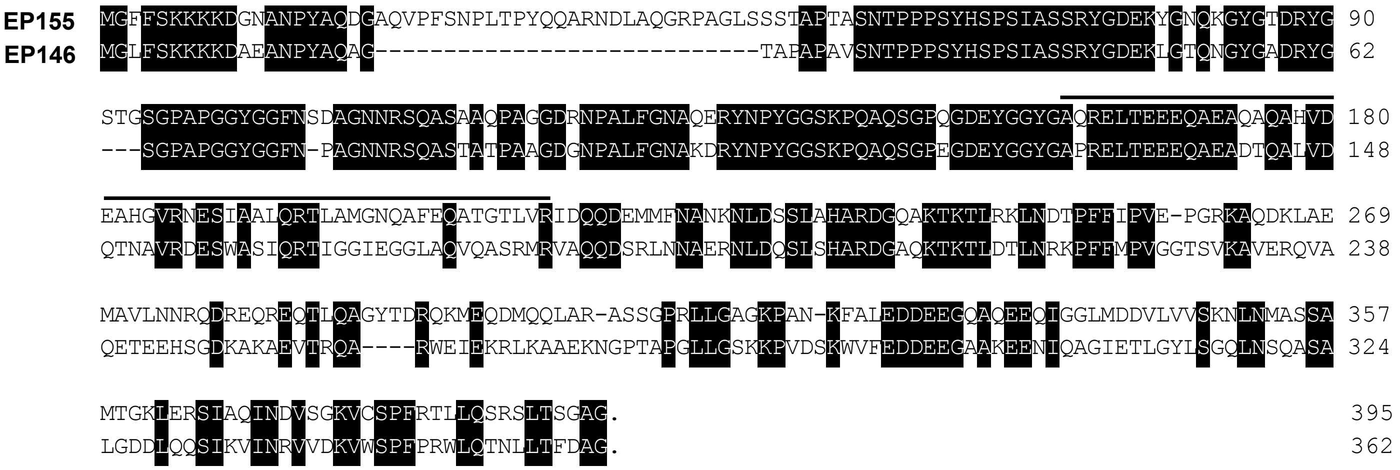

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EP155 MGFFSKKKKDGNANPYAQDGAQVPFSNPLTPYQQARNDLAQGRPAGLSSSTAPTASNTPPPSYHSPSIASSRYGDEKYGNQKGYGTDRYG 90
EP146 MGLFSKKKKDAEANPYAQAG----------------------------TAPAPAVSNTPPPSYHSPSIASSRYGDEKLGTQNGYGADRYG 62

      STGSGPAPGGYGGFNSDAGNNRSQASAAQPAGGDRNPALFGNAQERYNPYGGSKPQAQSGPQGDEYGGYGAQRELTEEEQAEAQAQAHVD 180
      ---SGPAPGGYGGFN-PAGNNRSQASTATPAAGDGNPALFGNAKDRYNPYGGSKPQAQSGPEGDEYGGYGAPRELTEEEQAEADTQALVD 148

      EAHGVRNESIAALQRTLAMGNQAFEQATGTLVRIDQQDEMMFNANKNLDSSLAHARDGQAKTKTLRKLNDTPFFIPVE-PGRKAQDKLAE 269
      QTNAVRDESWASIQRTIGGIEGGLAQVQASRMRVAQQDSRLNNAERNLDQSLSHARDGAQKTKTLDTLNRKPFFMPVGGTSVKAVERQVA 238

      MAVLNNRQDREQREQTLQAGYTDRQKMEQDMQQLAR-ASSGPRLLGAGKPAN-KFALEDDEEGQAQEEQIGGLMDDVLVVSKNLNMASSA 357
      QETEEHSGDKAKAEVTRQA----RWEIEKRLKAAEKNGPTAPGLLGSKKPVDSKWVFEDDEEGAAKEENIQAGIETLGYLSGQLNSQASA 324

      MTGKLERSIAQINDVSGKVCSPFRTLLQSRSLTSGAG.                                                    395
      LGDDLQQSIKVINRVVDKVWSPFPRWLQTNLLTFDAG.                                                    362
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Figure S2 Amino acid alignment of the Sec9-like protein candidate *vic2a* alleles in strain EP155 (*vic2a-2*) and EP146 (*vic2a-1*). Note the large indel near the N-terminus and the high level of polymorphism in the C-terminal half of the coding region. A Pfam DUF3359 domain, found only in the EP155 allele, is indicated by a line above the EP155 sequence. Amino acid identity is indicated by the solid background, while dashes indicate indels.