

**Caption of FIG.5 (next page).** DNA and amino acid sequence comparison of the putative *K. splachnirima* MAT1-1  $\alpha$ -box (FIG. 5A) and MAT1-2 HMG domain (FIG.5B) with other species: *Xanthoria polycarpa*, *Lobaria pulmonaria*, *Cladonia grayi*, *Dibaeis baeomyces*, *Aspergillus fumigatus* (non-lichenised), and *Cladonia galindezii*. Sequence portions are identical to those specified and illustrated in FIG. 3 of the main article. Amino acid sequences are depicted underneath corresponding DNA sequences, their orientation (5' to 3' and N to C terminal) is from left to right. Amino acid names are given in one-letter IUPAC nomenclature and were colour-coded according to polarity. Stretches of DNA sequence without translation are conserved introns; between 29 and 37 badly aligned nucleotides of the MAT1-2 intron were replaced by (...) to save space. Primer sites of the successfully used degenerate primers are indicated by green arrows below the alignments. Note that the sequences of the degenerate primers are based only on subsets of the illustrated alignments, which are *C. grayi*, *L. pulmonaria* and *X. polycarpa* for MAT1-1  $\alpha$ -box primers and *C. galindezii*, *L. pulmonaria*, *X. polycarpa*, *X. parietina* as well as *X. elegans* and *X. flammea* for MAT1-2 HMG domain primers. HMG sequences of *X. elegans* and *X. flammea* were omitted from this illustration, because they are very similar to the other *Xanthorias* and contribute no additional ambiguous positions to the degenerate primer sites. The alignment images were generated with Geneious R7 and manually edited in GIMP.

FIG. 5A.

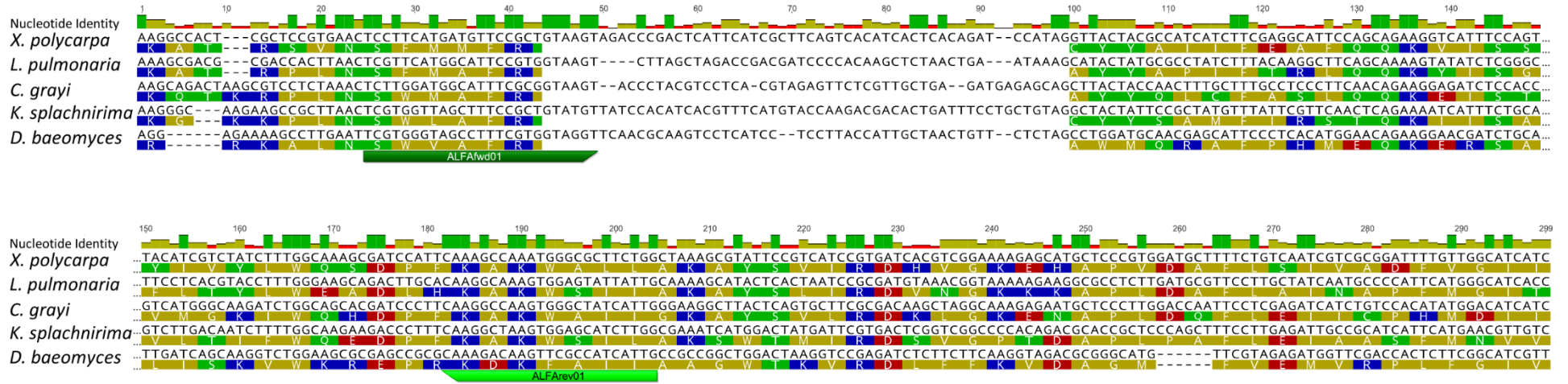


FIG. 5B.

