





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 (%) ^a	B (%) ^b	H (%) ^c	N (%) ^d	RPG recovered (%)	Total (cM)	Recombinant ^e	H-segments ^f
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

Continue Table S1

Individual*	A (%) ^a	B (%) ^b	H (%) ^c	N (%) ^d	RPG recovered (%)	Total (cM)	Recombinant ^e	H-segments ^f
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	0	1492.8	0	0

* The arrangement was based on the percentage of genetic similarity with TNG82

^a the percentage of genetic similarity with IRBB66

^b the percentage of genetic similarity with TNG82

^c the percentage of heterozygous

^d the percentage of missing data

^e the number of chromosome recombination

^f the number of heterozygous segments in sample