

Review of: "High-Quality Genome Assembly of the Endemic, Threatened White-Bellied Sholakili *Sholicola albiventris* (Muscicapidae: Blanford, 1868) From the Shola Sky Islands, India"

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Potential competing interests: No potential competing interests to declare.

The authors present the first genome assembly of the White-bellied Sholakili. This assembly was performed using Nanopore and Illumina reads to build and polish contigs, which were then organized into chromosomes with RagTag, using the *Taeniopygia guttata* assembly (GCA_003957565.4) as a reference.

The article is well-written and simple to read.

The methods are mostly state-of-the-art and well-described.

The assembly is not publicly available at the NCBI and therefore could not be correctly assessed.

Six rounds of polishing is a high number, which could lead to over-polishing, meaning haplotype chimeras. POLCA is not haplotype-aware. This could be checked by verifying the haplotypes' conservation in the assembly using Nanopore long reads.

Material and methods: mitoHiFi is known to work with HiFi reads. The authors should present how they have used it with Nanopore reads.