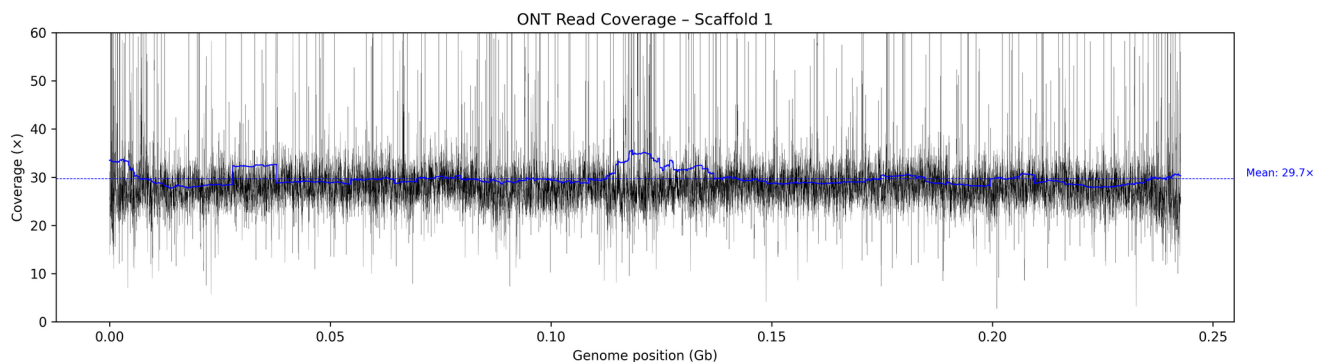


Additional file 7

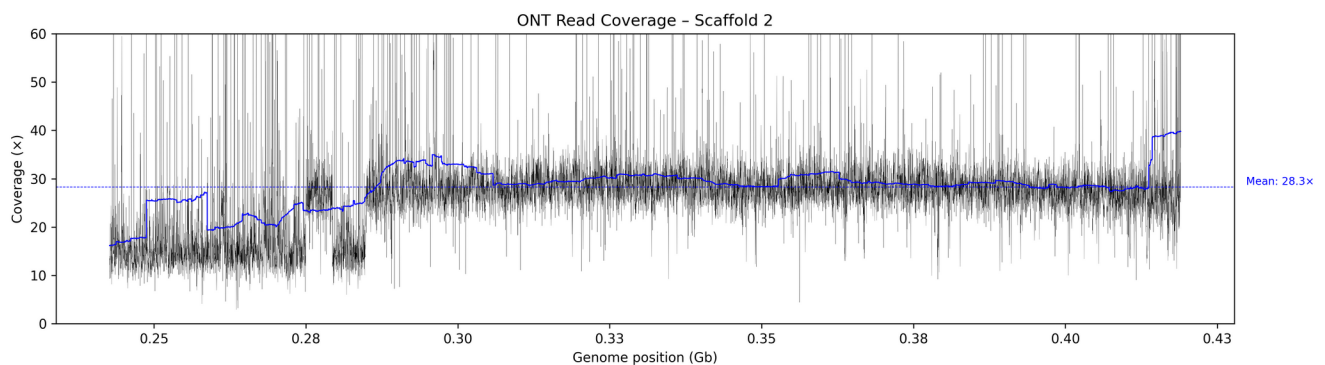
Supplementary results - read mapping and genome coverage analysis

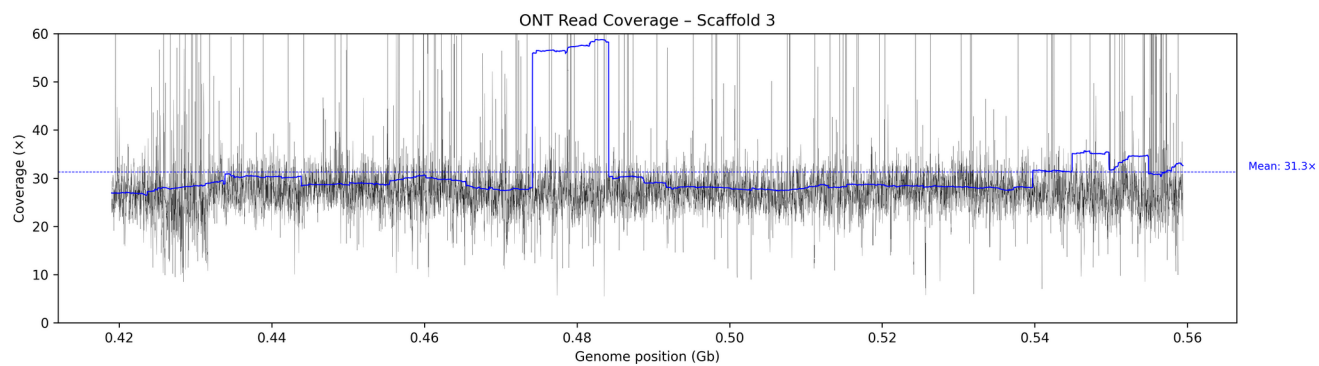
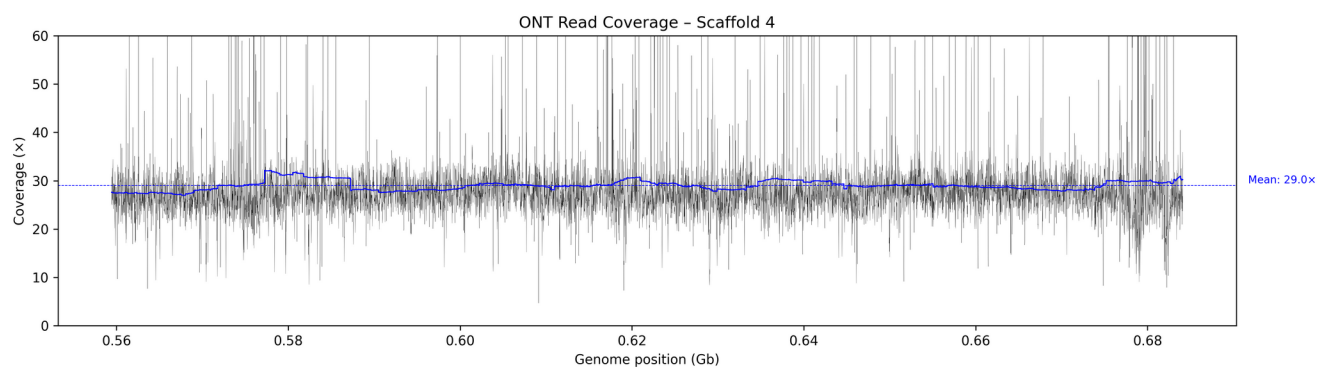
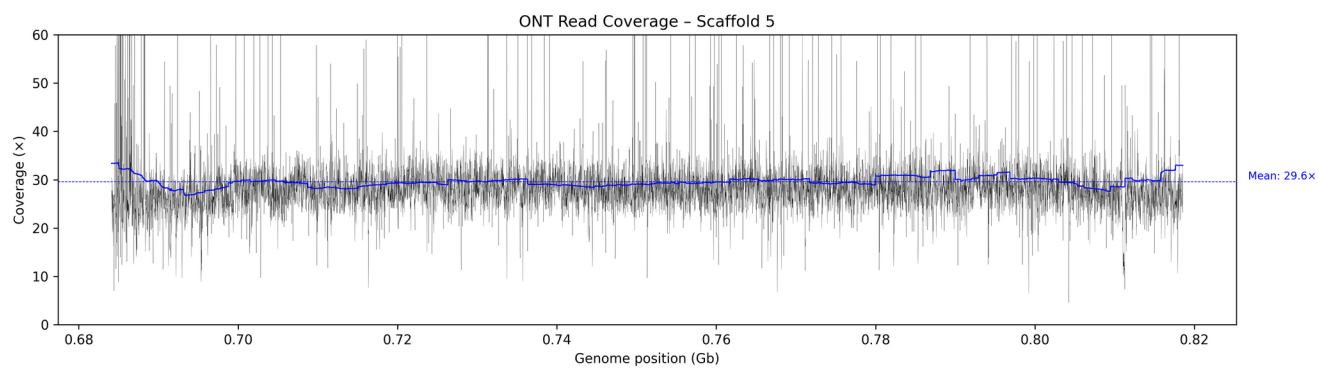
Figure. Individual scaffold coverage profiles for the 13 longest scaffolds of the *Pristimantis euphronides* genome assembly. Panels (A)-(M) correspond to scaffolds 1-13. Black line: read coverage smoothed over 2×10 kb windows. Blue line: long-range smoothed trend (1000×10 kb windows). Blue dashed horizontal line: per-scaffold mean coverage, annotated to the right of each panel. X-axis: genome position in gigabases (Gb). Y-axis: read depth ($\times$), range 0-60 $\times$. Scaffold numbers follow *Eleutherodactylus coqui* chromosome size order. Read depth computed with mosdepth v0.3.11 [1] from Minimap2 [2] alignments of high-accuracy (HAC) basecalled Nanopore reads to the RagTag v2.1.0 [3] scaffolded assembly.

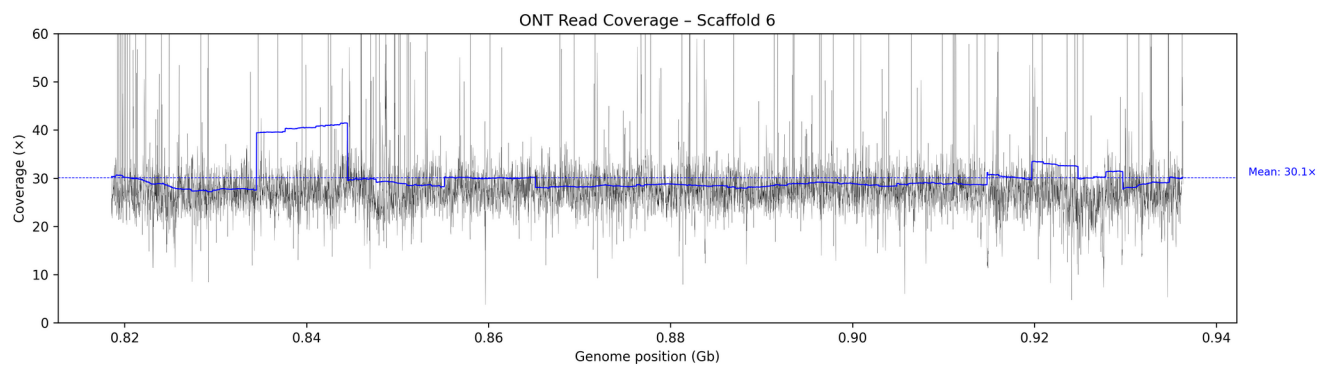
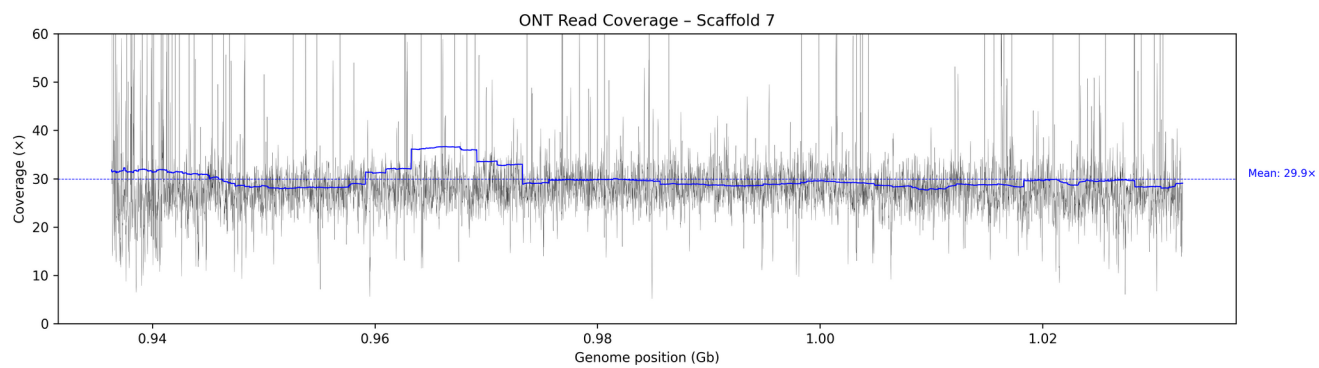
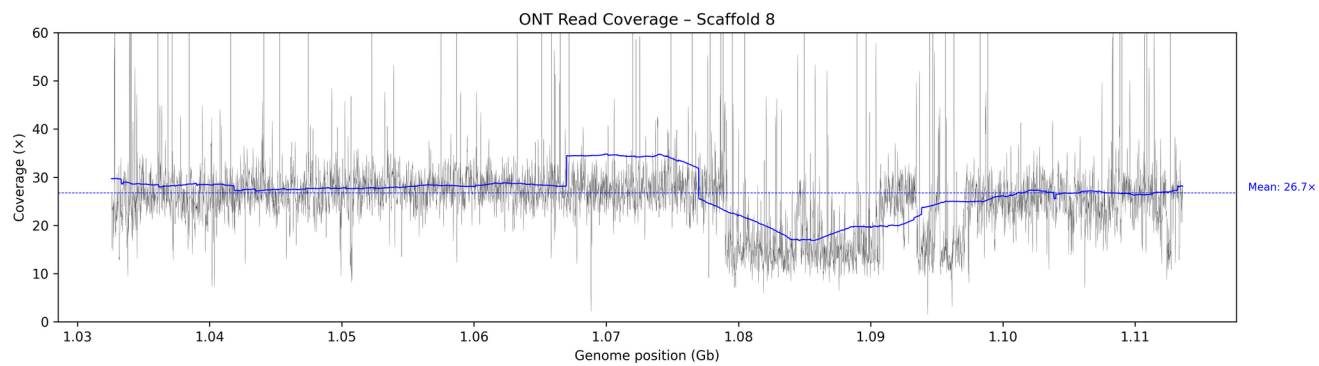
A

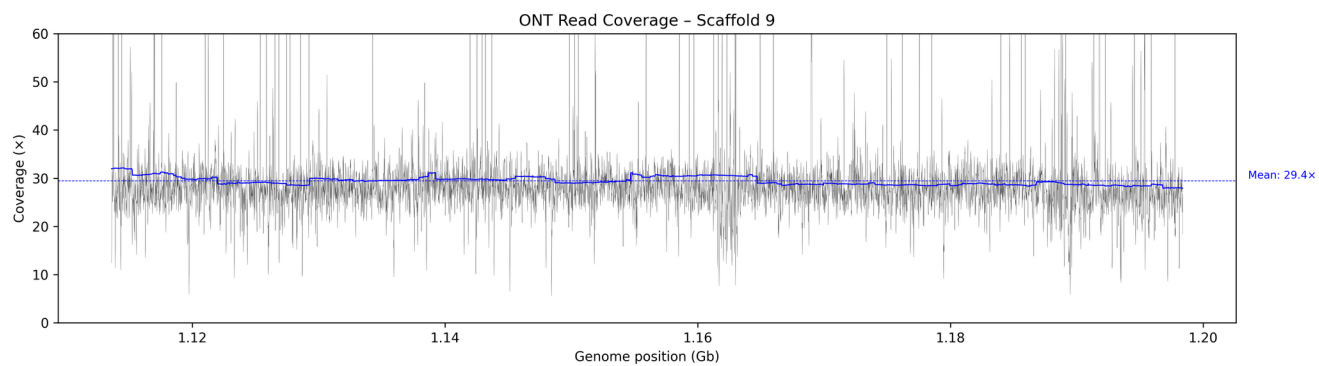
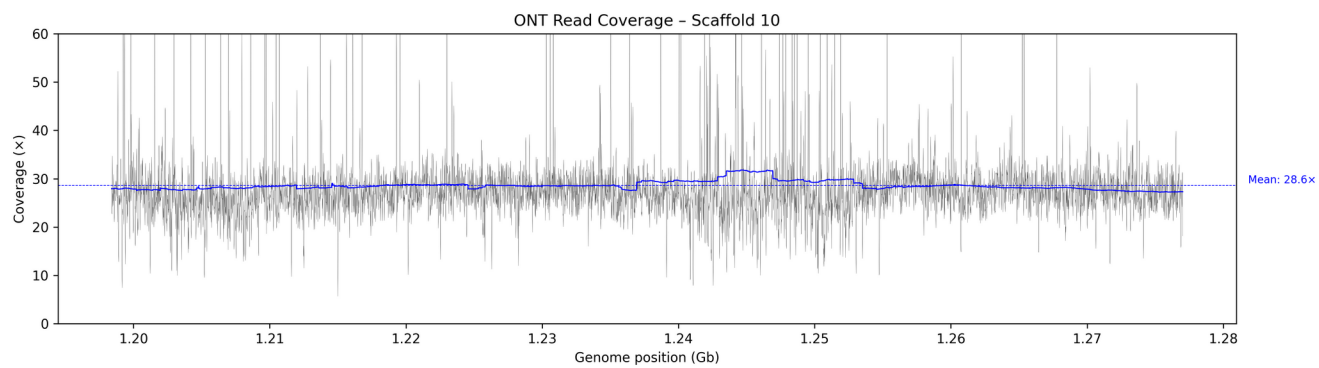
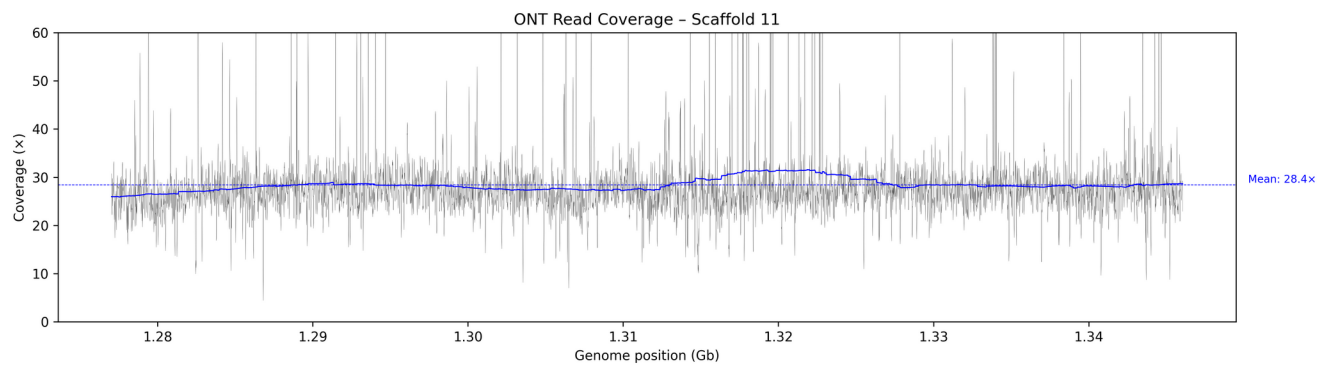


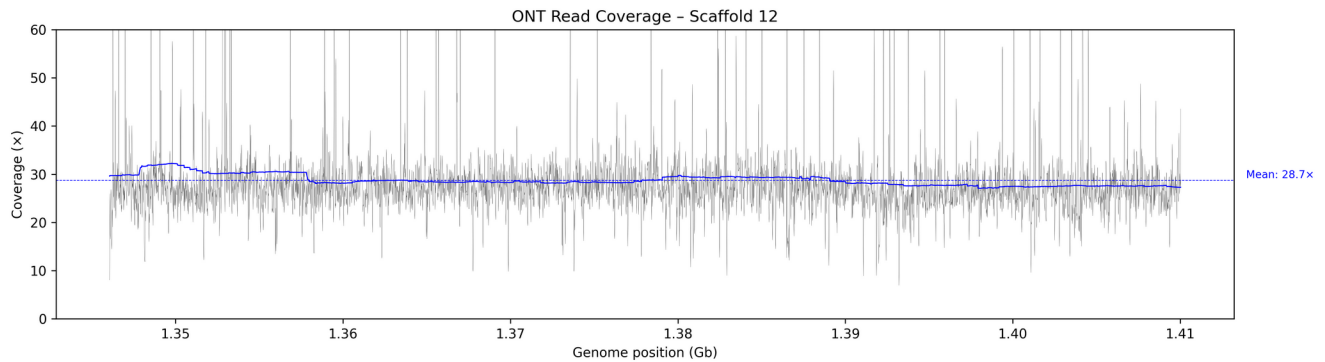
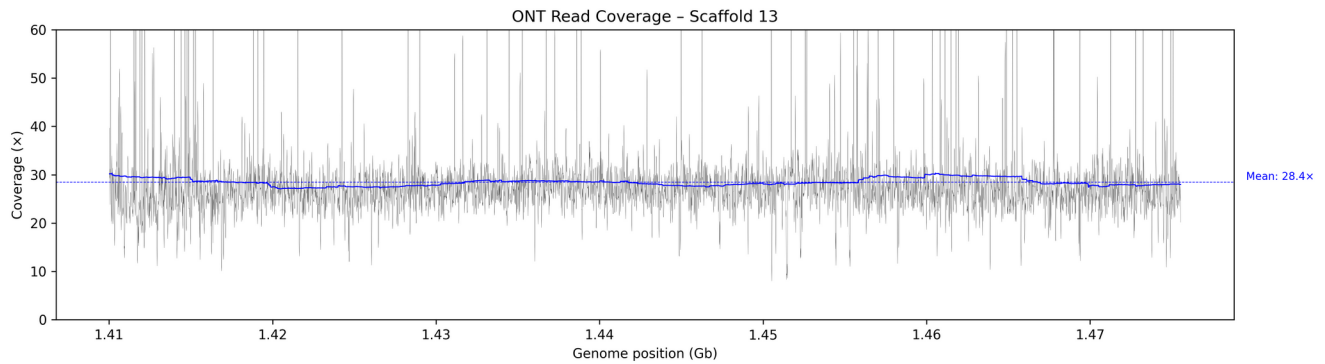
B



C**D****E**

F**G****H**

I**J****K**

L**M**

References

1. Pedersen BS, Quinlan AR. Mosdepth: quick coverage calculation for genomes and exomes. *Bioinformatics*. 2018;34(5):867-868.
2. Li H. Minimap2: pairwise alignment for nucleotide sequences. *Bioinformatics*. 2018 Sep 15;34(18):3094-3100.
3. Alonge M, Lebeigle L, Kirsche M, Jenike K, Ou S, Aganezov S, et al. Automated assembly scaffolding using RagTag elevates a new tomato system for high-throughput genome editing. *Genome Biol*. 2022;23(1):258.