Table S11. Comparison of the phages in the O55:H7 and the 2 O157:H7 strains

CB9615				Sakai				EDL933				Comparisons	
name	**site**	**Type[c]**	**length**	**name**	**site**	**Type[c]**	**length**	**name**	**site**	**Type[c]**	**length**	**CB9615 / Sakai[d]**	**EDL933 / Sakai[d]**
Ep1	302638-351615	Lambda-like	48,949	Sp1	300041-310626	Lambda-like	10,586	CP-933H	300042-310627	Lambda-like	10,586	replacement	100% 2kb inv
Ep2	351616-364486	P4-like	12,871	Sp2	310627-323513	P4-like	12,887	CP-933I	310628-323514	P4-like	12,887	12.9kb rec	100%
Ep3	697268-746682		49,415	-	-			-	-			ins	-
Ep4	980716-1026738	Lambda-like	46,023	Sp3	891123-929708	Lambda-like	38,586	CP-933K	892772-931359	Lambda-like	38,588	99.17% 4.4kb rec, 7.4kb ins	99.97% 0.3kb rec
-	-			Sp4	1161091-1210740	Lambda-like	49,650	CP-933M	1250314-1294565	Lambda-like	44,252	-	99.97% 1.1kb rec, 28.2k ins, 32.6k del
-	-			Sp5	1246012-1308719	Lambda-like	62,708	BP-933W	1330829-1392491	Lambda-like	61,663	-	99.99% 5.4kb rec, 10.6k ins, 11.6k del
-	-			Sp6	1541470-1589892	Lambda-like	48,423	CP-933N	1626566-1673868	Lambda-like	47,303	-	99.96% 1.1kb rec, 20k ins, 21.1k del
Ep5	1444732-1455388	P4-like	10,657	Sp7	1594570-1610032		15,463	CP-933C	1678546-1694005		15,460	replacement	99.95%
elbA-ypjA[a]	1463904-1478380		14,477	Sp8	1618153-1665049	Lambda-like	46,897	CP-933X	1702126-1756455	Lambda-like	54,330	replacement	99.96% 1.3kb rec, 15.1kb ins, 7.7kb del
Ep6	1574754-1627761	Lambda-like	53,008	Sp9	1757506-1815680	Lambda-like	58,175	CP-933O-1 & CP-933P[b]	1849445-1868506 2292538-2271497	Lambda-like	40,104	99.78% 1.3kb rec, 40.7kb ins, 27.8~45.9kb del	99.99% 0.7kb rec, 4k ins, 22.1kb del
Ep7	1732190-1777066	Lambda-like	44,877	Sp10	1921414-1972525	Lambda-like	51,112	CP-933R	2165752-2115956	Lambda-like	49,797	99.83% 1.3kb rec, 37.8kb ins, 43~44kb del	99.99% 1.4kb rec, 22.8kb ins, 24.2kb del
-	-			Sp11	2158174-2203951	Lambda-like	45,778	CP-933O-2	1930297-1878765	Lambda-like	51,533	-	99.97% 6.1kb rec, 32.9kb ins, 27.2kb del
Ep8	1967051-1988518	Lambda-like	21,468	Sp12	2203952-2250093	Lambda-like	46,142	CP-933O-1 & CP-933P[b]	1878764-1872344 2280925-2325378	Lambda-like	50,875	replacement	99.96% 0.2k rec, 4.1kb ins, 8.9kb del
Ep9	1988519-2009859	Lambda-like	21,341	-	-			-	-			ins	-
Ep10	2152246-2187996	P2-like	35,751	-	-			-	-			ins	-
-	-			Sp13	2592901-2614020	P2-like	21,120	CP-933T	2668112-2689231	P2-like	21,120	-	99.96%
Ep11	2437795-2486743	Lambda-like	48,949	Sp14	2668007-2712035	Lambda-like	44,029	CP-933U	2743224-2788400	Lambda-like	45,177	replacement	99.97% 5kb rec, 25.6kb ins, 24.4 kb del
-	-			Sp15	2895926-2943804	Lambda-like	47,879	CP-933V	2966157-3015071	Lambda-like	48,915	-	99.97% 17.2kb rec, 21.2kb ins 20.2kb del
Ep12	2934049-2942599	P22-like	8,551	Sp16	3192983-3201533	P22-like	8,551	CP-22	3262939-3271489	P22-like	8,551	99.94%	99.96%
Ep13	3161159-3202641		41,483	-	-			-	-			ins	-
Ep14	3258501-3337894	Lambda-like	79,394	Sp17	3475965-3500163	Lambda-like	24,199	CP-933Y	3545814-3567453	Lambda-like	21,640	99.85% 8.7kb rec, 35.1kb ins, 7.8~10.3kb del	99.97% 0.1kb rec, 1.5kb ins 4kb del
-	-			Sp18	5040843-5079601	Mu-like	38,759	-	-			-	-
Ep15	5306033-5355424	Lambda-like	49,392	-	-			-	-			ins	-
-	-			SpLE1	1370456-1456704	CP4-like	86,249	SpLE1	1454228-1541789	CP4-like	87,562	-	99.97% 0.1kb rec, 1.3kb ins
-	-			-	-			SpLE1 copy	1058621-1146183	CP4-like	87,563	-	99.98%
EpLE1	2510337-2531200		20,864	SpLE2	2738079-2751537		13,459	SpLE2	2814443-2821749		7,307	replacement	99.99% 0.4kb rec, 6.1kb del
EpLE2	3675949-3704076		28,127	SpLE3	3852036-3875489		23,454	SpLE3	3919348-3942802		23,455	99.92% 0.04kb rec, 8.4kb ins, 3.4kb del	99.97%
EpLE3	4470809-4511806		40,998	SpLE4	4580864-4624313		43,450	SpLE4	4649847-4693296		43,450	99.93% 2.4kb del-ISEc8	99.99%
-	-			SpLE5	5347085-5357319	CP-4 like	10,235	SpLE5	5377088-5387322	CP-4 like	10,235	-	99.99% 9bp rec
EpLE4	5195636-5229783		34,148	SpLE6	5357371-5391518		34,148	SpLE6	5387374-5421521		34,148	99.94%	99.98%

[a] This region is not the phage and was deleted in O157 lineage.

[b] These 2 phages at the ends of the inversion in EDL933.

[c] The phage type in Sakai was based on the Hayashi *et al.*[25]. The phage types in other 2 genomes were based on similarity to known phages in GenBank.

[d] Replacement: the phages are inserted at the same site but different in sequence; The percentage ratio shows the divergence in conserved region. rec: recombination region. ins: insert in phages; del: deletion in phages compared to phages in Sakai