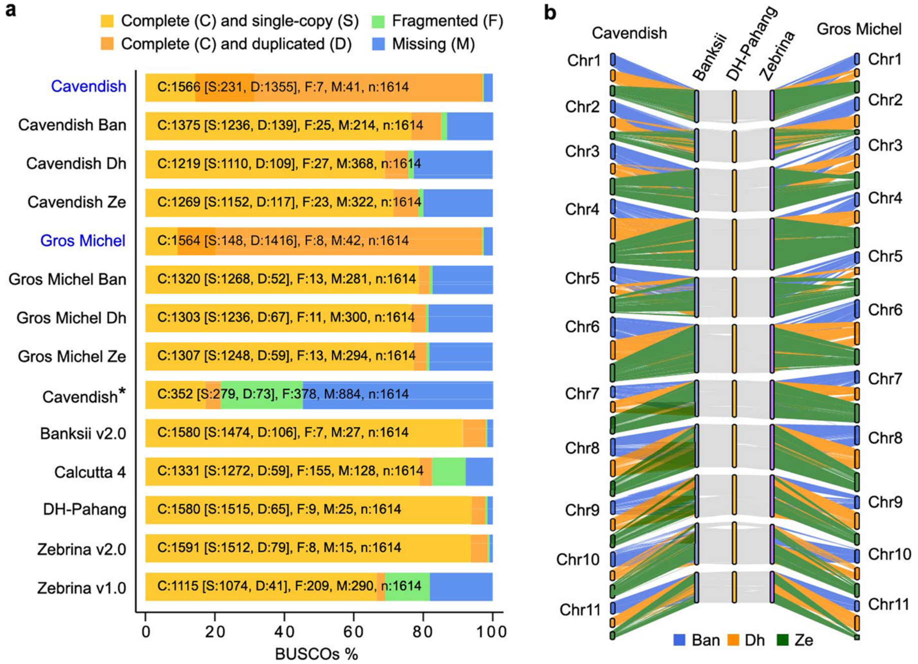
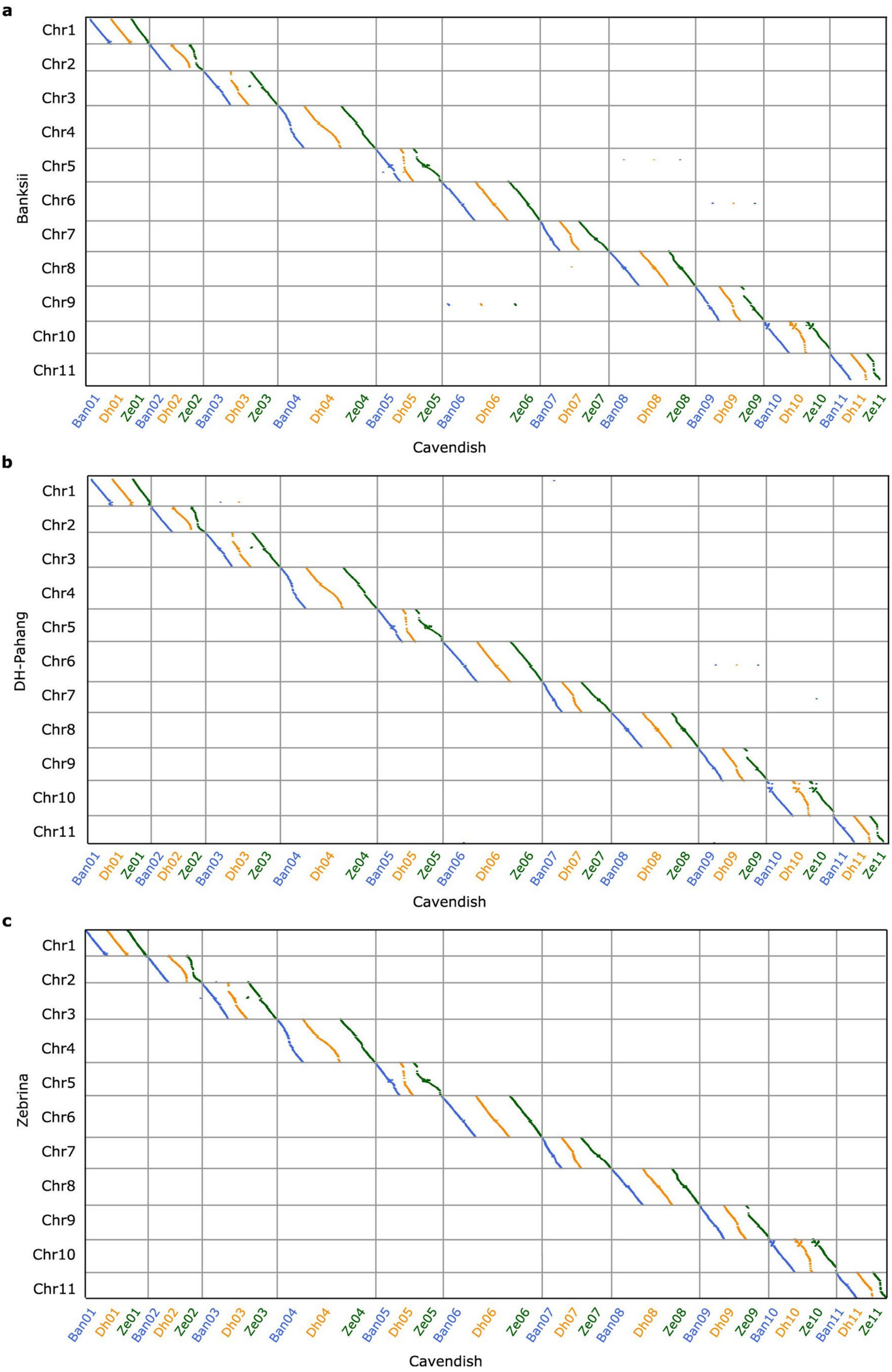
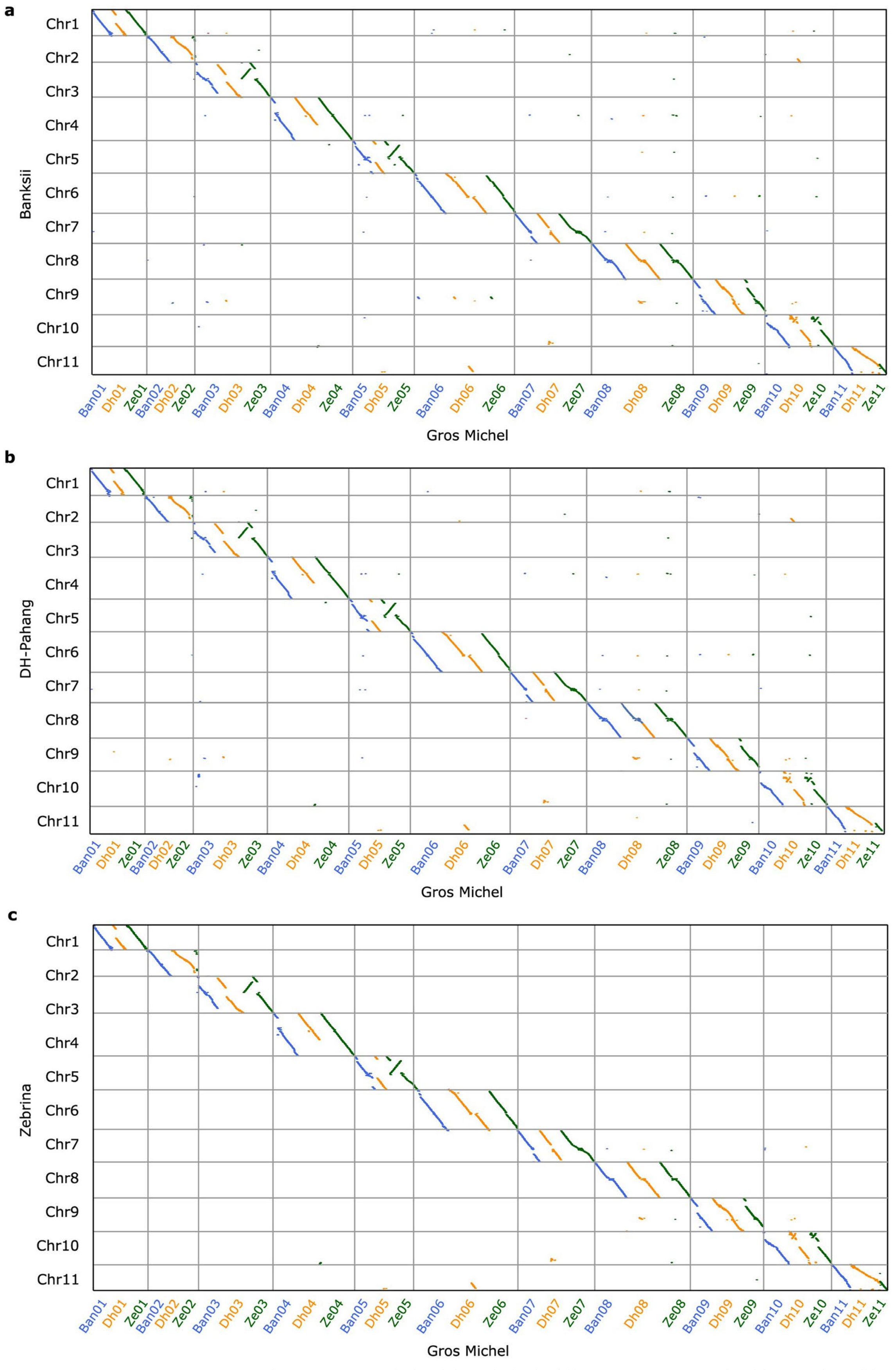


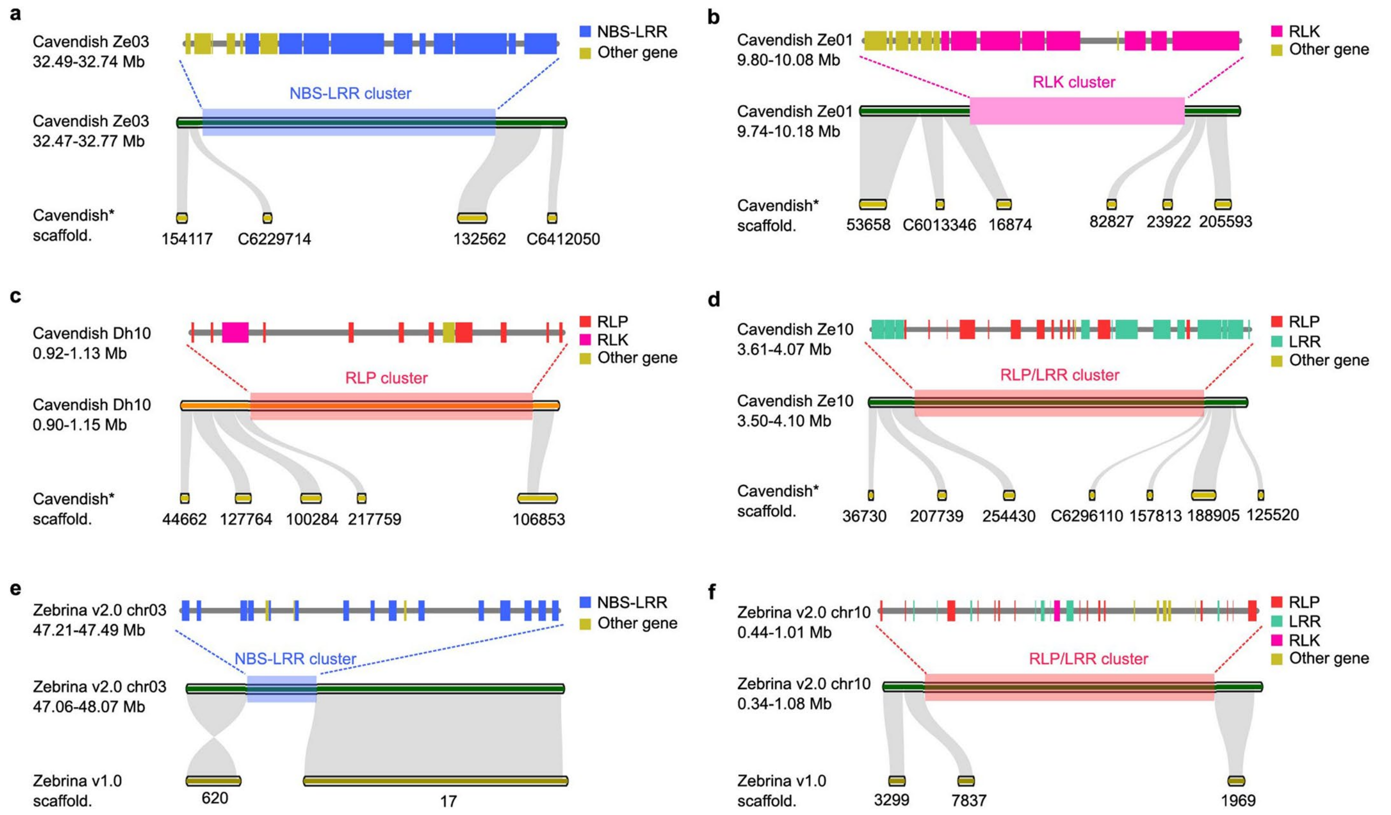
Extended Data Fig. 1 | Genome assemblies of Cavendish and Gros Michel. **a**, BUSCO completeness assessments of the genome assemblies of Cavendish, Gros Michel, and four diploid wild banana species (Banksii, DH-Pahang, Zebrina, and Calcutta 4). Cavendish* was assembled by Busche et al.[18]. Zebrina v1.0 was assembled by Rouard et al.[1], and Zebrina v2.0 was our assembly based on nanopore long-reads. The abbreviations of banana species refer to Fig. 1a. **b**, Macrosyntenic comparison of the entire Cavendish, Gros Michel and three diploid wild banana genomes (Banksii, DH-Pahang, and Zerbina), with each chromosome colored according to sub-genomes (Ban in blue, Dh in orange, and Ze in green).



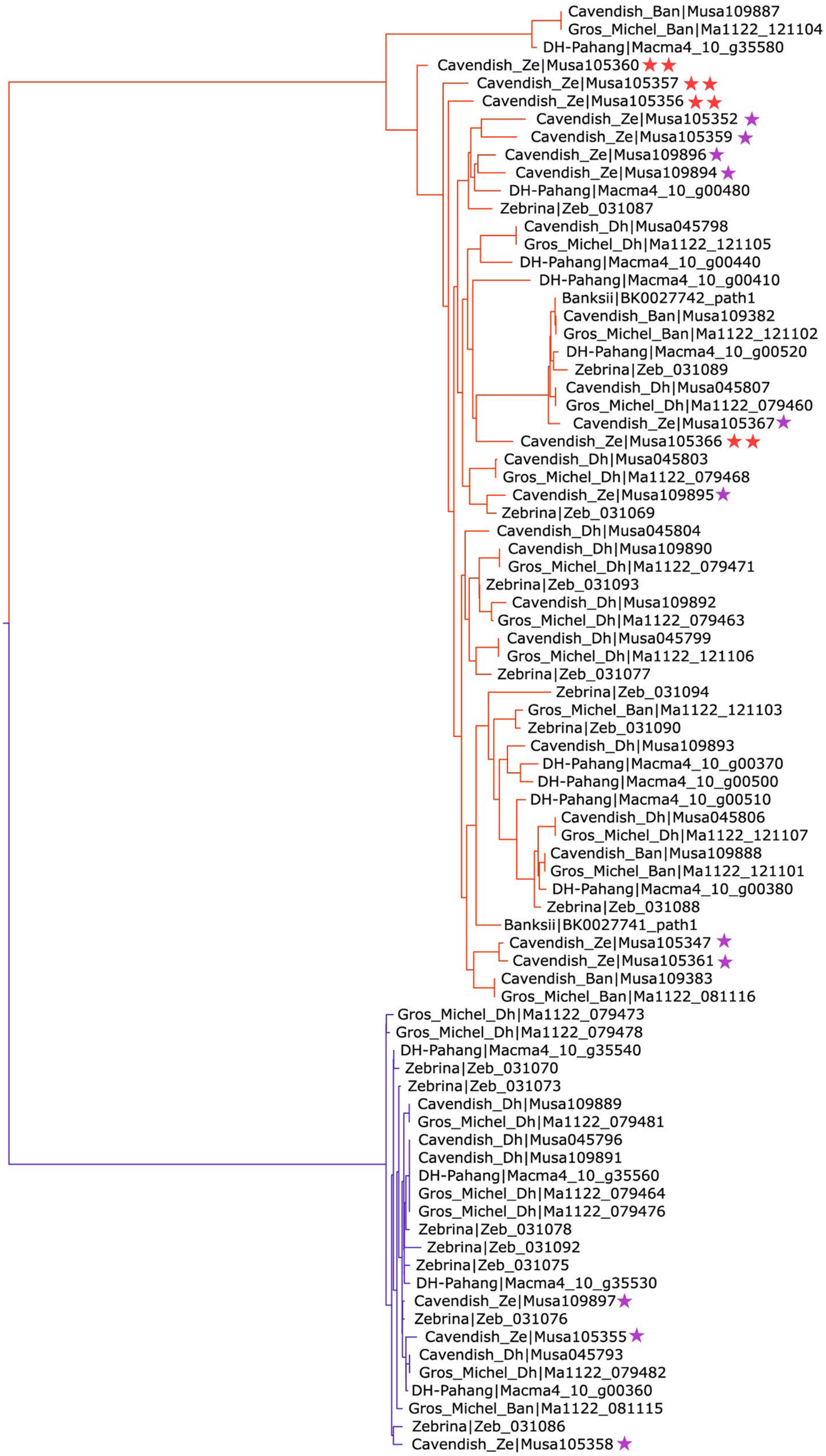
Extended Data Fig. 2 | Macrosyntenic comparison of the entire Cavendish and three diploid wild banana genomes: Banksii (a), DH-Pahang (b), and Zebrina (c). Each chromosome set colored according to sub-genomes (Ban in blue, Dh in orange, and Ze in green). The abbreviations of banana species refer to Fig. 1a.



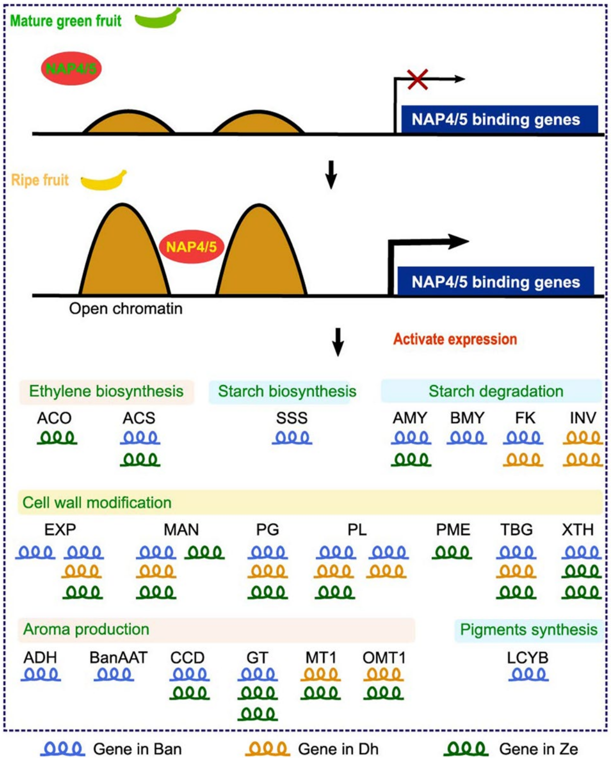
Extended Data Fig. 3 | Macrosyntenic comparison of the entire Gros Michel and three diploid wild banana genomes: Banksii (a), DH-Pahang (b), and Zebrina (c). Each chromosome set colored according to sub-genomes (Ban in blue, Dh in orange, and Ze in green). The abbreviations of banana species refer to Fig. 1a.



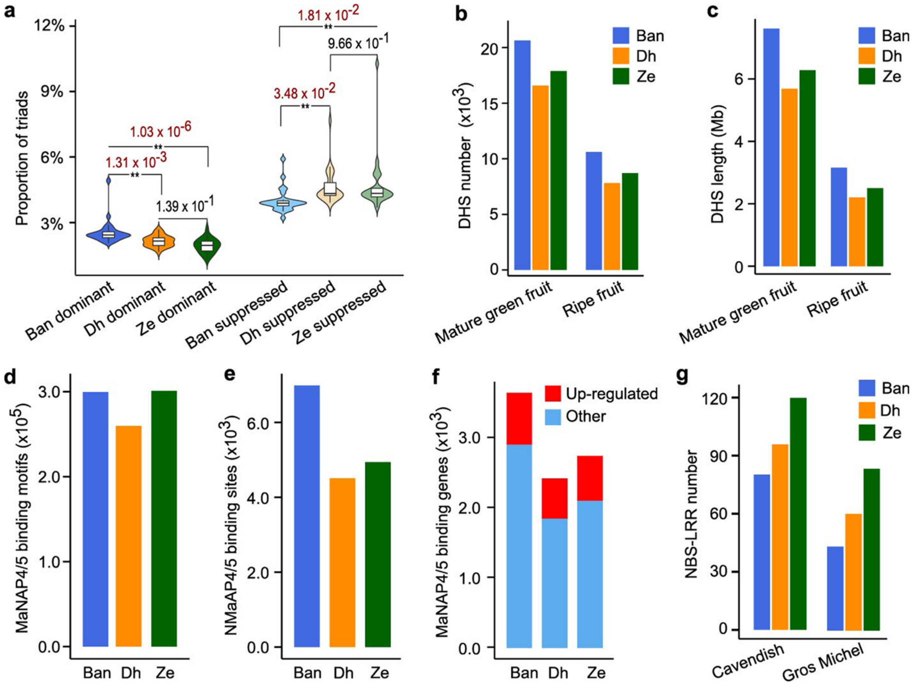
Extended Data Fig. 4 | Examples of high-quality Cavendish and Zebrina genome assemblies. a-d, NBS-LRR cluster, RLK cluster, RLP cluster, and RLP/LRR cluster on Ze03, Ze01, Dh10, and Ze10 of Cavendish, while not assembled in the previously published Cavendish assembly. Cavendish* was assembled by Busche et al.[18]. **e** and **f**, NBS-LRR cluster on chromosome 3 and RLP/LRR cluster on chromosome 10 of our assembled Zebrina v2.0 with length of 280 kb and 370 kb, while being two big gaps in the published Zebrina v1.0 (ref. 1). Each resistance gene was colored on micro-synteny plot (NBS-LRR in blue, RLK in pink, RLP in red, LRR in green, and other gene in yellow). The abbreviations of banana species refer to Fig. 1a.



Extended Data Fig. 5 | Phylogenetic tree of banana RLPs involved in *Foc* race1-associated QTL (named as RLP locus)[25]**.** The purple stars denote RLPs located in the Ze sub-genome, while the two red stars denote RLPs found only in the Ze sub-genome of Cavendish. The abbreviations of banana species refer to Fig. 1a.



Extended Data Fig. 6 | A model of MaNAP4/5' regulation of banana fruit ripening. In the model, these genes directly regulated by MaNAP4/5 are key genes in the fruit ripening process.



Extended Data Fig. 7 | Sub-genome dominance in the triploid banana genome. a, Statistical comparison of categories of syntenic triad homoeolog expression bias. P-values were determined by one-way ANOVA with Tukey's HSD test (n = 26 tissues of each category) within the suppression and dominance categories, and P-values less than 0.05 was highlighted in red. For boxplot in this study, the middle line represents the median, the lower and upper edges of the box represent the first and third quartiles, the end of the lower whisker represents the smallest value at most 1.5× inter-quartile range from the lower edge of the box, the end of the upper whisker represents the largest value at most 1.5× inter-quartile range from the upper edge of the box. **b** and **c**, Total number (b) and length (c) of DNase-hypersensitive sites (DHSs) detected in mature green and ripe fruits. **d-f**, Sub-genome distribution of MaNAP4/5 binding motifs (d), sites (e) and genes (f). **g**, Distribution of NBS-LRR resistance genes in the sub-genomes.