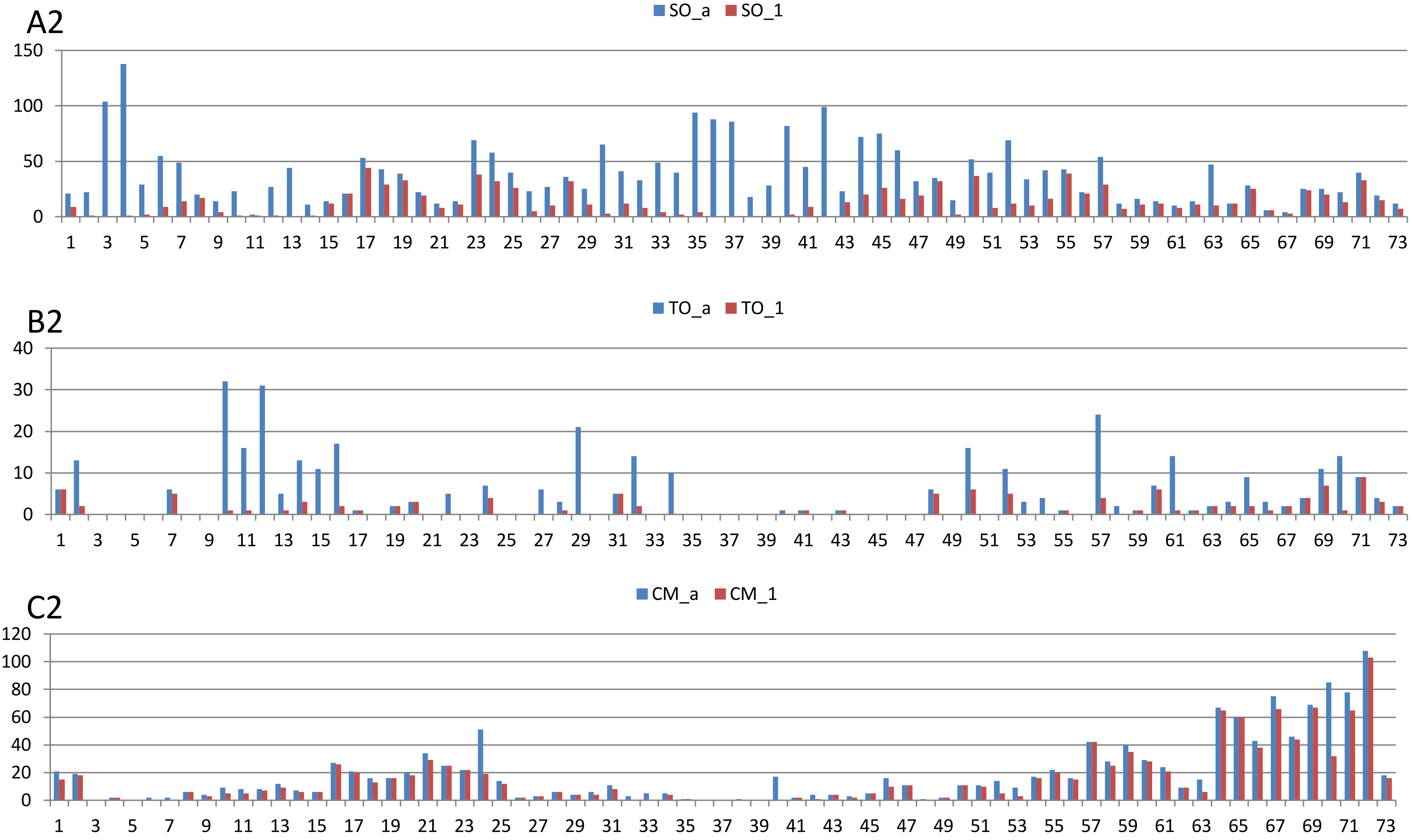
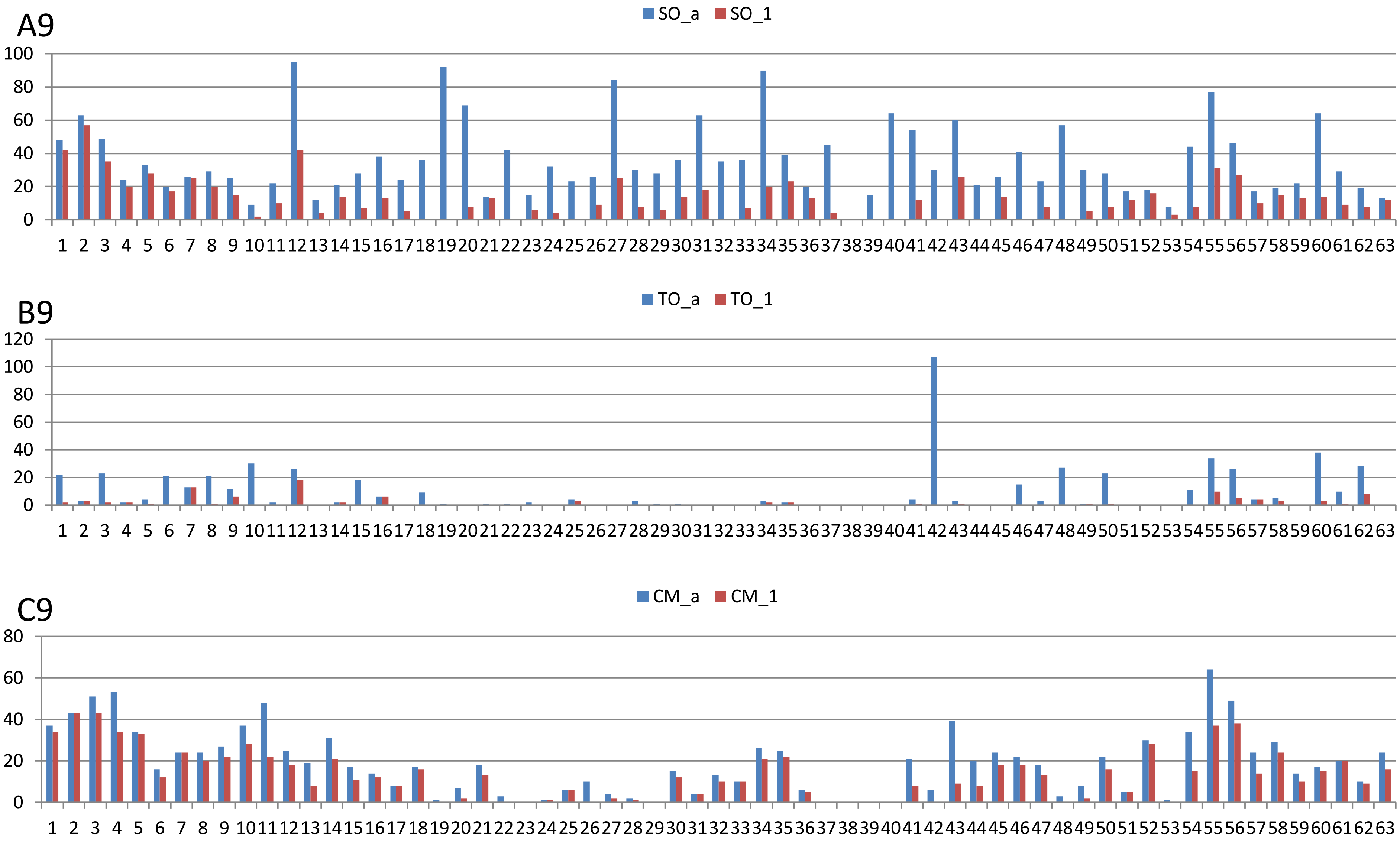


Additional File 3 Figure S1. SNP distribution on the Clementine reference genome Scaffold_2. Each interval of the x-axis represented 500kb of the scaffold, and the y-axis represented the number of SNPs in each 500kb on the scaffold. SO – sweet orange (**A2**); TO – trifoliate orange (**B2**); CM – Clementine mandarin (**C2**); "_a" – counts of all alignments generated by all SNPs; "_1" – counts of SNPs of only 1 unique hit/alignment in the genome. Differences between the "_a" and "_1" numbers were observed in several regions of each cultivar.



Additional File 3 Figure S1. SNP distribution on the Clementine reference genome Scaffold_9. Each interval of the x-axis represented 500kb of the scaffold, and the y-axis represented the number of SNPs in each 500kb on the scaffold. SO – sweet orange (**A9**); TO – trifoliate orange (**B9**); CM – Clementine mandarin (**C9**); "_a" – counts of all alignments generated by all SNPs; "_1" – counts of SNPs of only 1 unique hit/alignment in the genome. Differences between the "_a" and "_1" numbers were observed in several regions of each cultivar.