Table S3. Statistics and general features of A-394^T (=LMG 27910^T=CAIM 1892^T) genome determined in RAST environment:

Features	**as uploaded**	**after splitting into scaffolds**
Size (bp)	5,725,370	5,718,047
Contigs	1,805	1,830
Shortest contig size	100	100
Median contig size	2,005	1,988
Mean sequence size	3,172.0	3,124.2
Longest contig size	27,307	24,391
Content GC (%)	48.1	48.1
Subsystems (n=499)		
RNAs (t,rRNAs)	58	
Predicted ORFs	5,008	
Features (%)	In Subsystem=47	Not in subsystem=53
Total (n$\underline{^0}$)	2,353	2,655
Hypothetical Proteins (n$\underline{^0}$)	144	1,301
Non-Hypothetical (n$\underline{^0}$)	2,209	1,354