

Figure S4. Schematic representation of the motifs contained in the N-terminal domain of the avocado CC-type NLR proteins. (A) The consensus sequence pattern of the MADA motif, which was identified in a total of 30 avocado CC-NLR proteins. Red boxes refer to residues that were highly conserved and previously reported in plant species (Adachi et al., 2019a). (B) Three clearly distinguishable major groups (A, B and C) were identified after aligning and resolving their phylogenetic relationships based only on the CC domain, which contains a conserved array of amino acids known as the EDVID motif or the EDVID-corresponding area (Wróblewski et al., 2018). WebLogo (Crooks et al., 2004) with small-sample correction (Schneider et al., 1986) was used to generate the graphical representations of both domains (N-terminal domain CC-type and NBS, respectively).