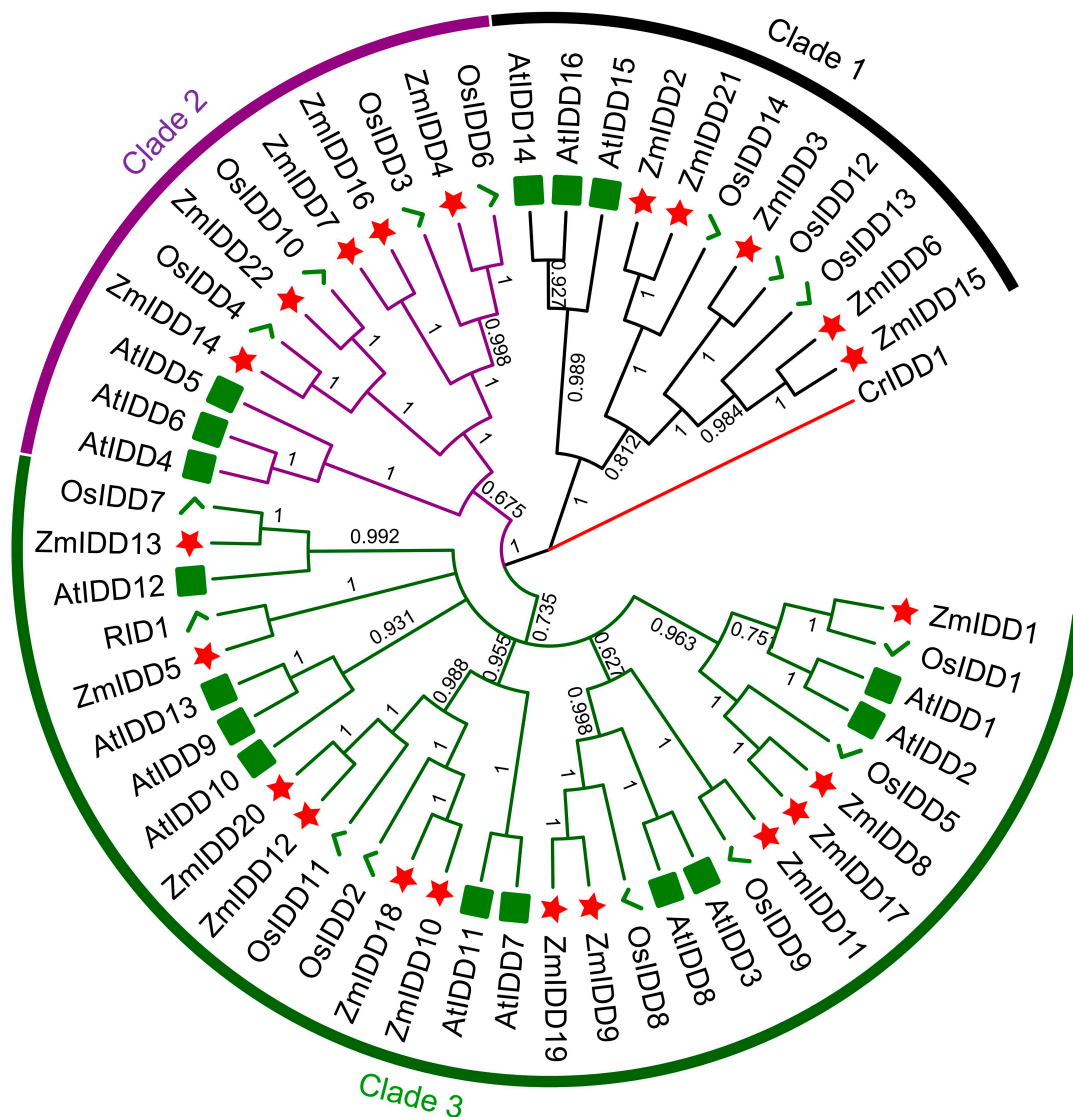**Figure S1**. Phylogenetic tree of full-length ZmIDD, AtIDD and OsIDD proteins using the Minimum Evolution method. The optimal tree with the sum of branch length = 3.31299193 is shown. The analysis involved 54 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 94 positions in the final dataset. The different colored arcs indicate subfamilies of the IDD proteins. Different colour shapes represent IDDs from maize (☆), rice (√), and Arabidopsis (□). IDD in *Chlamydomonas reinhardtii* was selected as outgroup.

Figure S2. Phylogenetic tree of full-length ZmIDD, AtIDD and OsIDD proteins using the Neighbor-Joining method. The optimal tree with the sum of branch length = 3.31299193 is shown. The analysis involved 54 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 94 positions in the final dataset. The different colored arcs indicate subfamilies of the IDD proteins. Different colour shapes represent IDDs from maize (☆), rice (√), and Arabidopsis (□). IDD in *Chlamydomonas reinhardtii* was selected as outgroup.

Figure S3. Interaction networks between ZmSnRK and ZmIDD proteins.