Table S2. Assembly statistics for the whole genome sequence of strain CCUG 66741^T and the other type strains of the family *Enterobacteriaceae* sequenced in the present study.

Strain	**Accession number**	**Ion Torrent platform**	**Coverage**	**No. of contigs**	**G+C (%)**	N_{50} **(bp)**	**Total length (bp)**	**No. of CDS**[a]
Scandinavium goeteborgense CCUG 66741^T	LYLP00000000	PGM	43x	192	54.31	74,823	4,539,908	4,384
Lelliottia nimipressuralis CCUG 25894^T	SDDX00000000	S5	36x	67	54.85	236,780	4,616,251	4,446
Buttiauxella izardii CCUG 35510^T	QZWH00000000	S5	280x	91	51.26	91,315	4,769,981	4,389

a CDS, coding sequences.