

TABLE S2. Putative deletions in the genomes of CU strains relative to 35000HP.

<b>Feature</b>	<b>Reference position</b>	<b>Length (bp)<sup>a</sup></b>
Intergenic	213,567	30
HD1034	825,958	388
HD1278	1,040,857	69
HD1528-HD1565	1,265,042	20,193
HD1715	1,429,444	196
<i>insB</i> & HD1973	1,645,354	767

<sup>a</sup>These deletions were present in all the 5 cutaneous ulcer strains sequenced in this study.