

Fragaria vesca g12690	G I P D R V T T E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Arabidopsis thaliana At4g14210	G V P E R V T D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Capsicum annuum	G V P D R V T D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Solanum lycopersicum	G V P D R V T D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Glycine max PDS1	G V P E R V T D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Zea mays	G V P D R V N D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q
Oryza sativa Osl_010044	G V P D R V N D E V F I A M S K A L N F I N P D E L S M Q C I L I A L N R F L Q

Fig. S7. Amino acid sequences for published plant *PDS* genes aligned against *Fragaria vesca*.

The extraction shown is the alignment for exon 7 of *F. vesca* g12690 (Fv assembly v4). The solid line above the alignment indicates the position of the CRISPR/Cas9 edited nucleotide target sequence.