



Figure 2: Phylogenomic tree based on the AHE dataset. **A.** Maximum likelihood tree of the AHE dataset. Nodes poorly supported (SH-aLRT < 80% or UFBS < 95%) are respectively highlighted with gray triangles and circles. For graphical purposes, some branches were shortened to half of their length (//). Pictures of weevils are linked to corresponding species. **B.** Partitioning scheme of a theoretical AHE loci. Flanking and inserted partitions (f1-3) are highlighted in grey and coding partitions (c1-3) are highlighted in green. The region targeted by the probes (P) is shown in red but does not appear in the final supermatrix. Credits: JH.