Table 2. Summary of the initial whole genome PCR scanning data of the eight O157 chromosomes

Segments*	Total (*n* = 4,392)	Loop unrelated (*n* = 2,712)	Loop related (*n* = 1,680)		
			Sp-related (*n* = 536)	SpLE-related (*n* = 168)	Others (*n* = 976)
Conserved	4,006 (91%)	2,651 (98%)	296 (55%)	138 (82%)	921 (94%)
Size-difference [Y]	144 (3%)	33 (1%)	53 (10%)	15 (9%)	43 (4%)
Not amplified [R]	242 (6%)	28 (1%)	187 (35%)	15 (9%)	12 (1%)

*Conserved, [Y], [R] segments correspond to gray, yellow, and red rectangles in Fig.2, respectively.