

Table S1 Whole-genome sequencing, assembly, and preliminary species annotation results for the candidate functional strain

Metric	Strain 11-9
Sequencing sample ID	L11_9
Isolation source	Throat swab sample from TB close contact #11
Primary species annotation	<i>Streptococcus oralis</i>
Proportion of reads assigned to the primary species (%)	80.99
Clean Q30 (%)	96.77
Total assembly length (bp)	1,853,872
Number of contigs	20
N50 (bp)	195,969
Assembly GC content (%)	40.84
Predicted coding genes	1,808

The primary species annotation was based on the classification of valid whole-genome sequencing reads using the Kraken2/PlusPF database. Clean Q30 was obtained from the sequencing quality-control results. The total assembly length, number of contigs, N50, and GC content were derived from the Unicycler assembly results. The number of coding genes was predicted using Prokka. ANI, dDDH, and core-genome phylogenetic comparisons with type strains were not available in the current report; therefore, this table supports the preliminary species annotation and description of the basic genomic features of strain 11-9.

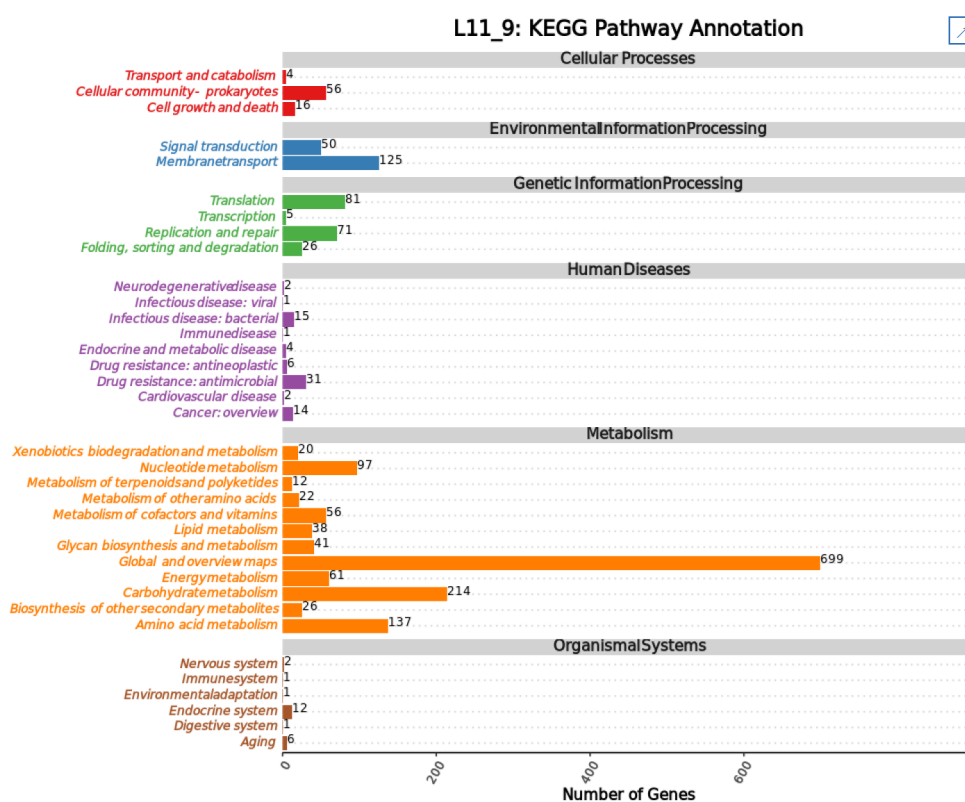


Figure S1 Whole-genome KEGG functional annotation of strain 11-9. KEGG pathway annotation showed that genes related to carbohydrate metabolism, amino acid metabolism, membrane transport, energy metabolism, and cell wall-related biosynthetic processes were abundant in the strain genome, suggesting that strain 11-9 has the genetic basis to produce and transport diverse metabolites.