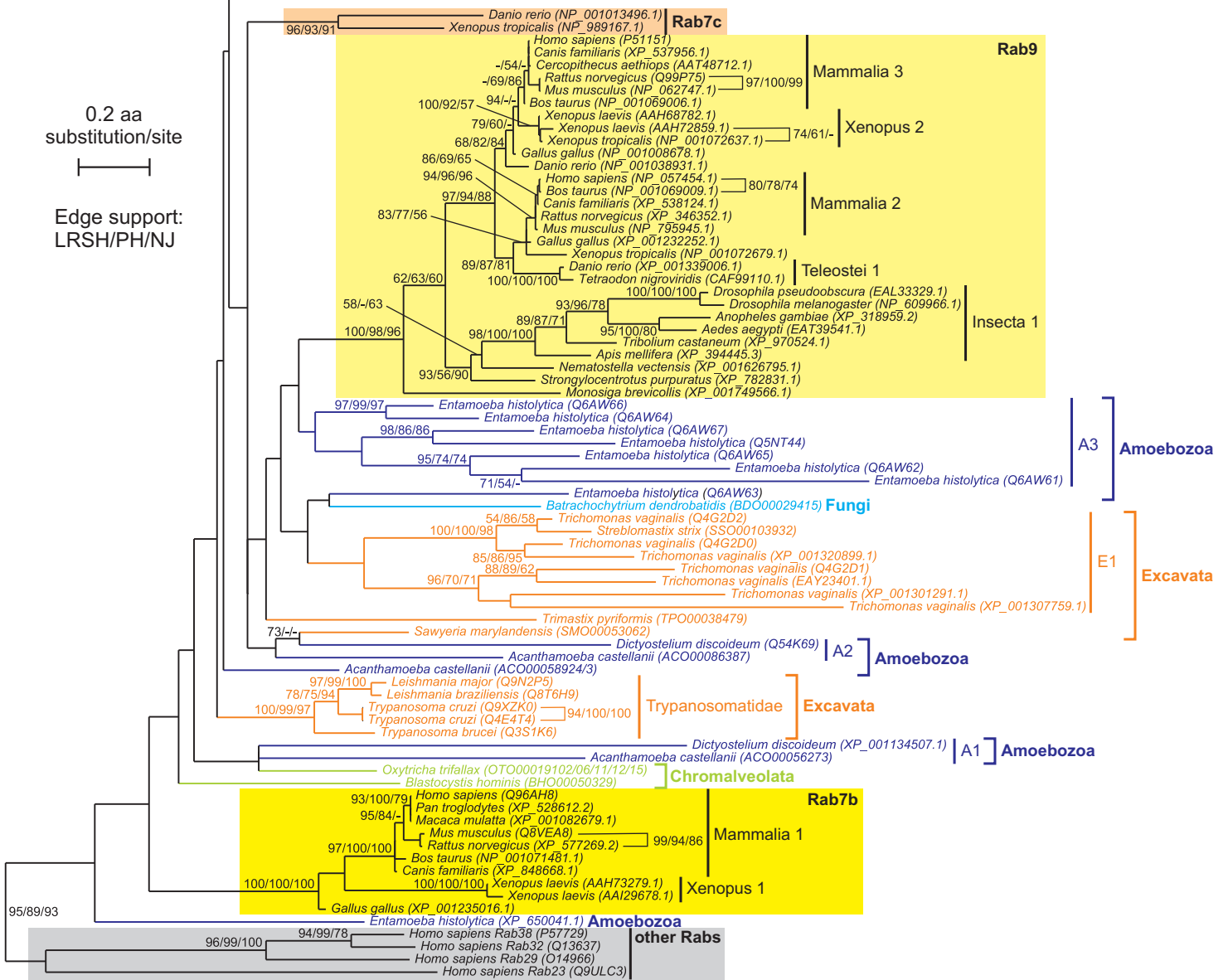


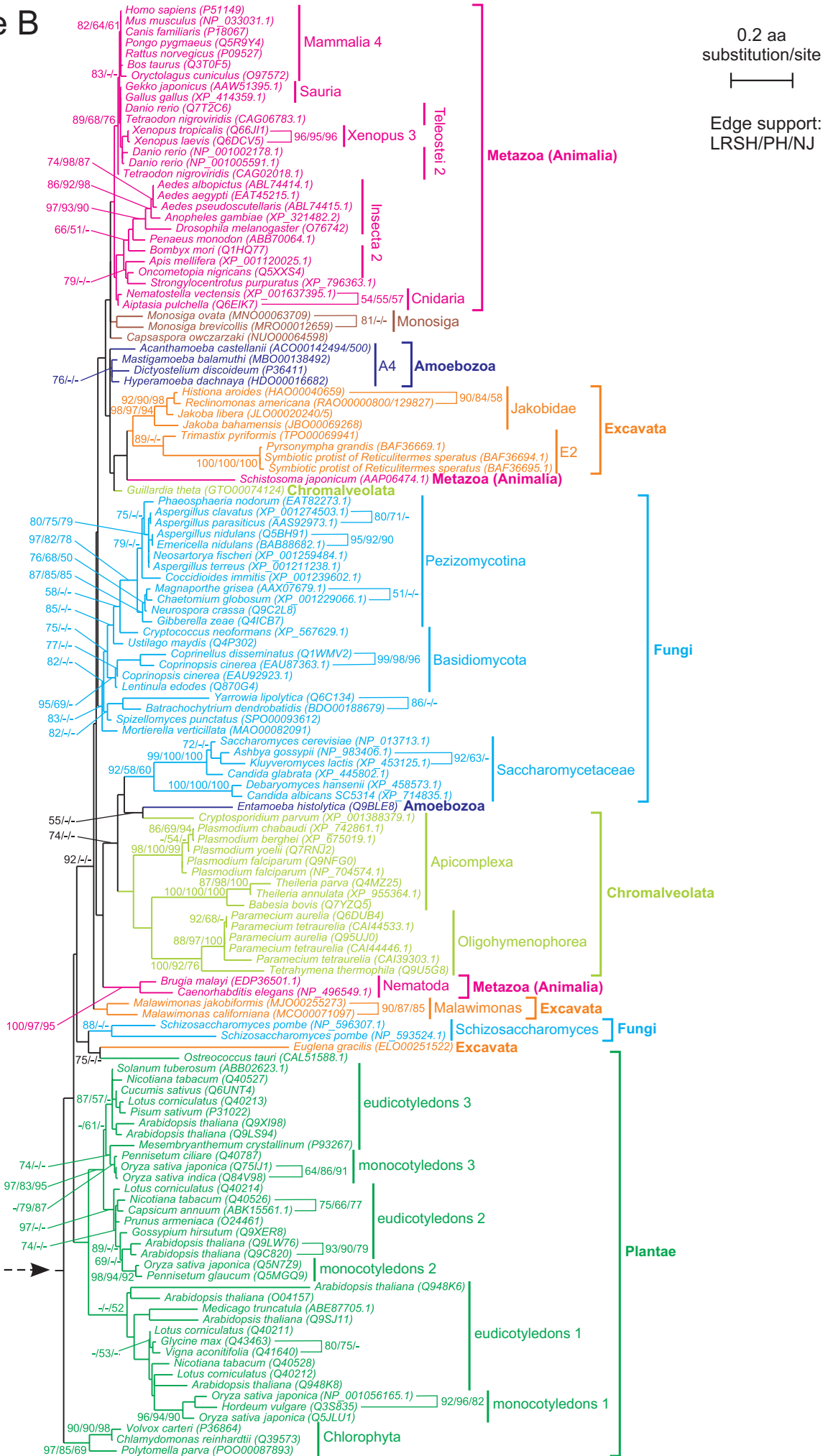
The maximum likelihood tree obtained in PHYML under the JTT+I+ $\Gamma$ (7) model for 210 amino acid sequences of Rab7 proteins and proteins classified in Rab7b and Rab9 subfamily (placed in the yellow rectangles). 'Rab7c', in the orange rectangle, contains very divergent Rab7 proteins of vertebrates. 'Other Rabs', in the grey rectangle, represents four human members of Rab23, Rab29, Rab32 and Rab38 subfamilies used as an out-group. Numbers at nodes, in the shown order, correspond to support values obtained for 1000 replicates in: the local rearrangement paired-sites method performed in TreeFinder (LRSH), the bootstrap analysis made in PHYML (PH) and bootstrap analysis based on neighbor joining method (NJ). Values of the bootstrap percentages lower or equal to 50% were omitted or indicated by a dash “-“. Names at thick vertical lines denote sequences that were contracted in the competitive tree presented in Additional file 3. The contracted clades show a high bootstrap support or contain sequences belonging to well defined taxonomical groups.

subtree A

continued in subtree B



subtree B



continued from subtree A