

Background:

Infectious disease is a major force of natural selection and a prime cause of yield loss in agriculture. In plants, NOD-like receptors (NLRs), also known as the intracellular nucleotide-binding site leucine-rich repeat receptors, can recognize the pathogen effectors and confer disease resistance to hosts. NLR genes exhibit high diversity among different species, but the true extent of intraspecific NLR diversity remains unclear. As one of the most economically important crops in the world, a better understanding of the evolution and diversity of NLR genes in soybeans can provide insights into breeding and molecular engineering for disease resistance.

Result 1: The identification of NLR genes in 29 wild and cultivated soybeans.

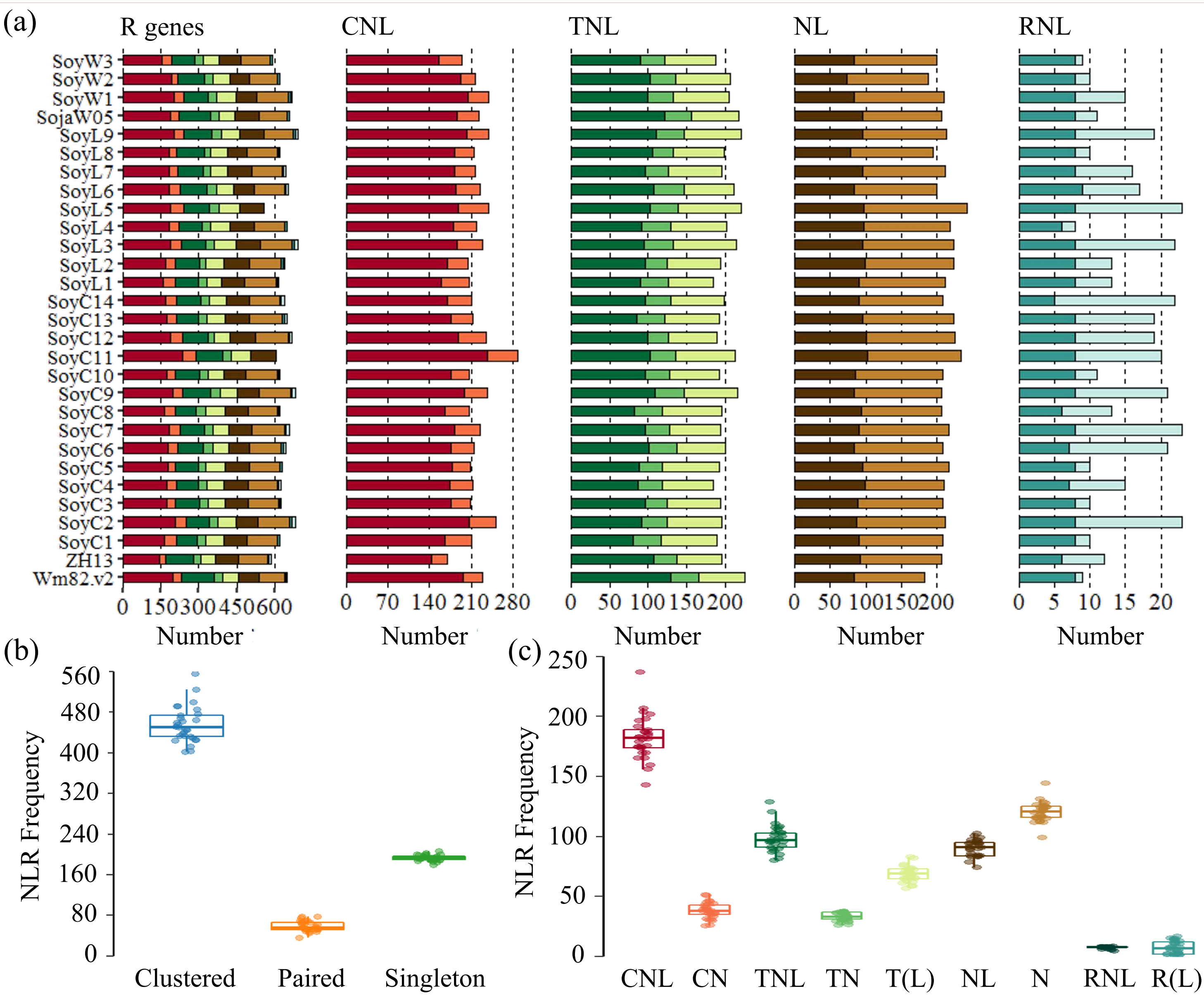


Fig 1. (a) comparison of NLR copy numbers in 29 soybean accessions. CNL: $CN+CNL$; NL: $N+NL$; TNL: $T+TN+TNL$; RNL: $R+RNL$. (b) NLR frequency of different subclasses. (c) Number of clustered, paired, and single NLRs in each accession.

Result 2: The varying extent of copy number variations (CNVs) in different NLR subclasses was detected among 29 soybean accessions.

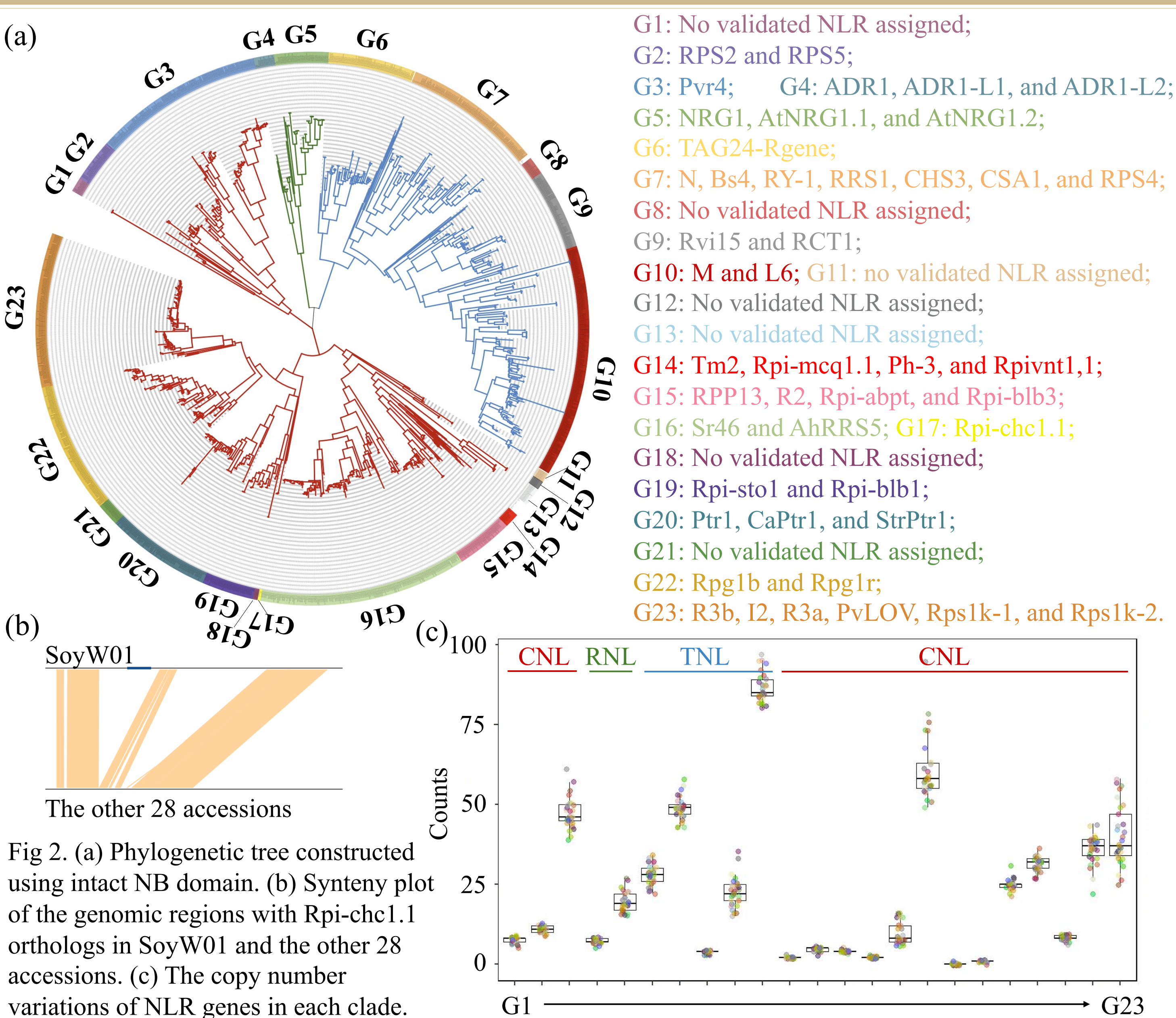


Fig 2. (a) Phylogenetic tree constructed using intact NB domain. (b) Synteny plot of the genomic regions with Rpi-cha1.1 orthologs in SoyW01 and the other 28 accessions. (c) The copy number variations of NLR genes in each clade.

Result 3: The CNVs of different NLR subclasses are driven by various modes of duplication events following the recent WGD event.

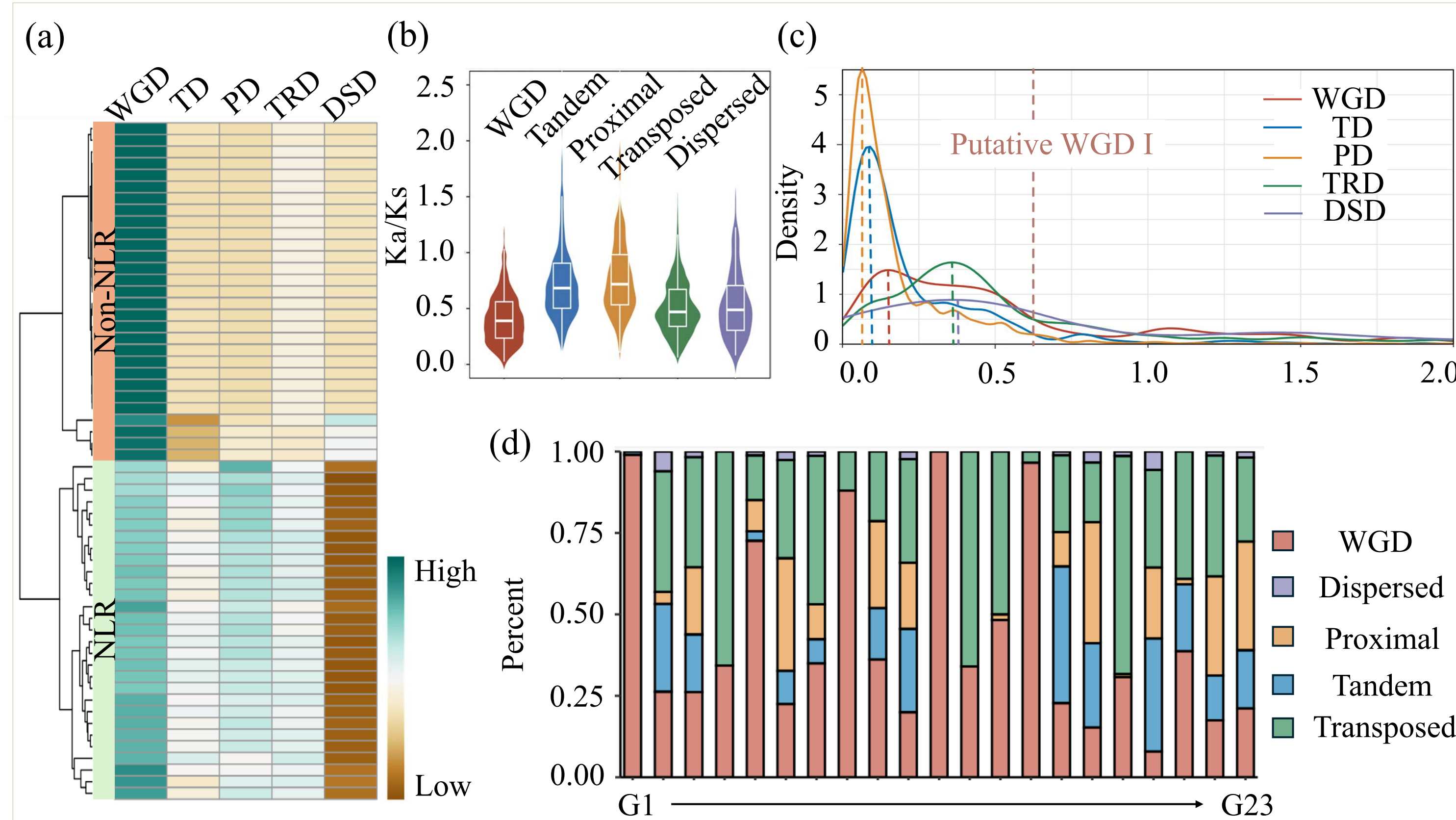


Fig 3. (a) The composition of NLR and non-NLR genes in each accession. (b) Comparison of Ka/Ks value of NLR gene pairs between different modes of duplication. (c) Ks distribution of NLR gene pairs from different modes of duplication. (d) Composition of NLR genes in each clade.

Result 4: The genomic recombination events preferentially occurred in regions with NLR clusters in the course of evolution.

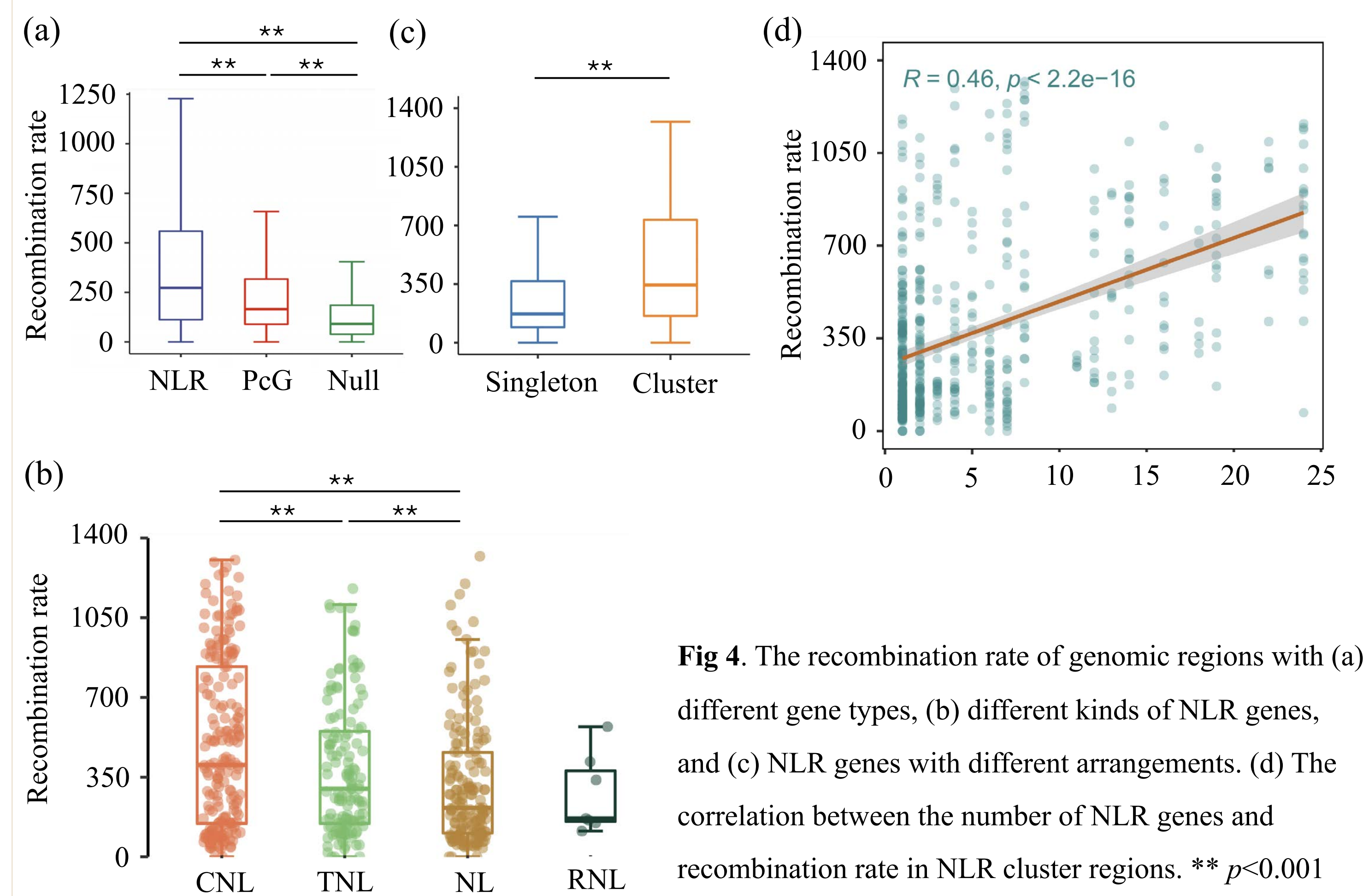


Fig 4. The recombination rate of genomic regions with (a) different gene types, (b) different kinds of NLR genes, and (c) NLR genes with different arrangements. (d) The correlation between the number of NLR genes and recombination rate in NLR cluster regions. ** $p < 0.001$

Future work:

- Detect the impact of 3D genomic architecture on the expansion of NLR genes in soybeans.
- Investigate the influence of dramatic CNVs of NLR genes on the evolution of flanking PcGs.
- Detect the impact of miRNAs on CNVs of NLR genes.

Result 5: Non-redundant functional profile of microRNAs in regulating the expression of NLR genes.

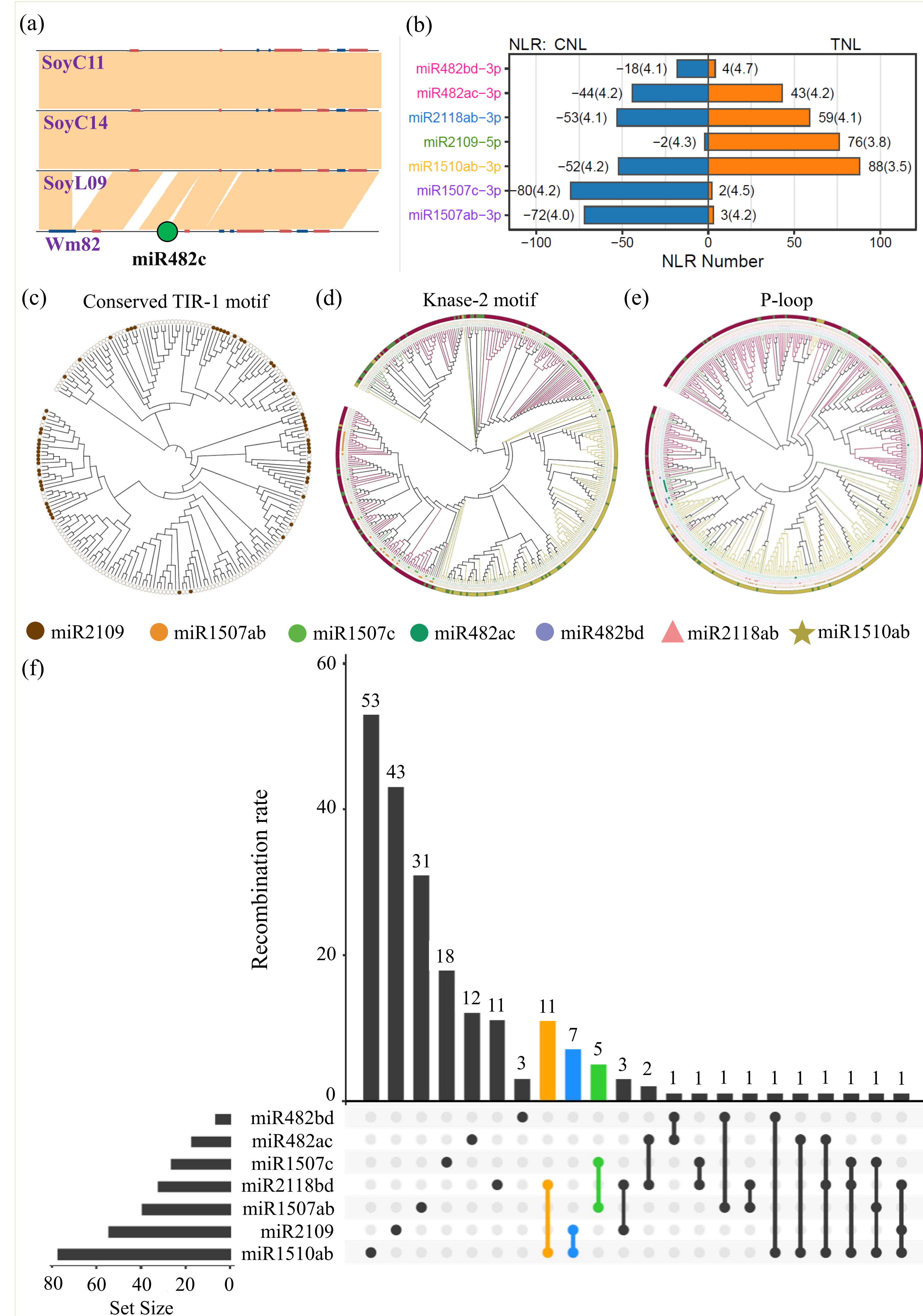


Fig 5. (a) 890 bp deletion induce the lost of miR482c. (b) Average number and penalty score of miRNA NLR targets. The conserved TIR-1 motif (c), Knase-2 motif (d), and P-loop (e) motif were used to construct the corresponding phylogenetic trees. The solid dots mean the genes were the predicted targets of miRNAs. (f) The overlap of NLR targets between different miRNA family.

References:

1. Van de Weyer, Anna-Lena, *et al.*, A species-wide inventory of NLR genes and alleles in *Arabidopsis thaliana*. *Cell* 178.5 (2019): 1260-1272.
2. Zhao, *et al.*, Evolutionary patterns and coevolutionary consequences of MIRNA genes and microRNA targets triggered by multiple mechanisms of genomic duplications in soybean. *The Plant Cell* 27.3 (2015): 546-562.
3. Liu, *et al.*, Pan-genome of wild and cultivated soybeans. *Cell* 182.1 (2020): 162-176.