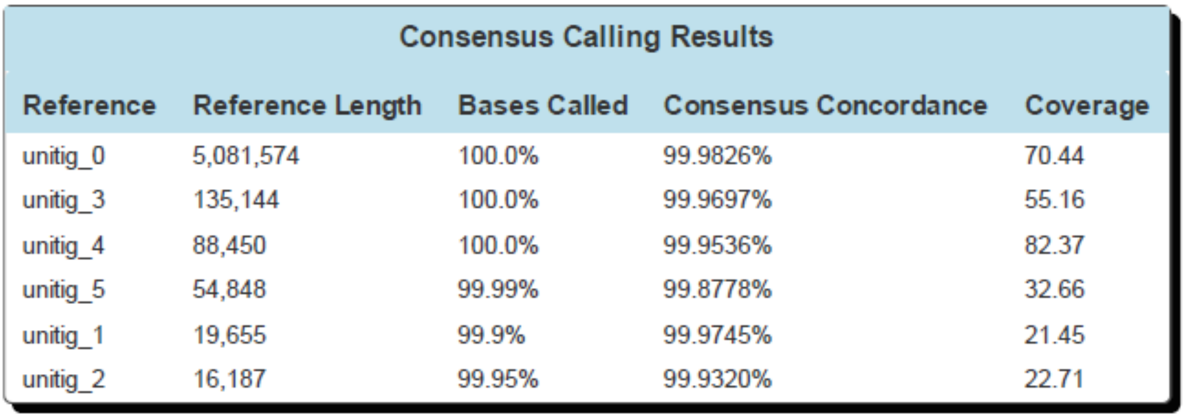
Table S1. Characteristics of the assembled reads of the *E. coli* ErtS genome.



Consensus Calling Results

Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
unitig_0	5,081,574	100.0%	99.9826%	70.44
unitig_3	135,144	100.0%	99.9697%	55.16
unitig_4	88,450	100.0%	99.9536%	82.37
unitig_5	54,848	99.99%	99.8778%	32.66
unitig_1	19,655	99.9%	99.9745%	21.45
unitig_2	16,187	99.95%	99.9320%	22.71

This table presents the characteristics of the assembled reads of the *E. coli* ErtS genome, which were obtained using the PacBio RS II platform. The other features of the assembly were : Polished Contigs 6 ; Max Contig Length 5,082,442 ; N50 Contig Length 5,082,442 ; Sum of Contig Lengths 5,397,004.