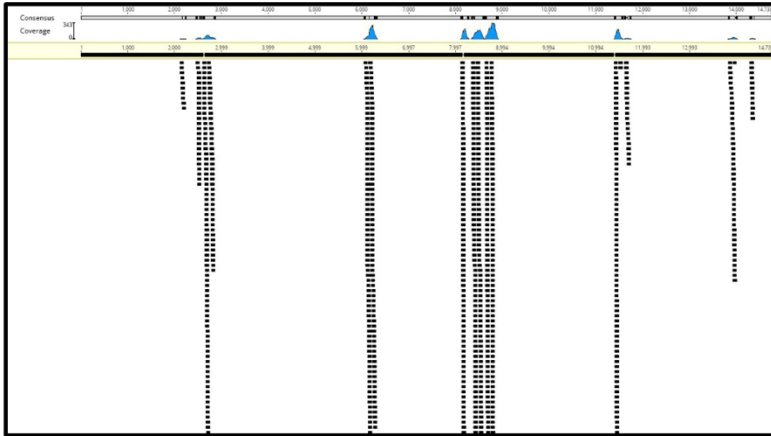
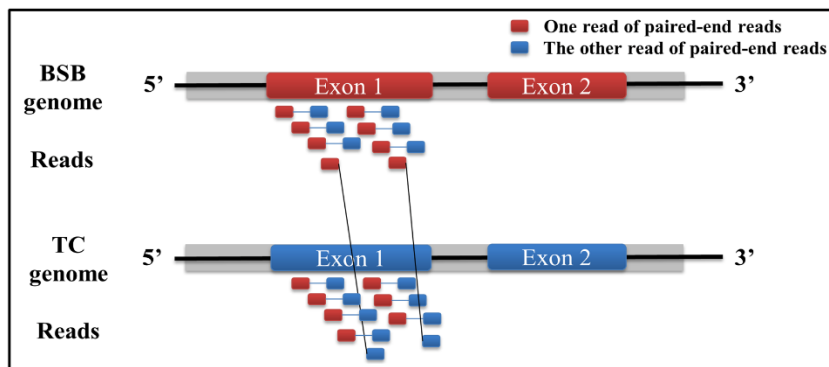


**A**



1. Splitting paired-end reads to single read
2. Mapping reads to the genomes of the two inbred

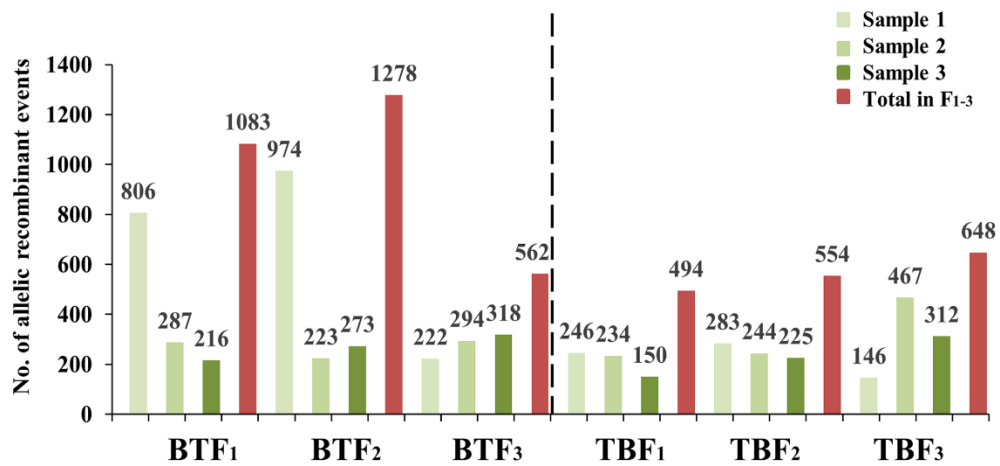
↓ Selecting the specific reads which belong to paired-end and are mapped to one genome of the two inbred parents, respectively



3. Detecting the allelic recombination reads

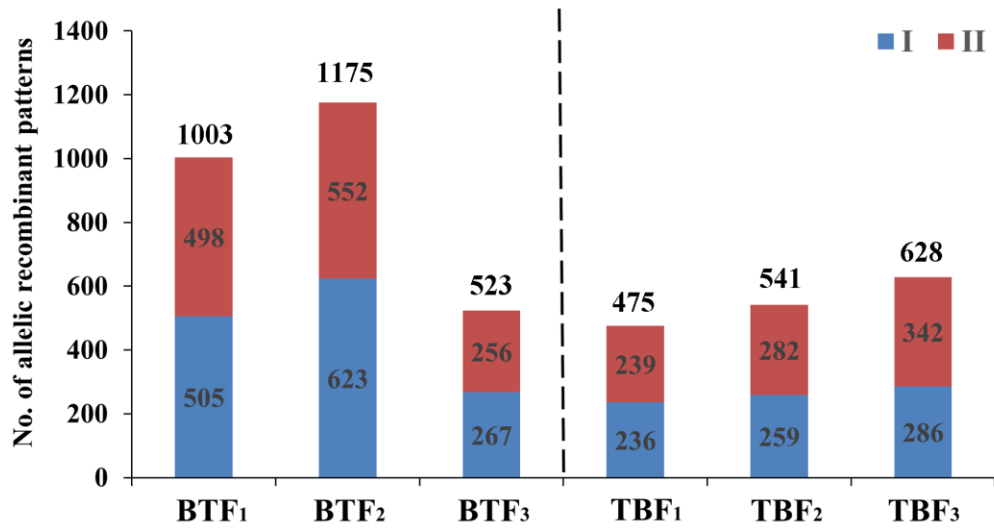
↓ Distribution of all allelic recombinant events

**B**



**C**



**D****E**

↓ Ten allelic recombinant genes verified by  
Illumina and Sanger sequencing methods

| No. | Gene symbol   | No. of supported reads |                  |                  |                  |                  |                  | Recombinant patterns |                  |                  |                  |                  |                  |
|-----|---------------|------------------------|------------------|------------------|------------------|------------------|------------------|----------------------|------------------|------------------|------------------|------------------|------------------|
|     |               | BTF <sub>1</sub>       | BTF <sub>2</sub> | BTF <sub>3</sub> | TBF <sub>1</sub> | TBF <sub>2</sub> | TBF <sub>3</sub> | BTF <sub>1</sub>     | BTF <sub>2</sub> | BTF <sub>3</sub> | TBF <sub>1</sub> | TBF <sub>2</sub> | TBF <sub>3</sub> |
| 1   | <i>ASXL1</i>  | 14                     | 16               | 10               | 10               | 19               | 15               | I                    | I + II           | I + II           | I + II           | I + II           | I + II           |
| 2   | <i>ELF2</i>   | 14                     | 16               | 10               | 10               | 19               | 15               | I                    | I + II           | I + II           | I + II           | I + II           | I + II           |
| 3   | <i>IGFALS</i> | 8                      | 19               | 12               | 5                | 13               | 9                | II                   | I + II           | I + II           | II               | II               | II               |
| 4   | <i>SLC43A</i> | 5                      | 15               | 7                | 14               | 7                | 17               | I                    | I                | I                | II               | II               | II               |
| 5   | <i>EPHX2</i>  | 8                      | 9                | 13               | 7                | 19               | 8                | I                    | I                | I                | II               | II               | II               |
| 6   | <i>GPI</i>    | 11                     | 7                | 7                | 5                | 15               | 6                | II                   | II               | II               | I                | I                | I                |
| 7   | <i>GPD1</i>   | 14                     | 5                | 8                | 11               | 10               | 14               | I                    | I                | I                | II               | II               | I + II           |
| 8   | <i>NOCT</i>   | 13                     | 11               | 12               | 11               | 12               | 8                | I                    | I + II           | I + II           | II               | II               | II               |
| 9   | <i>SLC8A1</i> | 13                     | 11               | 15               | 15               | 8                | 5                | I                    | I + II           | I + II           | II               | II               | II               |
| 10  | <i>NR1D2</i>  | 16                     | 9                | 5                | 15               | 6                | 15               | I                    | II               | II               | II               | II               | II               |

**Supplementary Fig. S6.** Analyses on the allelic recombination (AR) events in the two reciprocal cross hybrids. (A) The analysis pipeline is used to verify AR events in BTF<sub>1</sub> and TBF<sub>1</sub>. The AR reads of hybrids were obtained and supported our prediction of AR events, in which one of paired-end reads mapped to BSB subgenome, and the other read mapped to TC subgenome. (B) Three green columns with different green density represent the number of AR events in the three individuals of each generation. The red column represents the total number of AR events in each generation. (C) The identified AR sequences are classified into two patterns (I and II) in which the blue bars represent the TC-specific variants derived from TC, the red bars represent the BSB-specific variants derived from BSB. (D) Number of AR patterns in each gene (blue: I; red: II) was detected in successive generations. (E) Among 10 AR genes identified by Illumina and Sanger sequencing methods, two AR genes (gene order: No. 1-2) exhibited pattern I in each generation of the two hybrid lineages, and pattern I+II in BTF<sub>2</sub>-BTF<sub>3</sub> as well as TBF<sub>1</sub>-TBF<sub>3</sub>. One AR gene (gene order: No. 3) showed pattern II in each generation of the two hybrid lineages, and pattern I+II in BTF<sub>2</sub> and BTF<sub>3</sub>. Three AR genes (gene order: NO. 4-6) showed pattern I or pattern II in each generation of BT lineage or TB lineage. Three AR genes (gene order: NO. 7-9) presented pattern I or pattern II in each generation in BT lineage or TB lineage, and pattern I+II in BTF<sub>2</sub>, BTF<sub>3</sub> and TBF<sub>3</sub>. One AR gene (gene order: NO. 10) showed pattern II in each generation in BT lineage, but no regular model in BT lineage.