

Supplementary material:

Table 1: Parameter ranges used for data assembly with Velvet and Edena

Parameter	Initial value	Final value	Interval
k-mer	29	45	2
Coverage cutoff	5	15	2
Expected Coverage	60	300	40

Table 2: Results of the BLASTN program considering the contigs as query and the reference genome as subject

Criteria	Quantity
Contigs with single alignments	4774 (3,338,615 bp)
Contigs with alignments in more than one region of the genome	344 (1,195,432 bp)
Contigs without significant alignment	35 (37,138 bp)
Contigs that did not align	118 (52,536 bp)