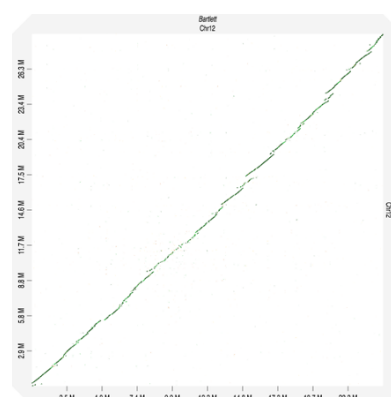
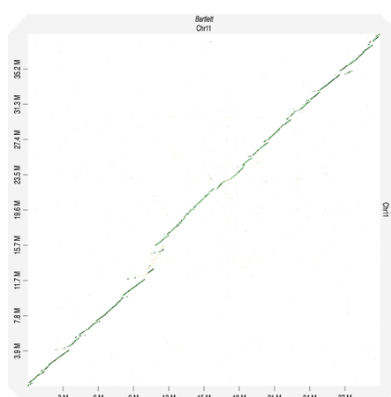
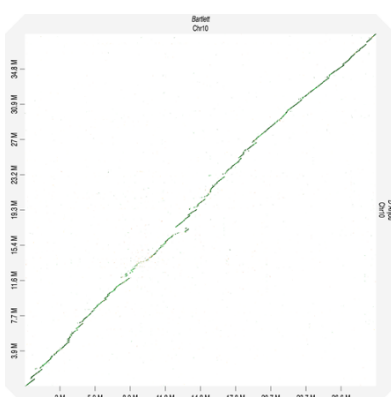
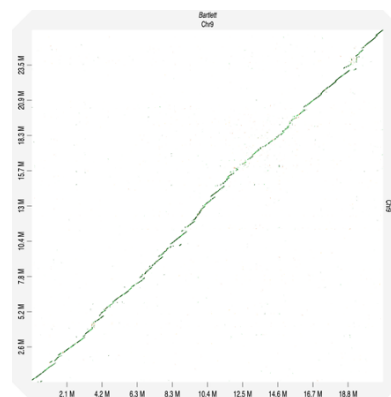
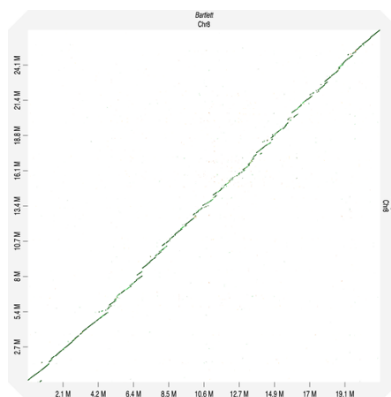
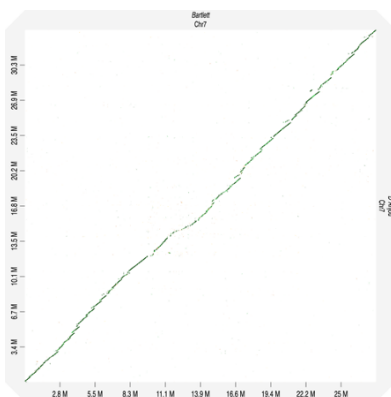
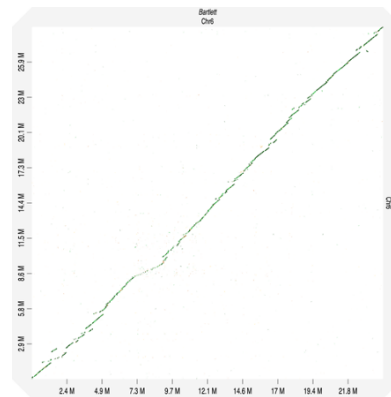
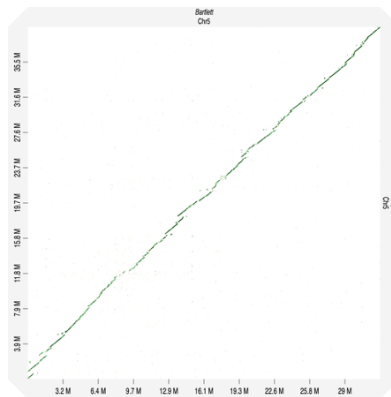
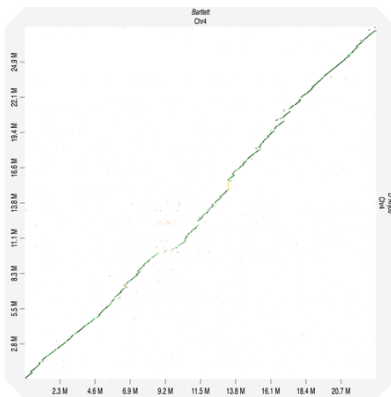
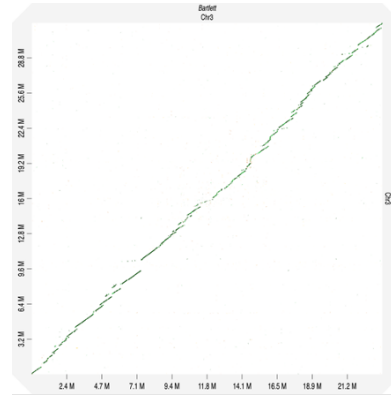
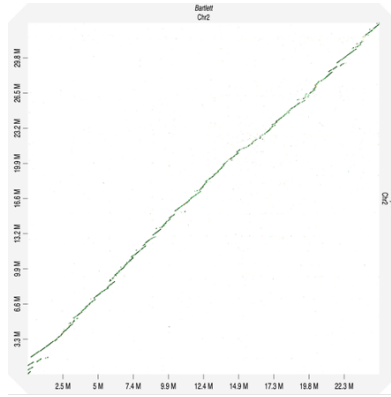
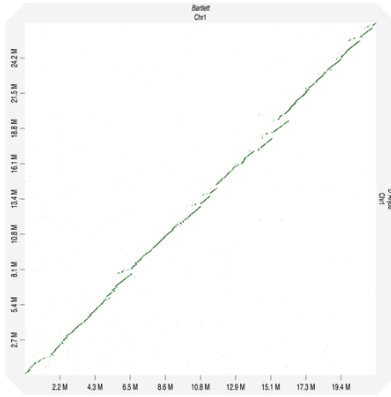
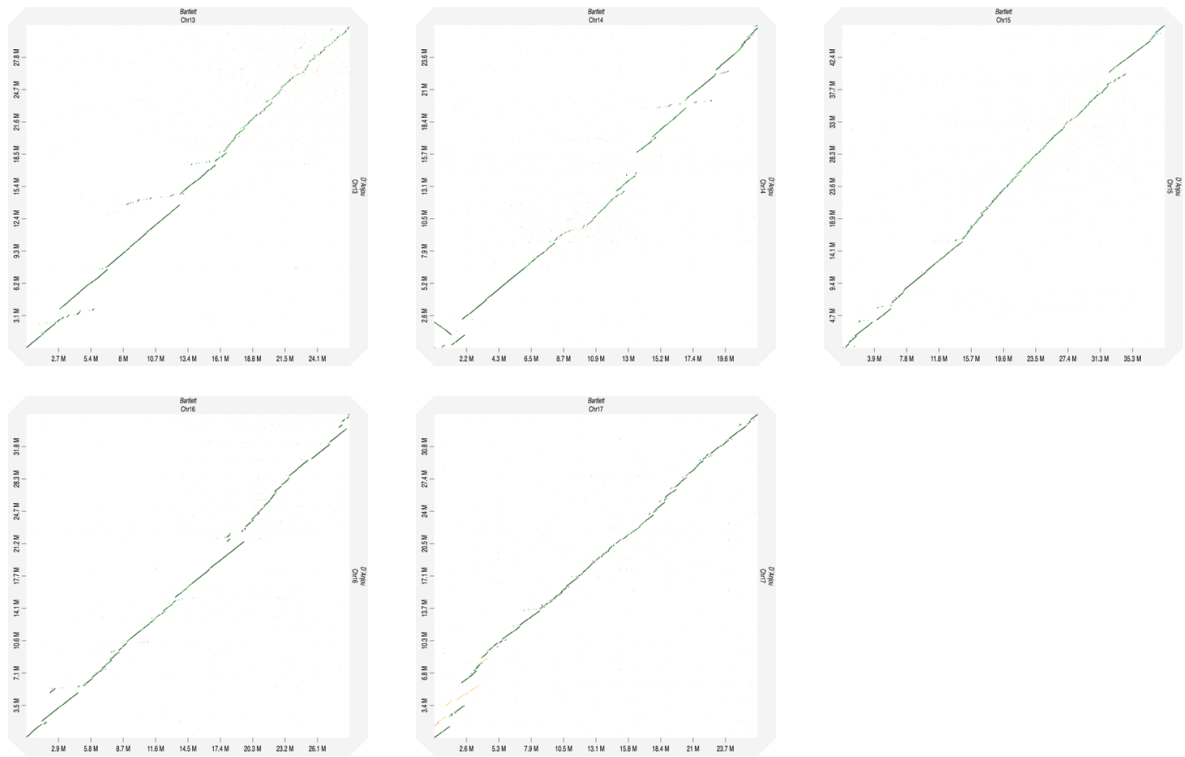
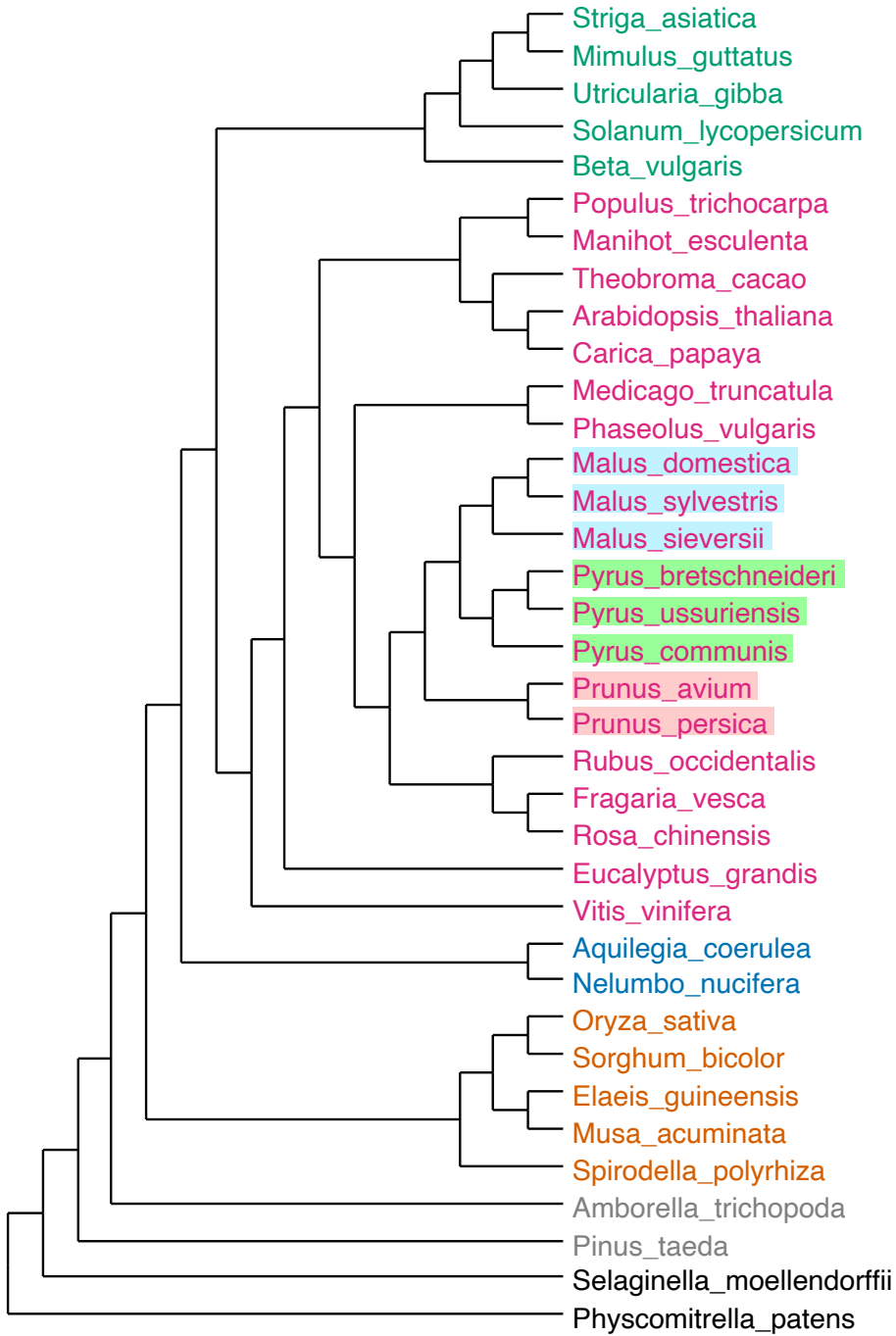


Supplementary Figure 1. A summary of the 'd'Anjou' genome assembly pipeline.





Supplementary Figure 2. Dot plot of chromosome alignments of Bartlett.DH_v2 (x axis) and d'Anjou_v1 (y axis).



Supplementary Figure 3. A cladogram of the plant species used in this study. Rosaceae species except *Prunus persica* were classified into the 26 genome scaffold version 2. Genes from these species followed the same color scheme in the phylogenetic trees in this manuscript.



Supplementary Figure 4. Sequence comparison of genomic fragments where an *IPT* gene is expected to be located in various *Pyrus* genomes. *Pyrcyco*: *Pyrus communis*; *Pyrcyco*: *P. bretschneideri*; *Pyrcusco*: *P. ussuriensis x communis*. Sequence 2 is the original Bartlett.DH_v2 assembly and Sequence 3 is the polished assembly.

Supplementary Figure 6.
Phylogeny of the *PIN* gene family inferred with the 26 genomes scaffold and *P. bretschneideri* *PIN* genes identified in reference Qi et al., 2020.

