

Supplementary Table 2 Structural features of insertion sequences

name	family ^{a)}	size ^{b)}	complete ^{c)}	partial ^{c)}
ISazl01	IS3	(1169)	0	6
ISazl02	IS3	1602	4	15
ISazl03	IS3	(964)	0	15
ISazl04	IS5	852	13	1
ISazl05	IS5	936	8	7
ISazl06	IS5	1312	9	1
ISazl07	IS5	(567)	0	3
ISazl08	IS21	2610	19	1
ISazl09	IS66	2633	2	14
ISazl10	IS66	2811	3	13
ISazl11	IS66	(653)	0	2
ISazl12	IS66	3233	2	5
ISazl13	IS110	1511	3	6
ISazl14	IS256	(1043)	0	5
ISazl15	IS256	(484)	0	6
ISazl16	IS256	1417	3	9
ISazl17	IS630	1180	9	4
ISazl18	IS701	(1119)	0	2
ISazl19	IS701	1388	8	2
ISazl20	IS1380	(1169)	0	2
ISazl21	IS1380	1620	27	4
ISazl22	ISAs1	1334	7	4
ISazl23	ISAs1	1225	6	1
ISazl24	ISAs1	1263	5	0
ISazl25	ISAs1	1270	4	3
ISazl26	ISAs1	1196	5	3
ISazl27	ISL3	1866	2	3
ISazl28	ISNCY	(545)	0	2
ISazl29	ISNCY	(539)	0	2

^{a)} Classification into IS family was subjected based on similarity of each transposase with the assistance of the ISFinder database. ^{b)} Size of intact IS are indicated with bp. For no intact, truncated ISs species, the figures of longest partial fragment are shown in parenthesis. ^{c)} Numbers of classified ISs are shown.