

Table S1. Allelic assignments using 7-gene multilocus sequence typing

Isolate ID	Species ^a	Sequence type for ^b							Sequence	Clonal
		atpD	fusA	glnS	gltB	gyrB	infB	pps	Type ^c	Complex ^d
FSL F6-023	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-024	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-025	<i>C. sakazakii</i>	1	1	1	1	1	1	1	1	1
FSL F6-027	<i>C. sakazakii</i>	3	15	28	22	5	38	54	128	6
FSL F6-028	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-029	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-032	<i>C. sakazakii</i>	11	8	7	5	8	15	10	8	NR
FSL F6-034	<i>C. sakazakii</i>	1	1	1	1	1	1	1	1	1
FSL F6-035	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-036	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-037	<i>C. sakazakii</i>	55	14	59	70	70	70	80	73	NR
FSL F6-038	<i>C. sakazakii</i>	3	15	28	22	5	38	19	40	6
FSL F6-039	<i>C. sakazakii</i>	3	3	3	5	3	3	3	3	NR
FSL F6-040	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-041	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-042	<i>C. sakazakii</i>	1	1	1	1	1	1	1	1	1
FSL F6-043	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-044	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-045	<i>C. sakazakii</i>	5	54	3	3	5	5	4	121	4
FSL F6-046	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-047	<i>C. sakazakii</i>	48	17	10	69	71	5	81	42	NR
FSL F6-048	<i>C. sakazakii</i>	15	14	15	13	22	5	16	13	8
FSL F6-049	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-050	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-051	<i>C. sakazakii</i>	5	1	3	3	5	5	4	4	4
FSL F6-030	<i>C. malonaticus</i>	10	13	18	7	17	23	8	62	NR
FSL F6-052	<i>C. malonaticus</i>	10	7	12	8	23	30	8	53	NR
FSL F6-031	<i>C. muytjensii</i>	26	25	3	-	33	39	-	49 ^e	NR
FSL F6-026	<i>Enterobacter</i>	53	52	51	-	68	68	79	UT	NA
FSL F6-033	<i>Enterobacter</i>	54	53	55	3	69	69	NEW	UT	NA

^aSpecies ID based on MLST results when available or 16S rDNA sequence when strain could not be sequence typed.

^b"-" indicates a gene that could not be amplified in a given strain; for FSL F6-031 both *gltB* and *pps* and for FSL F6-026 *gltB* could not be amplified; NEW - new allelic type.

^cUT = untypable (strains were designated as UT if at least one of the genes in the 7 gene MLST could not be amplified or if at least one gene had a new AT, thus not permitting assignment of an ST)

^dNA = not applicable (no ST was assigned and hence a CC cannot be determined); NR = non returned (No clonal complex returned from <http://pubmlst.org/cronobacter>)

^eThough both *gltB* and *pps* could not be amplified for F6-031 in our experiments, F6-031 was determined to be ST49 from the *Cronobacter* MLST database; see isolate 530 at <http://pubmlst.org/cronobacter/>