

Table S5: results of ANI and TETRA (r, raw data; s, sieved results in where the duplicates had been removed) of the partially sequenced strains and the comparison with the calculated DDH or ΔT_m values. The values of the aligned sequences are expressed in percentage of the total DNA used in the query and in brackets the complete nucleotide sequence used). DDH results were obtained from (18, 19).

