

# Identifying the causes and consequences of assembly gaps using a multiplatform genome assembly of a bird-of-paradise

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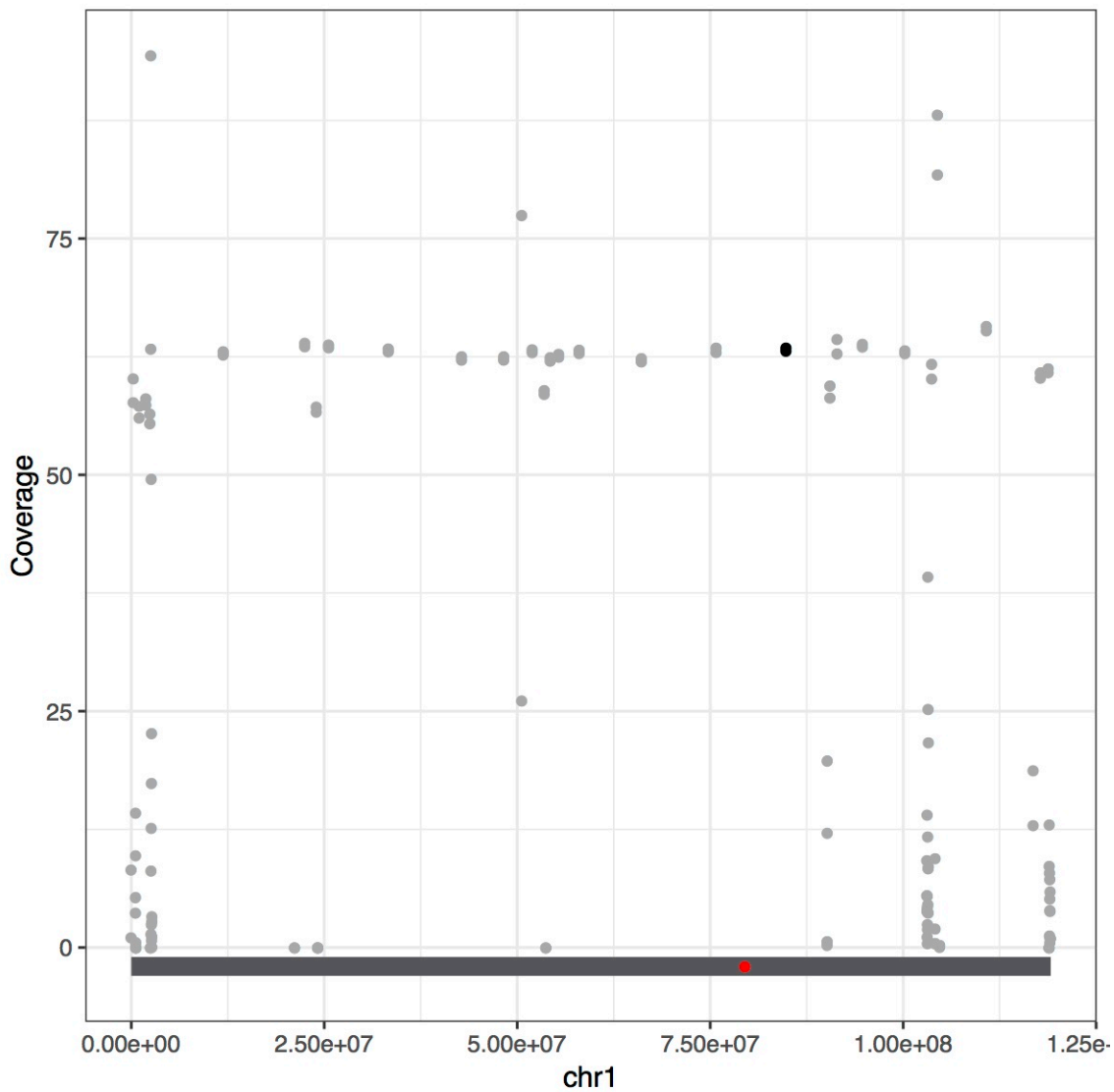
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**Figure S13.** Mean coverage of the lycPyr6 chromosome models or scaffolds/containing MHC genes. Coverage calculated using PacBio reads per contig, and plotted as a dot at each contig midpoint. Black dots: contigs with identified MHC genes; grey dots: contigs without identified MHC genes; red dot: contigs with coverage >100X (placed at the bottom).

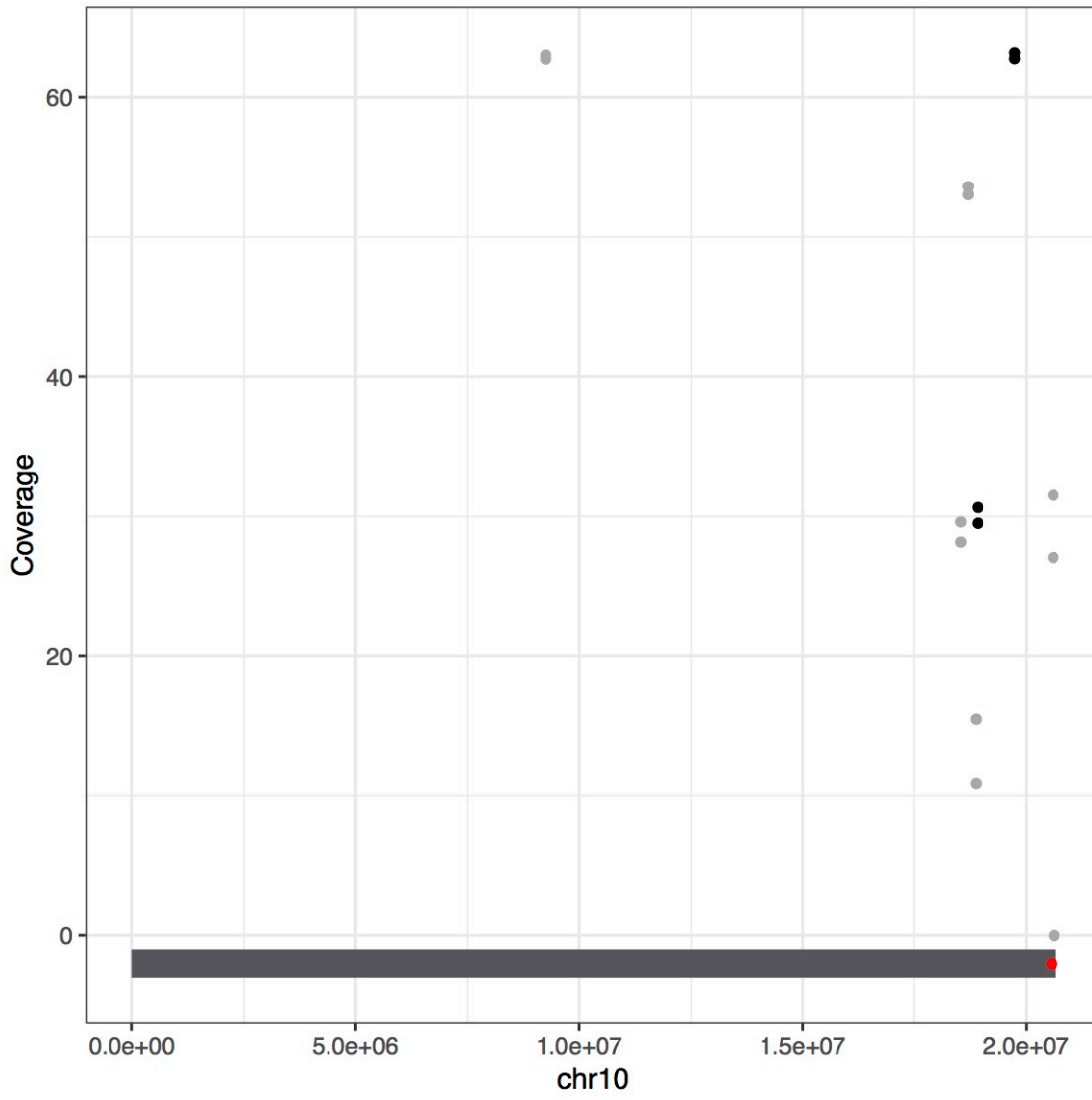


Figure S13. Continued.

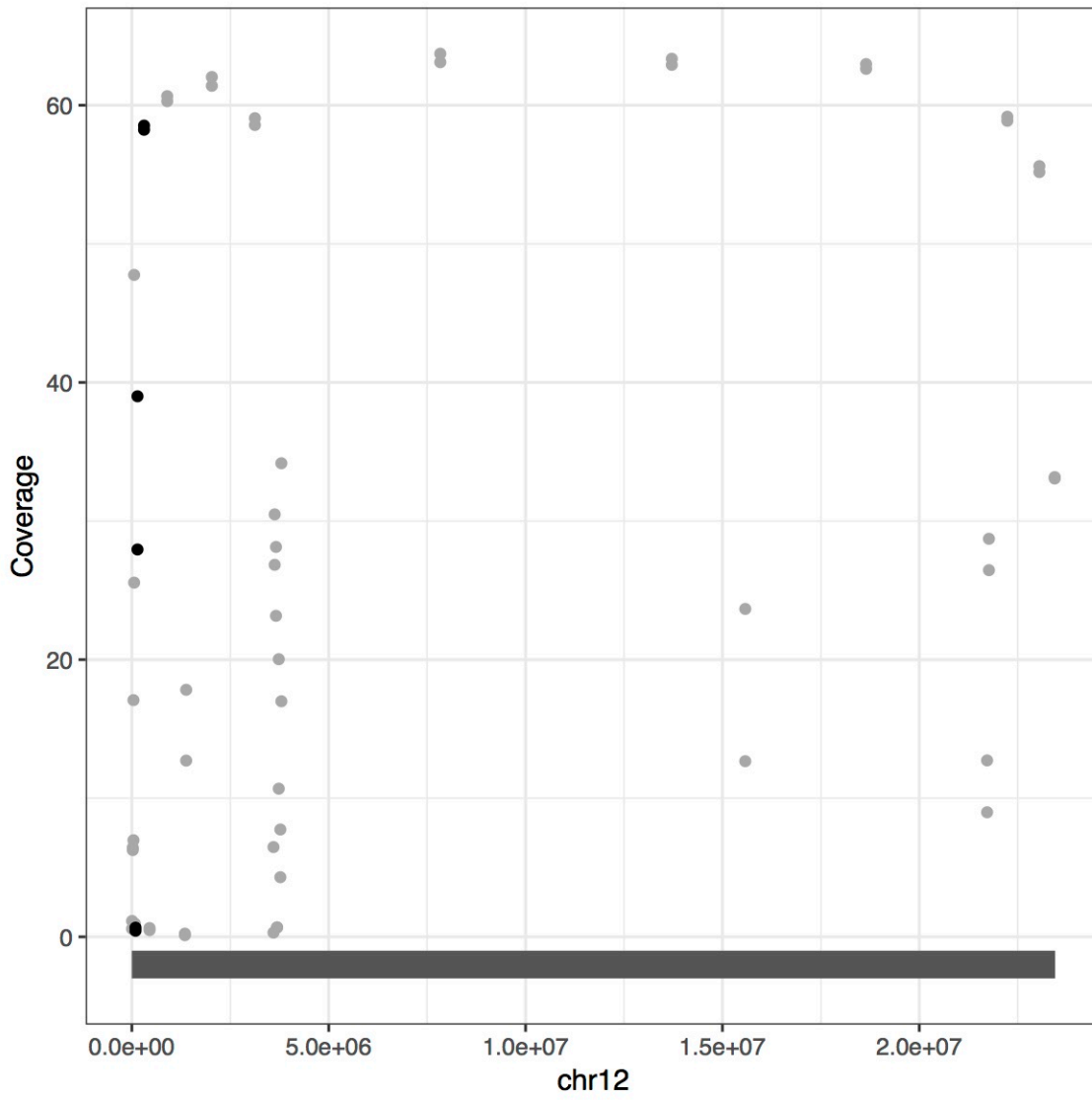
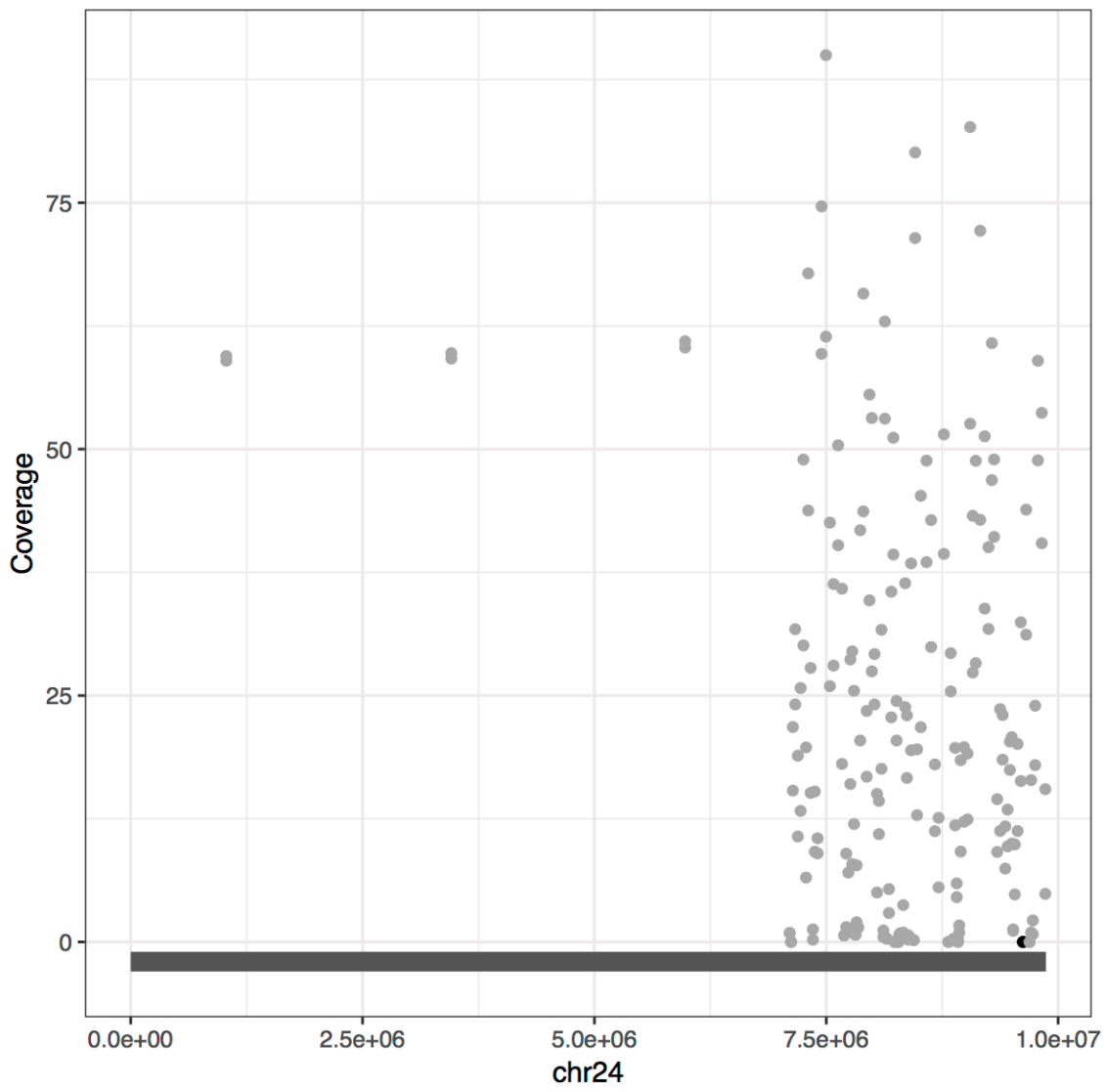


Figure S13. Continued.



**Figure S13.** Continued.

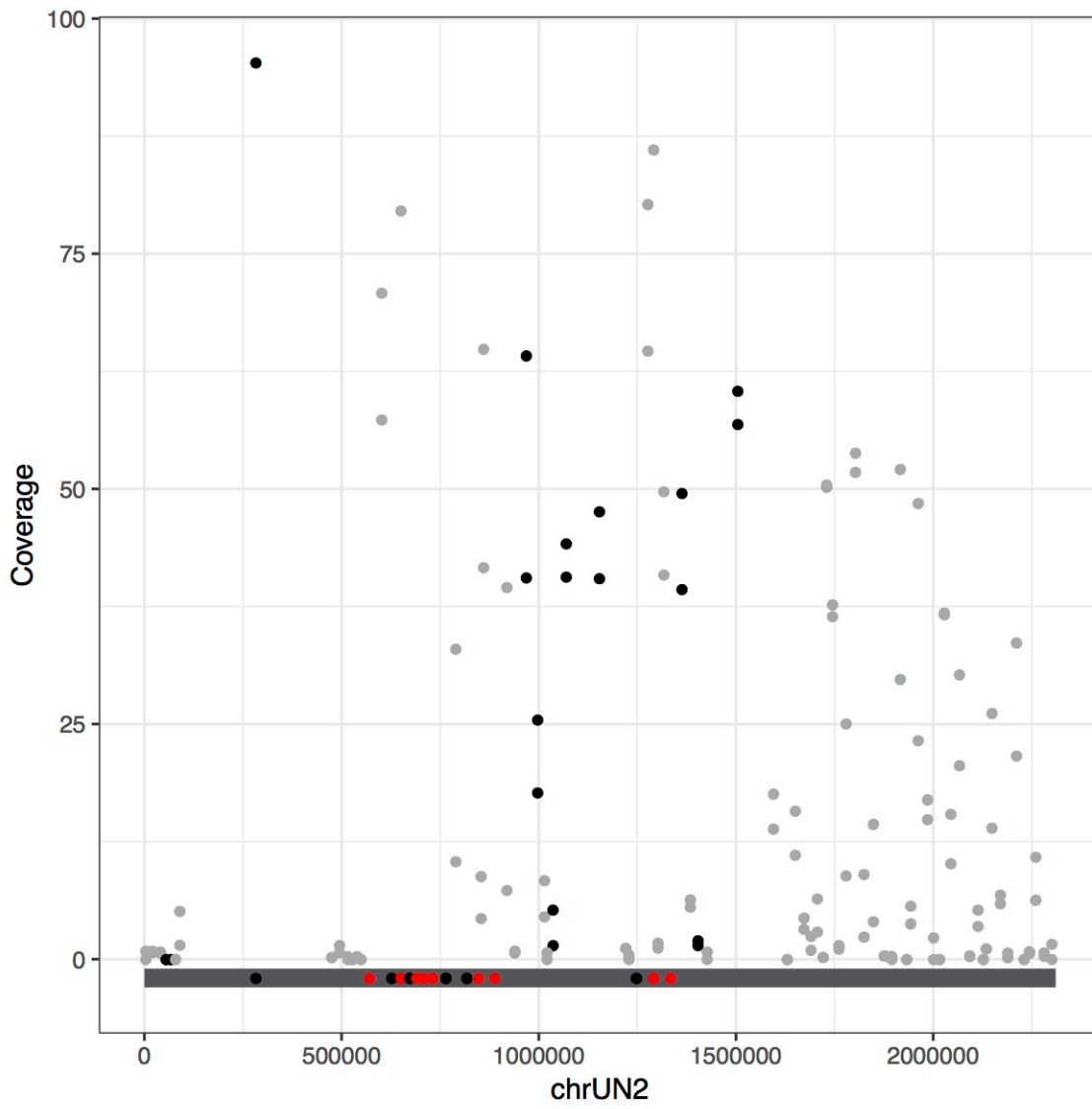


Figure S13. Continued.

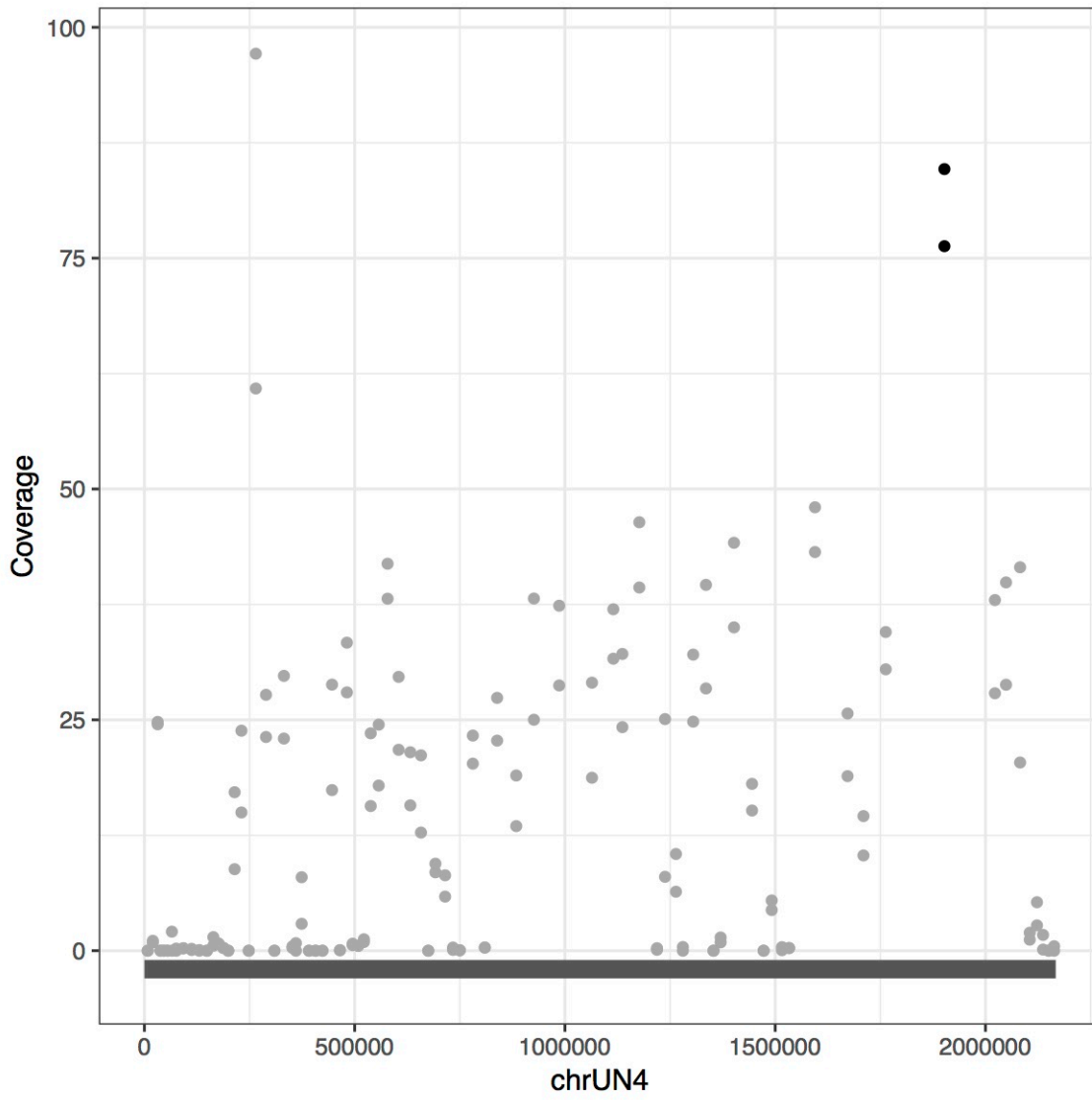


Figure S13. Continued.

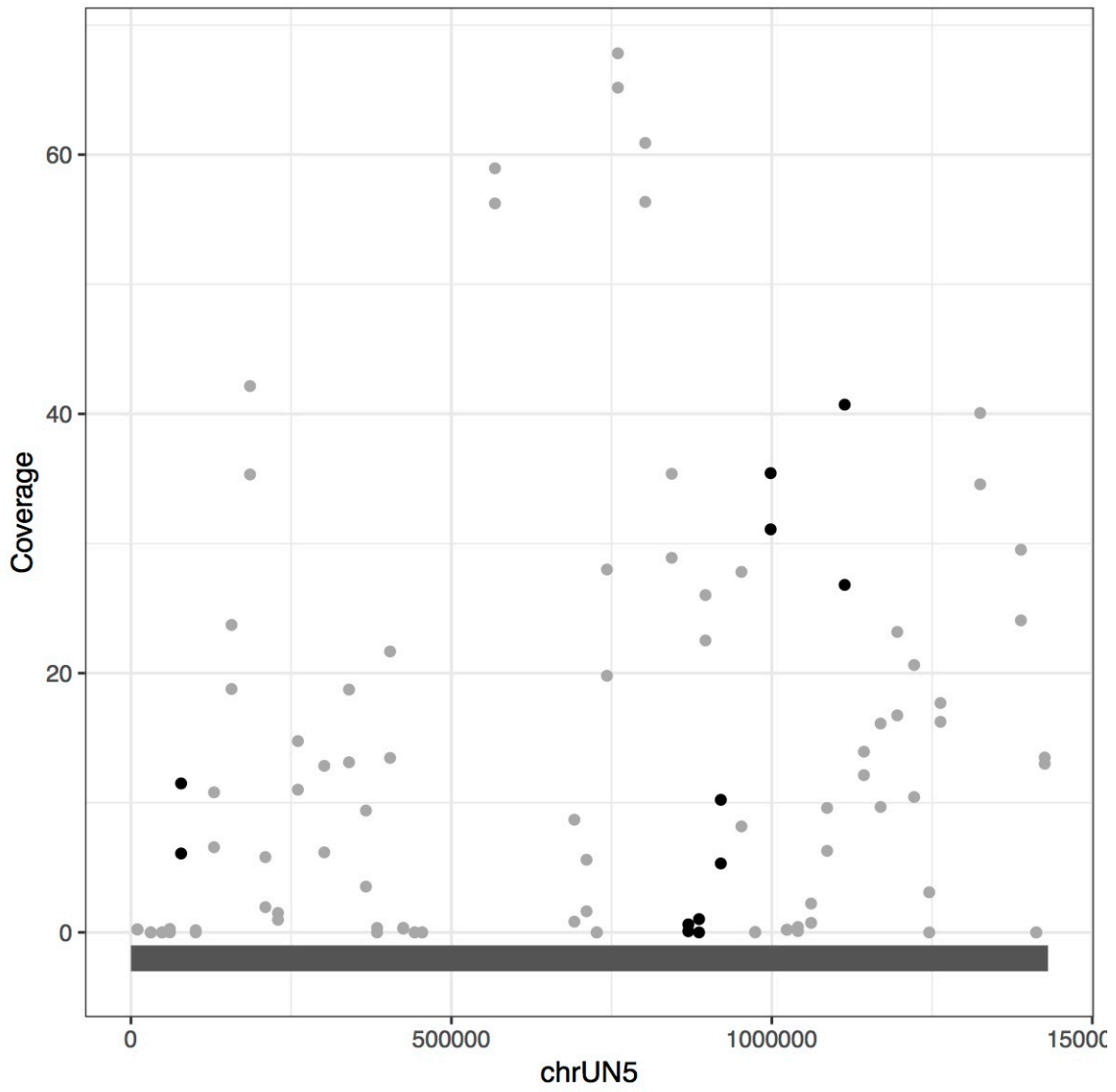
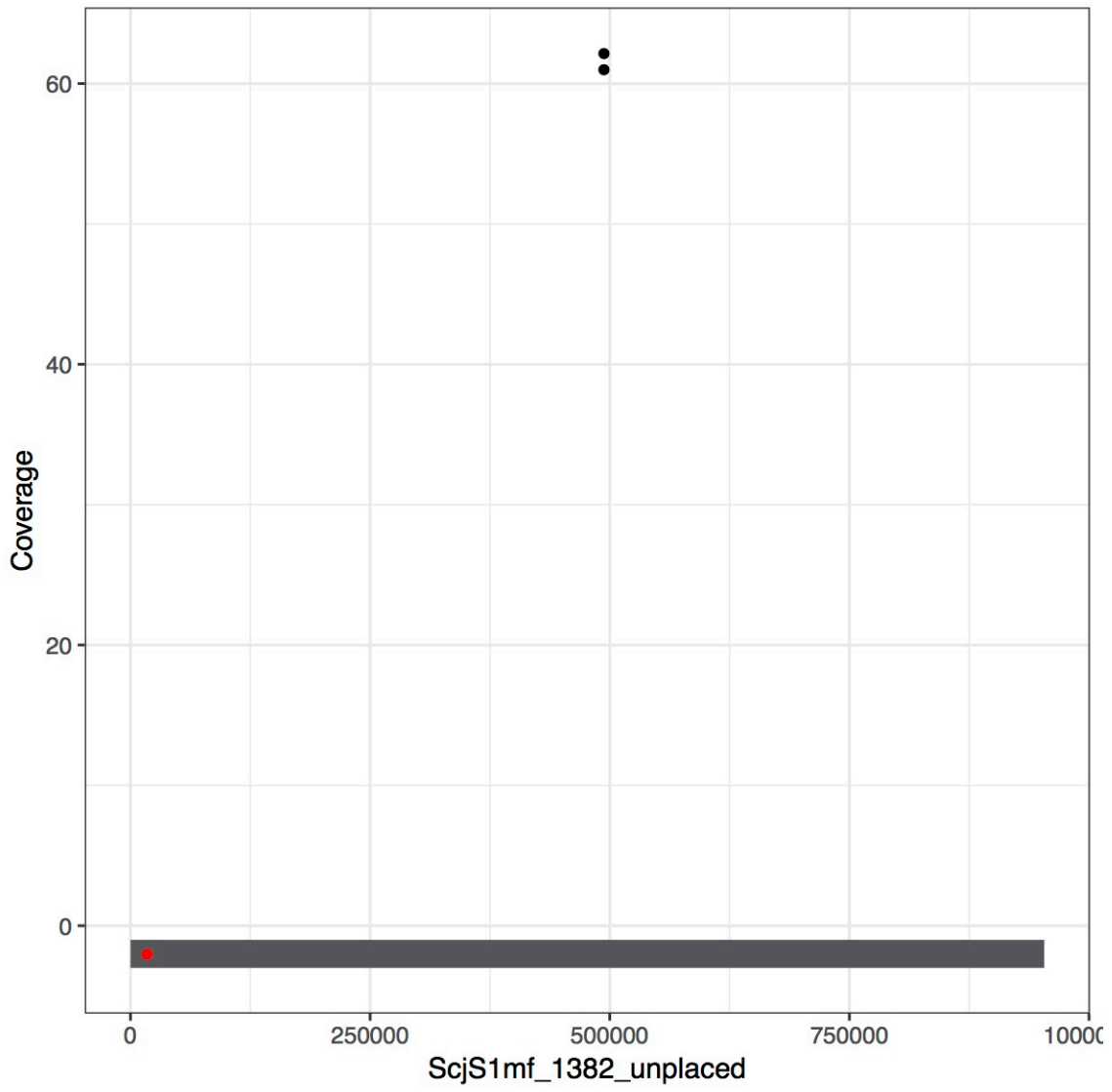


Figure S13. Continued.





**Figure S13.** Continued.