 (MW292452) and XM105 (MW292470) were isolated from *Rattus tanezumi*. The strains XM97 (MW292472) and XM102 (MW292471) were isolated from *Rattus losea*. BKV, bovine kobuvirus; BatKV, bat kobuvirus; CaKV, canine kobuvirus; CapKV, caprine kobuvirus; FKV, ferret kobuvirus; FeKV, feline kobuvirus; PKV, porcine kobuvirus; RKV, rabbit kobuvirus. (For better view of the sequences covered by different colors, the reader is referred to the web version of this article.)