Figure S1. The polymorphic markers used for background selection of TNG82/IRBB66 backcross population. 36 markers among all markers were applied to BC1F1 background selection (red star), 44 markers among all markers were applied to BC2F1 background selection (green circle), 117 markers among all markers were applied to BC2F2 background selection. The prefixes RM indicates SSR markers, C, R, S or E indicates STS markers, and CH, STS, SLS or RI indicates indel markers.
Table S1. The genome composition of BC2F2 derived from TNG82/IRBB66 by 117 polymorphic markers used for MAS.

| Individual | A (%) | B (%) | H (%) | N (%) | RPG recovered (%) | Total (cM) | Recombinant | H-segments |
|------------|-------|-------|-------|-------|-------------------|------------|-------------|------------|
| TNG82      | 0     | 100   | 0     | 0     | 100               | 1492.8     | 0           | 0          |
| 44         | 3.6   | 93    | 3.5   | 0     | 94.75             | 1492.8     | 8           | 2          |
| 21         | 5.5   | 92.7  | 1.8   | 0     | 93.6              | 1492.8     | 11          | 2          |
| 17         | 3.1   | 89.5  | 7.5   | 0     | 93.25             | 1492.7     | 9           | 3          |
| 30         | 4.1   | 90.1  | 5.8   | 0     | 93                | 1492.8     | 11          | 3          |
| 39         | 5.6   | 90.9  | 3.5   | 0     | 92.65             | 1492.8     | 9           | 3          |
| 40         | 3.6   | 88.2  | 8.2   | 0     | 92.3              | 1492.8     | 16          | 7          |
| 25         | 5.6   | 89.8  | 4.7   | 0     | 92.15             | 1492.8     | 8           | 2          |
| 29         | 6.8   | 90.9  | 2.3   | 0     | 92.05             | 1492.8     | 11          | 3          |
| 14         | 4.5   | 88.3  | 7.2   | 0     | 91.9              | 1492.8     | 9           | 4          |
| 8          | 6.6   | 90.3  | 3.1   | 0     | 91.85             | 1492.8     | 10          | 3          |
| 37         | 6.4   | 90    | 3.6   | 0     | 91.8              | 1492.8     | 13          | 4          |
| 32         | 4.5   | 87.9  | 7.6   | 0     | 91.7              | 1492.8     | 10          | 4          |
| 24         | 4.3   | 87.3  | 8.4   | 0     | 91.5              | 1492.8     | 15          | 4          |
| 36         | 5.2   | 87.5  | 7.4   | 0     | 91.2              | 1492.8     | 12          | 4          |
| 31         | 5.9   | 88.1  | 5.9   | 0     | 91.05             | 1492.7     | 12          | 4          |
| 10         | 7.8   | 87.8  | 4.5   | 0     | 90.05             | 1492.8     | 14          | 2          |
| 28         | 8.5   | 87.4  | 4.1   | 0     | 89.45             | 1492.7     | 13          | 4          |
| 20         | 8.3   | 87.1  | 4.6   | 0     | 89.4              | 1492.8     | 14          | 3          |
| 23         | 8     | 86.1  | 5.8   | 0     | 89                | 1492.8     | 11          | 3          |
| 46         | 8.9   | 85.2  | 5.9   | 0     | 88.15             | 1492.8     | 17          | 5          |
| 3          | 9.1   | 84.9  | 6     | 0     | 87.9              | 1492.8     | 16          | 4          |
| 22         | 9.3   | 85.3  | 4.5   | 1     | 87.55             | 1492.8     | 20          | 5          |
| 38         | 7.3   | 84    | 6.7   | 2.1   | 87.35             | 1492.8     | 18          | 5          |
| 7          | 6.9   | 81.4  | 11.7  | 0     | 87.25             | 1492.8     | 20          | 6          |
| 35         | 7.3   | 83.8  | 6.3   | 2.7   | 86.95             | 1492.8     | 23          | 5          |
| 33         | 9.7   | 81.4  | 8.9   | 0     | 85.85             | 1492.8     | 23          | 6          |
| 1          | 12.5  | 83.8  | 2.9   | 0.9   | 85.25             | 1492.8     | 20          | 2          |
| 12         | 9.4   | 79.4  | 11.2  | 0     | 85                | 1492.8     | 23          | 8          |
| 34         | 13.2  | 82.7  | 4.1   | 0     | 84.75             | 1492.8     | 18          | 4          |
| 45         | 10.7  | 79.7  | 9.7   | 0     | 84.55             | 1492.8     | 21          | 7          |
| 18         | 12.2  | 80.8  | 7     | 0     | 84.3              | 1492.8     | 20          | 5          |
| 41         | 10.5  | 79    | 10.5  | 0     | 84.25             | 1492.8     | 25          | 8          |
| 19         | 13.1  | 81.1  | 5.9   | 0     | 84.05             | 1492.8     | 18          | 4          |
| 6          | 7.8   | 75.6  | 16.7  | 0     | 83.95             | 1492.8     | 29          | 12         |
| 5          | 13.4  | 80.5  | 5.2   | 0.9   | 83.1              | 1492.8     | 23          | 4          |
| 27         | 11.6  | 76.4  | 12    | 0     | 82.4              | 1492.8     | 28          | 8          |
| 16         | 10.7  | 75.2  | 14.1  | 0     | 82.25             | 1492.8     | 29          | 8          |
| 15         | 12    | 76.4  | 11.6  | 0     | 82.2              | 1492.8     | 25          | 8          |
| Individual | A (%)<sup>a</sup> | B (%)<sup>b</sup> | H (%)<sup>c</sup> | N (%)<sup>d</sup> | RPG recovered (%) | Total (cM) | Recombinant<sup>e</sup> | H-segments<sup>f</sup> |
|------------|------------------|------------------|------------------|------------------|------------------|-----------|--------------------------|-------------------|
| 13         | 13.7             | 77.9             | 8.4              | 0                | 82.1             | 1492.8    | 25                       | 8                 |
| 9          | 15.3             | 79               | 5.7              | 0                | 81.85            | 1492.8    | 24                       | 4                 |
| 11         | 16               | 79.6             | 4.4              | 0                | 81.8             | 1492.8    | 20                       | 3                 |
| 42         | 17.2             | 76.1             | 6.7              | 0                | 79.45            | 1492.8    | 28                       | 6                 |
| 43         | 15.7             | 75.3             | 8.2              | 0.8              | 79.4             | 1492.8    | 28                       | 7                 |
| 26         | 19.2             | 71.4             | 9.4              | 0                | 76.1             | 1492.8    | 26                       | 6                 |
| 4          | 19.6             | 71.5             | 8.9              | 0                | 75.95            | 1492.8    | 23                       | 5                 |
| IRBB66     | 100              | 0                | 0                | 0                | 1492.8           | 0         | 0                        | 0                 |

<sup>a</sup> The arrangement was based on the percentage of genetic similarity with TNG82
<sup>b</sup> the percentage of genetic similarity with IRBB66
<sup>c</sup> the percentage of genetic similarity with TNG82
<sup>d</sup> the percentage of heterozygous
<sup>e</sup> the percentage of missing data
<sup>f</sup> the number of chromosome recombination
<sup>f</sup> the number of heterozygous segments in sample