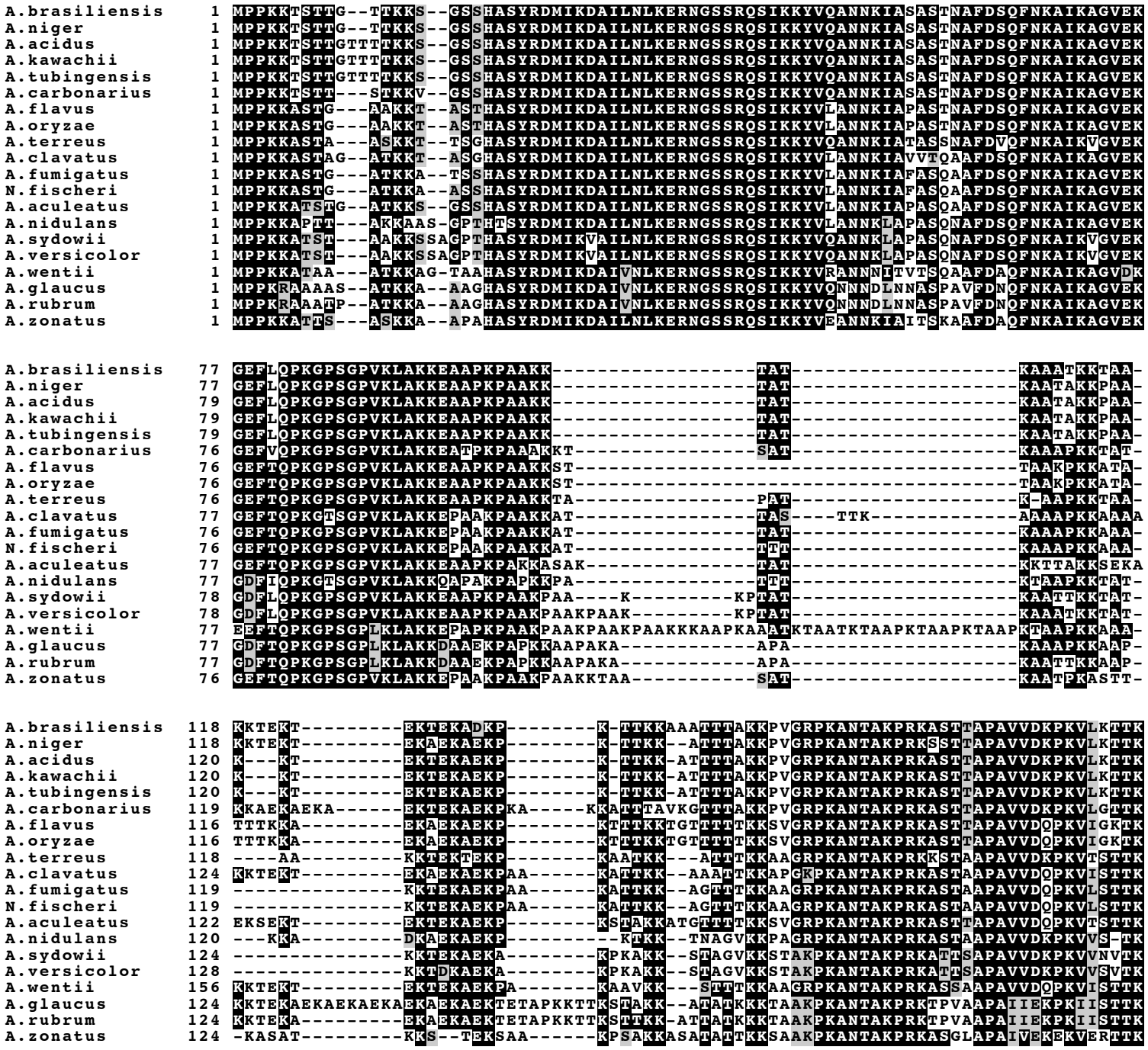
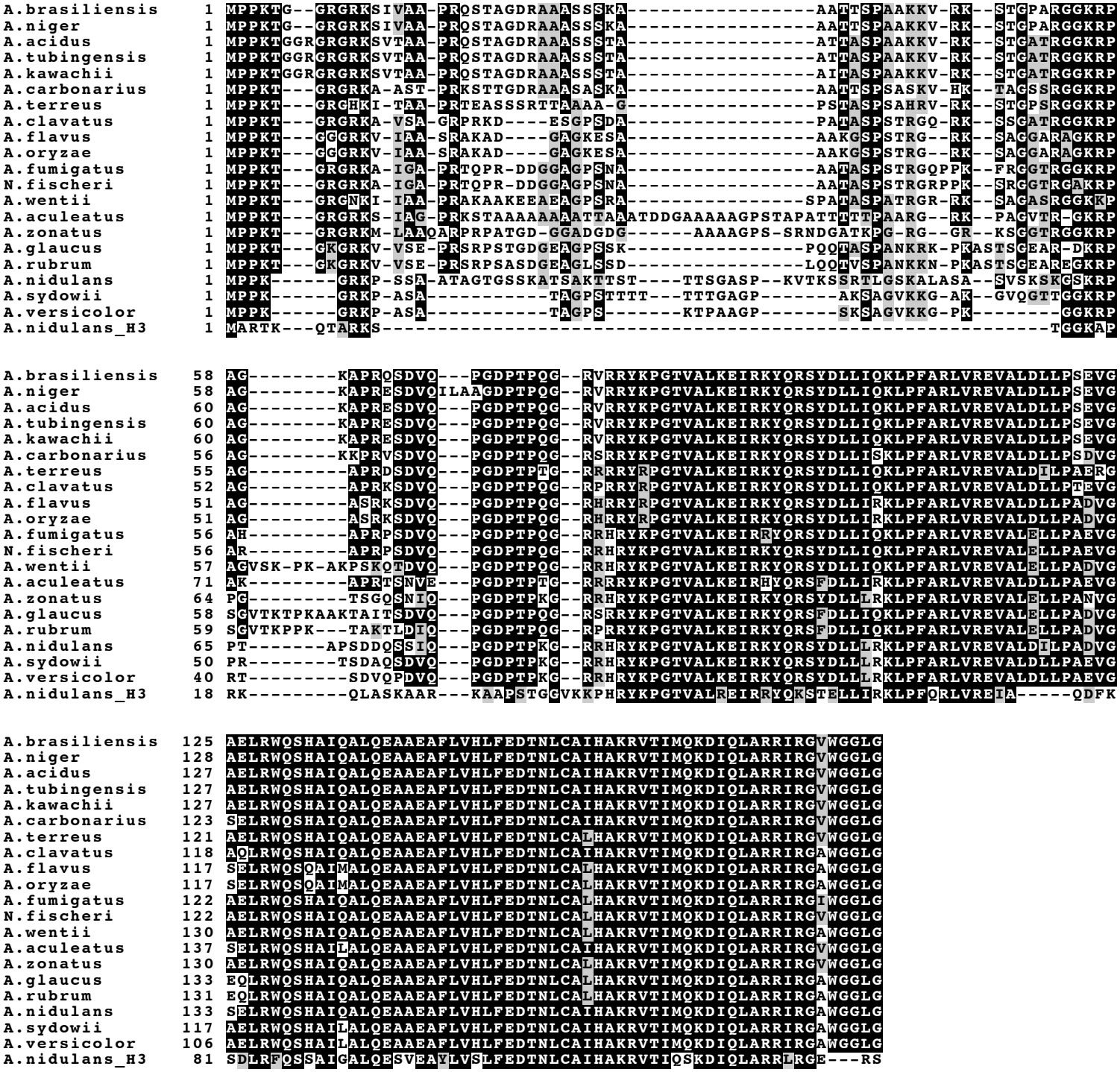
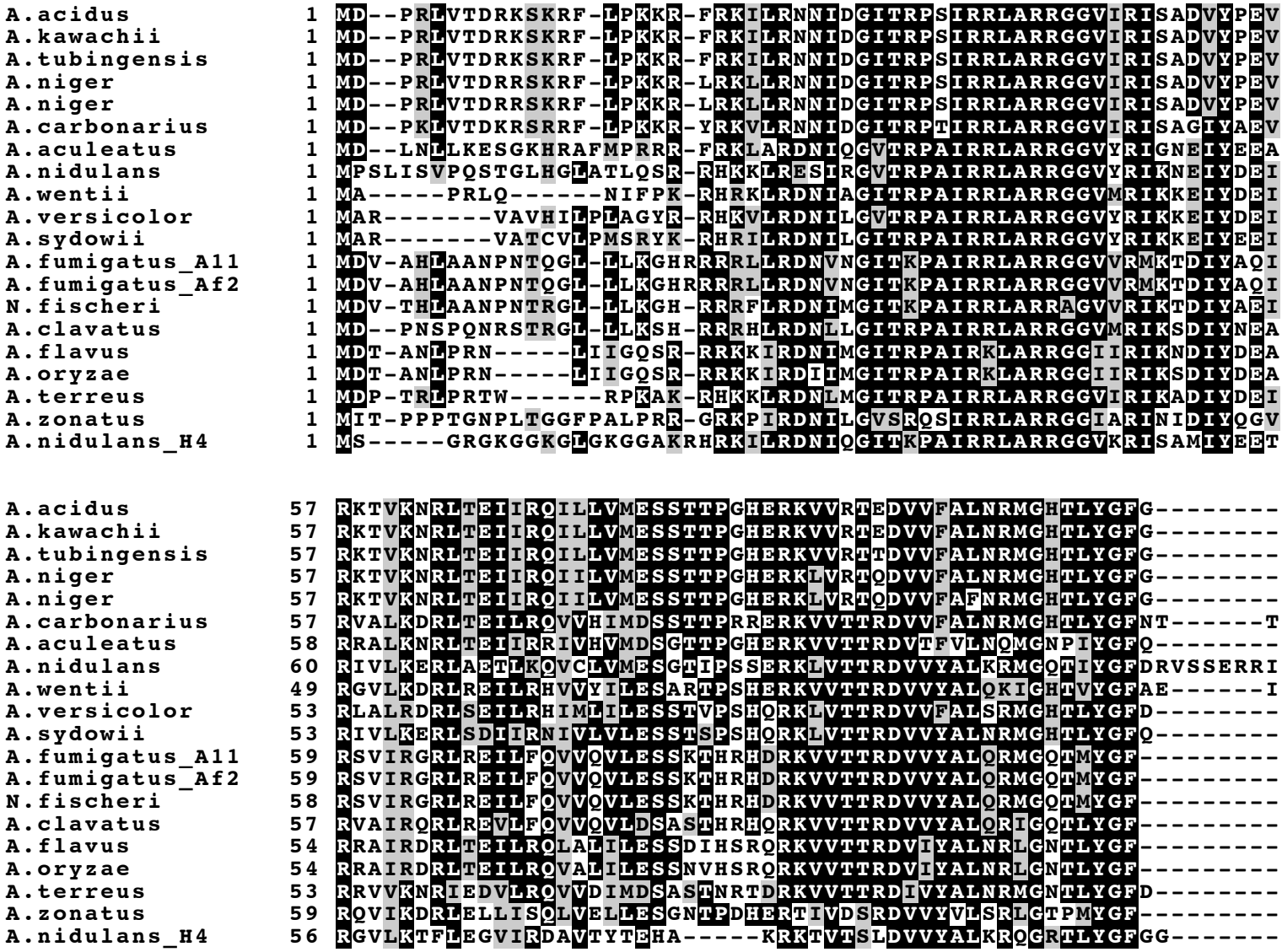


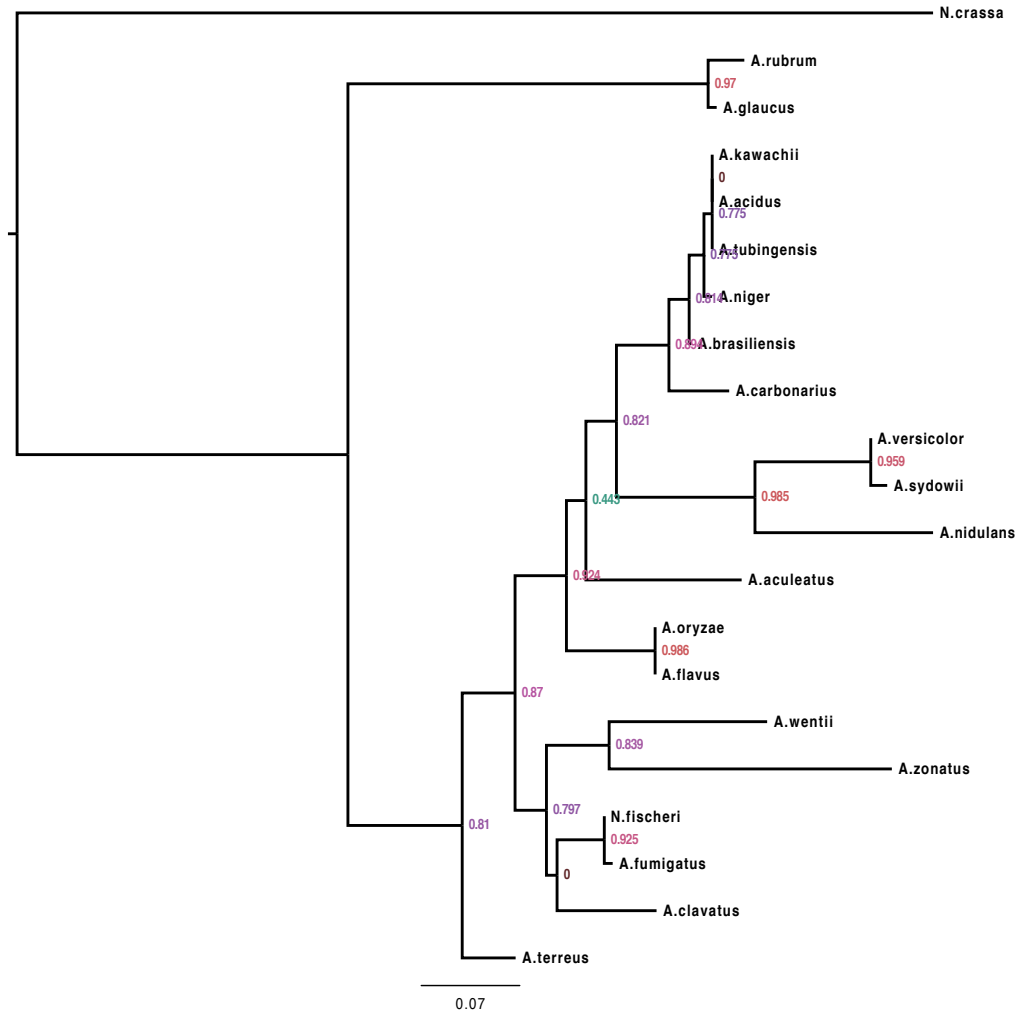
Histone H1 Alignment



Centromeric Histone H3
Alignment



Putative H4 Homologue
Alignment



H1

CenH3

Maximum likelihood phylogenetic trees

Additional File 34. Histones of the Aspergilli

This file shows alignments of the histone H1, the centromeric histone H3 and the putative histone showing similarity with histone H4 for different species of *Aspergillus*. Alignments carried out with MAFFT (G-ins-i) (http://mafft.cbrc.jp/alignment/server/) and visualised with BoxShade . (http://www.ch.embnet.org/software/BOX_form.html). The last page of this file compares the phylogenetic trees of the two most variables histones, H1 and CenH3. Trees are maximum likelihood trees derived from a MAFFT (G-ins-i) alignment curated with BMGE (http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::BMGE) with default settings. Maximum likelihood trees with PhyML (http://phylogeny.lirmm.fr/phylo_cgi/alacarte.cgi). Digits at the nodes are aLTRs (approximate likelihood ratio test values).