Table 3. Primer pairs used to detect multiple inversions in region 31, and their predicted and measured product sizes

Primer pair [*]	Genome organization [†]	Estimated size, kb	Measured sizes, kb
AI-1R	1-X-X-X-P	4.6	4.7
A2-4F	X-X-X-4-P	4.9	5.0
A2-4R	X-X-X-(4)-P	2.8	3.0
A2-3R	2-(3)-X-X-P	20.9	20.7
	X-X-(3)-4-P	14.4	15.2
	X-X-X-(3)-P	4.4	4.7
A2-2R	X-X-(2)-4-P	12.4	12.2
	X-X-X-(2)-P	4.5	5.0
A2-1R	X-X-X-(1)-P	5.5	6.1

[*] The nucleotide sequence of each primer is shown in Table 1.

[†] The genome organization of region 31 (the order of segments, 1, 2, 3, 4, and the promoter region shown in Fig. 11) to be detected by each primer pair is shown. X or the number represents a segment (X indicates a segment other than the numbered segment), and P indicates the promoter region. Parentheses indicate the reverse orientation.