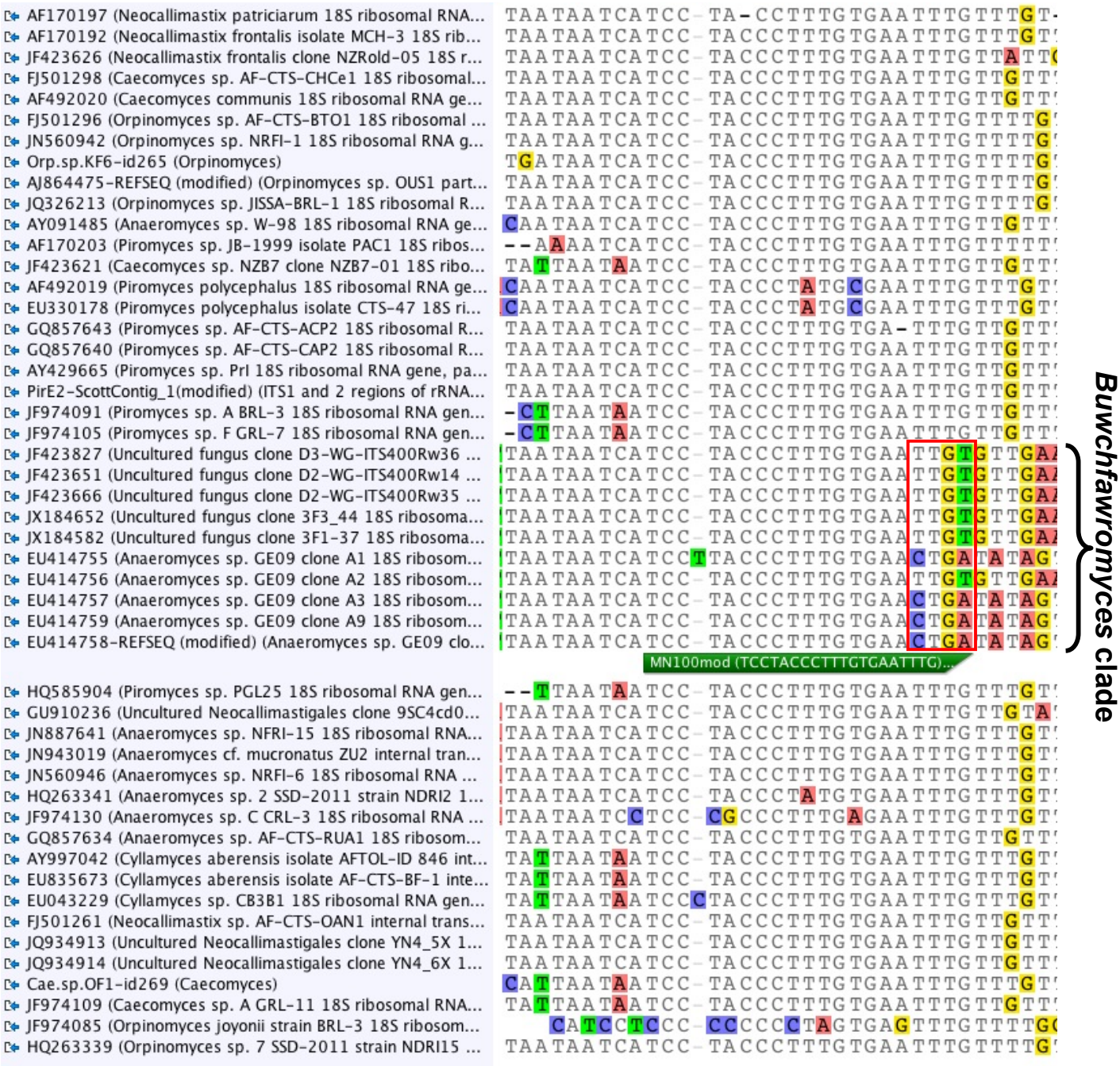

SuppFig. 2. Alignment of part of the ITS1 region across a range of anaerobic fungi from all the known genera. The sequences of the modified MN100 primer used by Liggenstoffer et al. (2010) (TCCTACCCTTTGTGAATTTG) is indicated (green). For all clades except *Buwchfawromyces*, there is a good match for this primer. However, for members of the *Buwchfawromyces*, there are several mismatches at the 3' end of the primer binding site (red square) which are likely to impede PCR amplification.