



**Supplementary Figure S1.** Results of multi-sequence alignment of Pag\_A\_036054-RA with a different fungus named VeA. Fungal sequences are named after their genus names and UniProtKB numbers, with the Pag\_A\_036054-RA protein sequence located at the bottom.



**Supplementary Figure S2.** The BLASTp result of Pag\_A\_036054-RA in *P. alba*. The similarity between the amino acids from 126th to 507th in the protein sequence of TKR79117.1 in *P. alba* and the amino acids from 80th to 498th in the protein sequence of Pag\_A\_036054-RA *P. alba* × *P. glandulosa* is as high as 89%.