

# The high-quality genome assembly of *Prunus mume* 'Nanko' reveals a chromosomal inversion associated with natural variation in dormancy and bud break

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**Abstract**

Bud dormancy is a critical process in woody perennials, allowing them to adapt to seasonal environmental changes. Fulfillment of the genotype-dependent chilling requirement (CR) and heat requirement (HR) through exposure to specific cold and warm temperatures, respectively is necessary to overcome dormancy and to resume growth. However, the genetic mechanisms underlying bud dormancy and bud break in *P. mume* remain incompletely understood. By using F1 segregating population derived from the cross between Japanese collection 'Nanko' (CR = approx. 600-1100 CH) and low-chill 'SC' (CR = approx. 0-400 CH) that adapt to subtropical condition, we identified a significant QTL for CR, HR and bud break in chromosome 4 (LG4 QTL) of the 'Nanko' genome. To decipher LG4 QTL, we generated a high-quality reference genome assembly of 'Nanko' by employing PacBio HiFi long reads and 10x Chromium linked reads technologies. Within the LG4 QTL interval, a substantial large-scale chromosome inversion spanning 5.6 Mb was identified in one of 'Nanko' genomes and compared with other *Prunus* species genomes. Intriguingly, the region covering inverted chromosome fragment was consistently overlapped with LG4 QTL for multiple seasons, indicating the close association of chromosome inversion with LG4 QTL. Results from fine mapping analysis and differentially expressed genes identified within LG4 QTL will be discussed.