

TABLE S3. Putative deletions in the genomes of class I strains relative to 35000HP.

Feature	Reference position	Length (bp)	82-029362	6644	HD183	HMC46	HMC56
HD0094 [pseudo]-HD0097	73898	3156	Δ	Δ	WT	Δ	Δ
HD0113 & HD0114	82733	129	WT	WT	Δ	WT	WT
HD0192	136845	111	Δ	Δ	WT	Δ	Δ
<i>nagZ</i>	412854	79	Δ	Δ	WT	Δ	Δ
Intergenic & HD0778	610591	85	Δ	Δ	WT	Δ	Δ
HD0897-Lys-1	719122	49457	WT	WT	WT	WT	Δ
<i>glpF</i> & <i>glpK</i>	914594	1424	WT	WT	Δ	WT	WT
<i>glpK</i>	915836	322	WT	WT	WT	WT	Δ
<i>glpQ</i> [pseudo]	921511	322	Δ	Δ	WT	Δ	Δ
<i>ompP2A</i> &/or <i>ompP2B</i>	1175494	1545	WT	WT	WT	WT	Δ
<i>InsB</i> & HD1973	1645353	768	Δ	Δ	Δ	Δ	Δ

<sup>Δ</sup>Deletion.

<sup>WT</sup>No deletion.