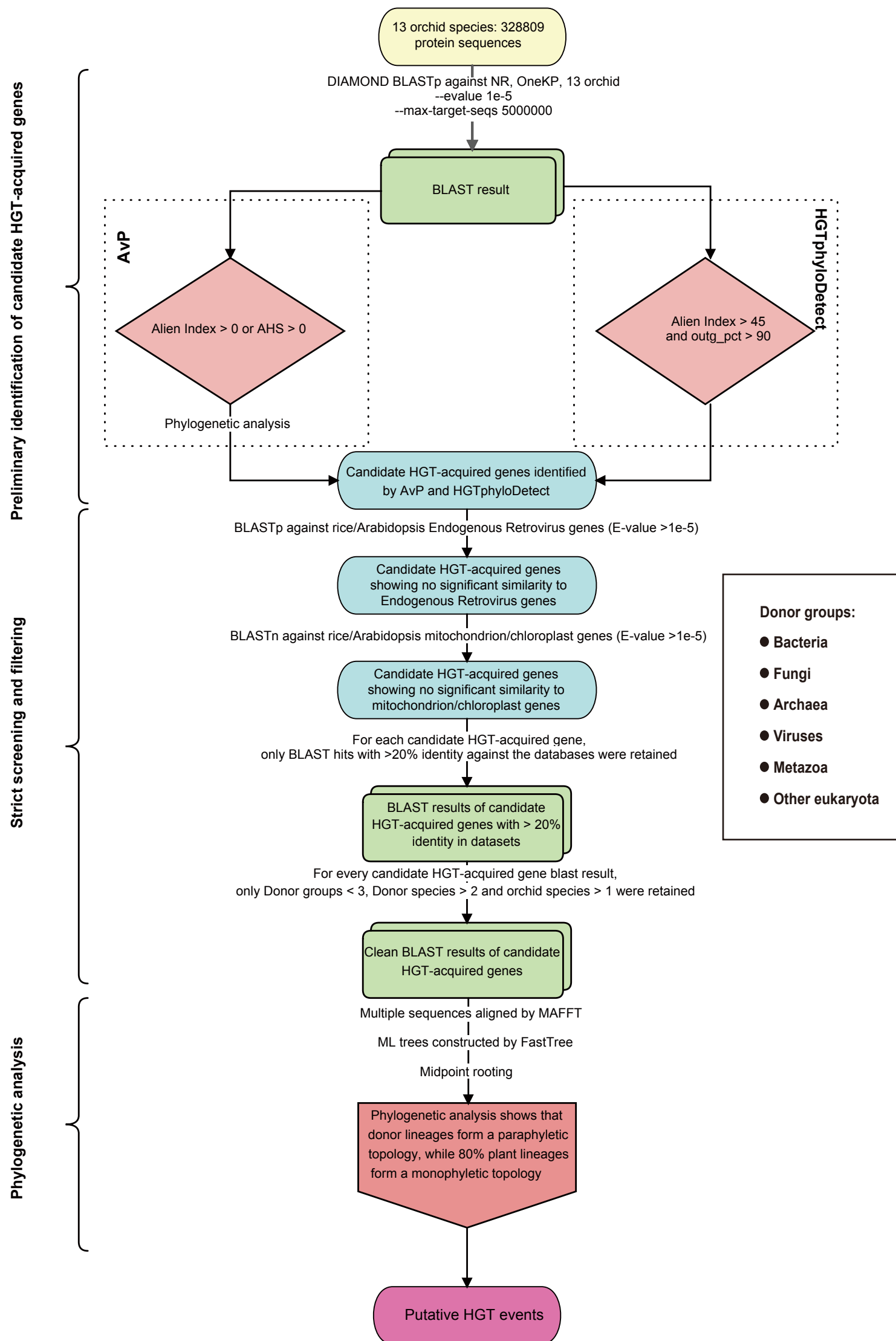




Supplementary figure15. Workflow for HGT identification. The HGT identification process in this study includes three main steps: (1) Preliminary screening of candidate HGT genes; (2) Multi-dimensional filtering; (3) Phylogenetic validation. Yellow oval boxes represent protein sequences, green boxes indicate BLAST result files, blue oval boxes denote the candidate HGT-acquired gene sets obtained at each filtering step, and red boxes represent the judgment criteria. The text on the arrows between each analytical step indicates the corresponding screening process.