

Gene regions included in the 15-locus phylogenetic analysis (Fig 1), with for every partition the number of sequences, total number of sites, informative sites, invariable sites, and model of nucleotide substitution as selected by ModelFinder.

Subset	gene	Model	Seqs	Sites	Infor	Invar
1	5.8S	TNe+R3	325	158	42	61
2	aTUB	GTR+F+R6	82	2056	1021	872
3	bTUB	GTR+F+R6	136	2139	1040	907
4	LSU	SYM+R6	337	898	399	393
5	MCM7	GTR+F+R6	117	732	386	302
6	mtSSU	GTR+F+R5	136	869	328	428
7	RPA1	GTR+F+R6	81	1079	647	362
8	RPA2	TIM3+F+R6	83	1744	979	660
9	RPB1	SYM+R7	212	1450	857	482
10	RPB2	GTR+F+R8	284	2026	1215	639
11	RPC2	GTR+F+R6	82	1569	947	498
12	SF3B1	GTR+F+R6	83	1103	491	570
13	SSU	TIM+F+R5	252	1152	341	575
14	TEF	GTR+F+R6	194	1135	507	485
15	TFB4	TVM+F+R5	79	1178	721	360