

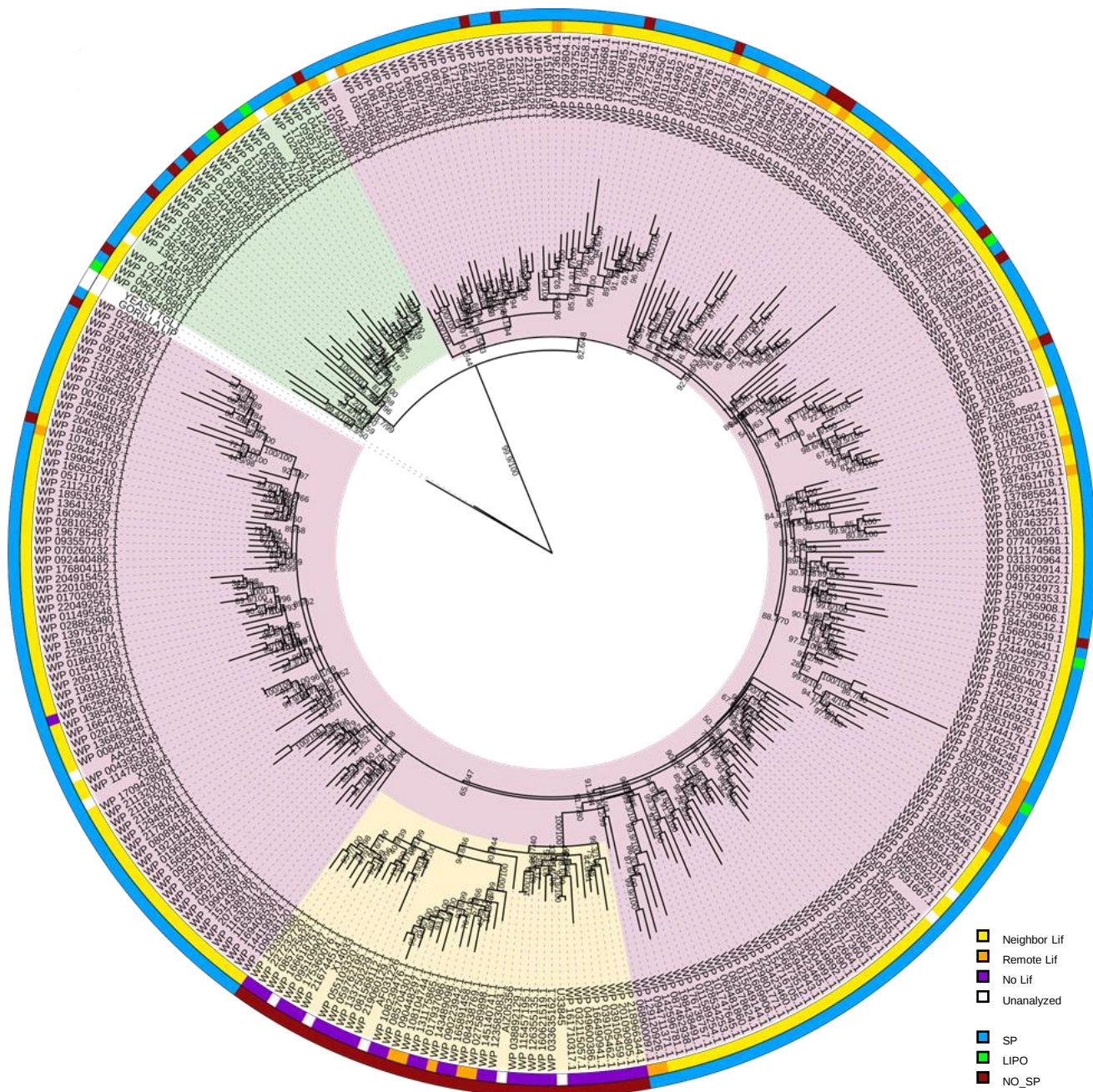


Figure S1: Phylogenetic tree and Lif coexistence of subfamily I.1 and I.2 lipases
 Accession numbers for all lipase sequences and confidence levels (SH-aLRT/UFboot) for all branches in Fig 2 are indicated.



Figure S2: Sequence comparison of the *P. fragil* *IP. vulgaris* clade and other clades of subfamily I.1

Comparison of full-length sequences of the *P. fragil* *IP. vulgaris* clade and other clades of subfamily I.1. Residue positions with particularly large differences (Fig. 3A) are indicated by a yellow background. The active centers (S82, D229, and H251 in PAL) are indicated by red triangles. The numbers of the corresponding amino acid residues of PML and PAL are shown below the logo. The background of the residue numbers predicted to interact with Lif in the predicted complex structure of PAL and its cognate Lif is shown in light blue.