

Concatenated ITS and LSU sequences used for analysis in Fig 2. Numbers of informative sites and model selected for each gene using ModelFinder.

Gene	Sequences	Sites	Informative	Invariable	Model
ITS	70	612	269	254	TIM2e+I+G4
LSU	60	855	157	619	TIMe+R3

```
#nexus
```

```
begin sets;
```

```
charset 1_ITS = 1-612;
```

```
charset 2_LSU = 613-1467;
```

```
charpartition mymodels =
```

```
  TIM2e+I+G4: 1_ITS,
```

```
  TIMe+R3: 2_LSU;
```

```
end;
```