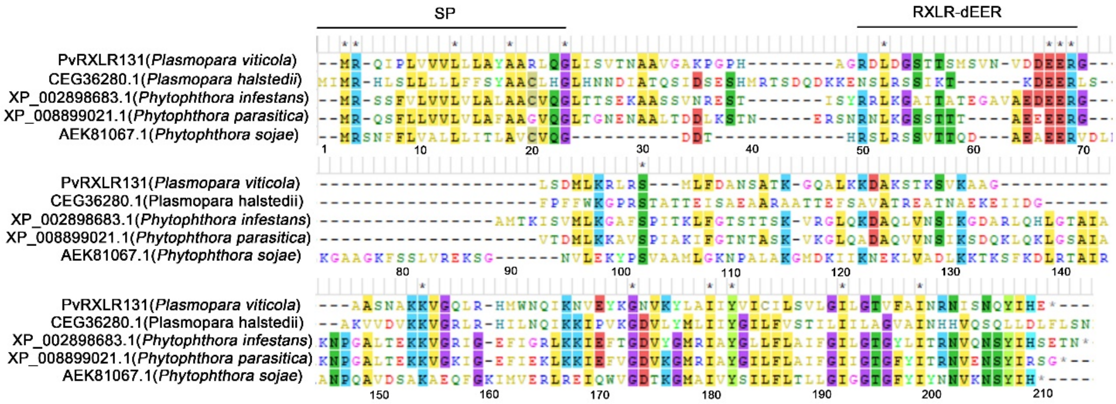
FIGURE S1



S1 Fig. Sequence alignment of PvRXLR131 and its homologs in oomycetes. The alignment was conducted by using ClustalW in MEGA7 software. Conserved sites at 60% level are shown in background color. The predicted signal peptide and RXLR-dEER motif are indicated. Species names are marked in the round brackets and the corresponding accession numbers are marked on the left.