

**Appendix S10. Target-capture alignment statistics.** Loci excluded refer to the number of excluded loci based on excessively long branch lengths, and loci retained is the final number of loci retained for both ML and coalescent analyses. Empty sequences inserted refers to amount of missing data. Min = minimum; Bp = base pairs.

	<b>TC Alignment 1 (min4)</b>	<b>TC Alignment 2 (min10)</b>	<b>TC Alignment 3 (min20)</b>
<b>Species</b>	40	40	40
<b>Minimum number of species per locus</b>	4	10	20
<b>Loci retained for ML analysis</b>	348	337	310
<b>Loci excluded</b>	10	7	7
<b>Loci retained for Astral analysis</b>	338	330	303
<b>Length of concatenated sequences (bp)</b>	261,975	257,519	244,272
<b>Empty sequences inserted</b>	3,147	2,781	2,092