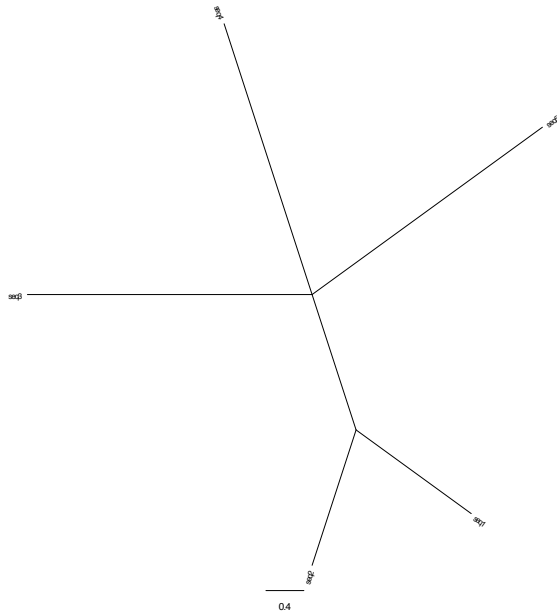


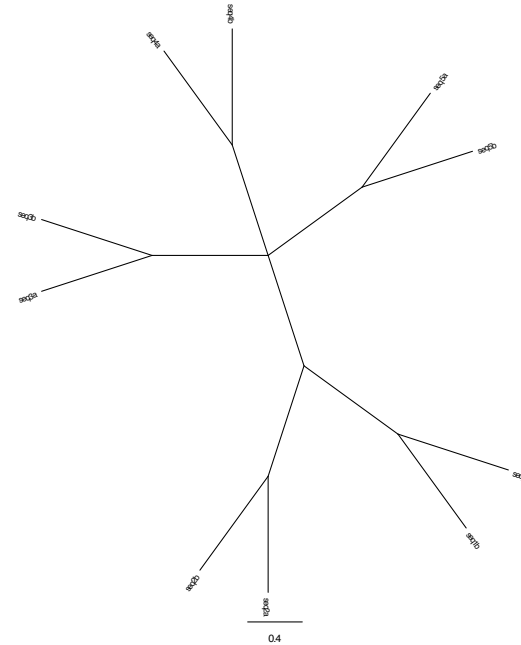
Additional file 2

The 10-taxon tree used in simulation 1c obtained by dividing each terminal taxon of the 5-Taxon tree (1a and 1b), and re-distributing the total tree length evenly among all branches.

5-taxon tree used in
scenarios 1a and 1b



10-taxon tree used in
scenarios 1C



Total tree length = 13.5 substitutions per codon for both trees

5-taxon tree (Simulation Study 1a and 1b):

```
((seq1:1.5, seq2:1.5):1.5, seq3:3, seq4:3, seq5:3);
```

* Note this the tree topology and branch lengths used in the simulation study of Wong et al. (2005) Genetics.168(2):1041-1051.

10-taxon tree (Simulation Study 1c):

```
(( (seq1a:0.85, seq1b:0.85):0.85, (seq2a:0.85, seq2b:0.85):0.85):0.85,  
 (seq3a:0.85, seq3b:0.85):0.85, (seq4a:0.85, seq4b:0.85):0.85, (seq5a:  
 0.85, seq5b:0.85):0.85);
```