

Supplementary Materials: Figures

Genome-wide analysis of genetic variations and the detection of rich variants of NBS-LRR encoding genes in common wild rice lines

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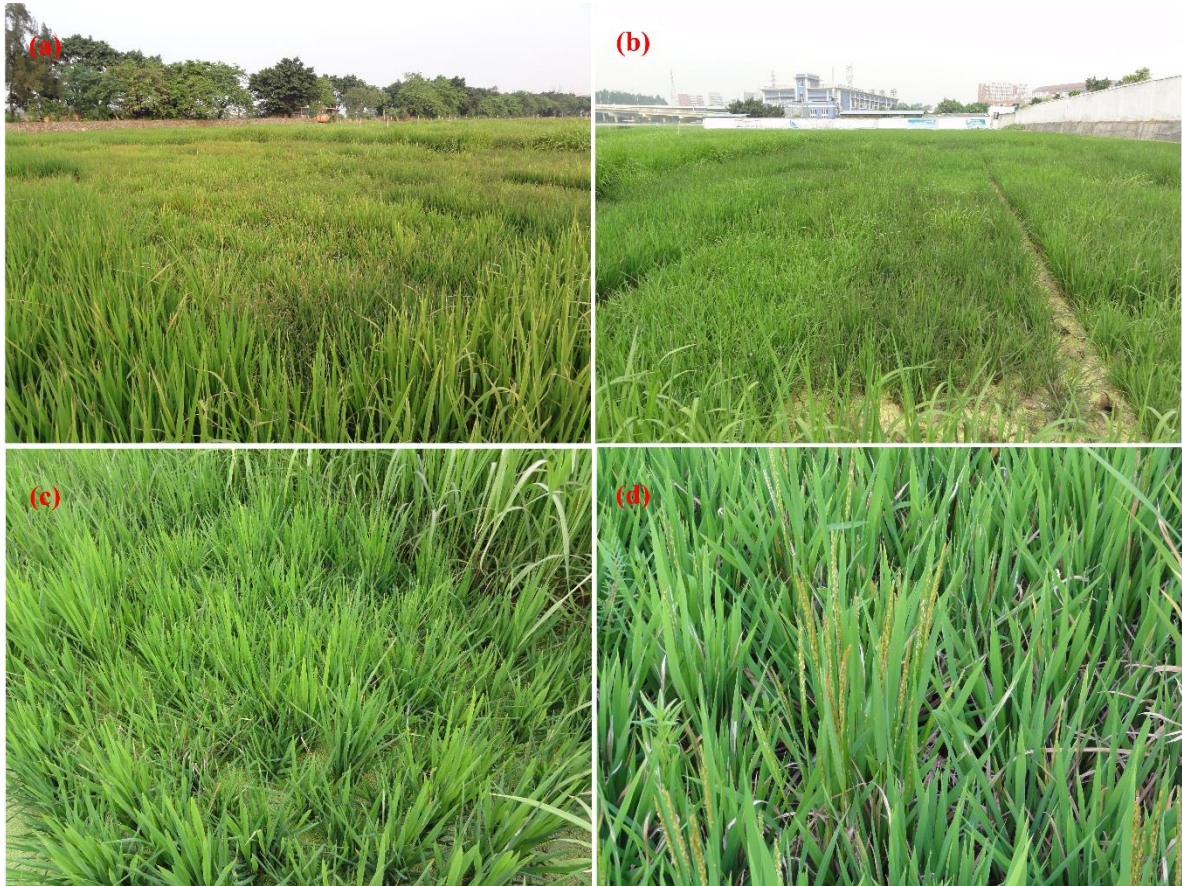


Fig.S1 Inbred lines derived from S24 common wild rice and segregation in their traits.

(a, b, c) 4th generation of inbred lines derived from S24 grown in the field during early season of 2011. (d)

Plants of 4th generation segregation population of S24 at heading stage.

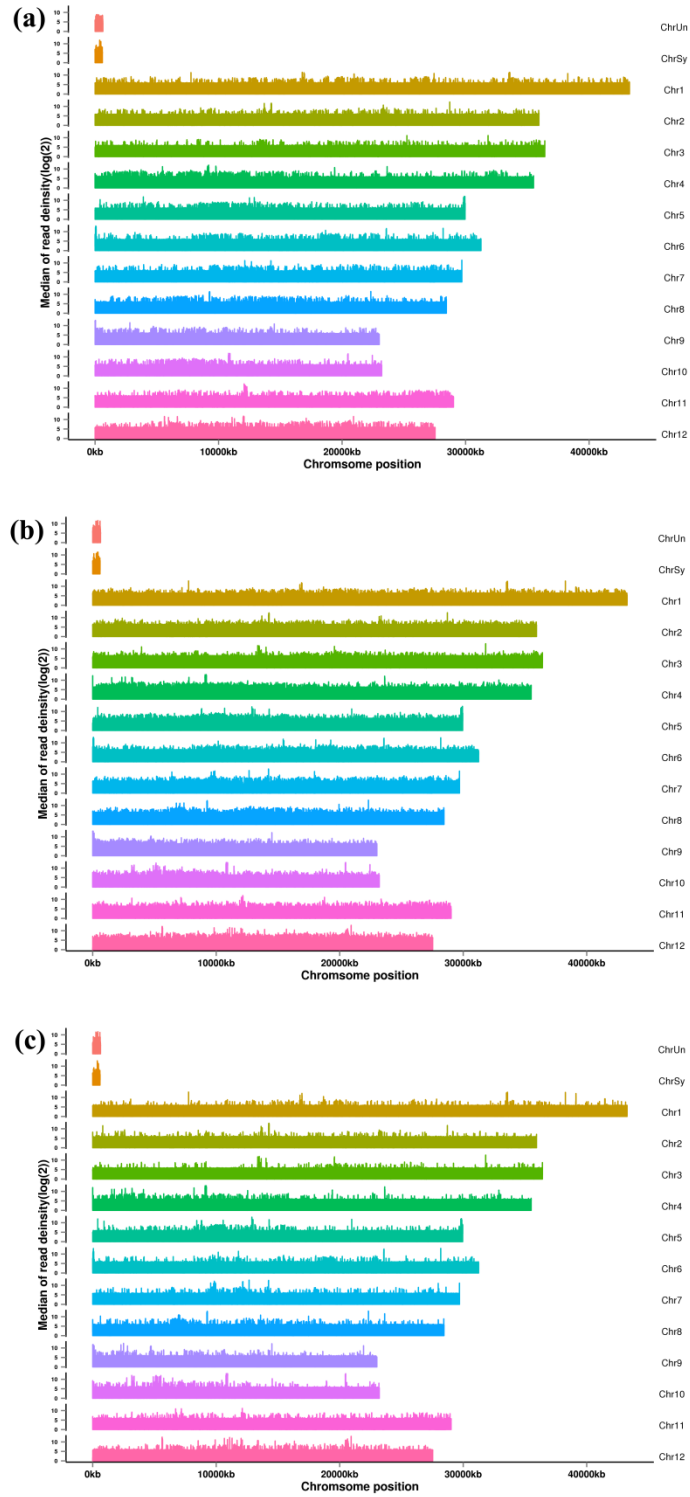


Fig.S2 Genome-wide distribution of reads mapping coverage in S24 (a), Huaye 3 (b) and Huaye 4 (c)

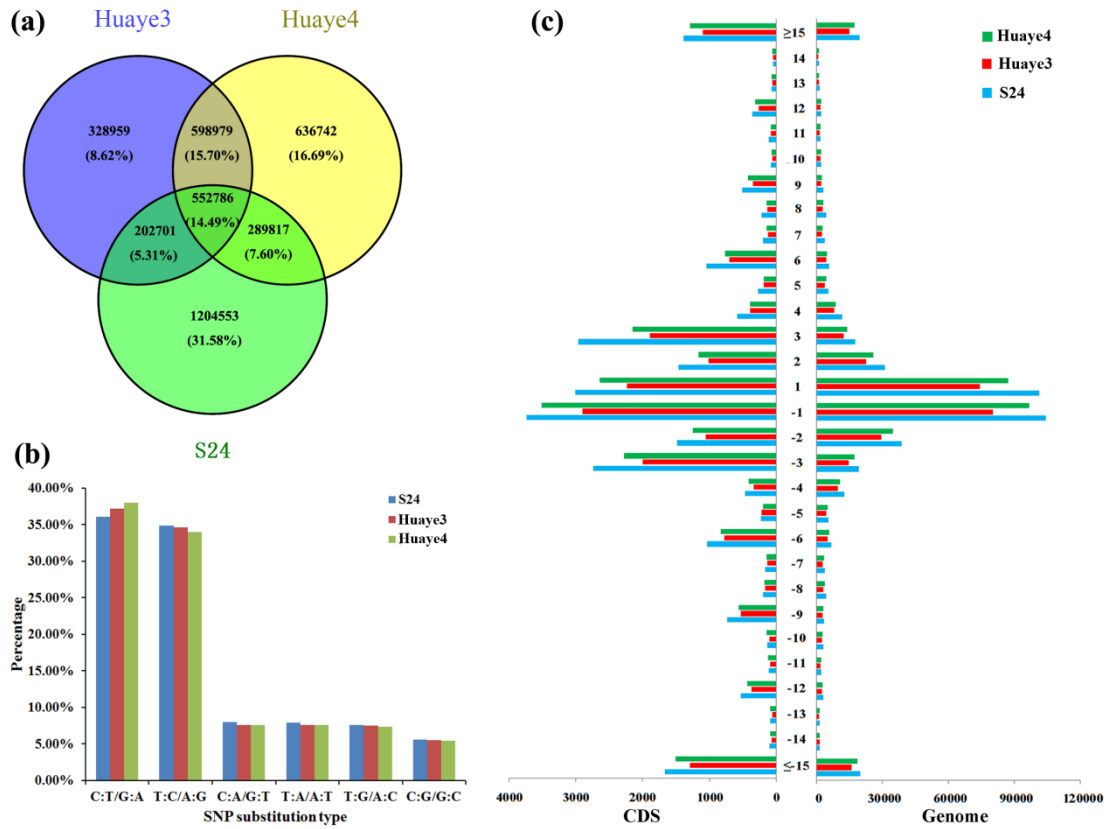


Fig.S3 Distribution of single nucleotide polymorphisms (SNPs) and insertion and deletions (InDels).

(a) Venn analysis of SNPs and InDels in S24, Huaye 3 and Huaye 4. (b) Frequency of six substitution types of SNPs. (c) Distribution of InDels in different length.

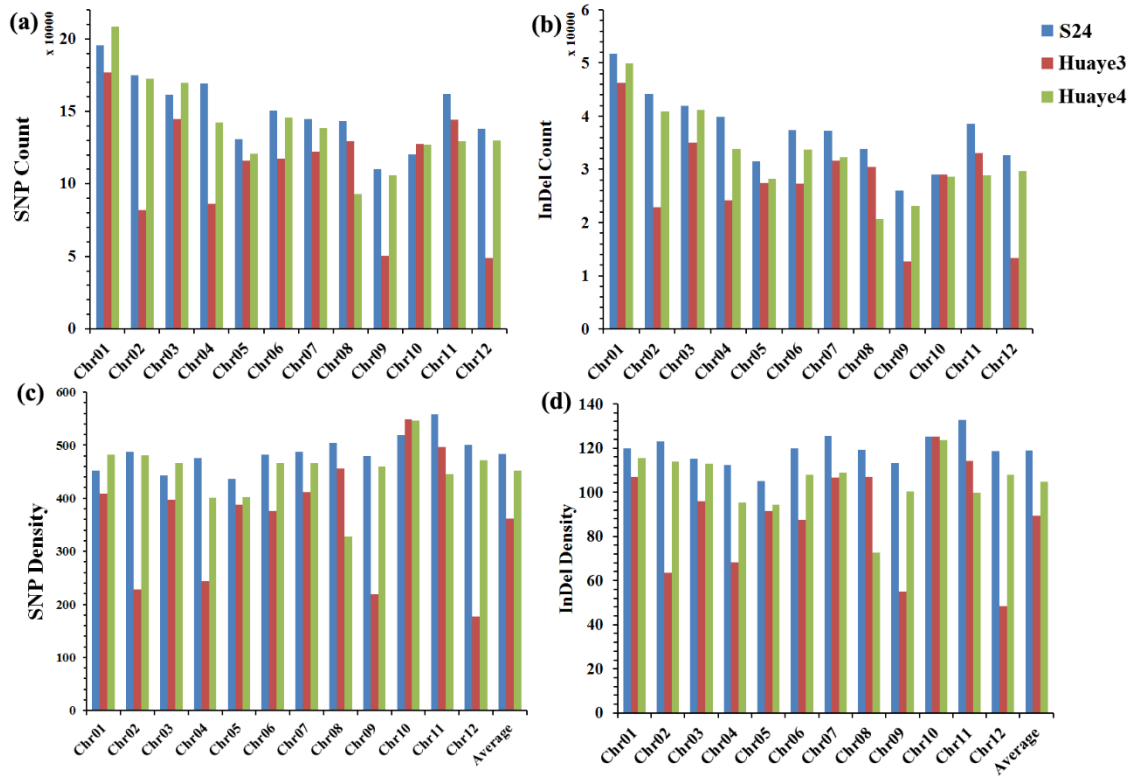


Fig.S4 Distribution of DNA polymorphisms number and density in common wild rice lines.

(a, b) Number of SNPs (a) and InDels (b) in different chromosomes. (c, d) Density of SNPs (c) and InDels (d) in different chromosomes.

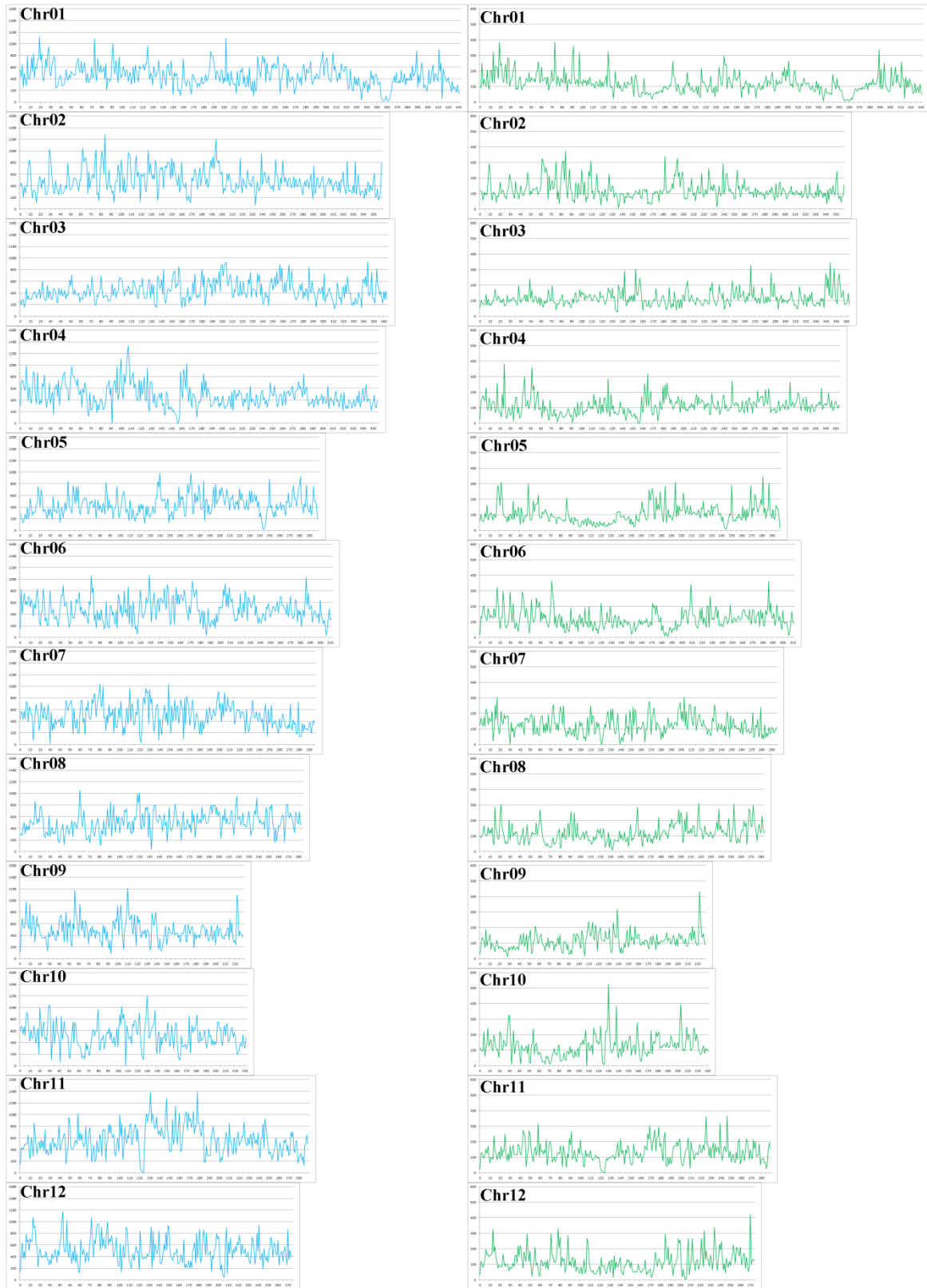


Fig.S5a Distribution of SNPs (blue lines) and InDels (green lines) in 100 kb windows across different chromosomes in S24.

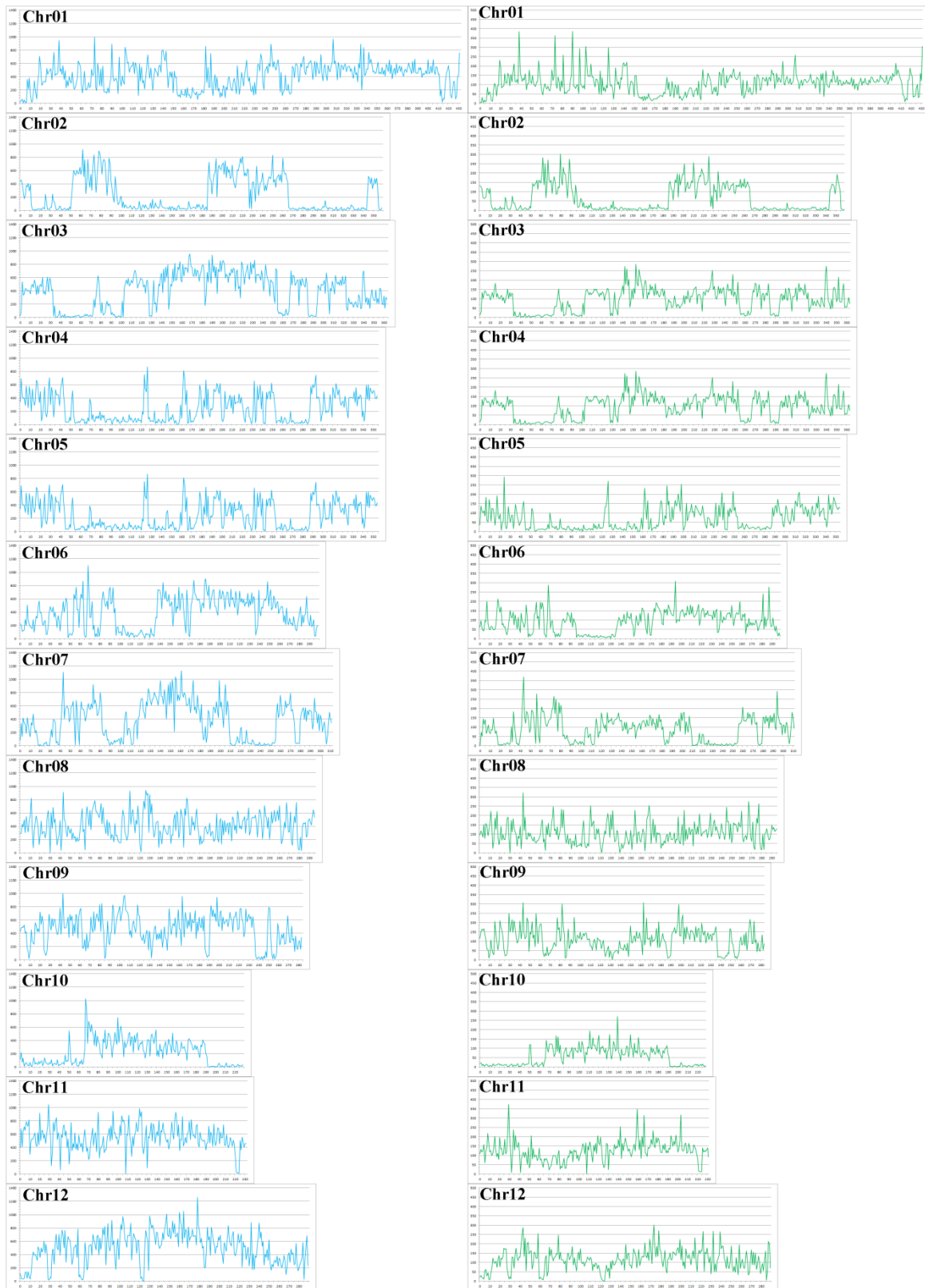


Fig.S5b Distribution of SNPs (blue lines) and InDels (green lines) in 100 kb windows across different chromosomes in Huaye 3.

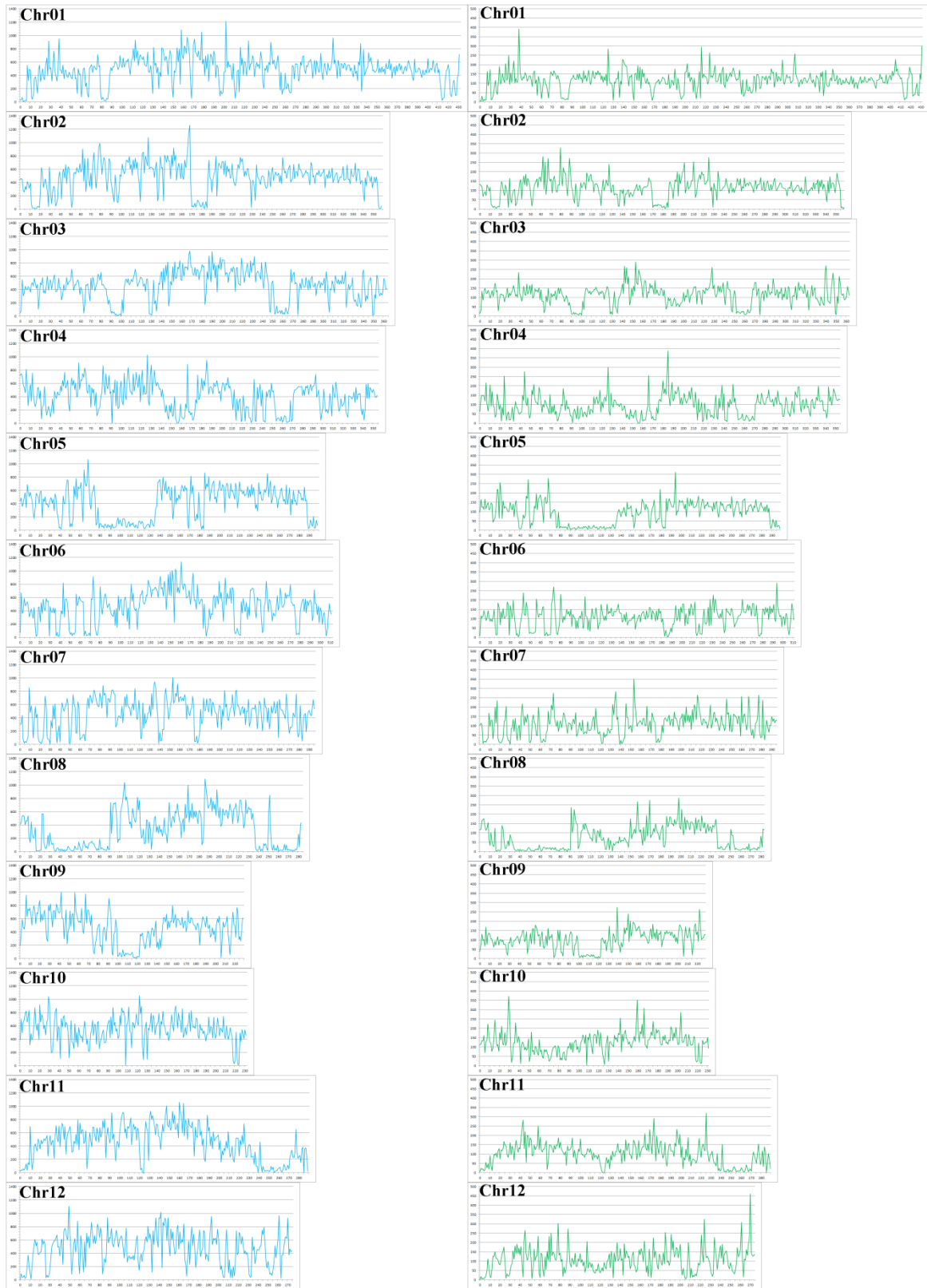


Fig.S5c Distribution of SNPs (blue lines) and InDels (green lines) in 100 kb windows across different chromosomes in Huaye 4.

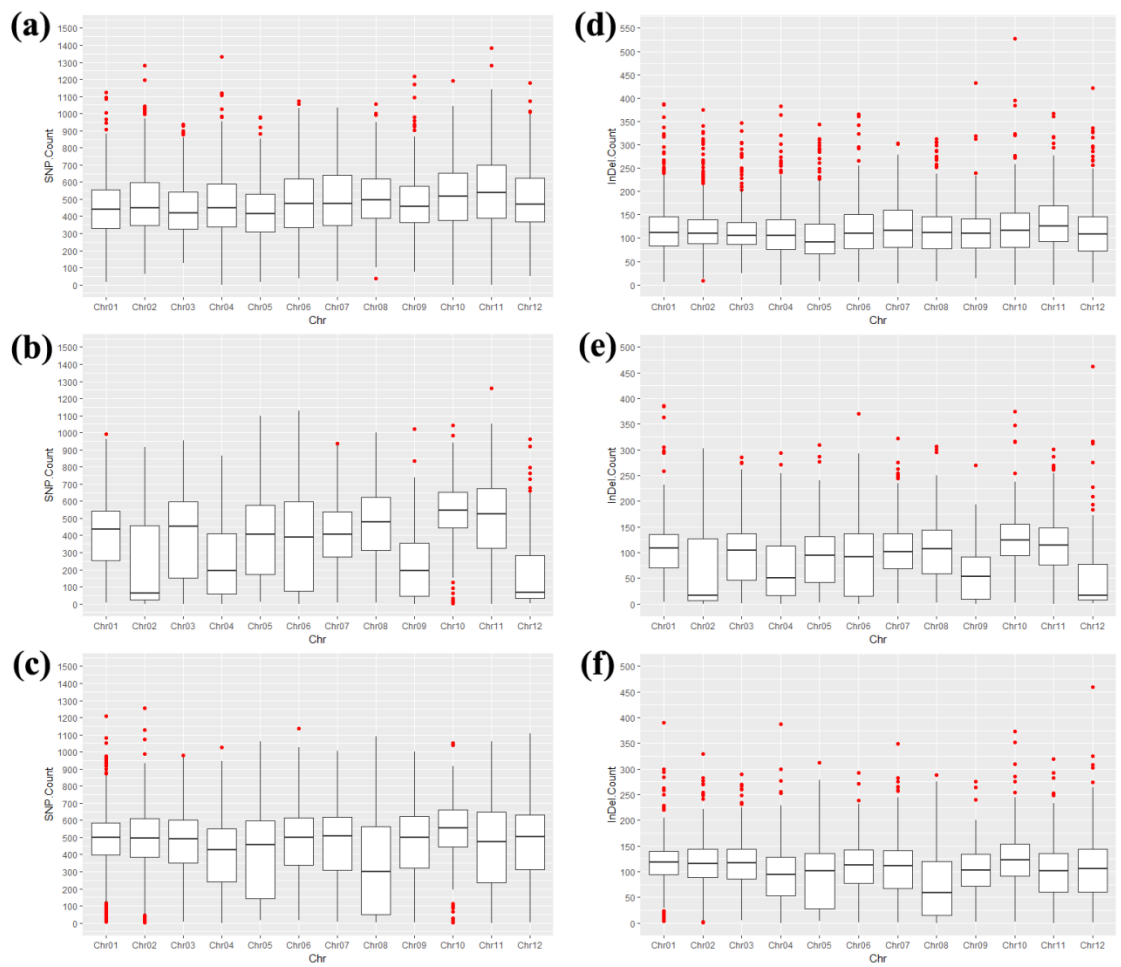


Fig.S6 Boxplot of DNA polymorphisms density in every 100 kb window.

(a, b, c) Boxplot of SNP density across the 12 chromosome in S24 (a), Huaye 3 (b) and Huaye 4 (c). (d, e, f)

Boxplot of InDel density across the 12 chromosome in S24 (d), Huaye 3 (e) and Huaye 4 (f).

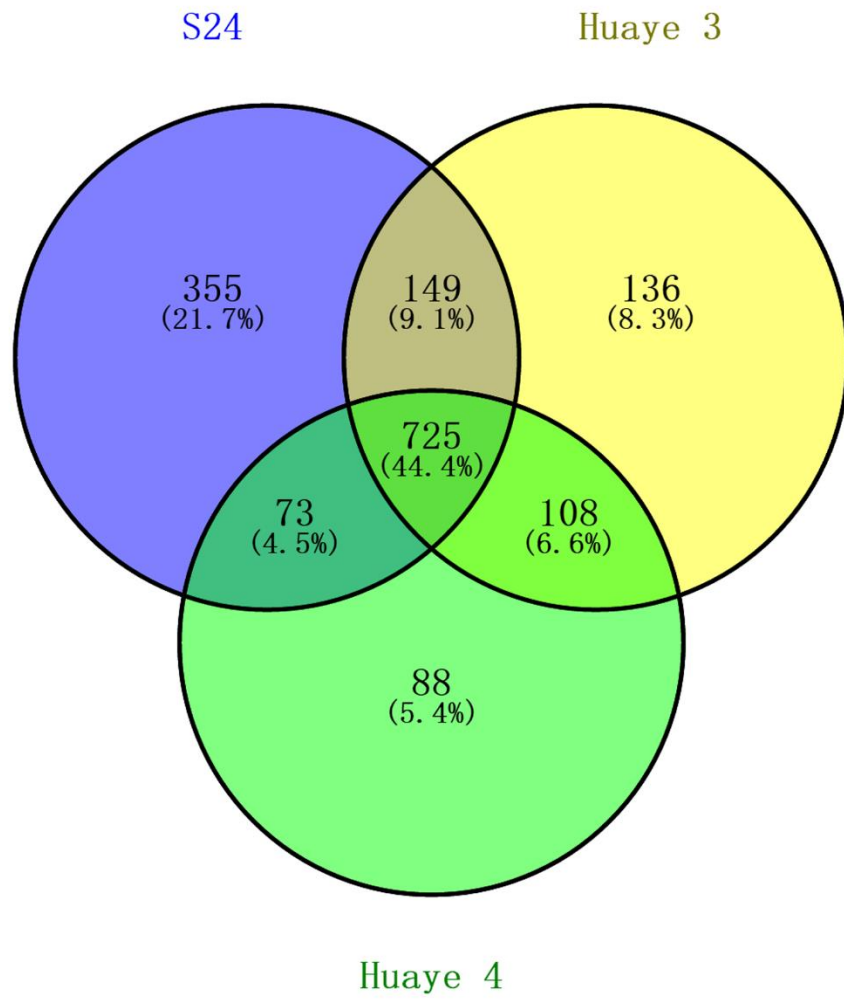


Fig.S7 Venn analysis of common wild rice unique genes detected in S24, Huaye 3 and Huaye 4.

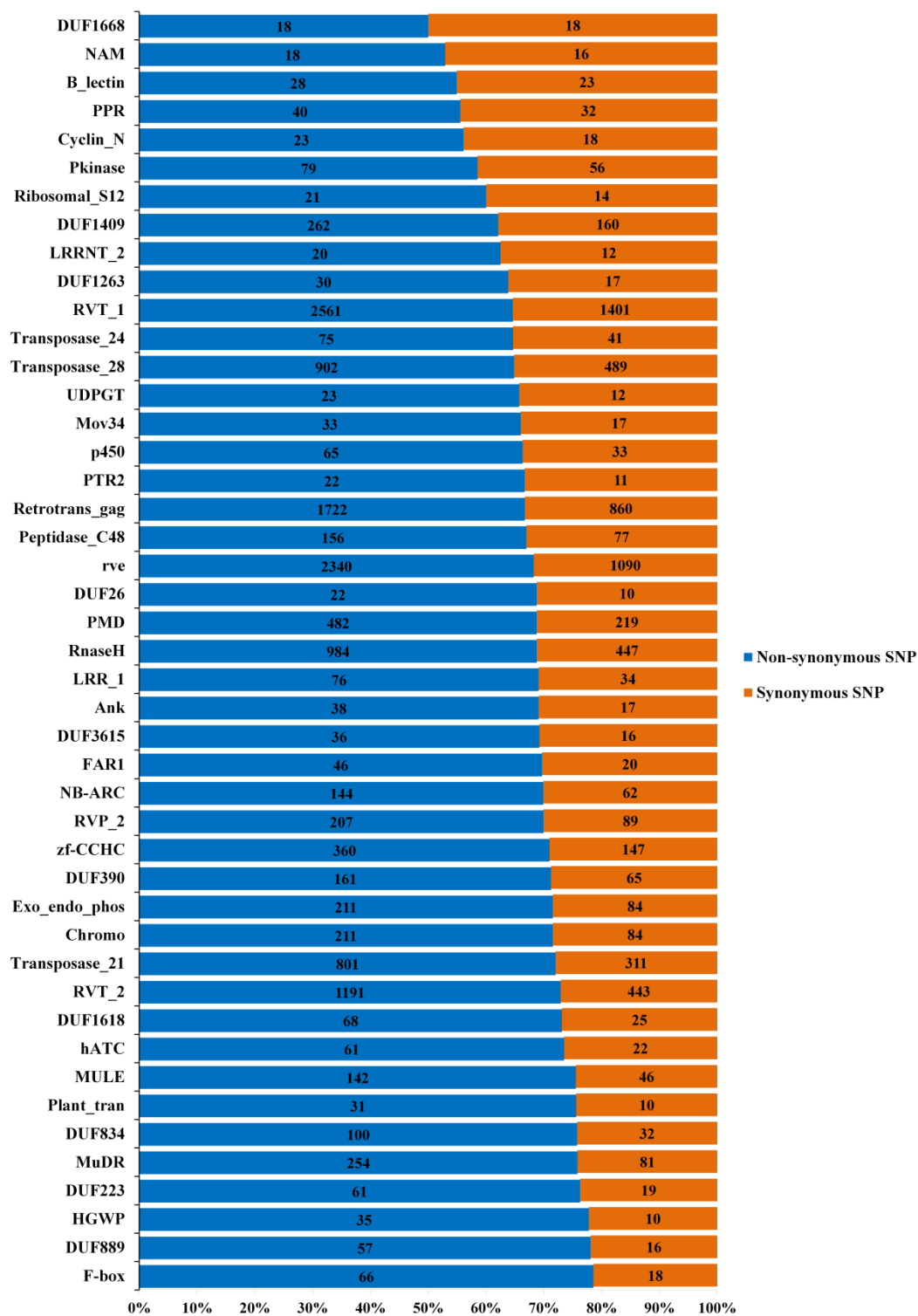


Fig.S8 Distribution of non-synonymous and synonymous SNPs in different Pfam domain families

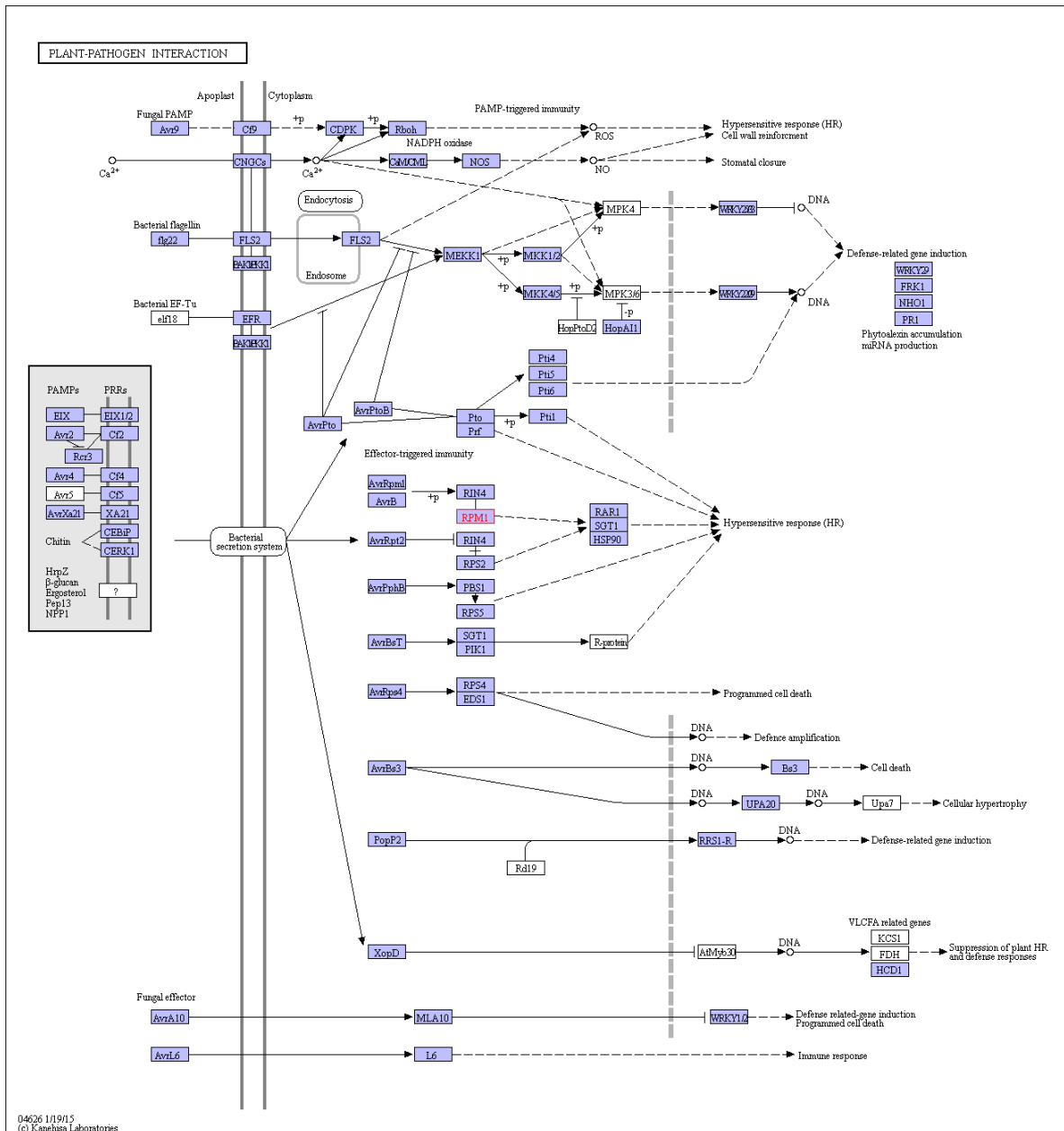


Fig.S9 KEGG pathway of a disease resistance protein RPM1 homologue. The RPM1 homologue was marked as red color.

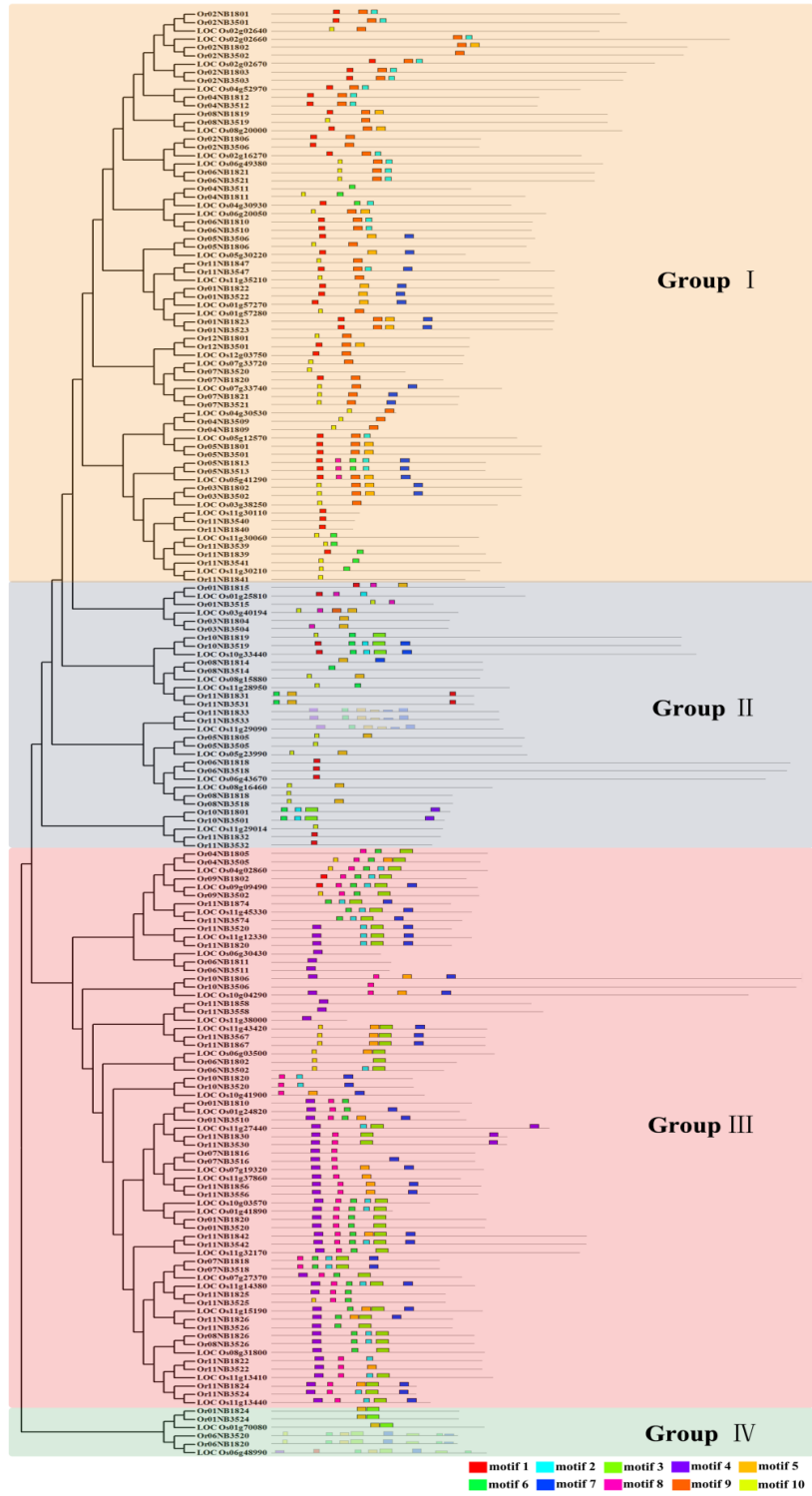


Fig.S10 Phylogenetic and MEME analysis of candidate genes and their homologs in the two inbred lines. The serial numbers of homologs in Huaye 3 and Huaye 4 were named as “Or-Chr-NB-18/35-No.”. “Or” represents *Oryza rufipogon*, “Chr” represents chromosome, “NB” represents NB-ARC, “18” represents Huaye 3, “35” represents Huaye 4 and “No.” represents serial number.

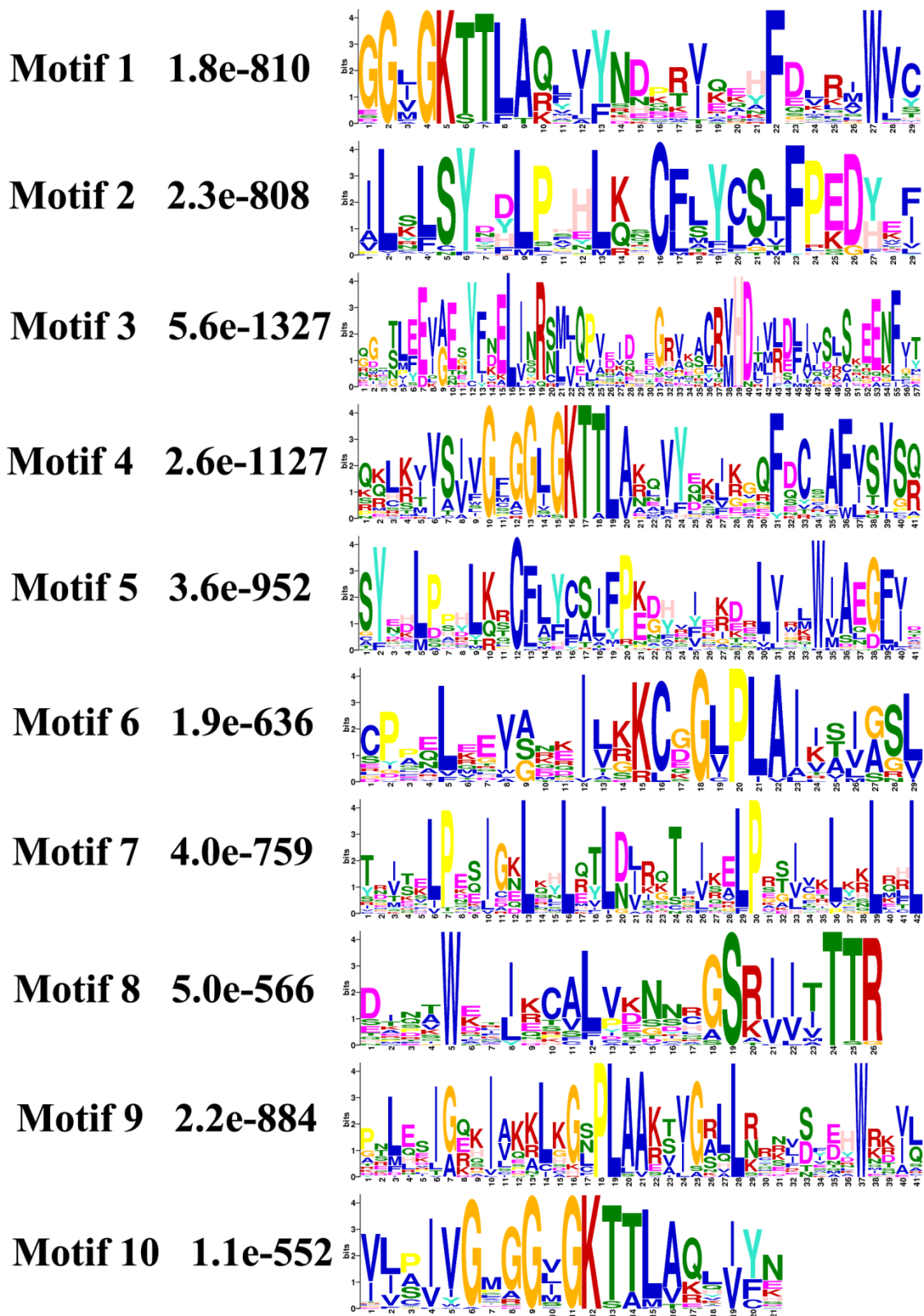


Fig.S11 Sequence logos of MEME motifs

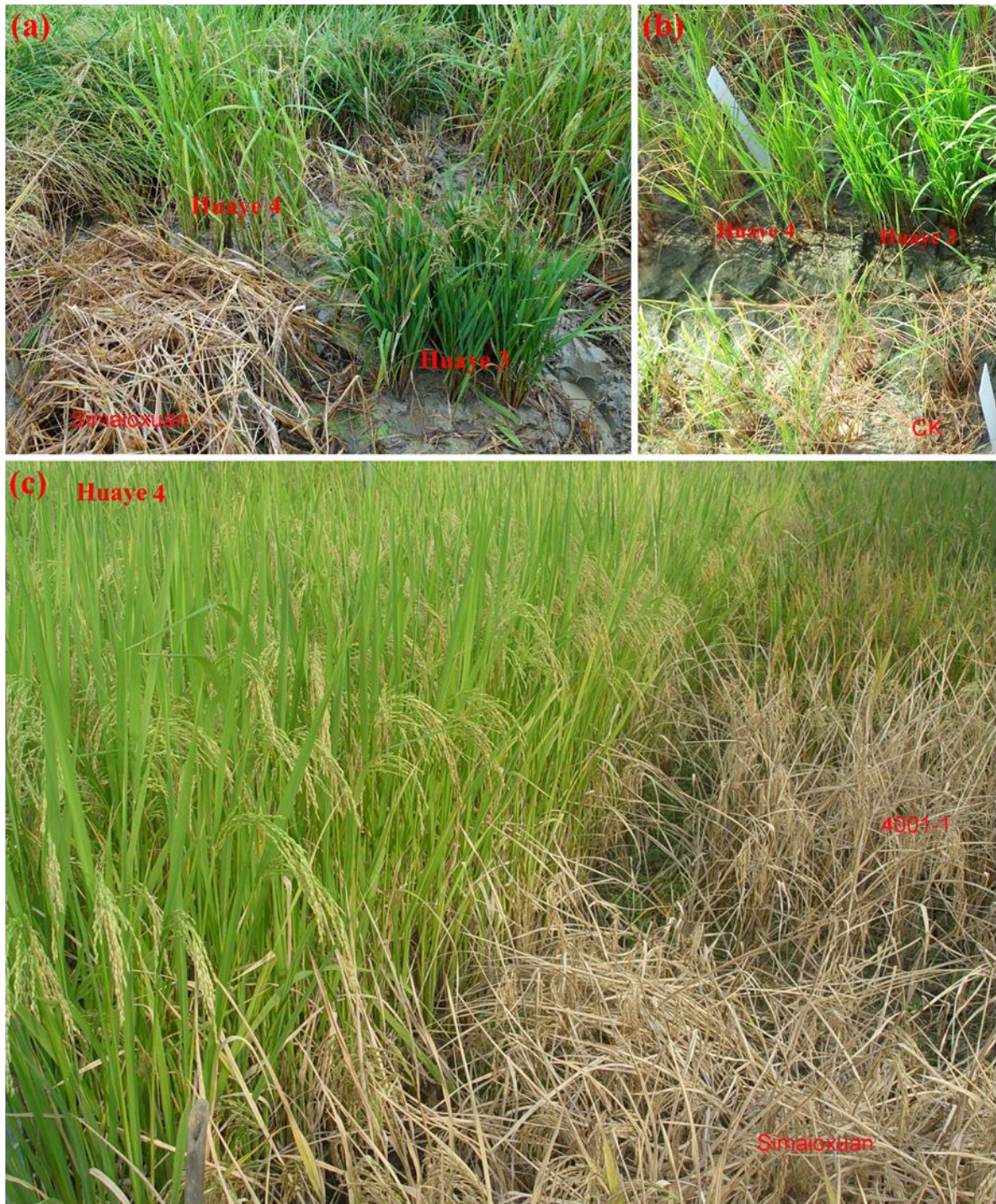


Fig.S12 Brown planthopper (BPH) resistance performance of Huaye 3 and Huaye 4.

(a) Resistance performance of Huaye 3 and Huaye 4 against BPH in epidemic year of 2017. Susceptible variety: Simiaoxuan. (b) The results of brown planthopper resistance assay of Huaye 3 by artificial inoculation. CK: Taichuang Native 1 (TN1). (c) Resistance performance of Huaye 4 against BPH in 2015. Susceptible varieties: Simiaoxuan and 4001-1.