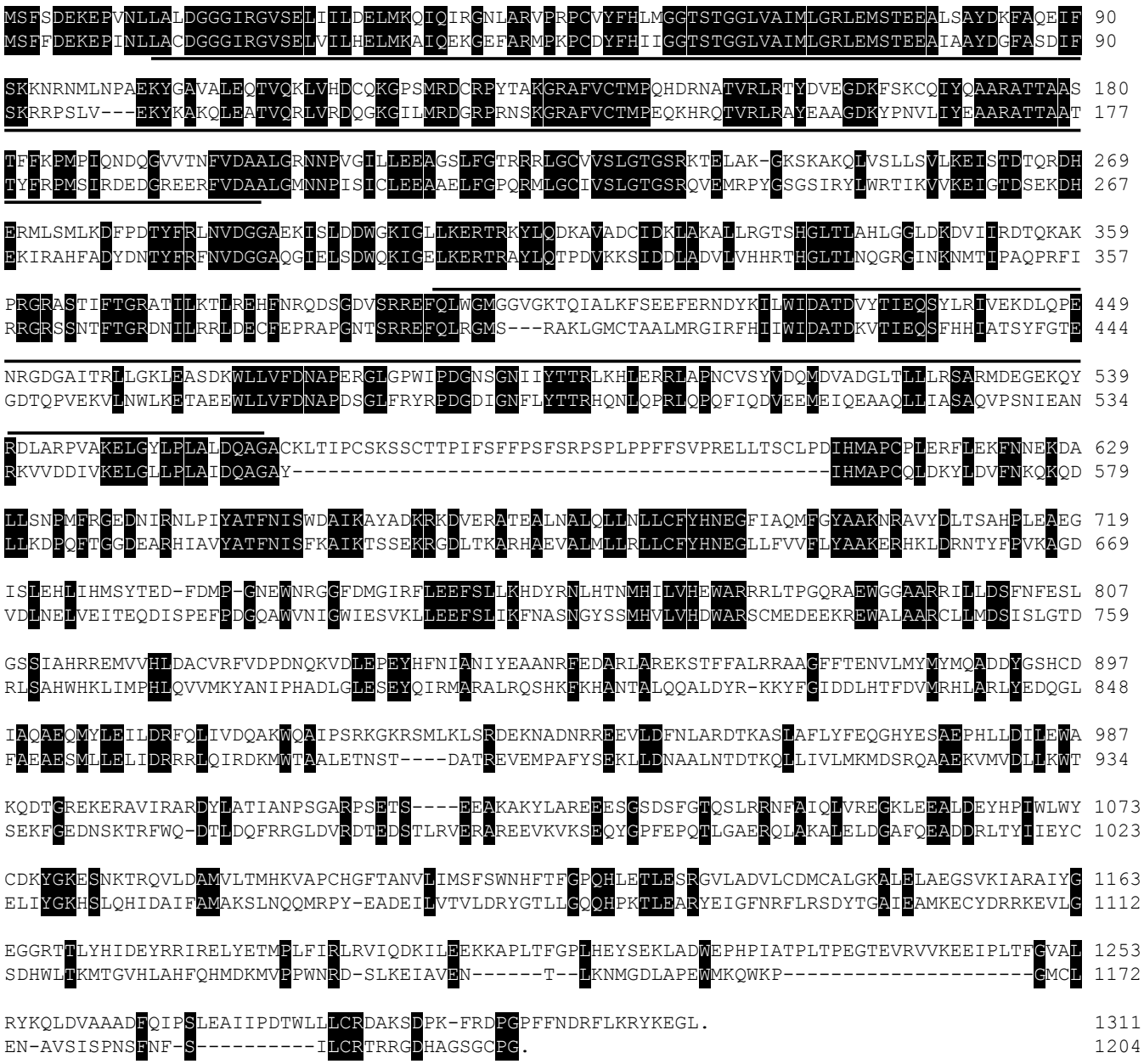

Figure S1 Amino acid alignment of candidate *vic2* alleles in strain EP155 (*vic2-2*) and in strain EP146 (*vic2-1*) performed using MegAlign in Lasergene (DNASTAR Inc. Madison WI). Note the high level of polymorphism that spans nearly all of the patatin-like protein (39% identity). A region in the N-terminal portion of the ORF (aa 13-212 in the EP155 sequence) containing a patatin-like phospholipase domain (PLA2; EC3.1.1.4) consisting of the esterase box GTSTG and anion binding element DGGGXRG (Scherer et al., 2010 Patatin-related phopholipase A: nomenclature, subfamilies and functions in plants. *Trends in Plant Science* **15**:693-700), and conserved in both the *vic2-1* and *vic2-2* alleles, is underlined. An NB-ARC, or P-loop NTPase domain, detected in the EP155 genome sequence but not in the EP146 sequence, is indicated by an overline extending from aa 396-561. Amino acid identity is indicated by the solid background, while dashes indicate deletion events.