Supplementary information

The gynoecious CmWIP1 transcription factor interacts with CmbZIP48 to inhibit carpel development.

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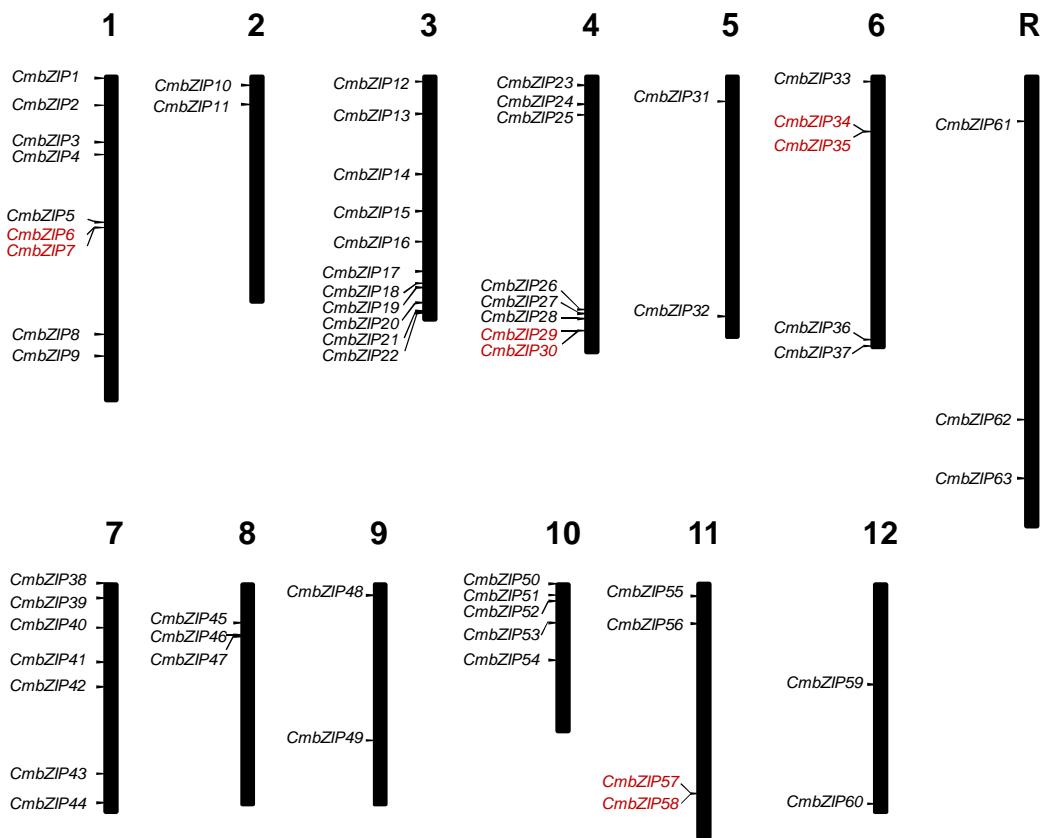
Supplementary Figure 1: Distribution of *CmbZIP* genes on melon chromosomes.

The scaled representation shows the physical locations of the *CmbZIPs* genes on the 12 melon chromosomes. Unanchored scaffolds are assembled in a random chromosome named R. Tandem-duplicated genes are indicated in dark red.
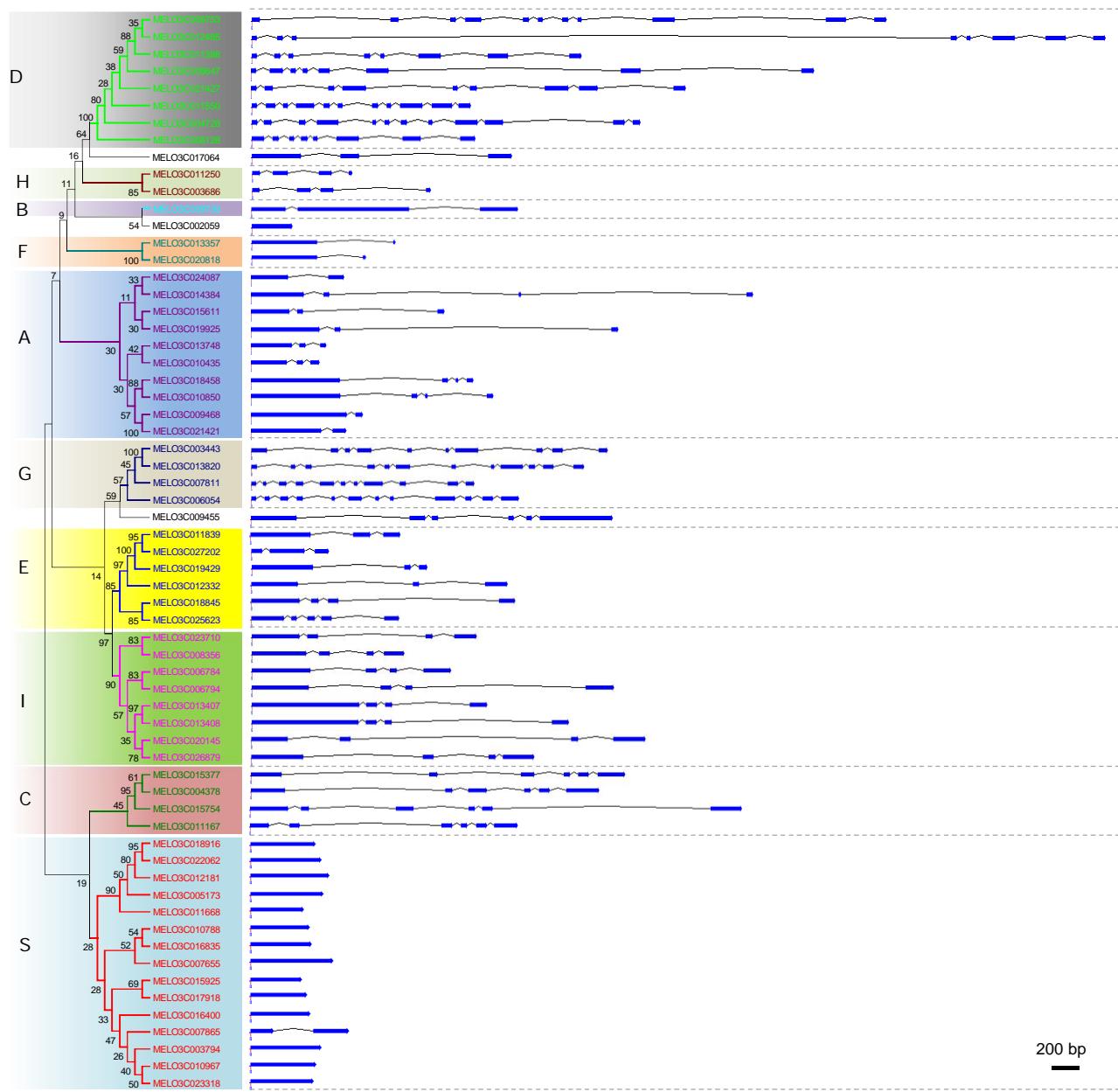
Supplementary Figure 2: Phylogenetic analysis and exon-intron structures of the melon CmbZIP genes.

(**Left**) Unrooted phylogenetic tree of the 64 CmbZIP proteins. Numbers on the tree branches indicated bootstrap values. (**Right**) Exon-intron structure of the melon CmbZIP genes. Blue boxes represent exons and black lines represent introns.
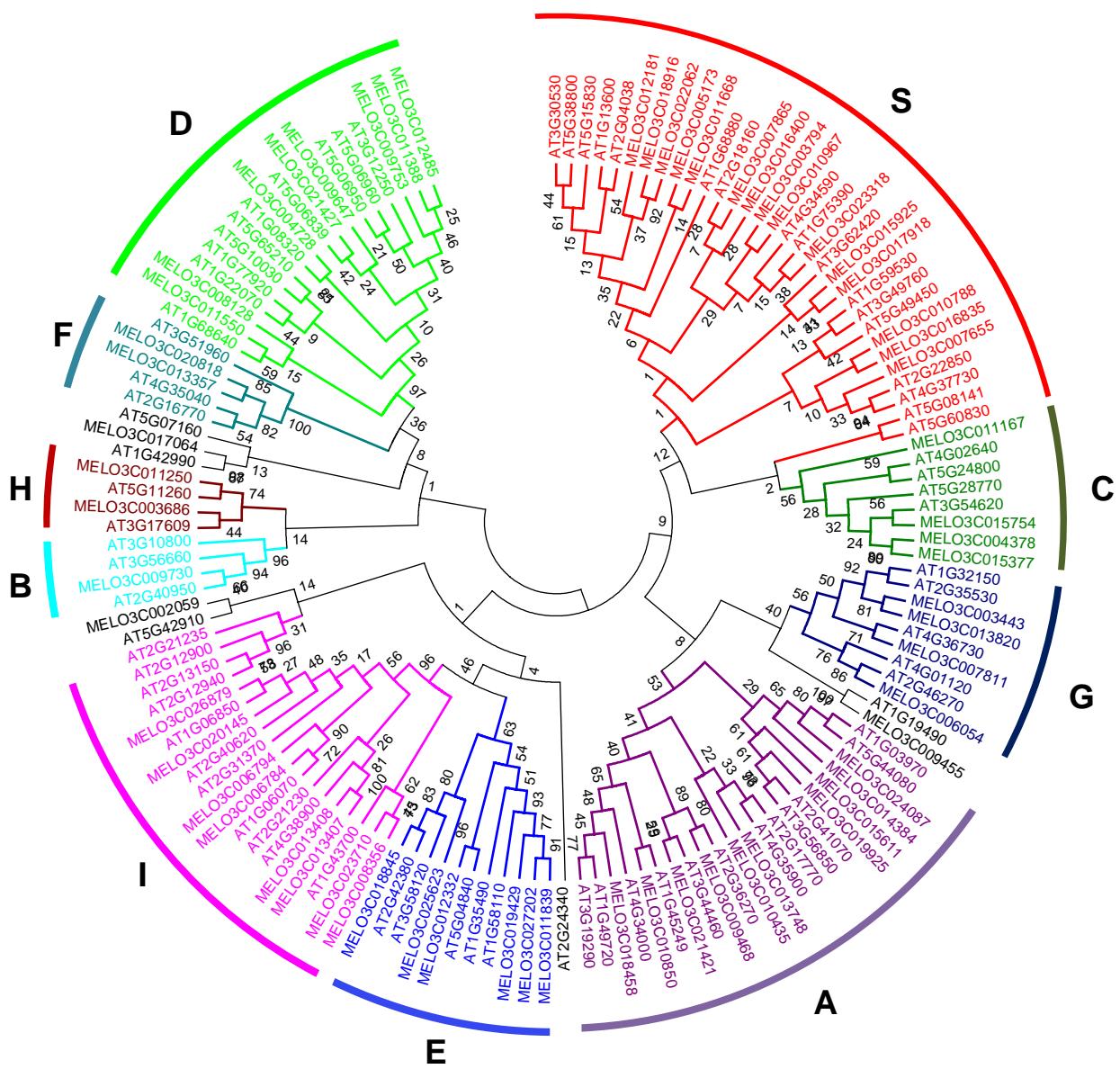
Supplementary Figure 3: Phylogenetic tree of melon and Arabidopsis bZIP proteins.
The bZIP protein sequences were aligned by CLUSTALW and the phylogenetic tree was
constructed using the Neighbor-Joining method by MEGA 7.0. Boostrap values from 1000
replicates are indicated in each node. The CmbZIP proteins are grouped into 10 groups (A-I
and S).

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MELO3C011668_CmbZIP14   ---ADERKQRRMISNRESARRSRMRKQKHVKELCSQLLRDCTQKHEDEEKLRVLMESQQRL
MELO3C018916_CmbZIP42   LSLINERKQRRMISNRESARRSRMRKQKHLDELWSQVLWLRNENHQDIDKLNQVSECHDRA
MELO3C005173_CmbZIP49   RIVVDERKQRRMISNRESARRSRMRKQKHLDELWSVVVRLRTENHSDMEKLNQLTDSEQQL
MELO3C022062_CmbZIP48   QSLINERKQRRMISNRESARRSRMRKQKHLDELWSQVLWLRNENHQDIDKLNQVSDCHDKV
MELO3C012181_CmbZIP52   KSIIDERKQRRMISNRESARRSRMRKQKHLDELWSQVLRLRTENHKDIDKLNHVSDNHEKV
AT3G30530_AtbZIP42      NNIINERKQRRMISNRESARRSRMRKQRHLDELWSQVMWLRIENHQDLDKLNNLSESHDKV
AT1G13600_AtbZIP58      -MVIDERKQRRMISNRESARRSRMRKQRHLDELWSQVIRLRTDNHCDMDKLNRVSESHELA
AT2G04038_AtbZIP48      -MVLDERKQRRMLSNRESARRSRMRKQRHLDELWSQVIRLRNENNCDIDKLNRVSETQNCV
AT5G38800_AtbZIP43      KEIINERKQKRKISNRESARRSRMRKQRQVDELWSQVMWLRDENHQDLRKLNCVLESQEKV
AT5G15830_AtbZIP3       IFVINERKQRRMVSNRESARRSRMRKQRHLDELLSQVAWLRSENHQDLDKLNQVSDNNDLV
AT5G08141_AtbZIP75      ----EEKRLRRMASNRESARRTRMRERMMKEGLQMQVKQDMAYNQFDYNKYISLLEYNHQI
AT5G60830_AtbZIP70      GLAPEERRARRMVSNRESARRSRMRKKKQIEELQQQVEQDMMLNHHDSEKVINLLESNHQI
AT1G68880_AtbZIP8       ----NERKRRRKVSNRESARRSRMRKQRHMEELWSMLVQDINKNKSDVDELSQAREEYEKV
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Supplementary Figure 4: Protein sequence alignment of the conserved bZIP domains of S2 sub-group proteins.

Sequences were aligned using ClustalW. Conserved amino acids are highlighted in black. Invariant residues within the bZIP domain are colored in red.