

*Table 1: Quality control checks for MitoCall tool.*

<b>Step</b>	<b>Tool/programming language used</b>	<b>What it does</b>
<b>Paired-end alignment</b>	bismark	Increases read depth, makes sure there are alignments in both directions, and removed less low quality reads
<b>deduplication</b>	bismark	Remove non-unique reads and low quality reads
<b>Mapping quality</b>	samtools	Removes reads with low read mapping quality
<b>Base quality</b>	bcftools	Removes reads with low base quality
<b>BAQ</b>	bcftools	Removes variants due to misalignments
<b>Multiallelic variant calling</b>	bcftools	Has the option to give more than one alternative allele
<b>Left-alignment normalization</b>	bcftools	Removes INDELS, and improves the alignments of mapped reads

<b>Variant calling quality</b>	python	Removes low confidence variant calling sites
<b>Minimum total reads</b>	python	Removes alignments with low total number of reads
<b>Minimum alternative reads</b>	python	Removes alignments with low total number of alternative reads