

Supplementary table 4 - EC071 whole genome sequencing metrics ^a.

Parameters	
Size (pb)	5 271 699
Contigs	262
Genes	5139
N50 ^b	86 427
N75 ^c	42 340
L50 ^d	19
L75 ^e	40
G+C (%)	50,53
Coverage	141x

^a Calculated using the QCAST platform (Gurevich et al., 2013).

^b Base pair (bp) size that contigs with this or bigger size include half the total of bases.

^c Base pair (bp) size that contigs with this or bigger size include $\frac{3}{4}$ of the total of bases.

^d Number of contigs that are bigger or have the same N50 size.

^e Number of contigs that are bigger or have the same N75 size.

Reference

Gurevich A, Saveliev V, Vyahhi N, Tesler G. QCAST: Quality assessment tool for genome assemblies. *Bioinformatics*, 2013;29:1072-1075.