

Table S1. Overall genome relatedness indexes between strain Iri35c^T and its closest relatives. Shaded box corresponds to unavailable genome. Average Nucleotide Identity scores were calculated using the ANI calculator tool provided by the EzBioCloud web server (<https://www.ezbiocloud.net/tools/ani>). Digital DNA-DNA hybridization (dDDH) estimate values were determined using the formula 2 of the genome-to-genome distance calculator GGDC v2.1.

	16S rRNA gene sequence similarity (%)	OrthoANIu (%)	dDDH (%)
<i>T. camini</i> Iri35c ^T (this study)	100	100	100
<i>T. celericrescens</i> TS2 ^T	99.66	88.20	35.10
<i>T. siculi</i> RG-20 ^T	99.26	79.72	22.40
<i>T. barossii</i> SHCK-94 ^T	98.79	81.09	23.70
<i>T. thioeducens</i> DSM 14981 ^T	98.79	83.58	26.40
<i>T. hydrothermalis</i> AL662 ^T	98.75		
<i>T. cleftensis</i> CL1 ^T	98.59	82.50	24.90
<i>T. pacificus</i> P-4 ^T	98.05	79.45	22.20

