

Fig. 1 Phylogenetic tree of BEL-1\_LVa-I and its homologues. Only those bootstrap values below 90% were shown (100 replicates); the same below. The *p-value* of approximately unbiased (AU) test is 0.729.

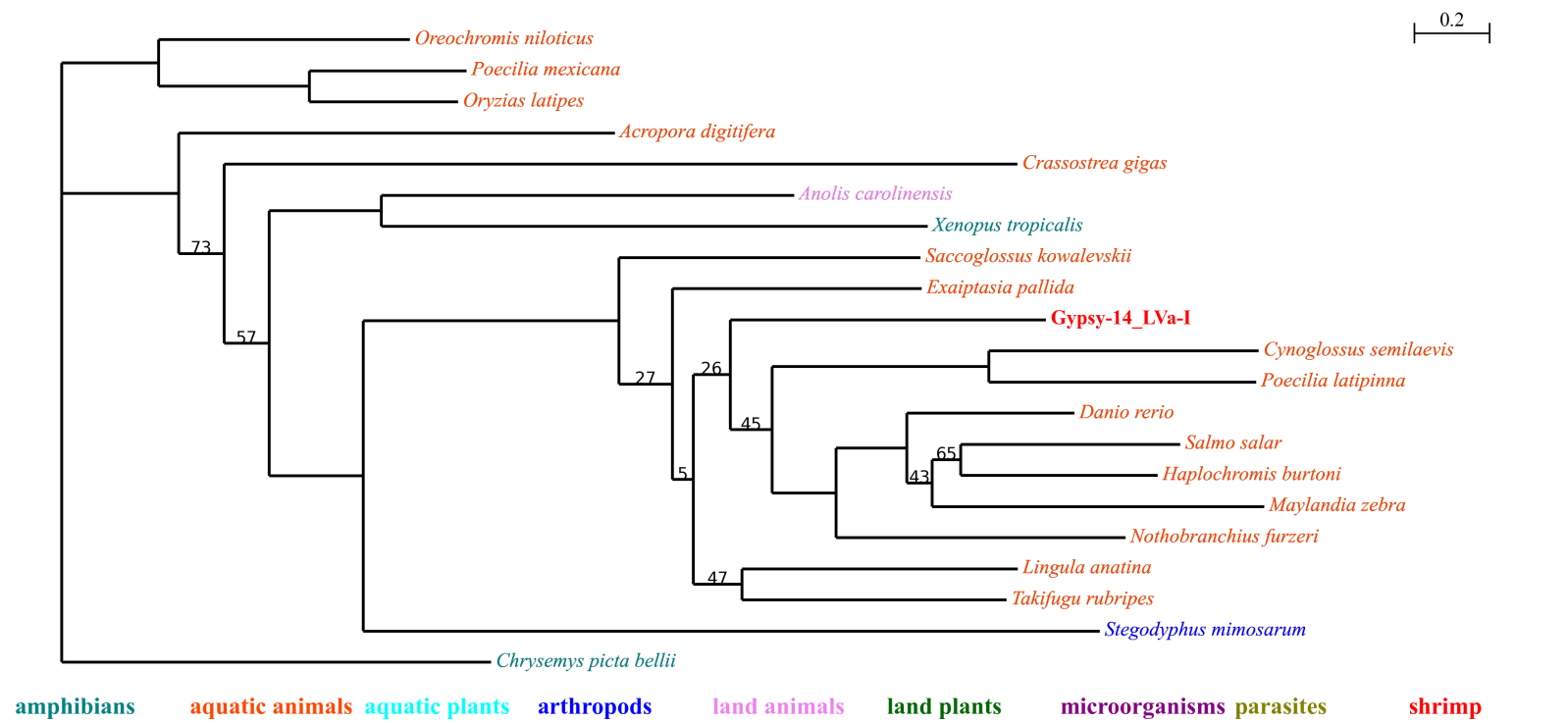


Fig. 2 Phylogenetic tree of Gypsy-14\_LVa-I and its homologues. The *p-value* of AU test is 0.770.



Fig. 3 Phylogenetic tree of Nimb-1\_LVa and its homologues. The *p-value* of AU test is 0.760.

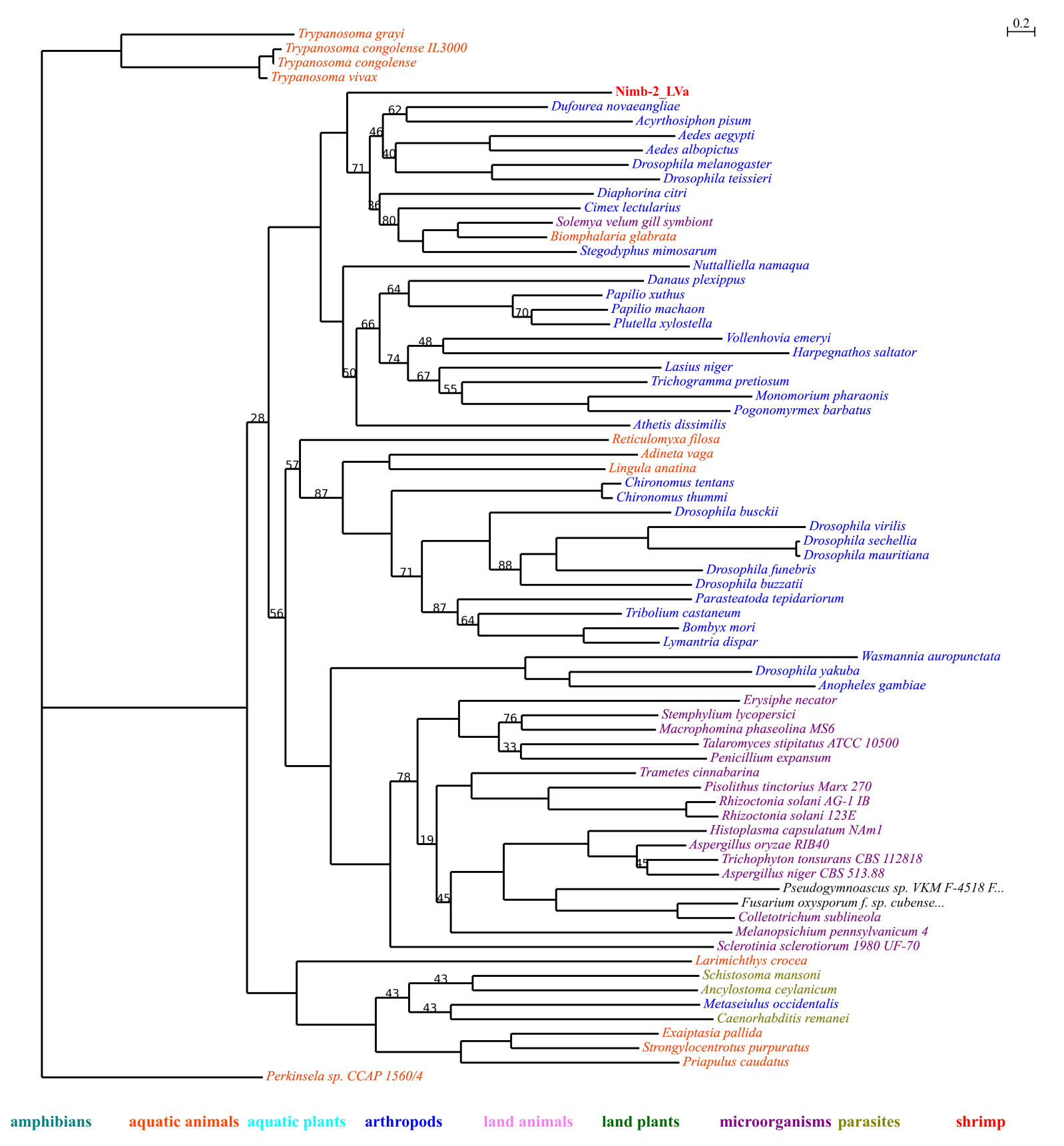


Fig. 4 Phylogenetic tree of Nimb-2\_LVa and its homologues. The *p-value* of AU test is 0.899.

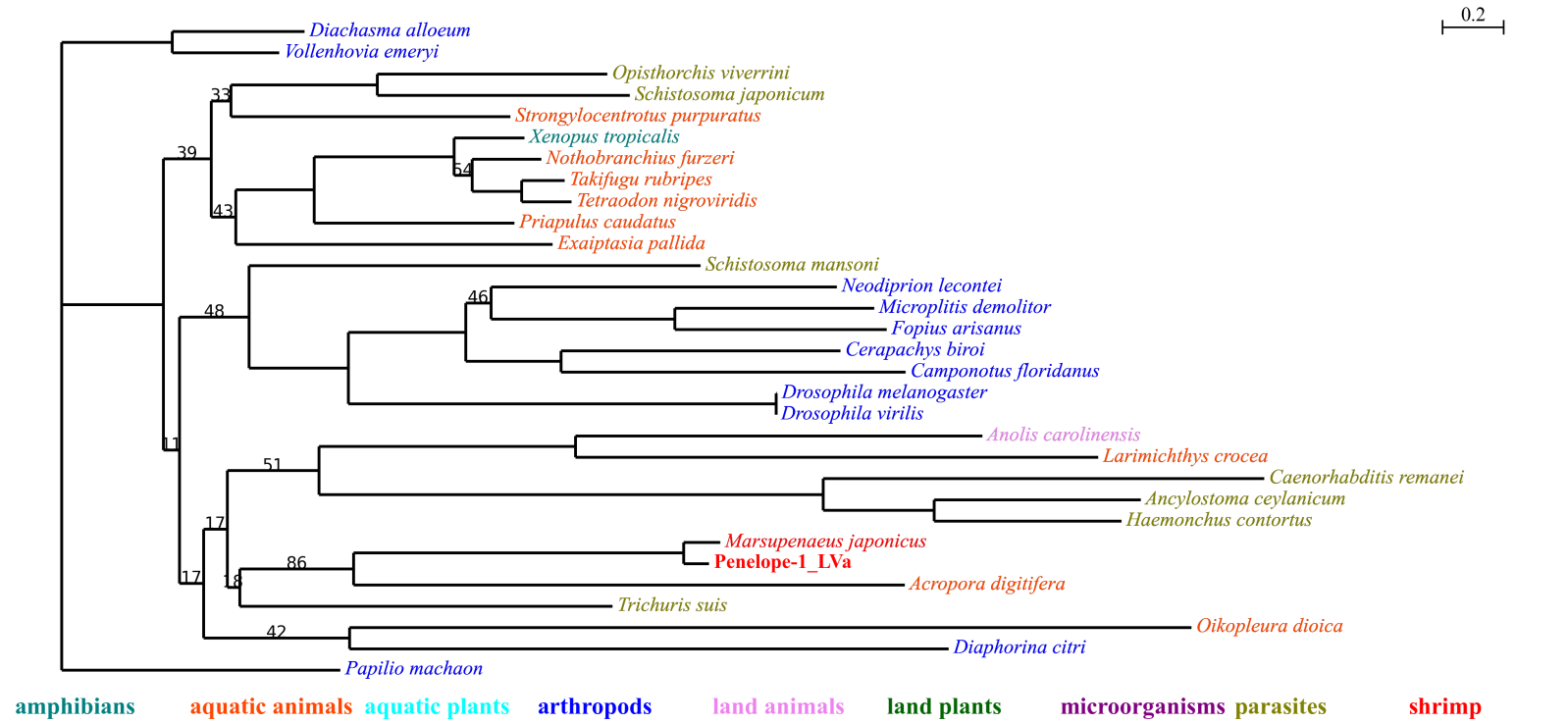


Fig. 5 Phylogenetic tree of Penelope-1\_LVa and its homologues. The *p-value* of AU test is 0.926.

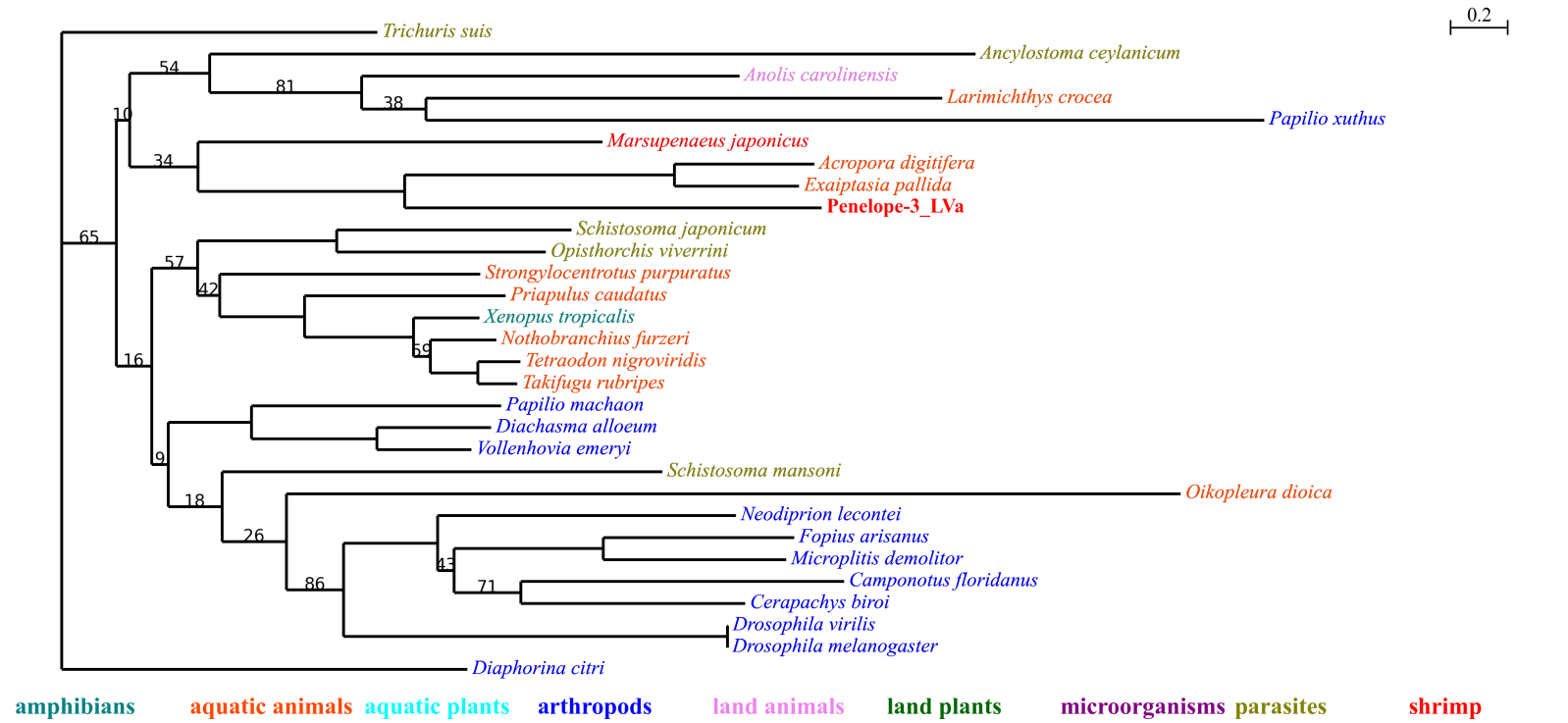


Fig. 6 Phylogenetic tree of Penelope-3\_LVa and its homologues. The *p-value* of AU test is 0.875.

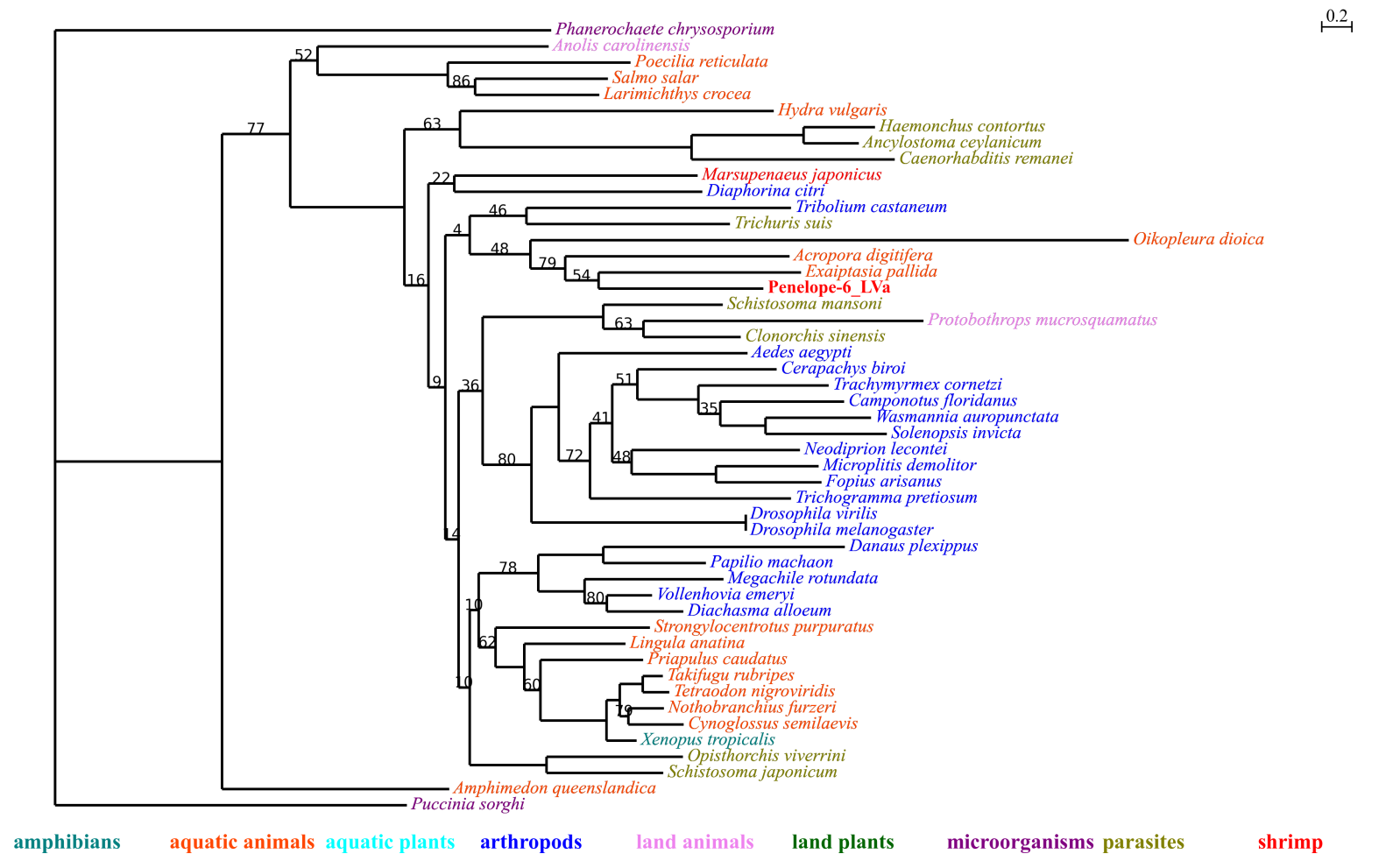


Fig. 7 Phylogenetic tree of Penelope-6\_LVa and its homologues. The *p-value* of AU test is 0.812.

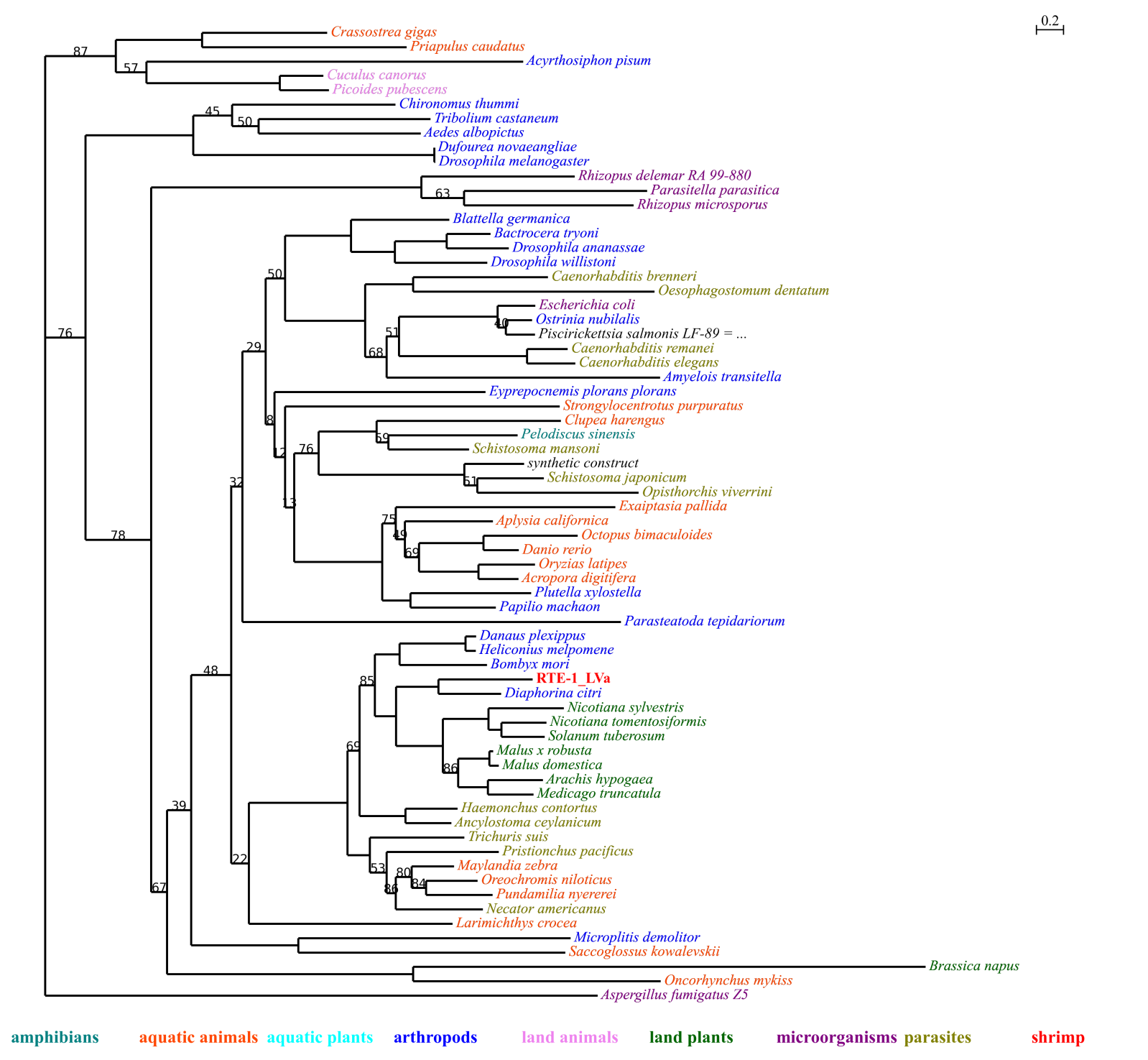


Fig. 8 Phylogenetic tree of RTE-1\_LVa and its homologues. The *p-value* of AU test is 0.893.



Fig. 9 Phylogenetic tree of RTE-2\_LVa and its homologues. The *p-value* of AU test is 0.805.

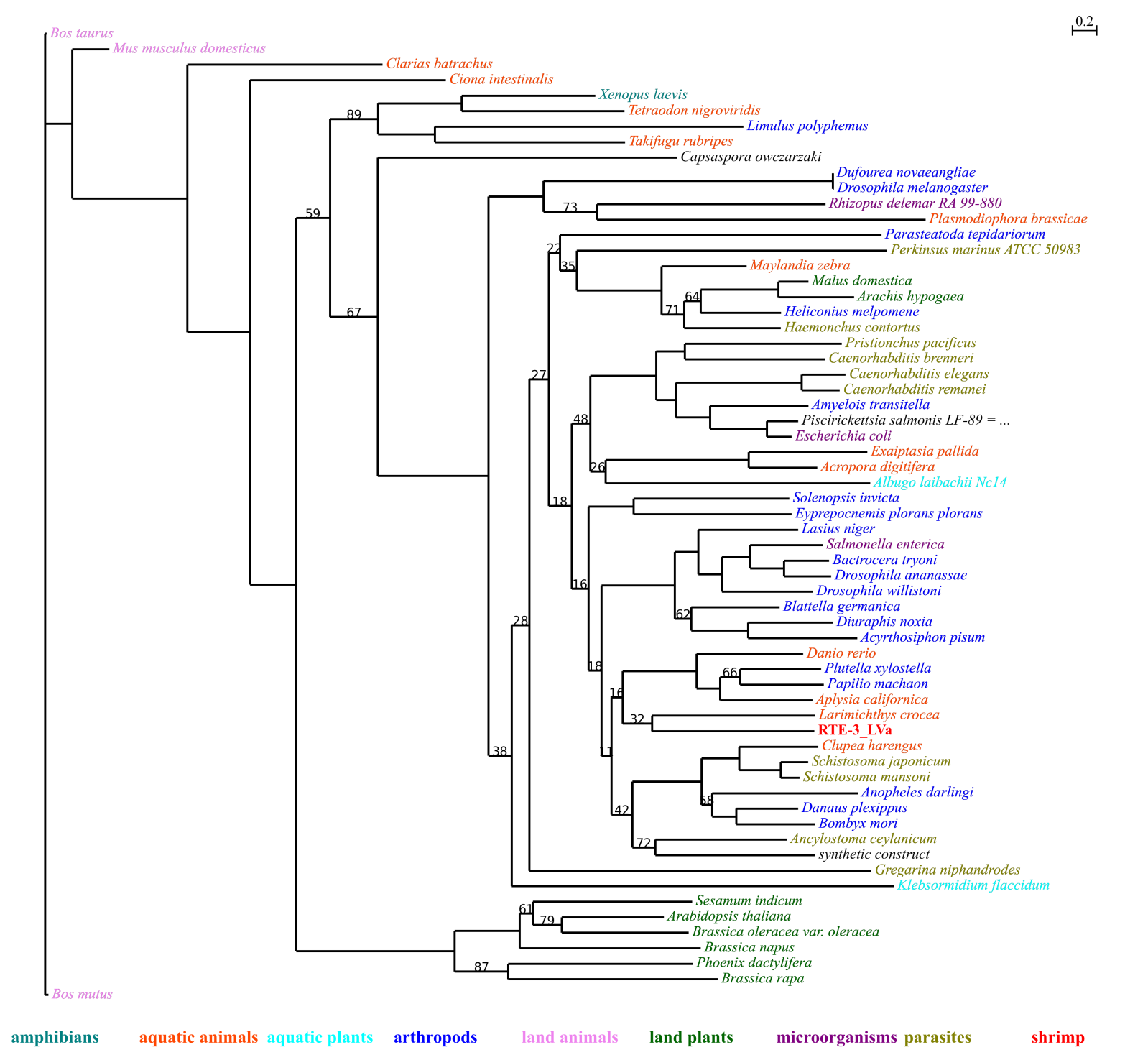


Fig. 10 Phylogenetic tree of RTE-3\_LVa and its homologues. The *p-value* of AU test is 0.813.