图表, 条形图

描述已自动生成**Supplementary Figure 1.**

The number of SNP within 1Mb window size

图表, 条形图

描述已自动生成**Supplementary Figure 2.**

Distribution of SNP position annotations

**Supplementary Figure** 图表, 条形图

描述已自动生成**3.**

The number of INDEL within 1Mb window size

图表, 条形图

描述已自动生成**Supplementary Figure 4.**

Distribution of INDEL position annotations

**Supplementary Figure 5.**

DeltaK calculated with *K* from 2 to 7.

图表, 条形图

描述已自动生成**Supplementary Figure 6.**

Treemix residual fit heatmap shows the standard error (SE) of pairwise comparisons between different *Pyrus* populations.

**Supplementary Figure** 图表, 折线图

描述已自动生成**7.**

Analysis of the optimal number of migration edges using OptM.R. The upper panel shows the mean likelihoods (Lm) with standard deviations (SD) for different numbers of migration edges (m), along with the percentage of variance explained, indicated by red dots. The 99.8% variance threshold is represented by the dotted line. The lower panel presents the changes in likelihood (Δm) across different migration edges.