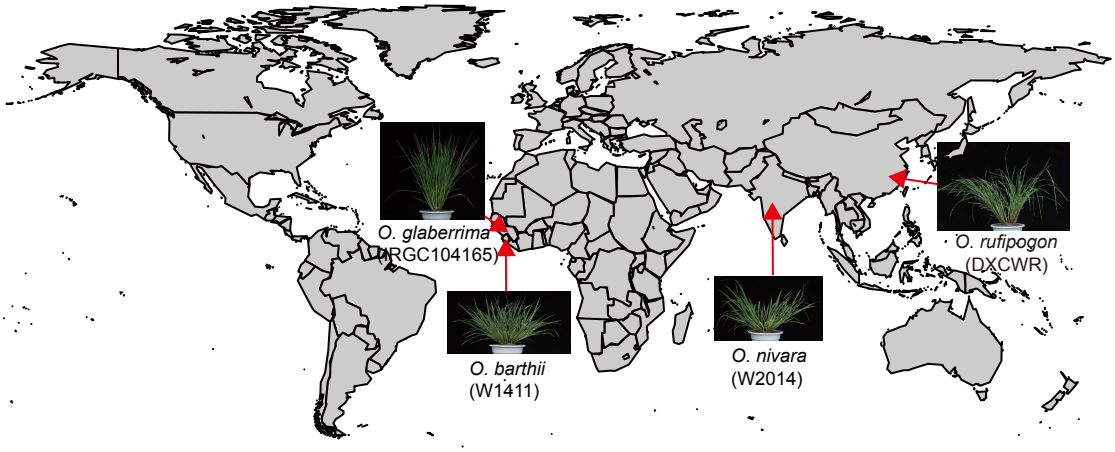

Figure S1. Geographical distribution of the four *Oryza* AA species for whole-genome *de novo* assembly.

O. rufipogon accession DXCWR, *O. nivara* accession W2014, *O. barthii* accession W1411, and *O. glaberrima* accession IRGC104165, originated from China, India, Sierra Leone, and Guinea, respectively.

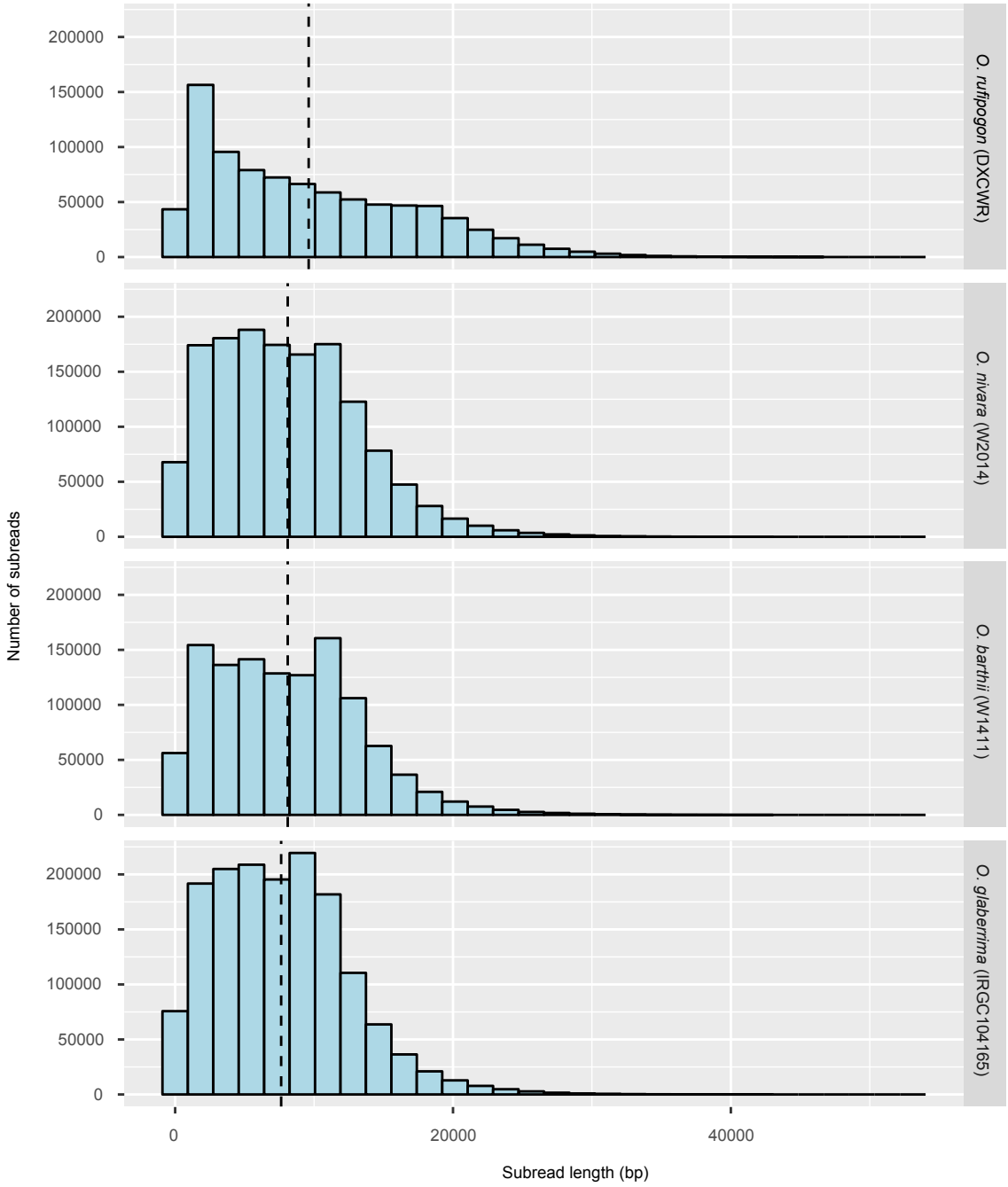

Figure S2. Frequency distribution of subread length for the four rice samples.

Vertical dashed lines indicate mean subread length.

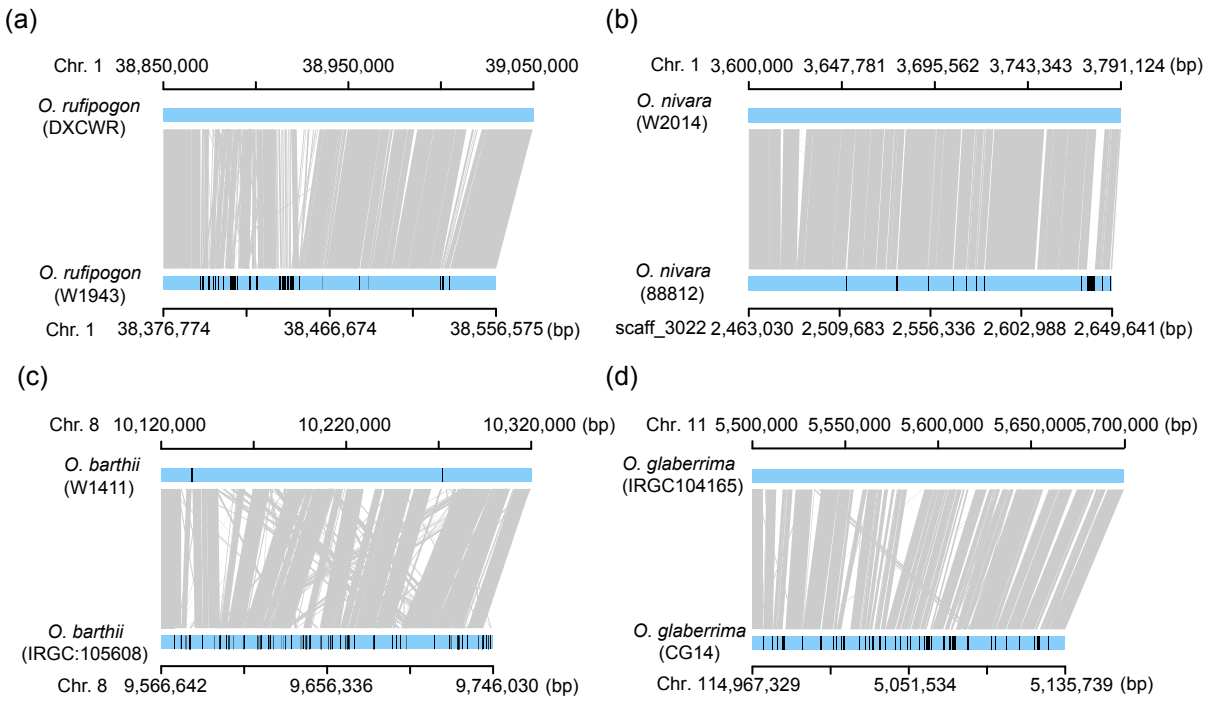

Figure S3. Sequence comparisons of *de novo* assemblies of *Oryza rufipogon* (a), *Oryza nivara* (b), *Oryza barthii* (c) and *Oryza glaberrima* (d) in the present and previous studies (Huang *et al*., 2012; Wang *et al*., 2014; Zhang *et al*., 2014; Stein *et al*., 2018).

The grey regions represent sequences sharing sequence collinearity. The black vertical lines indicate gap regions in the corresponding assembly.

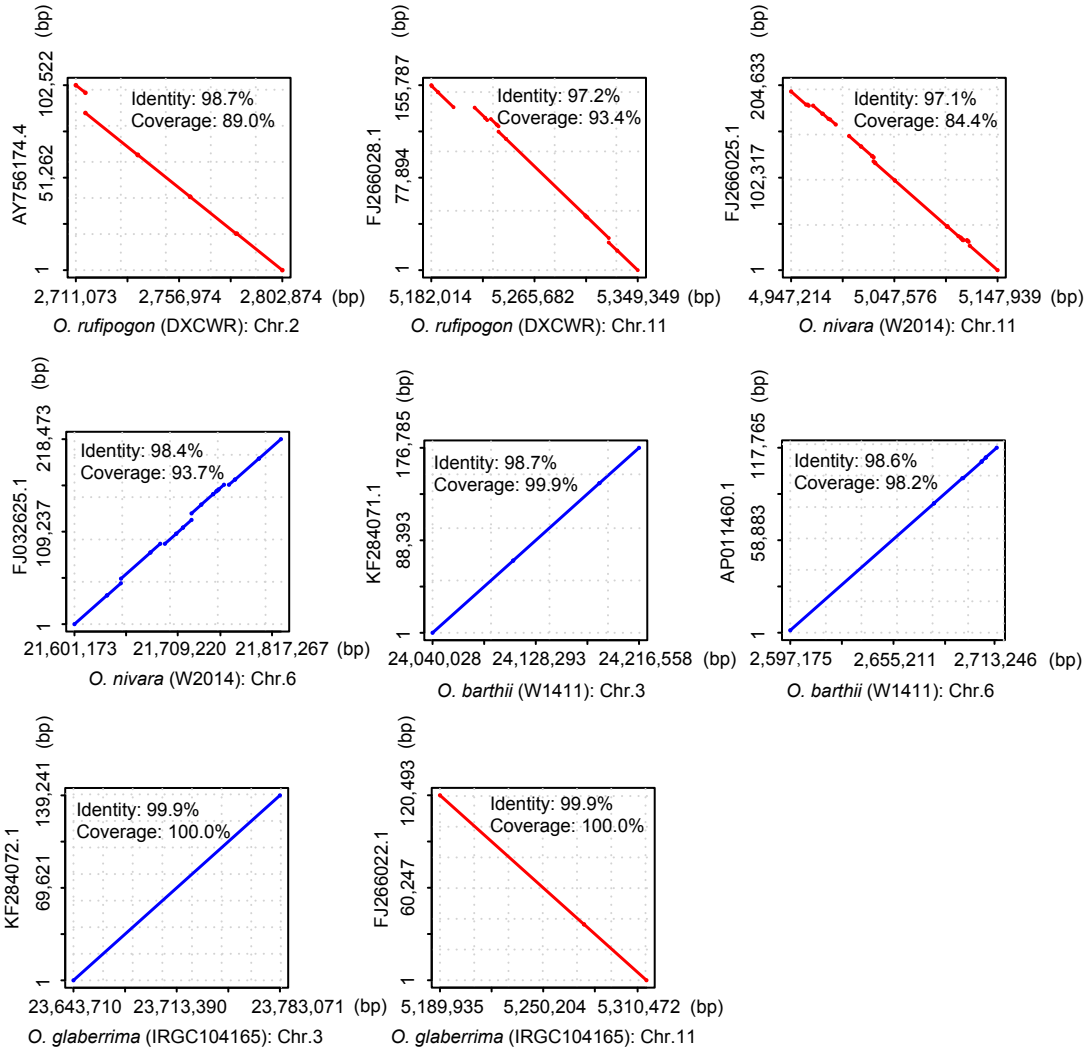

Figure S4. Confirmation of the four *de novo* assemblies using publicly available bacterial artificial chromosome (BAC) sequences.

All these BAC sequences were collected from GenBank.

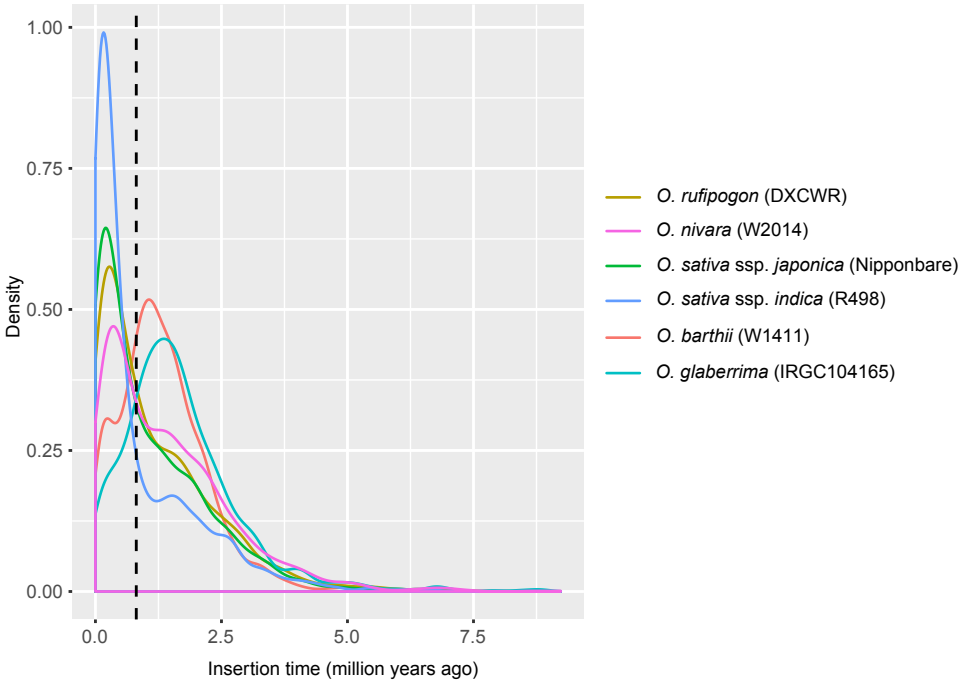

Figure S5. The insertion time of LTR/*Gypsy* elements in the African and Asian rice genomes. Black vertical dashed line represents estimated mean divergence time between African and Asian rice genomes (Stein *et al*., 2018).

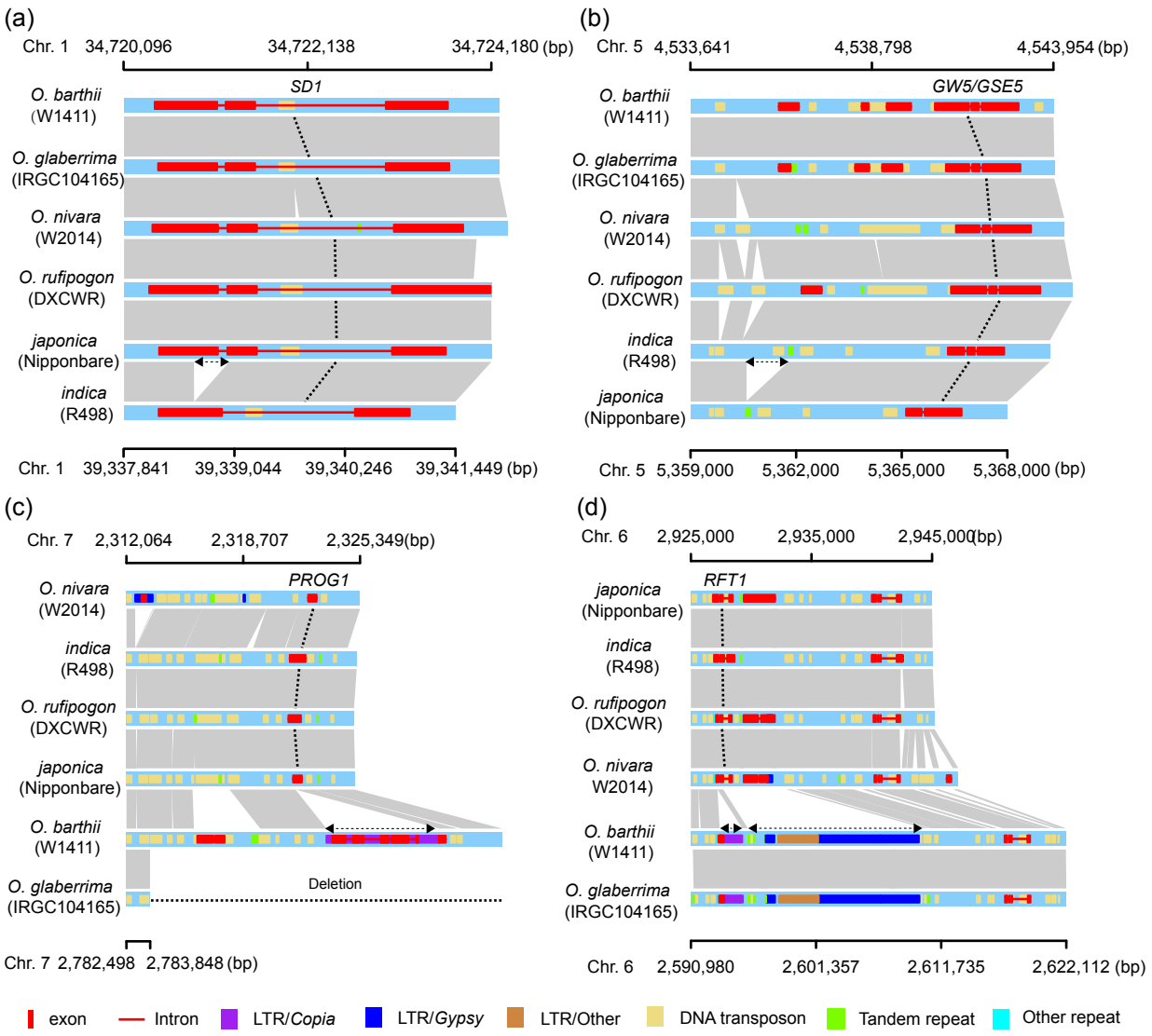

Figure S6. Identification of known and novel structural variations (SVs) in African and Asian rice genomes.

(a, b) Identification of known SVs in the coding region of the gene *SD1* (a) and the upstream regions of the gene *GW5/GSE5* (b).

(c, d) Identification of novel SVs in the coding region of the gene *prog1* (c) and the coding and downstream regions of the gene *RFT1* (d). Black dashed lines between arrows represent the SVs. The grey regions represent sequences sharing sequence collinearity.

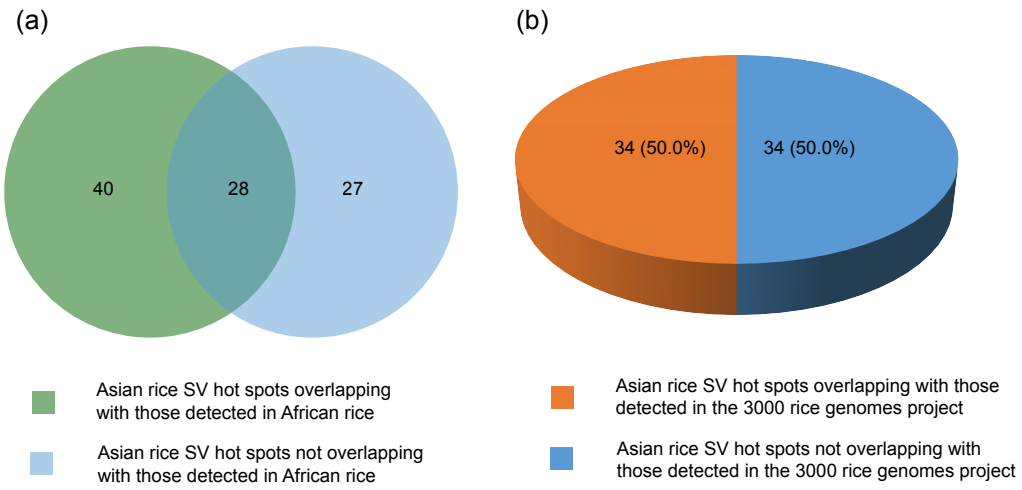

Figure S7. The proportion of common structural variation (SV) hot spots identified in the present and previous studies.

(a) The proportion of common SV hot spots identified in the present between African and Asian rice.

(b) The proportion of identical SV hot spots in Asian rice between the present study and the 3000 Rice Genomes Project (Fuentes *et al*., 2019).

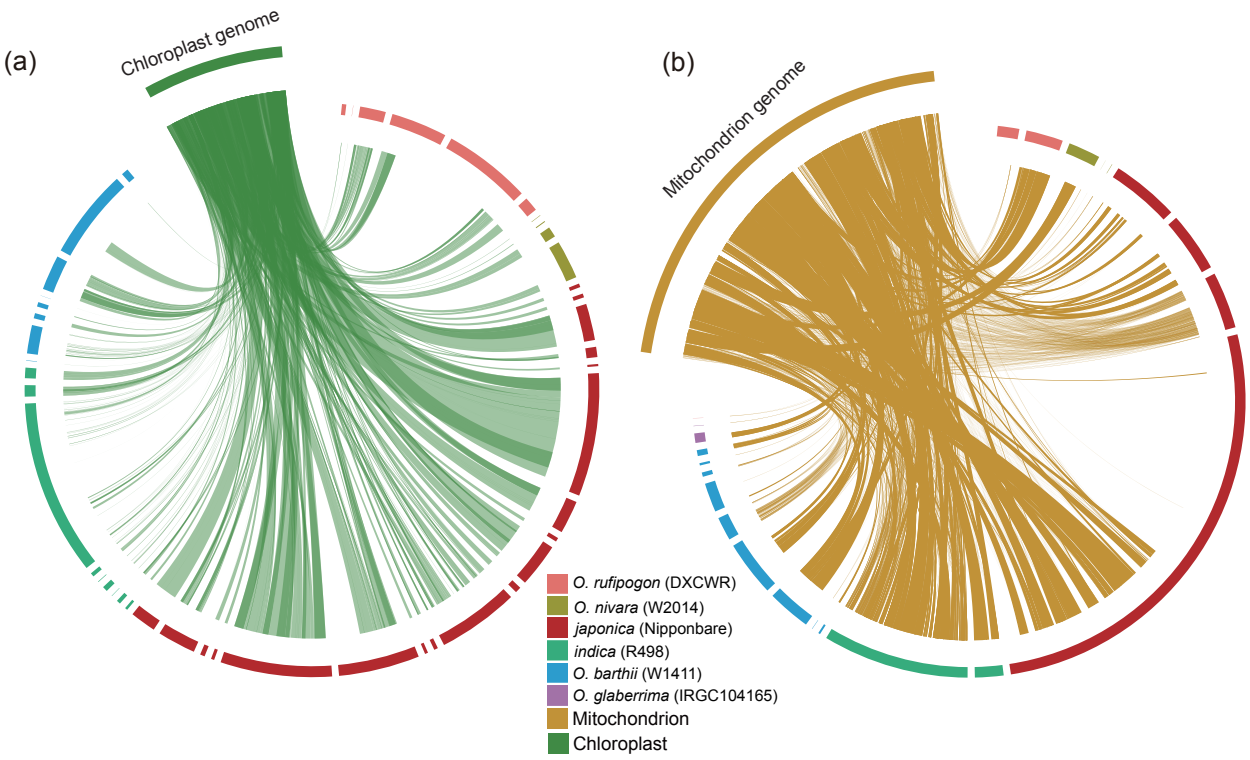

Figure S8. Organelle-to-nucleus DNA transfers generating structural variations (SVs).

(a, b) A subset of SVs contain chloroplast- (a) and mitochondrion-derived (b) genes.

Outer circles indicate chloroplast and mitochondrion genomes. Inner circle represents SVs.

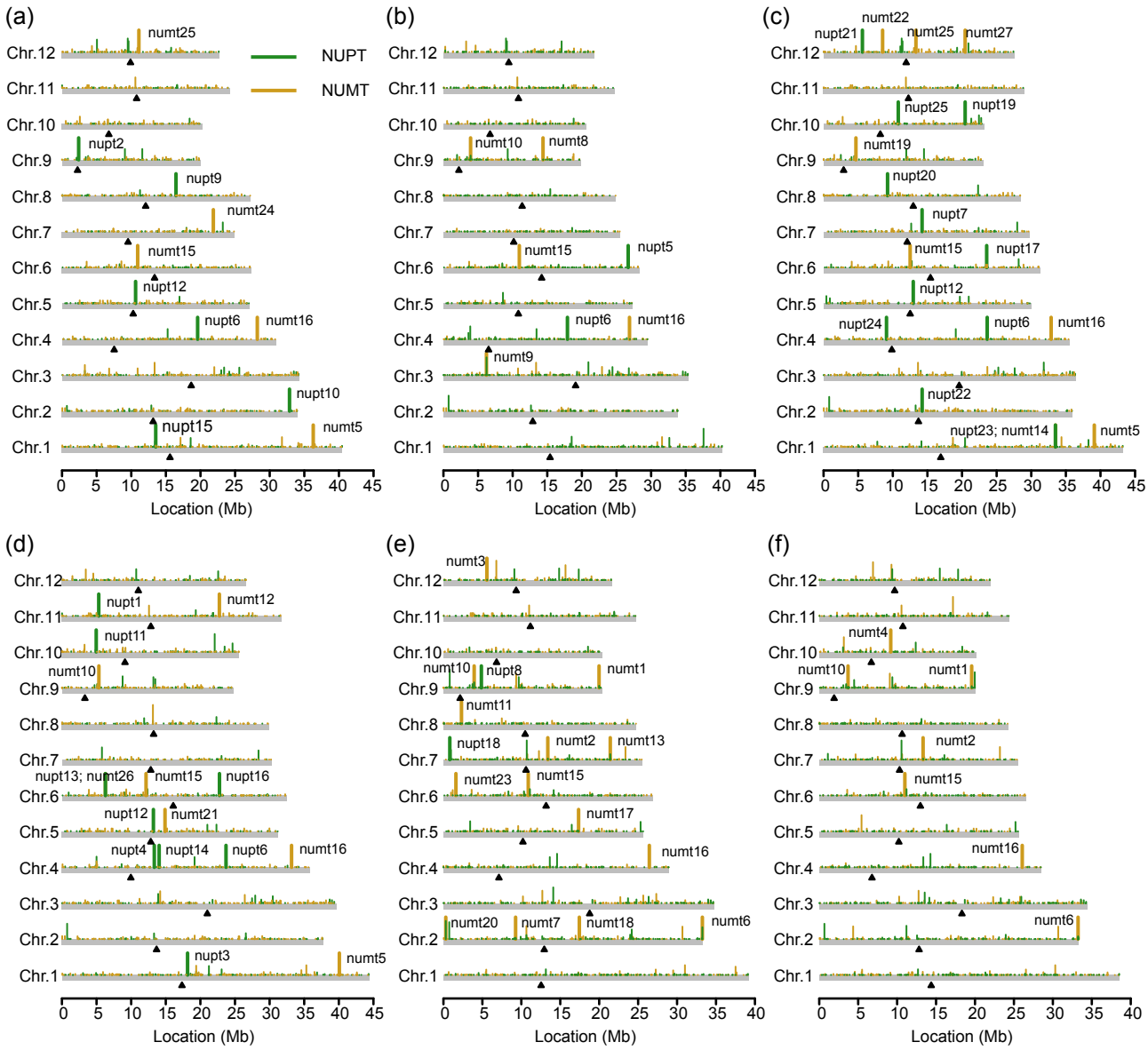

Figure S9. Genome-wide identification of nuclear integrants of plastid DNA (NUPTs) and mitochondrial DNA (NUMTs) in African and Asian rice genomes.

(a-f) Distribution of NUPTs and NUMTs in the *O. rufipogon* (a), *O. nivara* (b), *O. sativa* ssp. *japonica* (c), *O. sativa* ssp. *indica* (d), *O. barthii* (e), and *O. glaberrima* (f) nuclear genomes. The thin green and brown vertical lines denote NUPTs and NUMTs, respectively, with the heights of the lines indicating their sizes. The bold lines of fixed height represent the giant NUPTs and NUMTs (>10 kb). Black triangles denote centromeres.

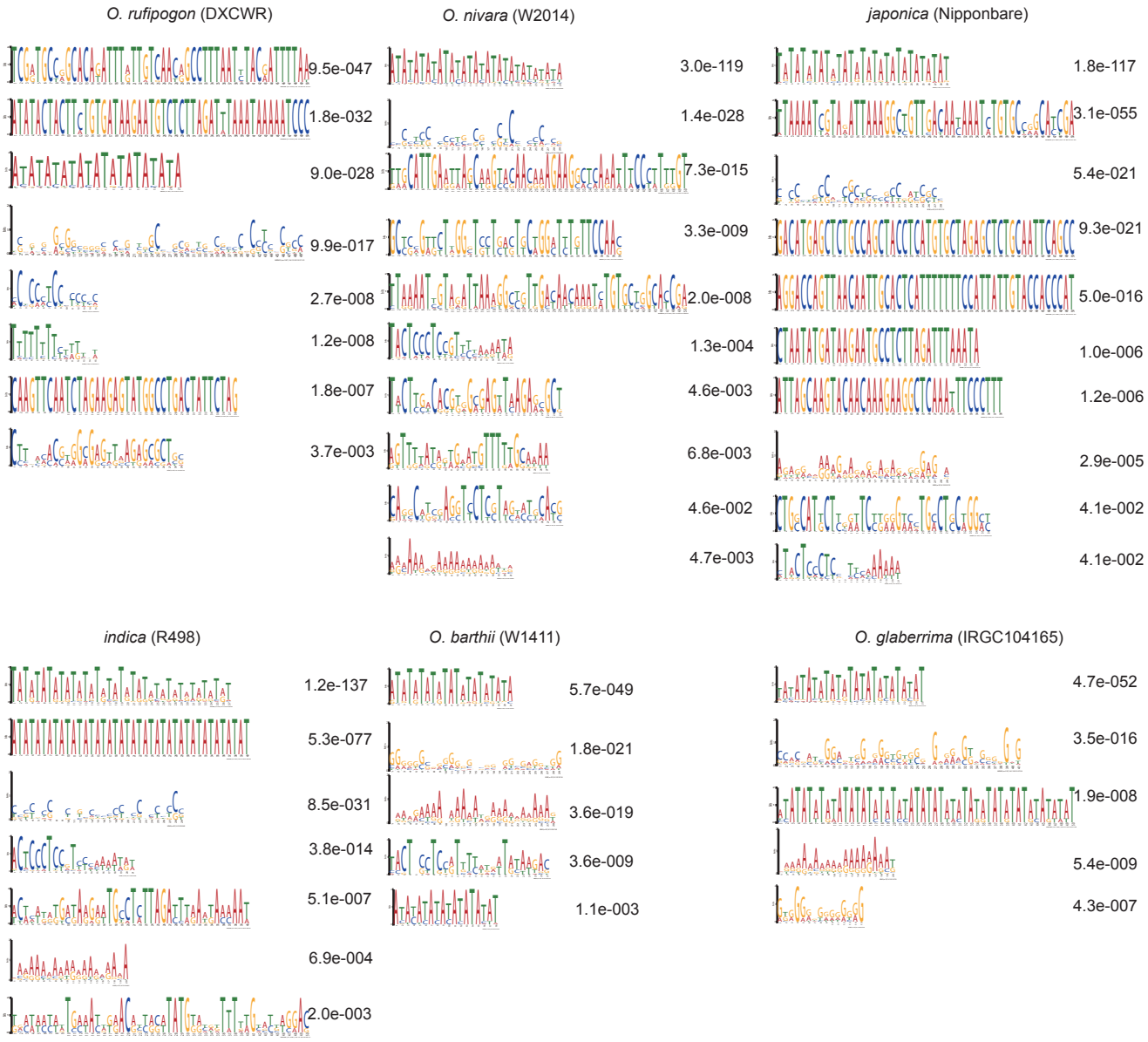

Figure S10. Sequence motifs identified in 100-bp flanking regions surrounding nuclear integrants of plastid DNA (NUPTs) in African and Asian rice genomes.

E-values of each motif were generated with the software MEME.

Figure S11. Sequence motifs identified in 100-bp flanking regions surrounding nuclear integrants of mitochondrial DNA (NUMTs) in African and Asian rice genomes.

E-values of each motif were generated with the software MEME.

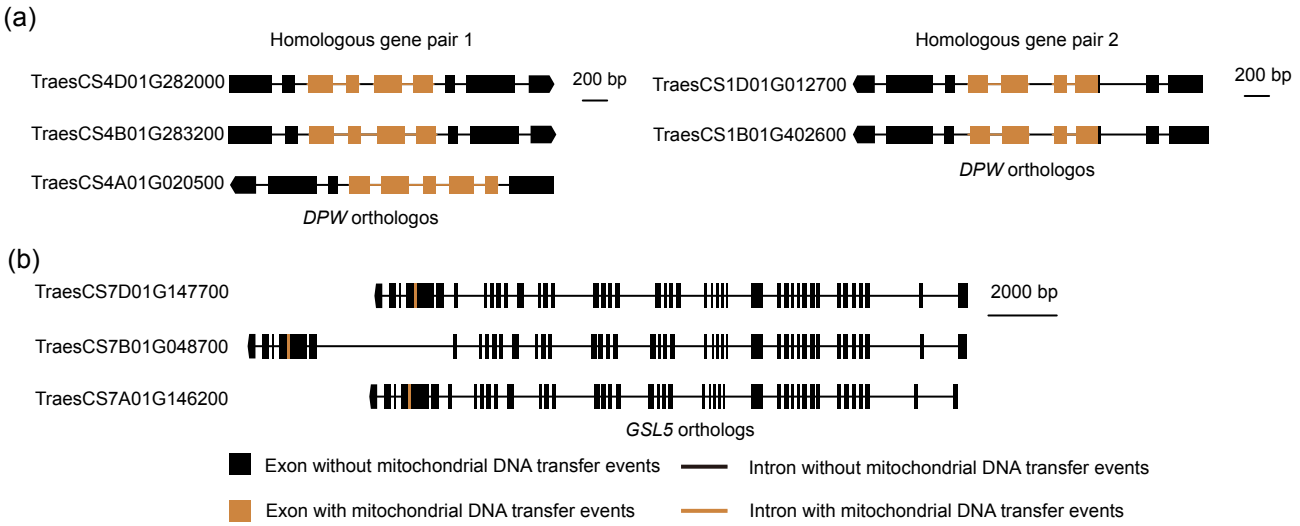

Figure S12. Ancient nuclear integrants of mitochondrial DNA (NUMTs) detected in *Triticum aestivum* (wheat) genome.

(a, b) Several NUMTs were found in exon and/or intron of *DPW* (a) and *GSL5* (b) orthologs in wheat.

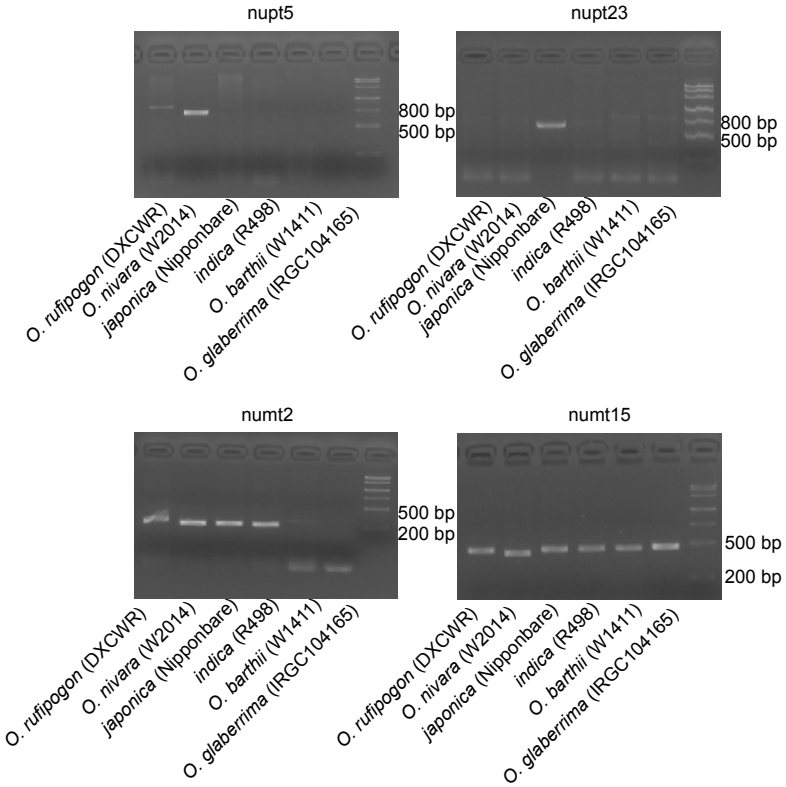

Figure S13. Confirmation of the giant nuclear integrants of plastid DNA (NUPTs) and mitochondrial DNA (NUMTs) identified in this study using PCR analysis.

PCR products spanned cpDNA-nuclear or mtDNA-nuclear DNA junctions.

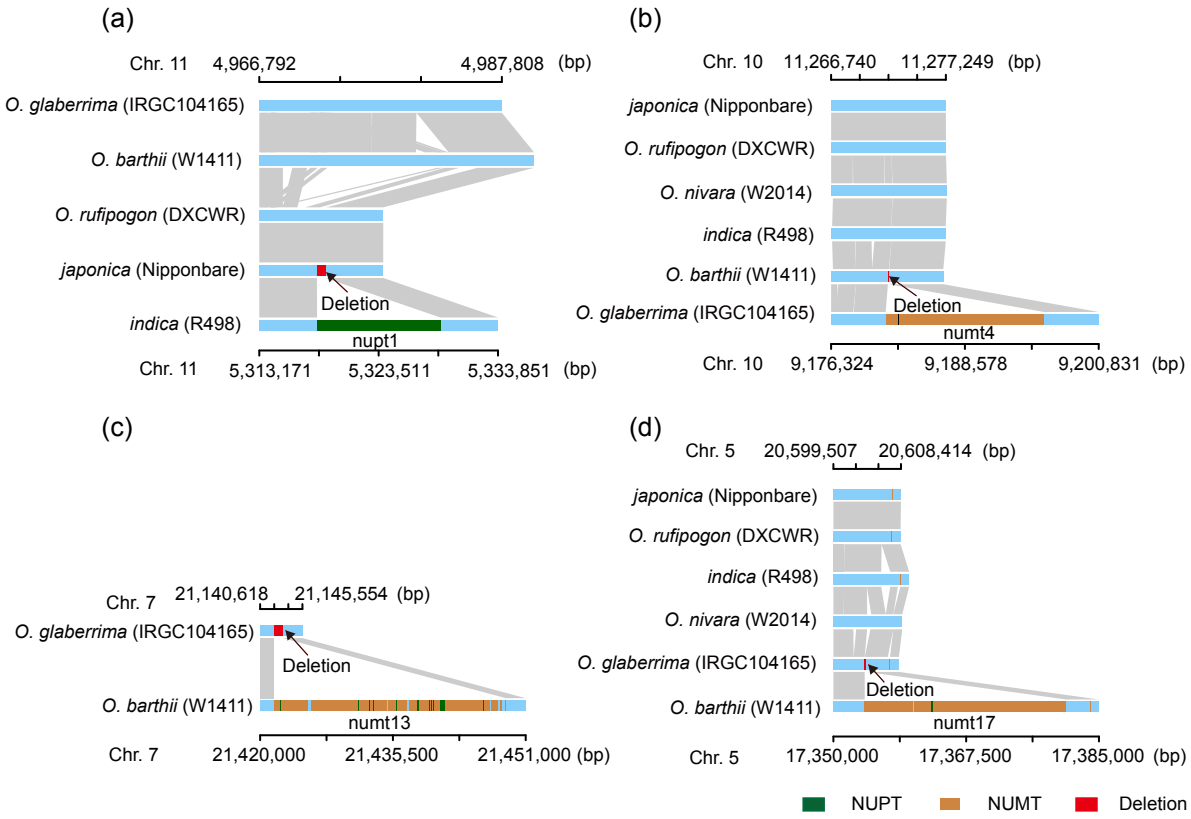

Figure S14. The nuclear integrant of organelle DNA (NORG) events coupled with the generation of structural variations (SVs).

(a-d) Shown are the four integration events, nupt1 (a), numt4 (b), numt13 (c), and numt17 (d), coupled with deletions. The grey regions represent sequences sharing sequence collinearity. The black vertical lines indicate gap regions in the corresponding assembly.

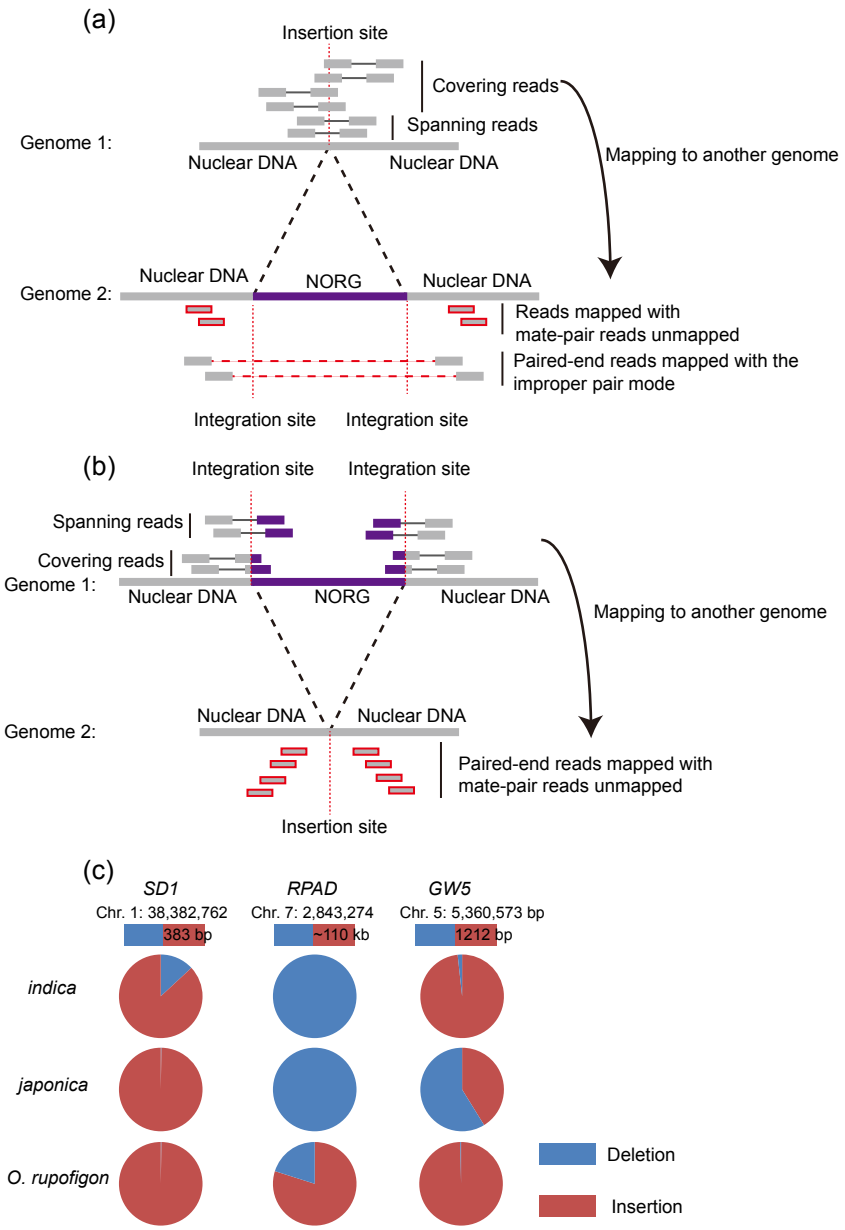

Figure S15. The method used for detection of chloroplast or mitochondrial DNA transfer events based on genome assembly in rice natural populations.

(a, b) Resequencing data for each rice accession were firstly aligned to the two analyzed genomes (genome1 and genome2). Based on the mapping status of reads derived from rice samples in the integration sites and insertion sites of NORGs, the specific transfer events were identified and genotyped as absence (a) or presence (b).

(c) The method we developed was used to genotype the well-characterized phenotypically meaningful SVs in the *SD1*, *RPAD*, and *GW5* genes using resequencing data from the previous study (Huang *et al*., 2012). The percentages of deletion/insertion in different rice populations is consistent with the previous reports (Duan *et al*., 2017; Liu *et al*., 2017; Wu *et al*. 2018; Zhao *et al*., 2018), suggesting the effectiveness and practicability of this method.

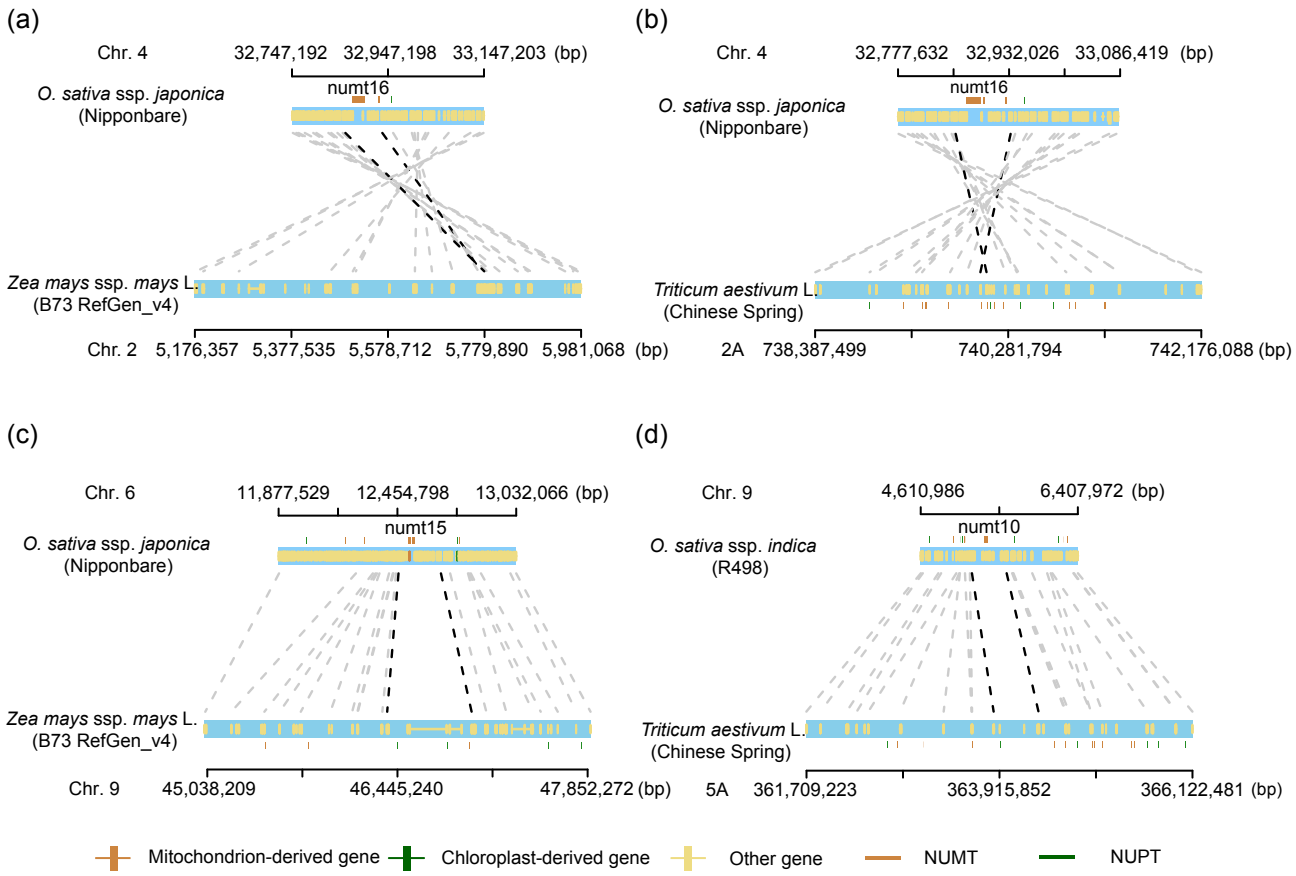

Figure S16. Collinearity analysis of the regions harboring giant nuclear integrants of mitochondrial DNA (NUMTs) between *Oryza sativa* (rice) and *Zea mays* (maize) (a and c) and between rice and *Triticum aestivum* (wheat) (b and d).

Collinear genes are connected by grey or black lines.

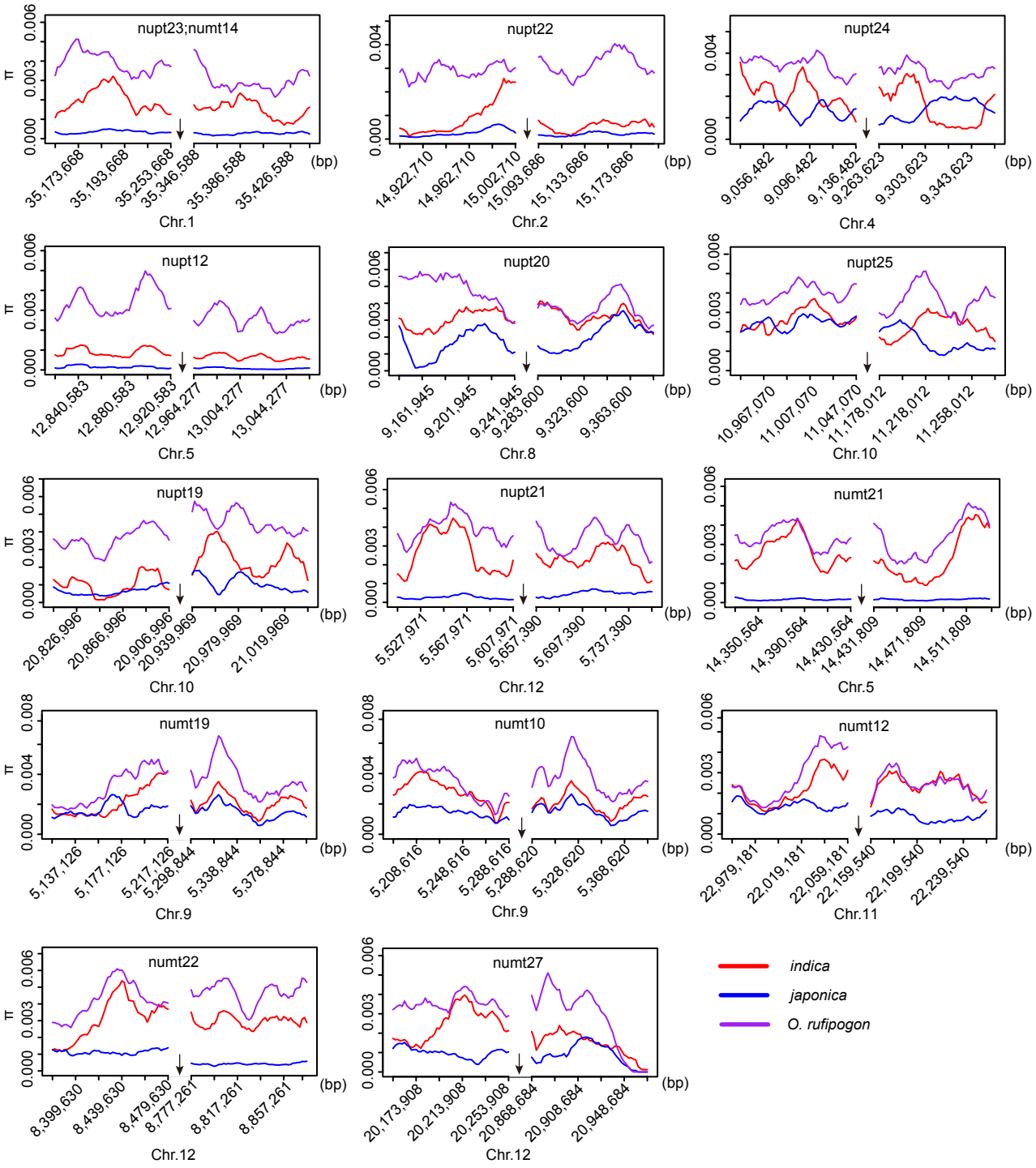

Figure S17. Comparison of the nucleotide diversity of highly differentiated giant nuclear integrants of plastid DNA (NUPTs) and mitochondrial DNA (NUMTs) (*Fst* values>0.3) among *Oryza sativa* ssp. *indica* and *japonica* and *Oryza rufipogon* using the public resequencing data (Huang *et al*., 2012).

Black arrows indicate the positions of NUPTs and NUMTs based on the *japonica* Nipponbare reference genome (IRGSP 4.0).

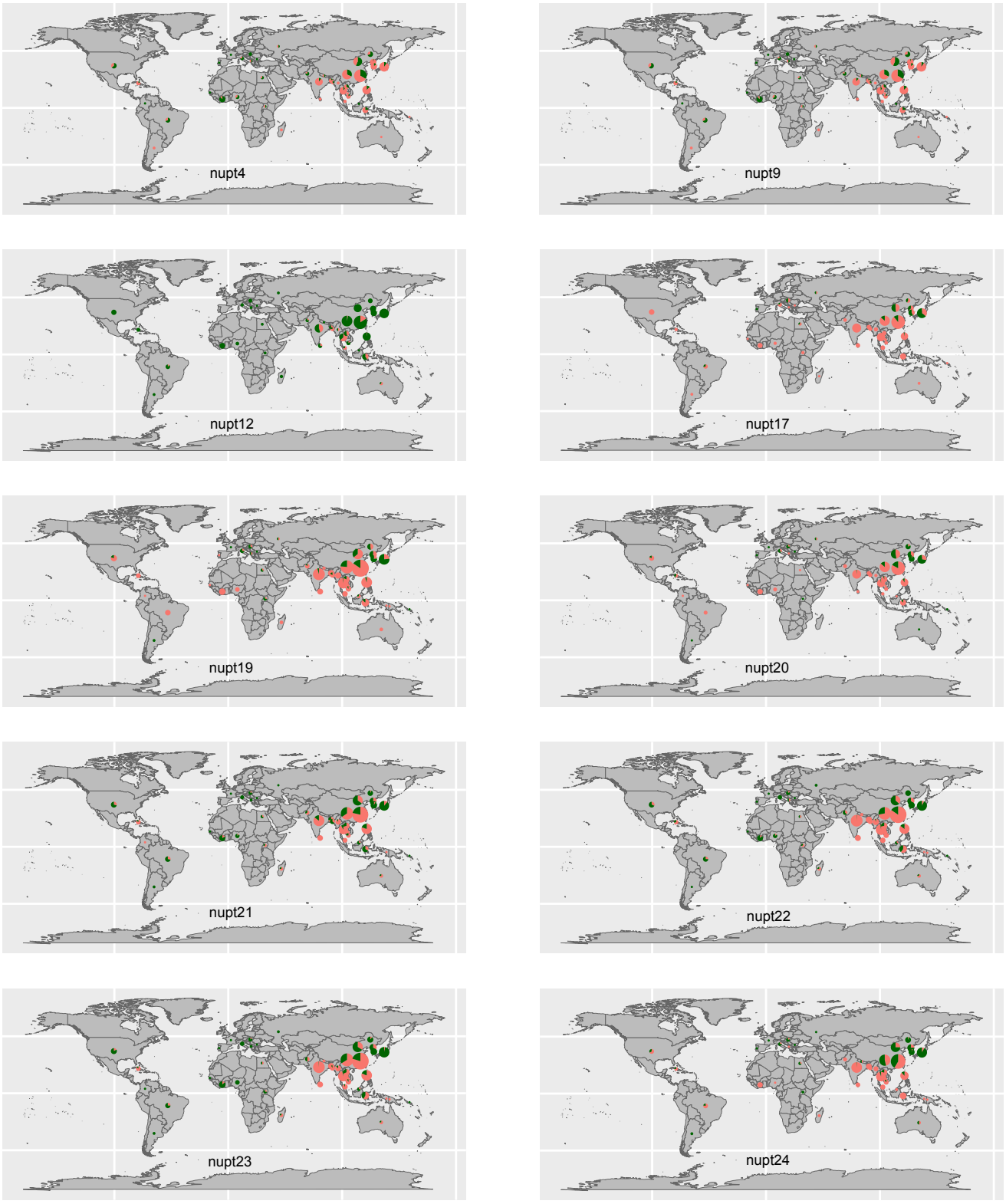

Figure S18. Geographical distributions of highly differentiated giant nuclear integrants of plastid DNA (NUPTs) in Asian rice natural populations.

The colors green and orange in the pie chart represent the presence and absence of NUPT, respectively. The circle size represents the number of rice accession with a logarithmic scale. On the map, China is represented by four regions: Southern China, Southwest China, Northern China and Northeast China.

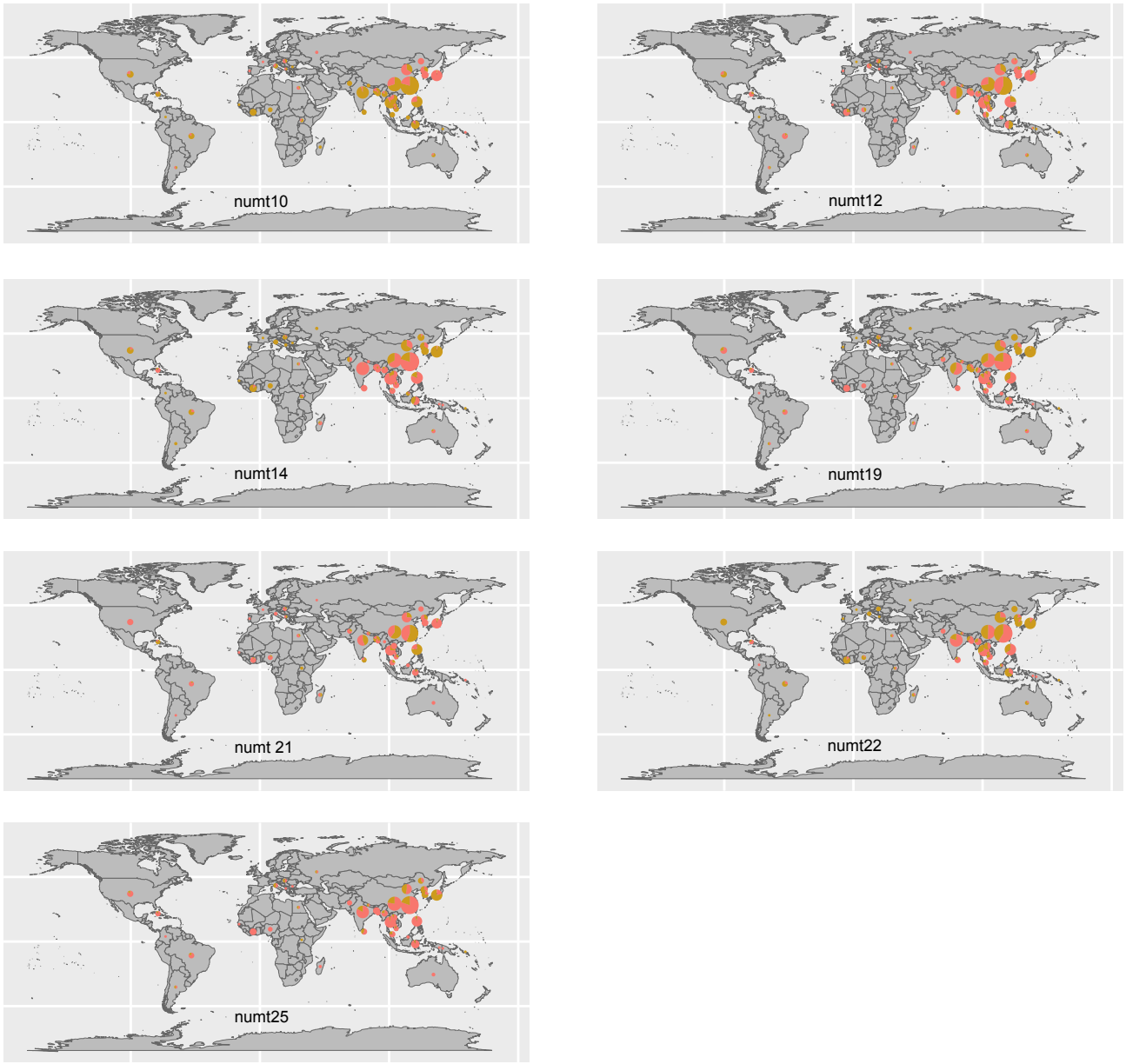

Figure S19. Geographical distributions of highly differentiated giant nuclear integrants of mitochondrial DNA (NUMTs) detected in the Asian rice population.

The circle size of each pie is proportional to number of rice accessions in a given region with a logarithmic scale. The color peru in each pie indicates a NUMT event, pink shows no transfer detected in each rice accession. On the map, China is represented by four regions: Southern China, Southwest China, Northern China and Northeast China.