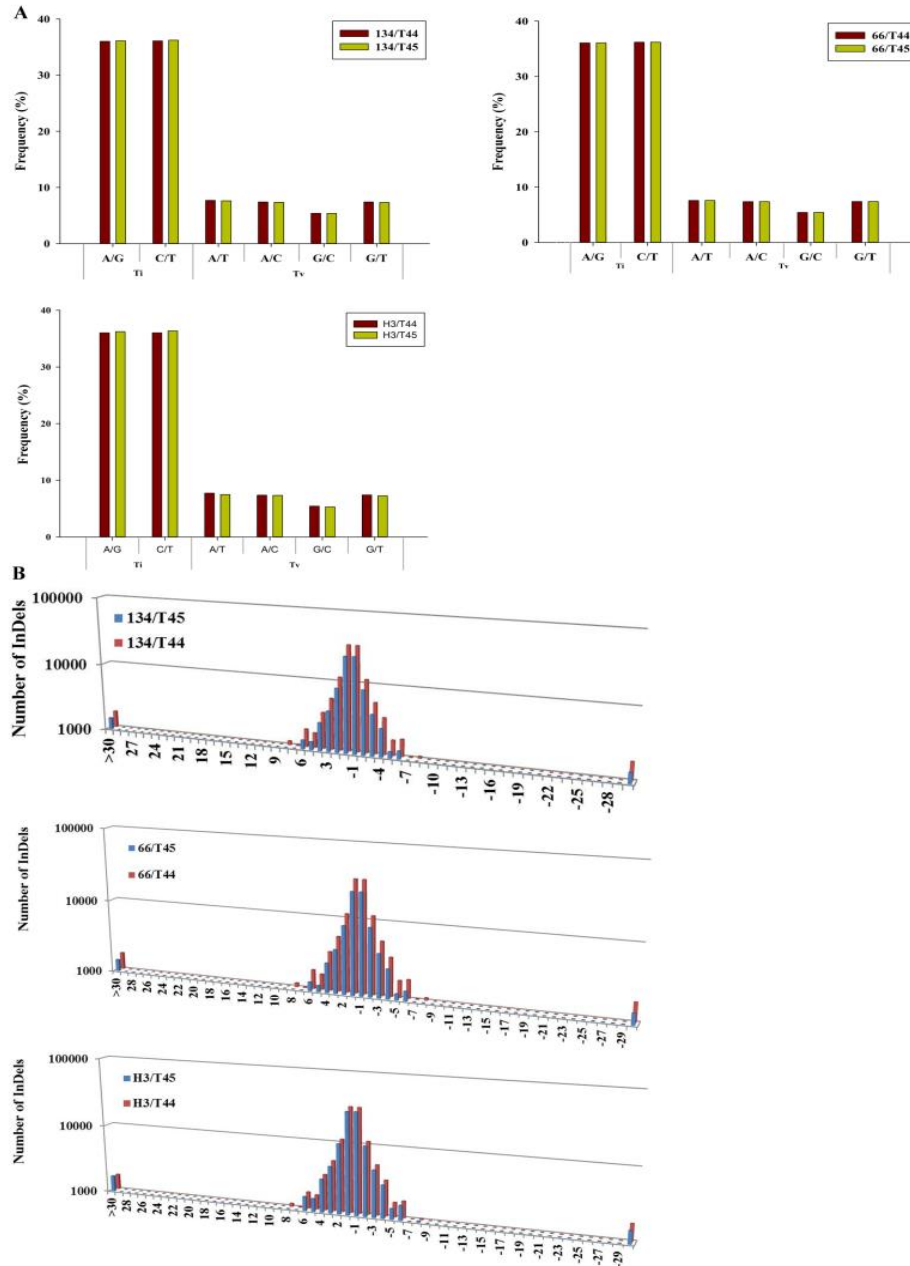


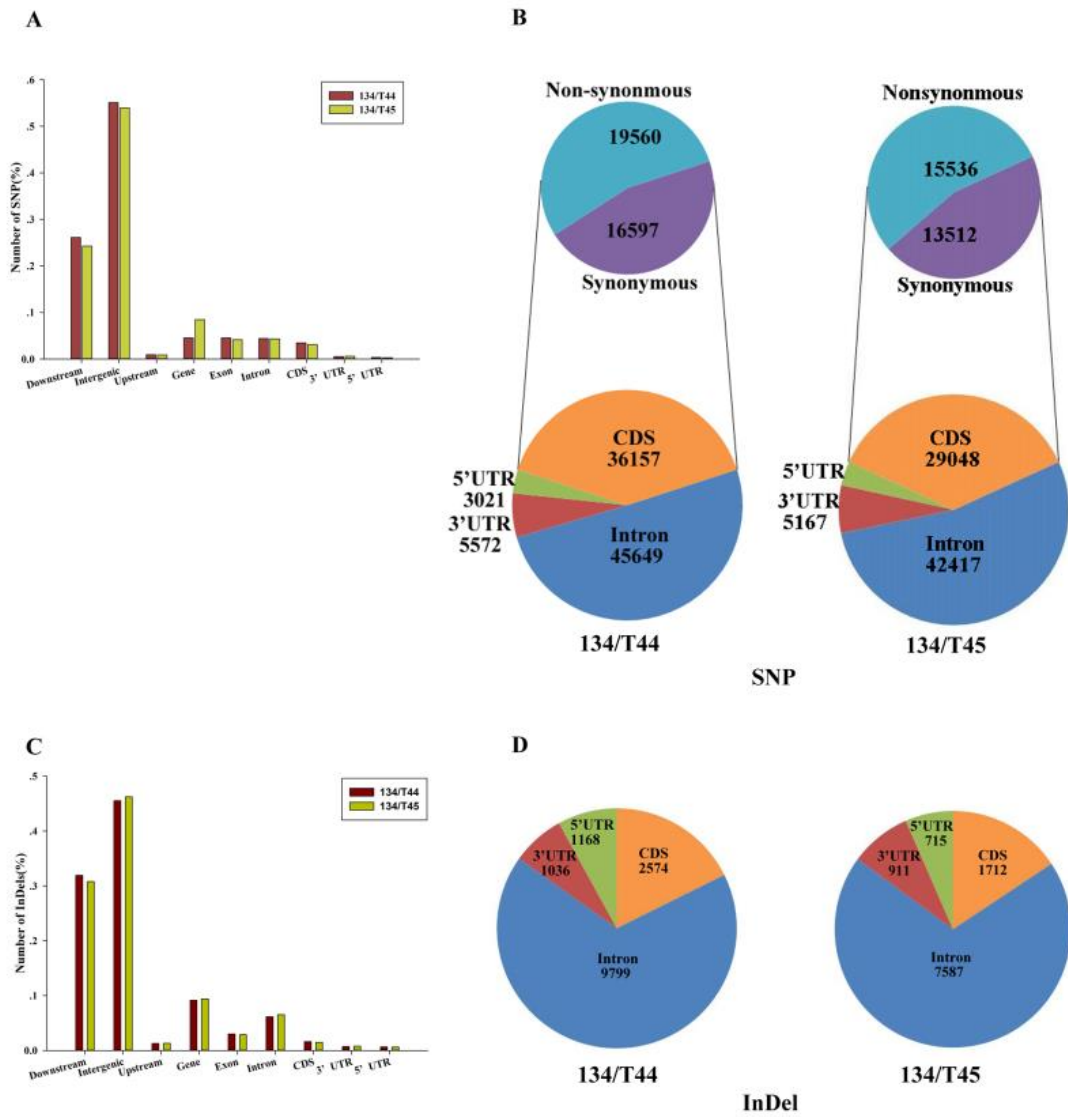
# Supporting Information

## S1 File. Additional figures about distribution and annotation of SNPs and InDels in this study.



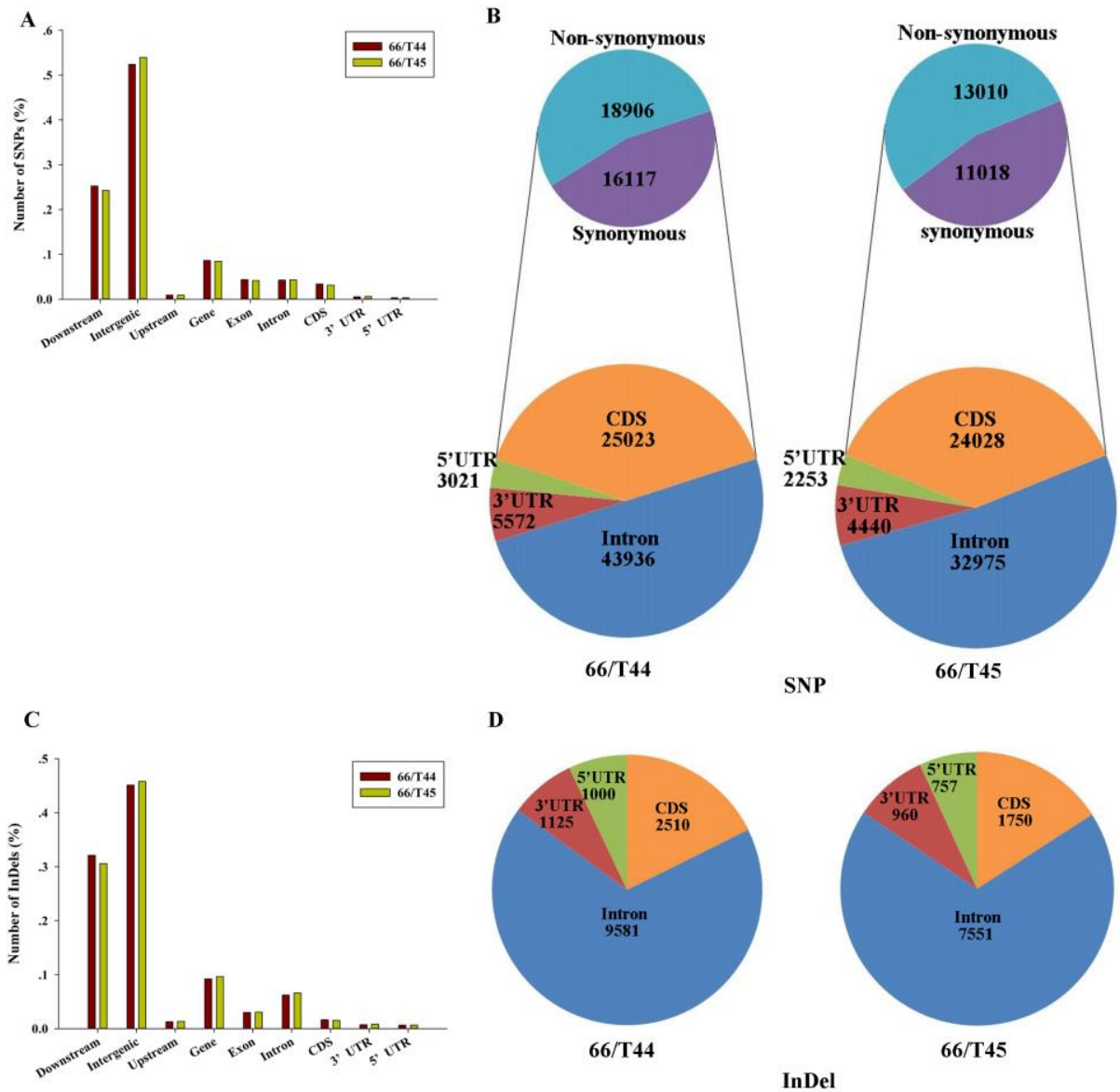
**Fig A. Frequency of SNPs substitutions and length distribution of InDels in Neo-tetraploid rice lines compared to their parents.**

(A) Frequency of SNPs substitutions in Neo-tetraploid rice lines compared to T45 and T44. (B) Length distribution of InDels. Number of insertions and deletions (y-axis) of various lengths (x-axis, in bp) are shown in the bar graph. Neo-tetraploid rice lines/T44 indicates InDels identified between neo-tetraploid rice and its autotetraploid parent (T44), neo-tetraploid rice lines/T45 indicates InDels identified between neo-tetraploid rice and its autotetraploid parent (T45).



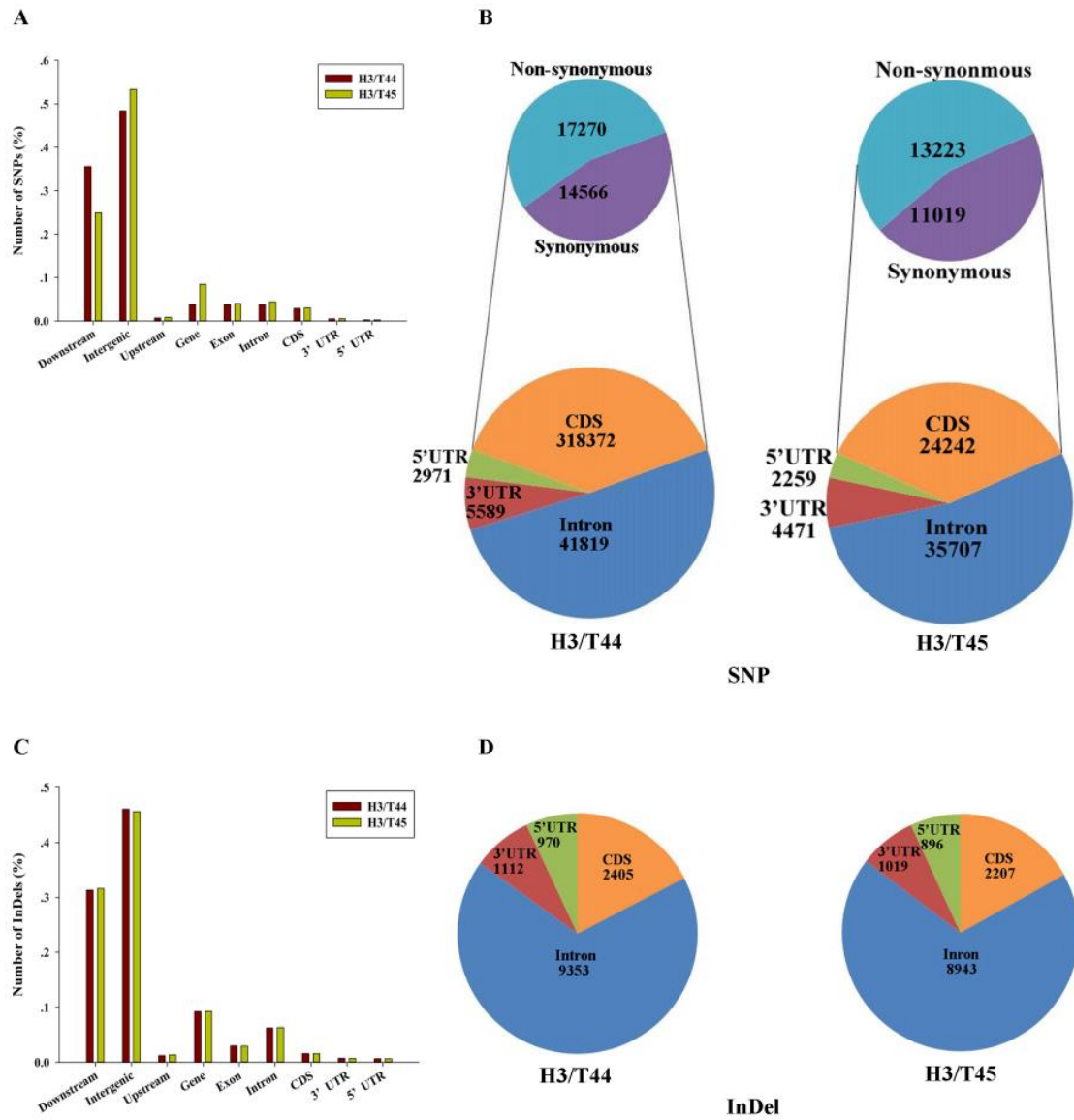
**Fig B. Annotation of SNPs and InDels.**

Distribution of SNPs (A) and InDels (C) in different genomic regions of 134/T44 and 134/T45. (B, D) Distribution of SNPs (B) and InDels (D) in different genic regions. The number of synonymous and nonsynonymous SNPs detected within the CDS region.



**Fig C. Annotation of SNPs and InDels.**

Distribution of SNPs (A) and InDels (C) in different genomic regions of 66/T44 and 66/T45. (B, D) Distribution of SNPs (B) and InDels (D) in different genic regions. The number of synonymous and nonsynonymous SNPs detected within the CDS region.



**Fig D. Annotation of SNPs and InDels.**

Distribution of SNPs (A) and InDels (C) in different genomic regions of H3/T44 and H3/T45. (B, D) Distribution of SNPs (B) and InDels (D) in different genic regions. The number of synonymous and non-synonymous SNPs detected within the CDS region.