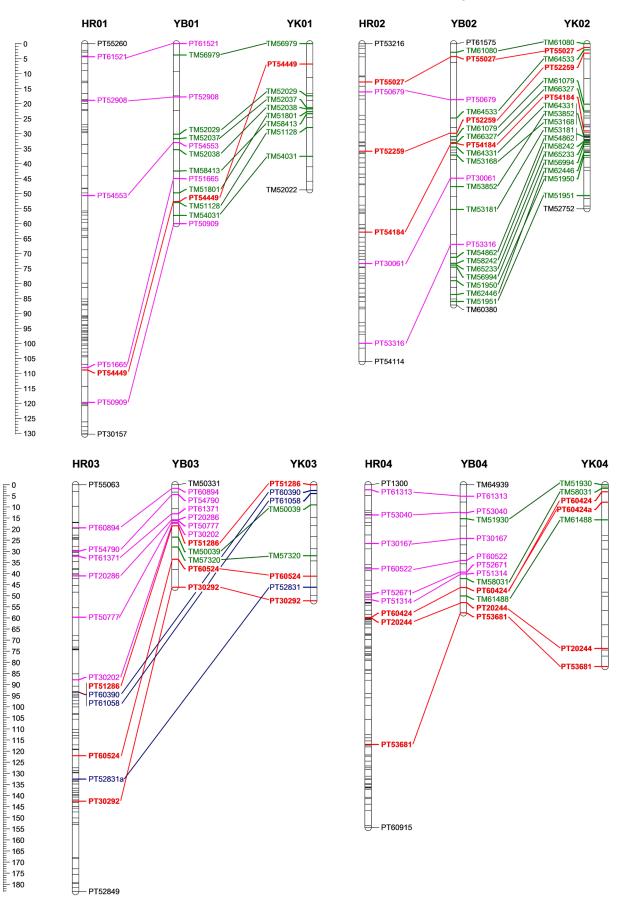
## Construction of a Genetic Linkage Map of Cigar Tobacco (Nicotiana tabacum L.) Based on SSR Markers and Comparative Studies

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**Electronic Supplementary Material (ESM)** 

Figure S1. Comparative genetic linkage map of cigar tobacco constructed from BC<sub>1</sub>F<sub>1</sub> population of  $\underline{Y}3 \times \underline{B}$ einhart1000-1 in this study (denoted as the YB, cigar type) (middle) and F<sub>2</sub> population derived from a dark tobacco cross  $\underline{H}$ icks Broadleaf  $\times \underline{R}$ ed Russian tobacco (denoted as the HR, dark type; BINDLER et al. 2011) (left) and BC<sub>1</sub>F<sub>1</sub> population derived from a flue-cured tobacco cross  $\underline{Y}3 \times \underline{K}326$  (denoted as the YK, flue-cured type; Tong et al. 2016) (right); only common markers as well as the start and end marker which were used to determine the full-length of each linkage groups are shown in the maps; positions of common marker loci in the three maps are connected with red solid lines while between each two maps (HR and YB map; YB and YK map; HR and YK map), the common marker loci are connected with pink, green and blue lines, respectively



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