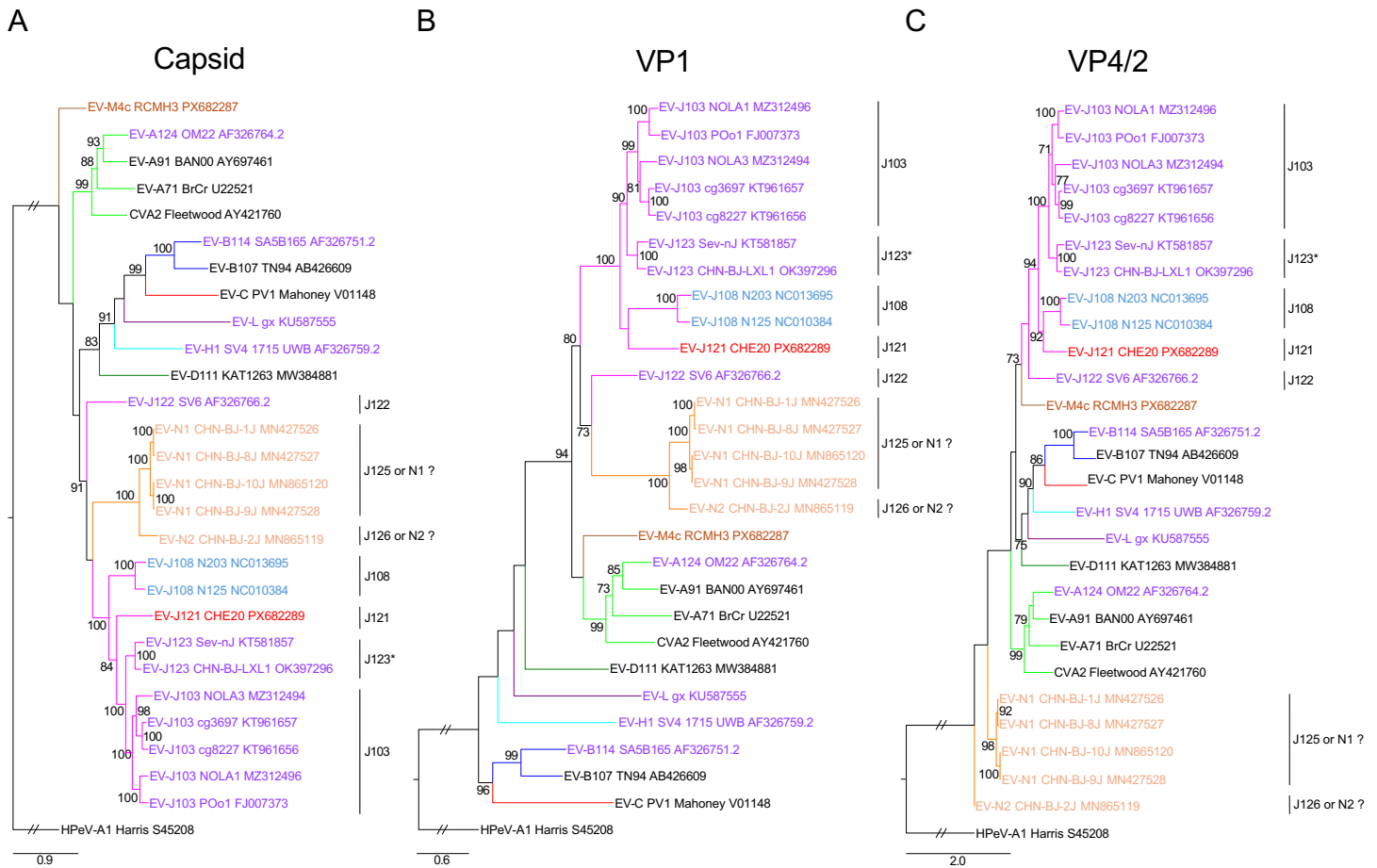




Phylogenetic analysis of enterovirus J species. The maximum-likelihood trees were constructed with all available (a) full capsid (length of alignment 2,640nt), (b) full VP1 (length of alignment 939 nt), and (c) full VP4/2 (length of alignment 1,020 nt) sequences. The trees were rooted with the HPeV-A1 Harris strain (S45208). The symbol * indicates proposed new virus types. The colours of the strain names indicate their host origins: *Mandrillus* (green), *Chlorocebus* (orange), *Cercopithecus* (brown), *Papio* (blue), *Macaca* (purple), and *Pan* (red). Bootstrap values greater than 70% (based on 1,000 pseudoreplicates) are shown at the corresponding nodes. The sequence alignments were performed using MAFFT, the phylogenetic trees were constructed with IQ-Tree, and the visualization was generated with FigTree. The trees are drawn to scale, with branch lengths measured in the number of substitutions per site.