

Supplementary Material

**Assembly of the largest squamate reference genome to date: the western fence lizard,  
*Sceloporus occidentalis***

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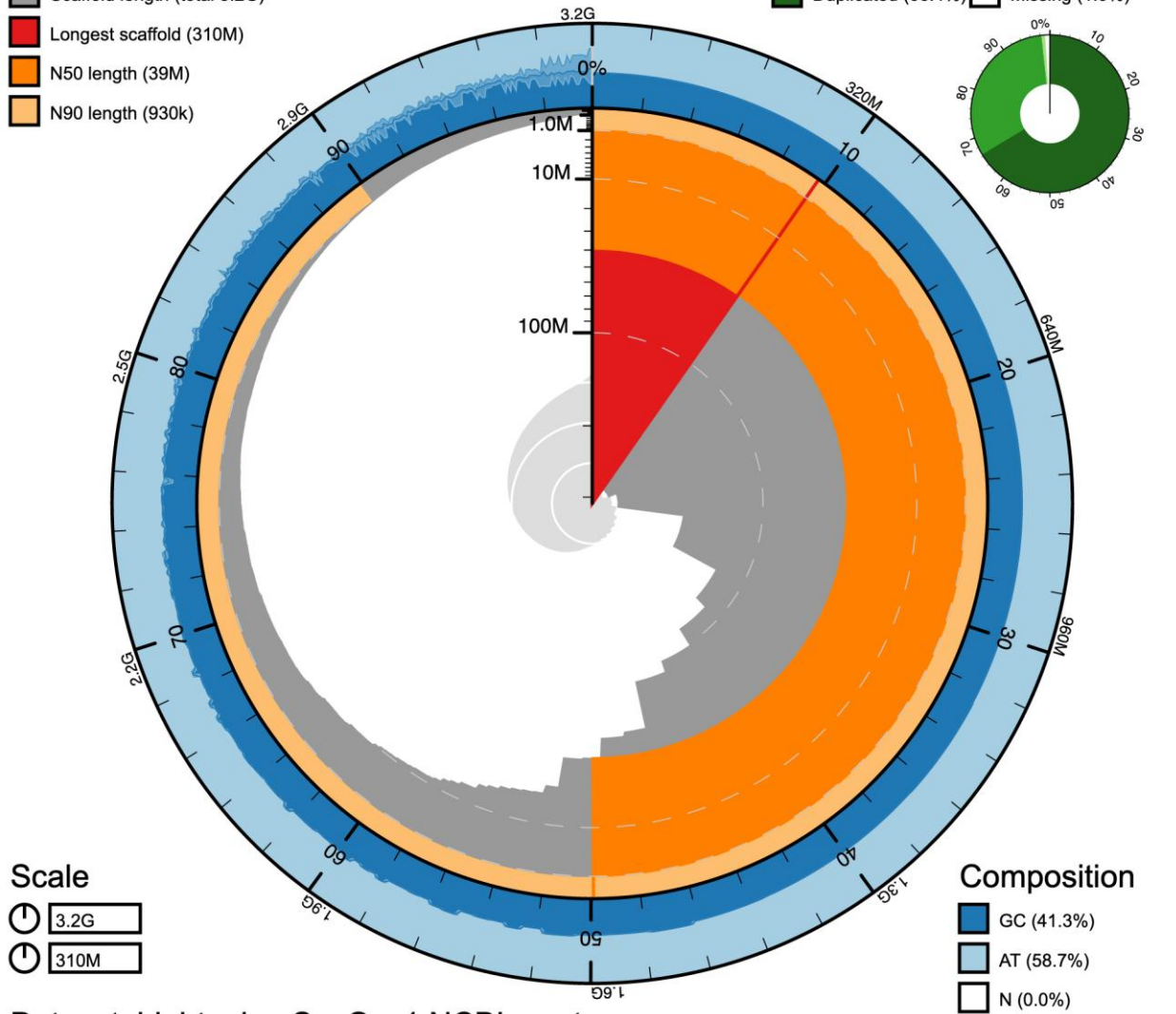
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### Scaffold statistics

- Log10 scaffold count (total 1.8k)
- Scaffold length (total 3.2G)
- Longest scaffold (310M)
- N50 length (39M)
- N90 length (930k)

### BUSCO tetrapoda\_odb10 (5310)

- Complete (98.3%)
- Fragmented (0.7%)
- Duplicated (66.4%)
- Missing (1.0%)



**Supplementary Fig. 1:** BlobToolKit Snail plot showing a graphical representation of the quality metrics for the *S. occidentalis* alternate assembly. The plot circle represents the full size of the assembly. From the inside out, the central plot covers length-related metrics. The red line represents the size of the longest scaffold; all other scaffolds are arranged in size-order moving clockwise around the plot and drawn in gray, starting from the outside of the central plot. Dark and light orange arcs show the scaffold N50 and scaffold N90 values. The central light gray spiral shows the cumulative scaffold count with a white line at each order of magnitude. White regions in this area reflect the proportion of Ns in the assembly; the dark vs. light blue area around it shows mean, maximum, and minimum GC vs. AT content at 0.1% intervals.