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Construction of high-density genetic map and QTL mapping in *Nicotiana tabacum* backcrossing BC4F3 population using whole-genome sequencing

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

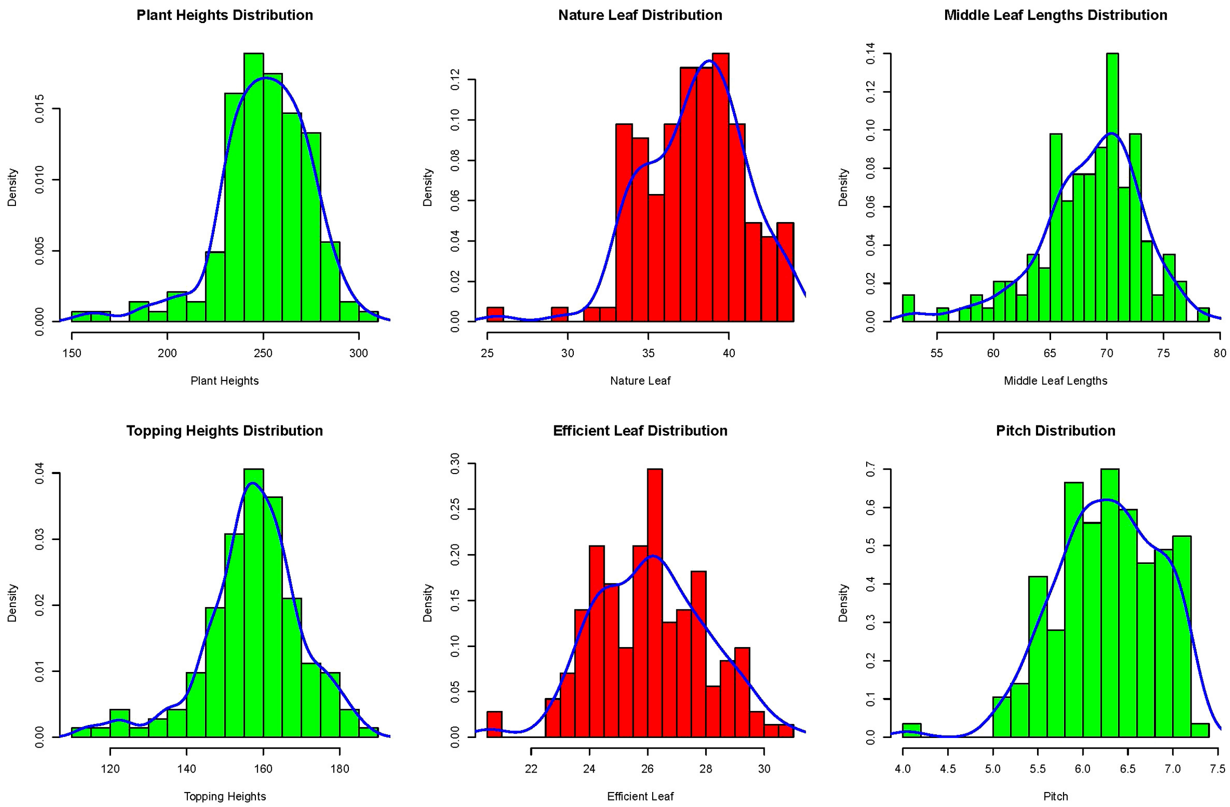

Figure S1. The frequency distribution histogram of the agronomic traits; six agronomic traits including the plant height (cm), nature leaf (cm), topping height (cm), efficient leaf (cm), pitch and middle leaf length (cm) were recorded

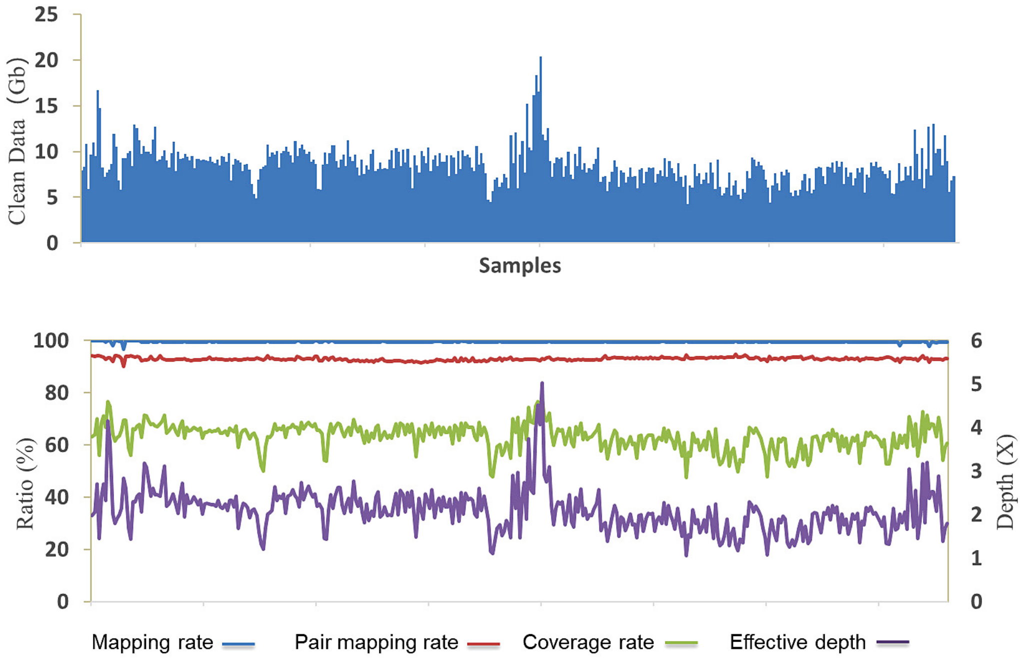

Figure S2. Statistic of clean data and alignment

The Y-axis stands for the quantity of the clean data (Gb) per the sample and ratios of the mapping; Mapping reads rate (%) = mapping reads/total reads; pair mapping rate (%) = properly paired reads/clean reads; total reads = clean reads; effective depth = mapped data bases/the effective genome size