P₁₂+T (BI/ML)	P₁₂₃+T (BI/ML)	P₁₂₃+T+R (BI/ML)	P₁₂+T+R (BI)	Node	P₁₂+T+R (ML)
1/94	1/94	1/87	1	I	85
1/100	1/100	1/100	1	II	100
1/98	1/100	1/100	1	III	99
1/100	1/100	1/100	1	IV	100
1/100	1/100	1/100	1	V	100
1/93	1/94	1/100	1	VI	100
0.91/63	1/83	0.99/70	0.72	VII	53
1/100	1/100	1/100	1	VIII	100
1/100	1/100	1/100	1	IX	100
1/100	1/100	1/100	1	X	100
1/100	1/100	1/100	1	XI	100
1/100	1/100	1/100	1	XII	100
1/100	1/100	1/100	1	XIII	100
1/100	1/100	1/100	1	XIV	100
1/97	1/92	1/91	1	XV	94
1/99	1/98	1/100	1	XVI	100
1/100	1/100	1/100	1	XVII	100
1/100	1/100	1/100	1	XVIII	100
1/100	1/100	1/100	1	XIX	100
1/100	1/100	1/100	1	XX	100
1/100	1/100	1/100	1	XXI	100
1/100	1/100	1/100	1	XXII	100
1/100	1/100	1/100	1	XXIII	100
1/100	1/100	1/100	1	XXIV	100
1/100	1/100	1/100	1	XXV	100
1/100	1/100	1/100	1	XXVI	100

Tree of consistent topology (Seven trees, BI / ML)

P₁₂+T+R (ML)

Note Summary of the major clades recovered by different datasets and analytical approaches.Roman numerals correspond to each node of the phylogenetic tree; The support values of the corresponding nodes are represented by Arabic numerals, the left side of "/" is bootstraps of BI, and the right side of "/" is posterior probability of ML.The topological inconsistencies of phylogenetic trees are marked in gray.