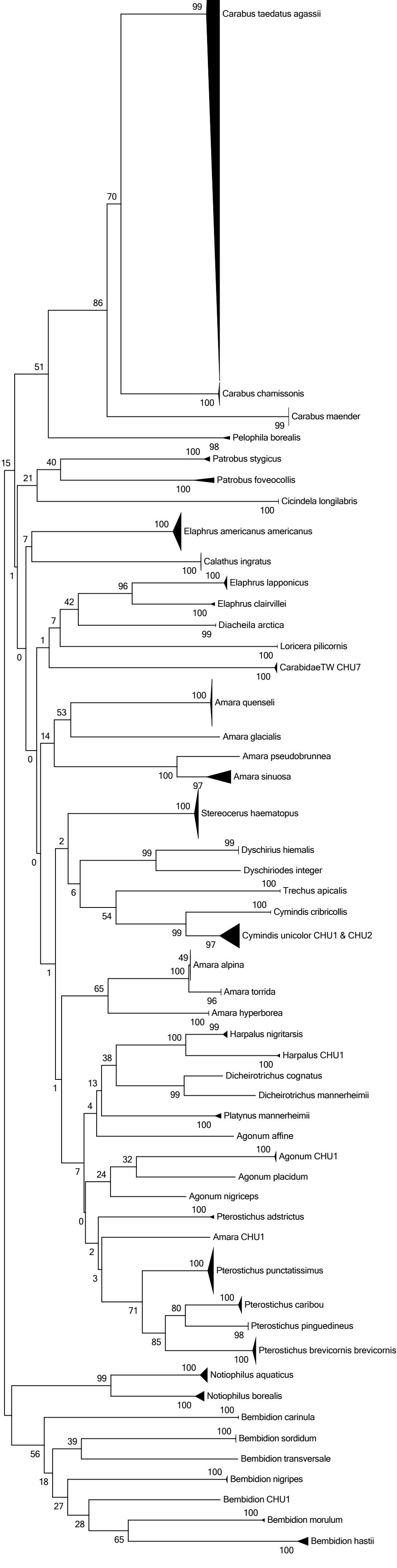


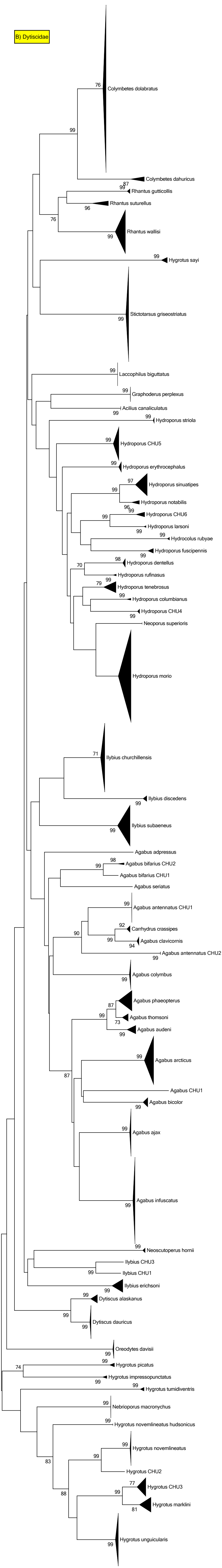
### **Additional file 3 – Neighbour-joining trees of barcode sequences of Coleoptera of Churchill.**

Neighbour-joining phenograms based upon Kimura-2-parameter genetic distances for 3194 COI sequences ( $\geq 300$ bp) from Coleoptera specimens from Churchill. Clusters representing species or provisional species (see Methods) are collapsed into triangles, with the vertical dimension corresponding to sample size and the horizontal dimension corresponding to intraspecific genetic variability. Bootstrap values are based on 1000 pseudoreplicates, with values shown for nodes having values  $\geq 70\%$ . All sequences of at least 300 bp were included, except in cases where there was a lack of overlapping nucleotides among sequences (ProcessIDs of specimens omitted from analysis: TWCOL605-10, TWCOL141-09, TWCOL005-09, TWCOL204-09, AWWBC026-09, HMCOC345-07, TWCOL286-09, TWCOL080-09, TWCOL402-10, EBCCH402-1, and HMCOC696-09). To enable bootstrap analysis, 4 data partitions were run separately: A) family Carabidae; B) family Dytiscidae; C) family Staphylinidae; and D) all other families together.

A) Carabidae

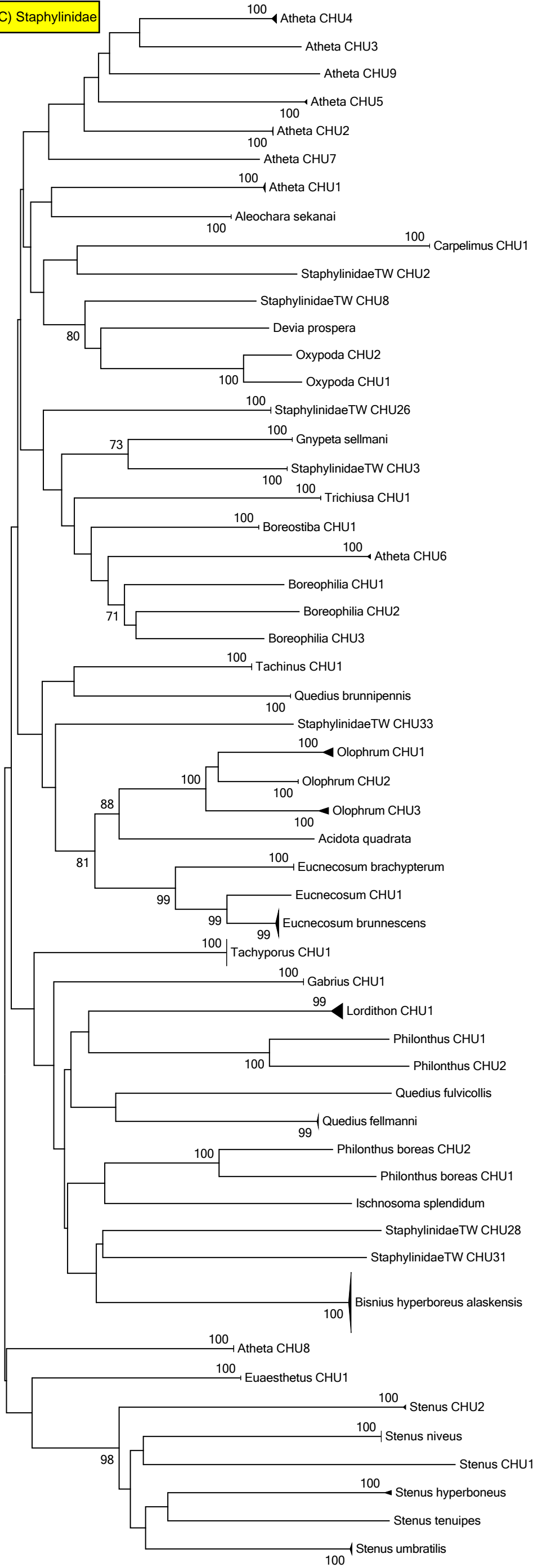


B) Dytiscidae



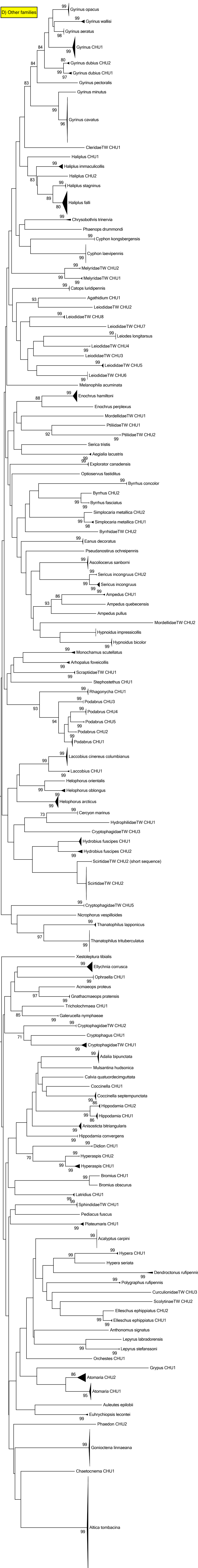
0.02

C) Staphylinidae



0.02

D) Other families



0.02