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

Feature	**Reference position**	**Length (bp)**[a]
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
insB & HD1973	1,645,354	767

[a]These deletions were present in all the 5 cutaneous ulcer strains sequenced in this study.