Guidelines for *Listeria monocytogenes* cgMLST typing (IPasteur scheme)

Genome quality parameters	
sequencing coverage (after trimming)	>40X
assembly N50	>20 Kb
cgMLST loci detected	>95% (>1660)

Allele scan parameters	
algorithm	BLASTN
similarity cut-off	70%
minimum alignment length	70%
word size	10

New allele quality parameters	
species identification	*L. monocytogenes*
start and stop codons	present[*]
non-GATC characters, truncations, frameshifts	absent

[*]within a range of +- 18 nt from the start/stop codons of reference allele

Reference:
Nature Microbiology (2016) 2:16185