

**Large-scale analyses of BES1 gene family reveal the distinct evolutionary patterns between  
*Brassicaceae* and *Poaceae* species**

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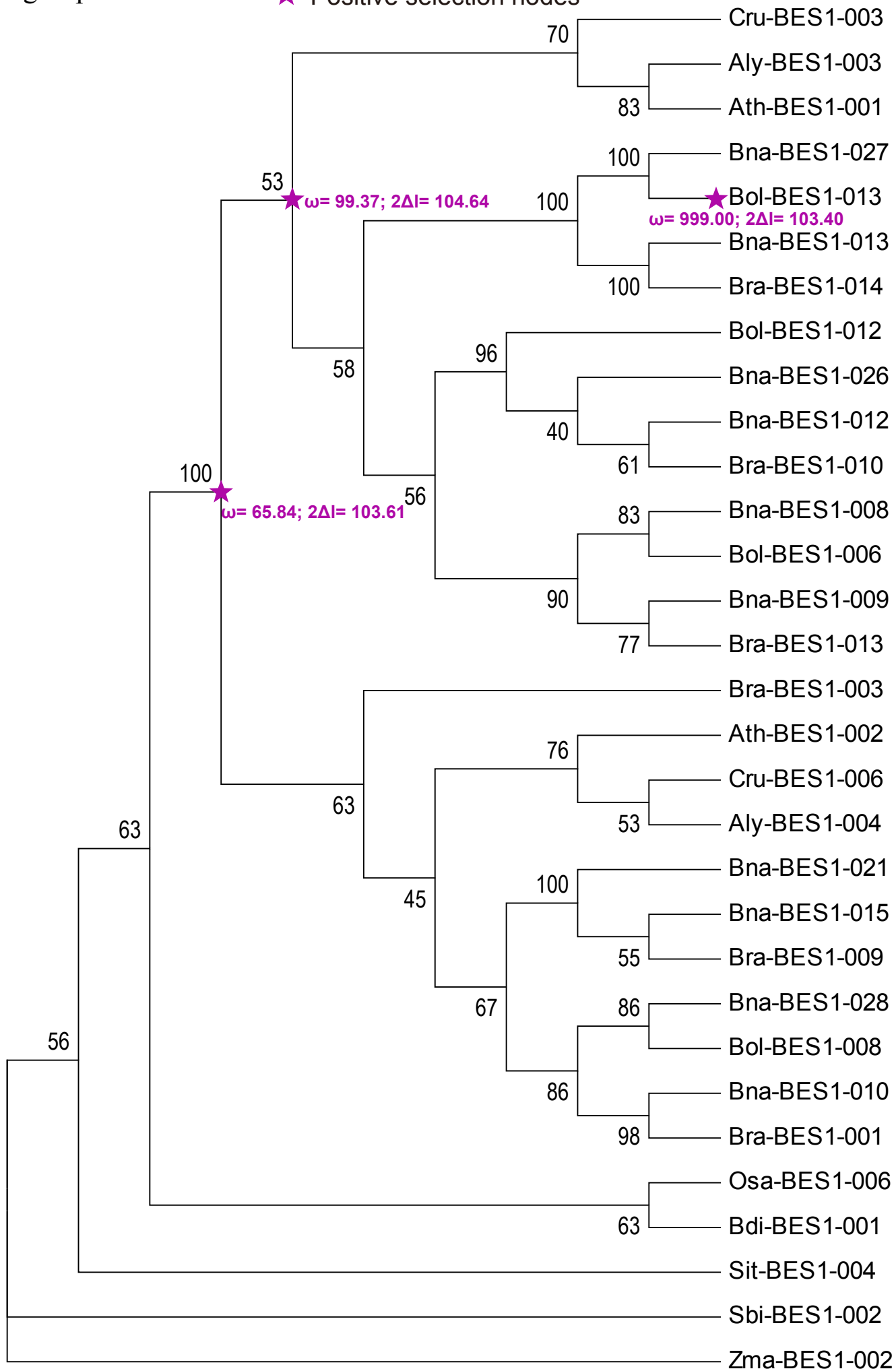
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**Figure S1.** The positive selection analyses for each group of BES1 gene family in representative species. The  $\omega$  on the clades is dn/ds value under M8 model of codeml, which indicates the positive selection nodes.

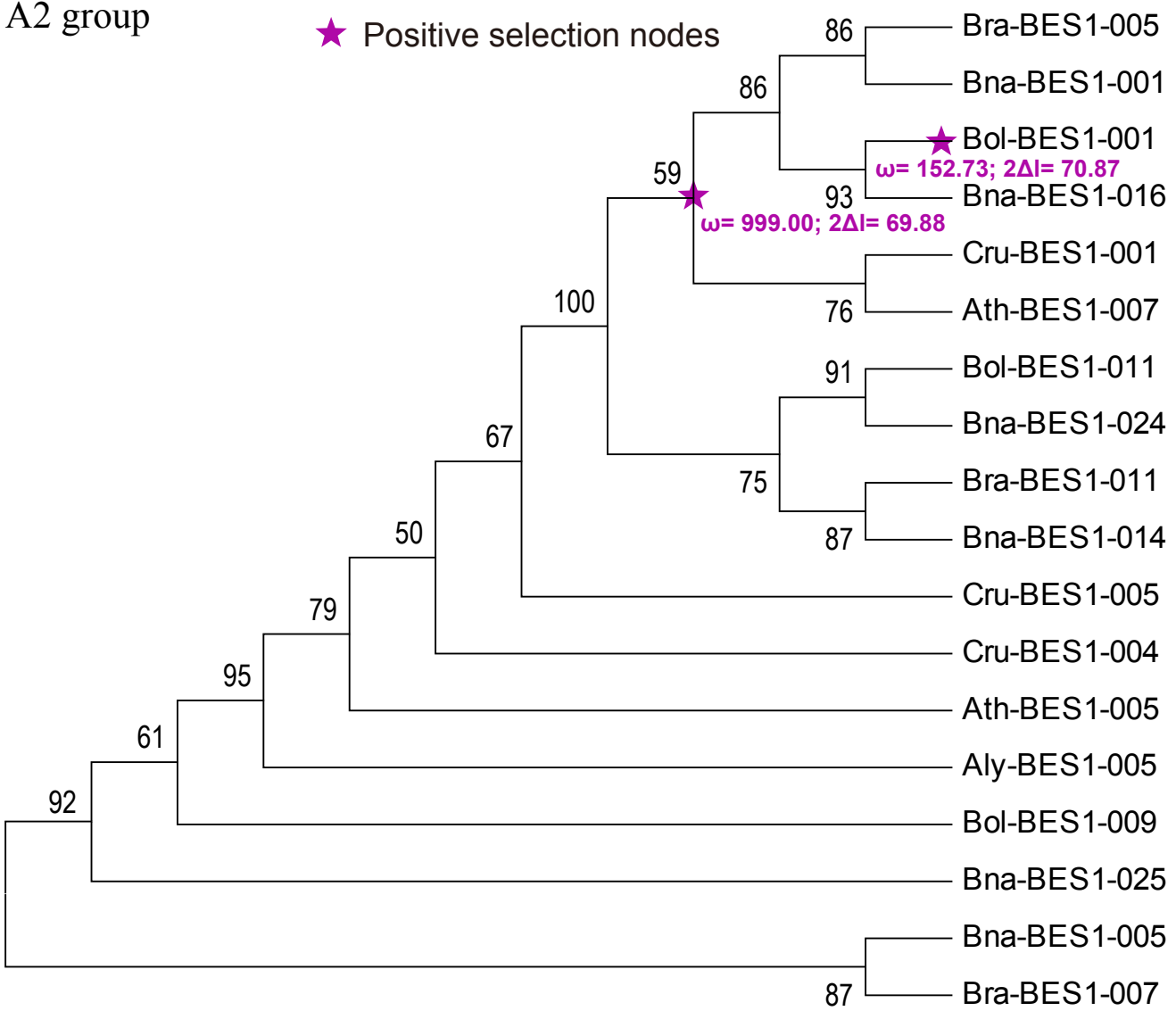
# A1 group

★ Positive selection nodes



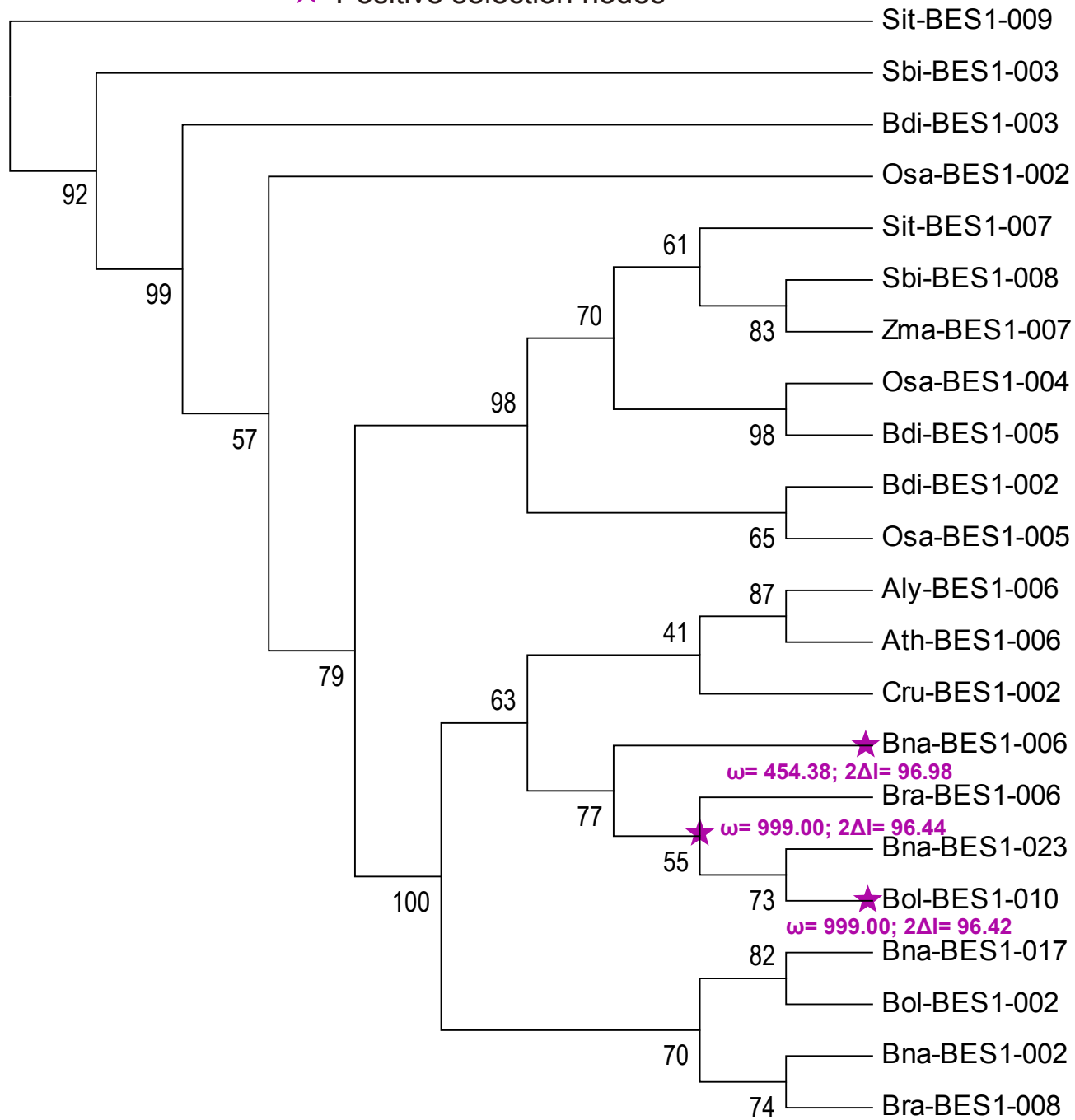
# A2 group

★ Positive selection nodes



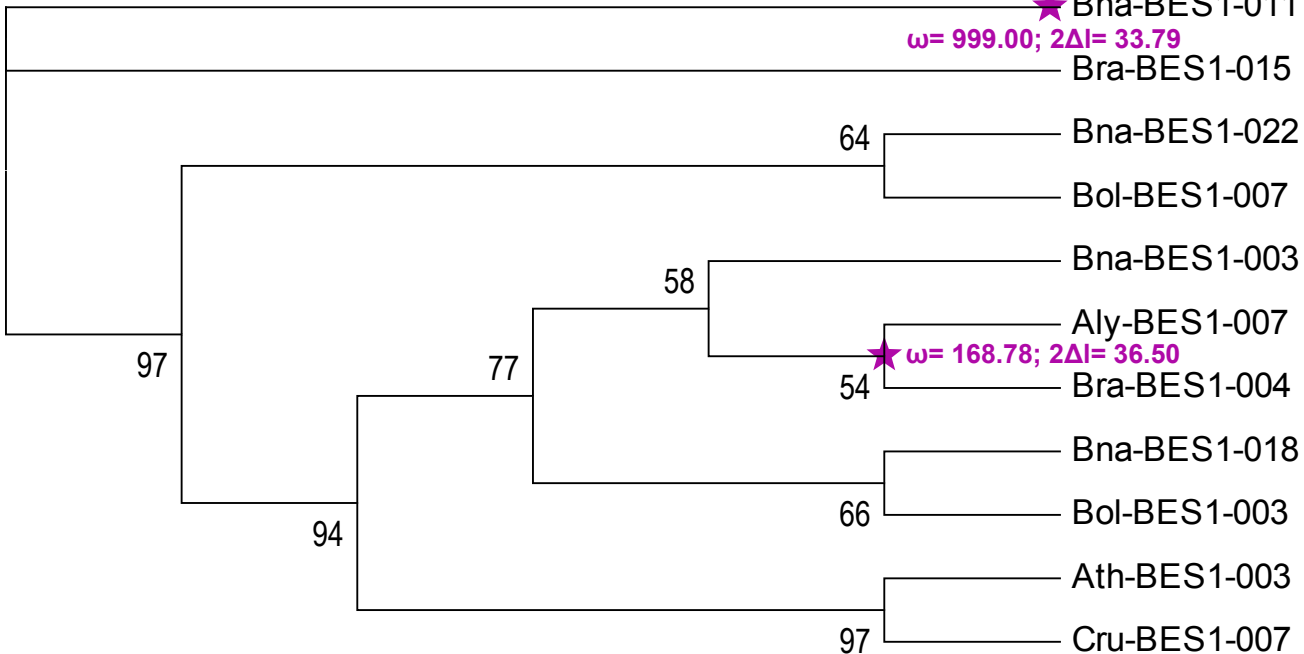
# B1 group

★ Positive selection nodes



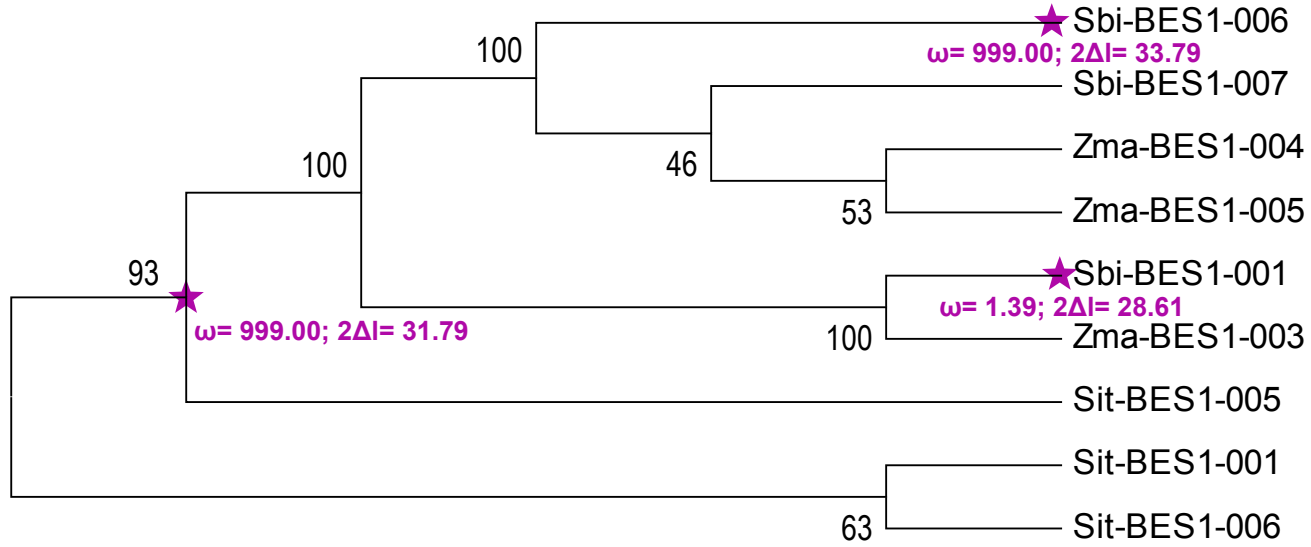
# B2 group

★ Positive selection nodes



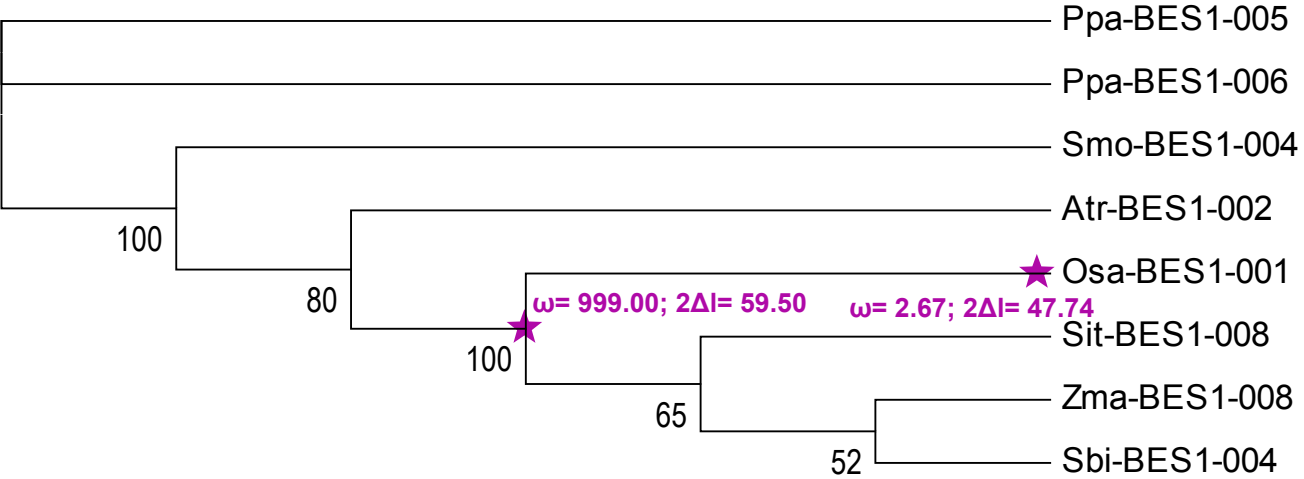
D group

★ Positive selection nodes



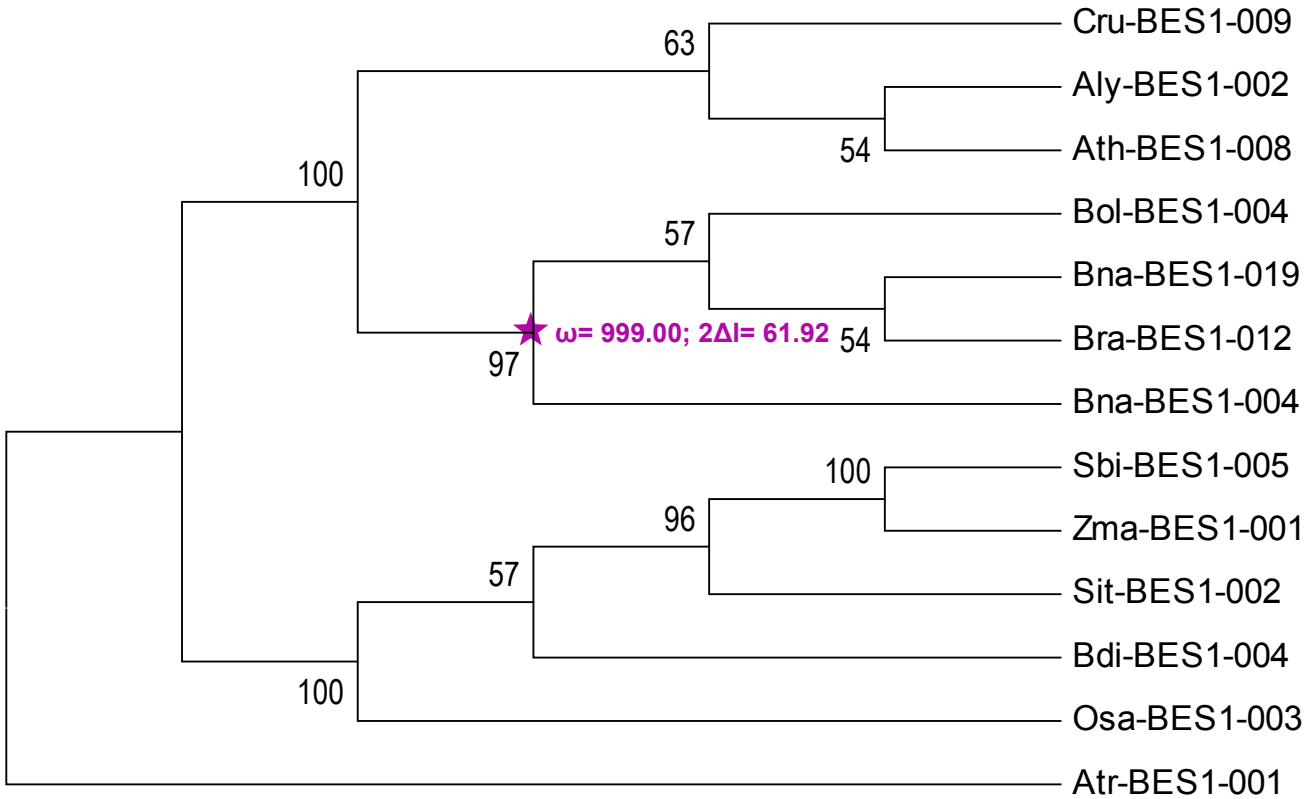
E group

★ Positive selection nodes



# F1 group

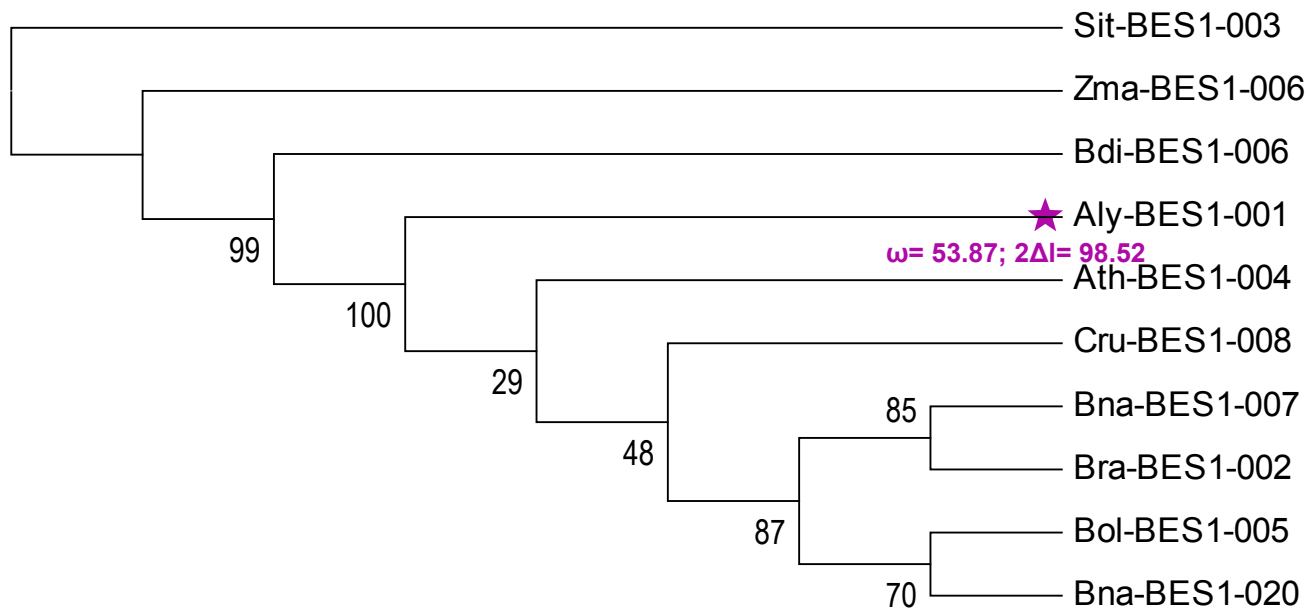
★ Positive selection nodes





F2 group

★ Positive selection nodes



# F3 group

★ Positive selection nodes

