

TABLE S6. Putative recombination points in the genomes of CU and GU strains as determined by the likelihood ratio test (LRT).

Gene	Description	Nucleotide position	LRT score
<i>argH</i>	Arginosuccinate lyase	664720	54.7
		664730	60.0
		664740	49.8
		664750	49.8
		664760	49.8
		664770	49.8
		664780	49.8
		664790	49.8
		664800	49.8
		664810	49.8
<i>lon</i>	ATP-dependent protease LA	741540	79.2
		741550	79.2
		741560	79.2
		741570	88.4
		741580	88.4
		741590	88.4
		741600	88.4
<i>HD0637</i>	Hypothetical protein	1400630	27.7
<i>flp3</i>	<i>flp</i> operon protein Flp3	1400800	19.4
		1400810	21.4
		1400820	22.5
		1400830	25.4
		1400840	27.5
		1400850	30.7
		1400860	32.3
		1400870	32.3
<i>HD1070</i>	Hypothetical protein	1424410	36.3
		1424420	36.7
		1424430	47.1
		1424440	47.5
		1424450	47.9
		1424460	47.9
		1424470	48.0
		1424480	48.4
		1424490	48.8
		1424500	49.1
		1424510	49.2
		1424520	49.2