

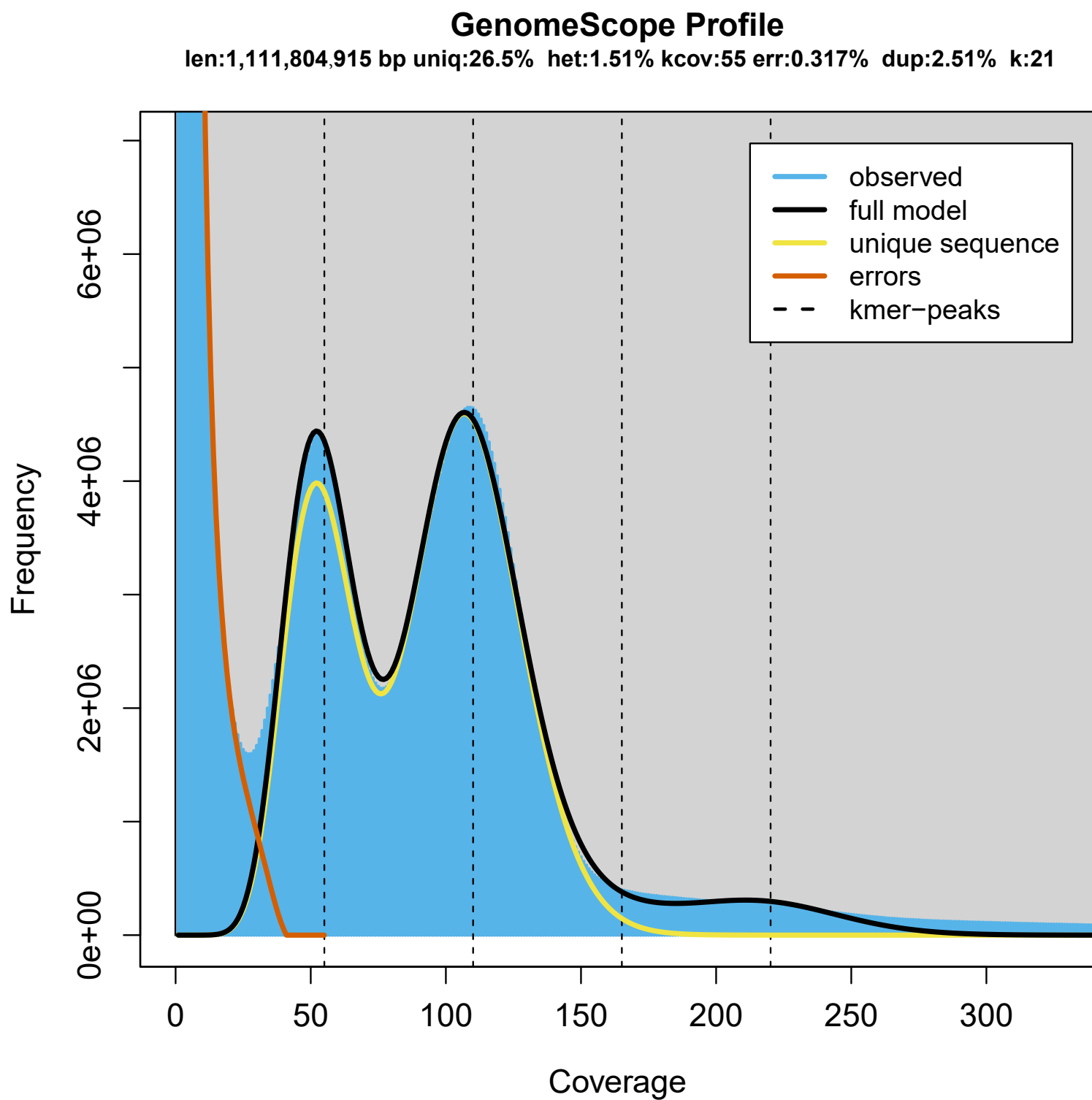


Figure S1. Genome survey of *S. guianensis* utilizing a k-mer-based approach.

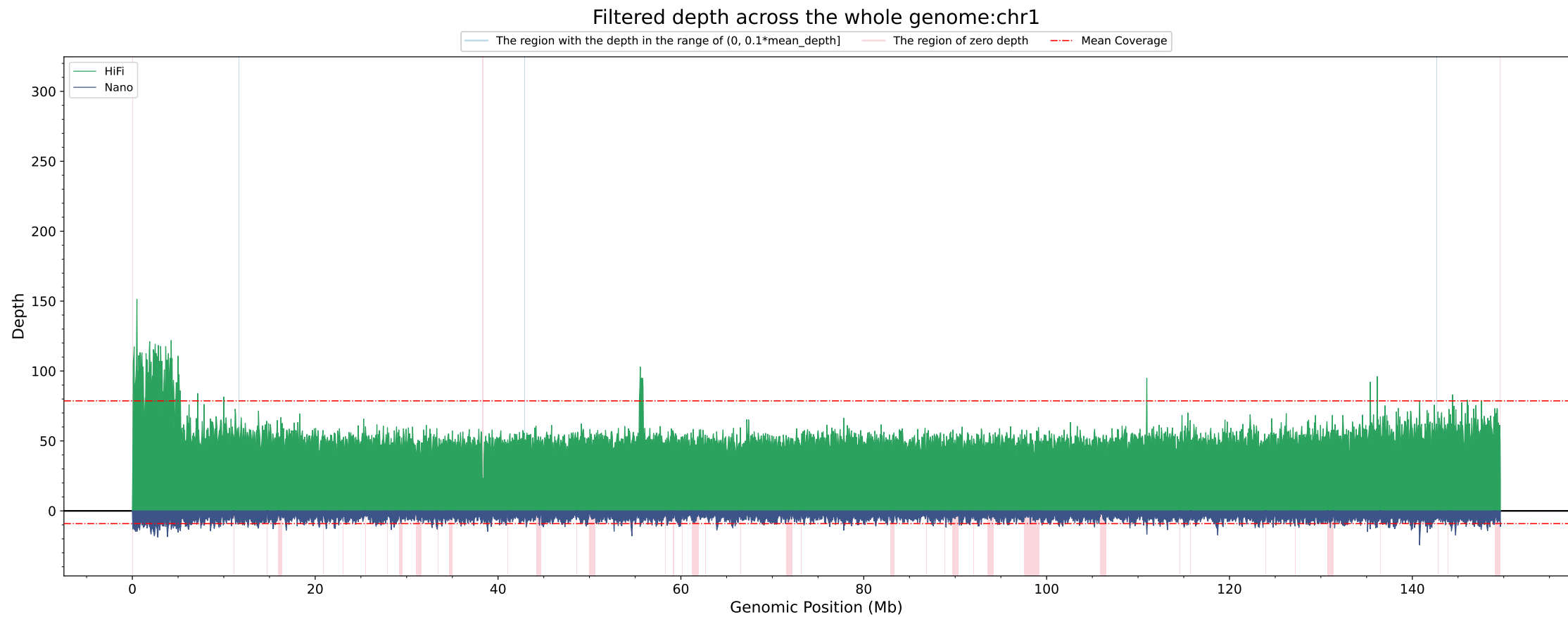


Figure S2. Genome continuity inspector (GCI) assessment analysis of chromosome 1 of *S. guianensis* based on ONT and PacBio HiFi reads.

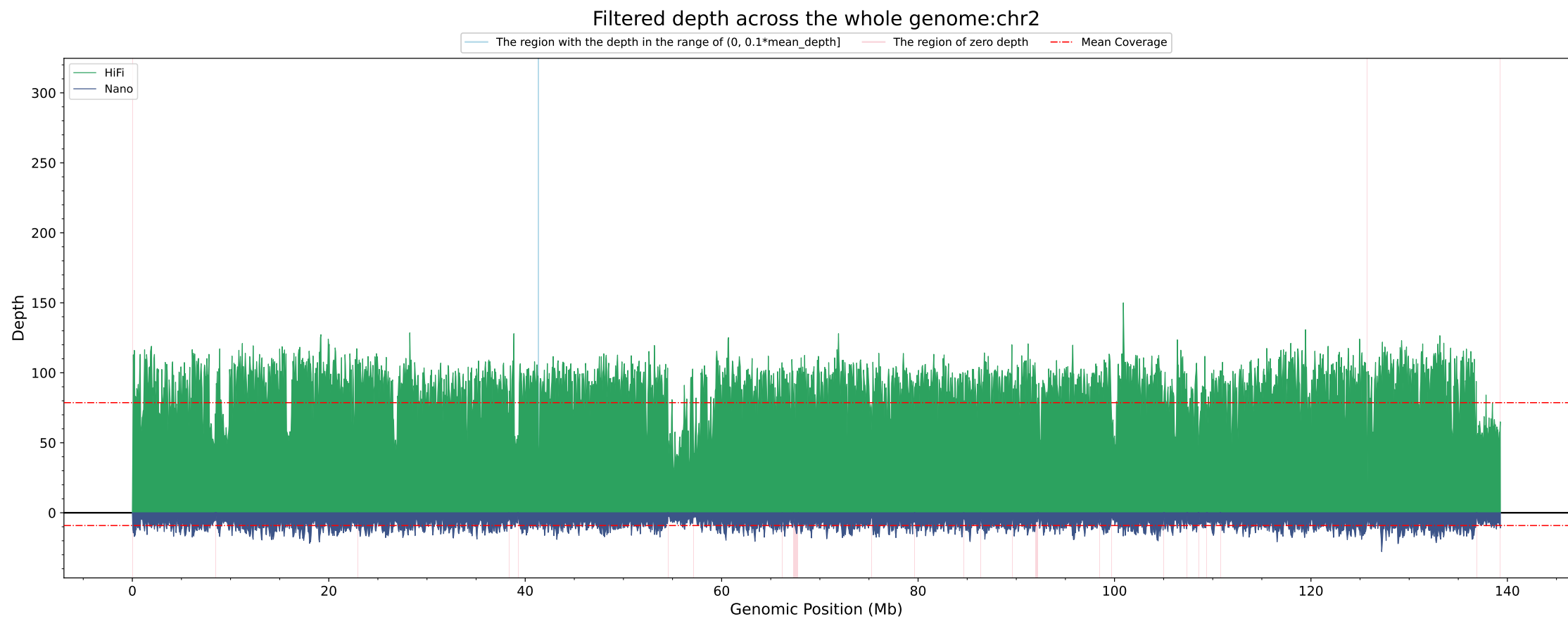


Figure S3. GCI assessment analysis of chromosome 2 of *S. guianensis* based on ONT and PacBio HiFi reads.

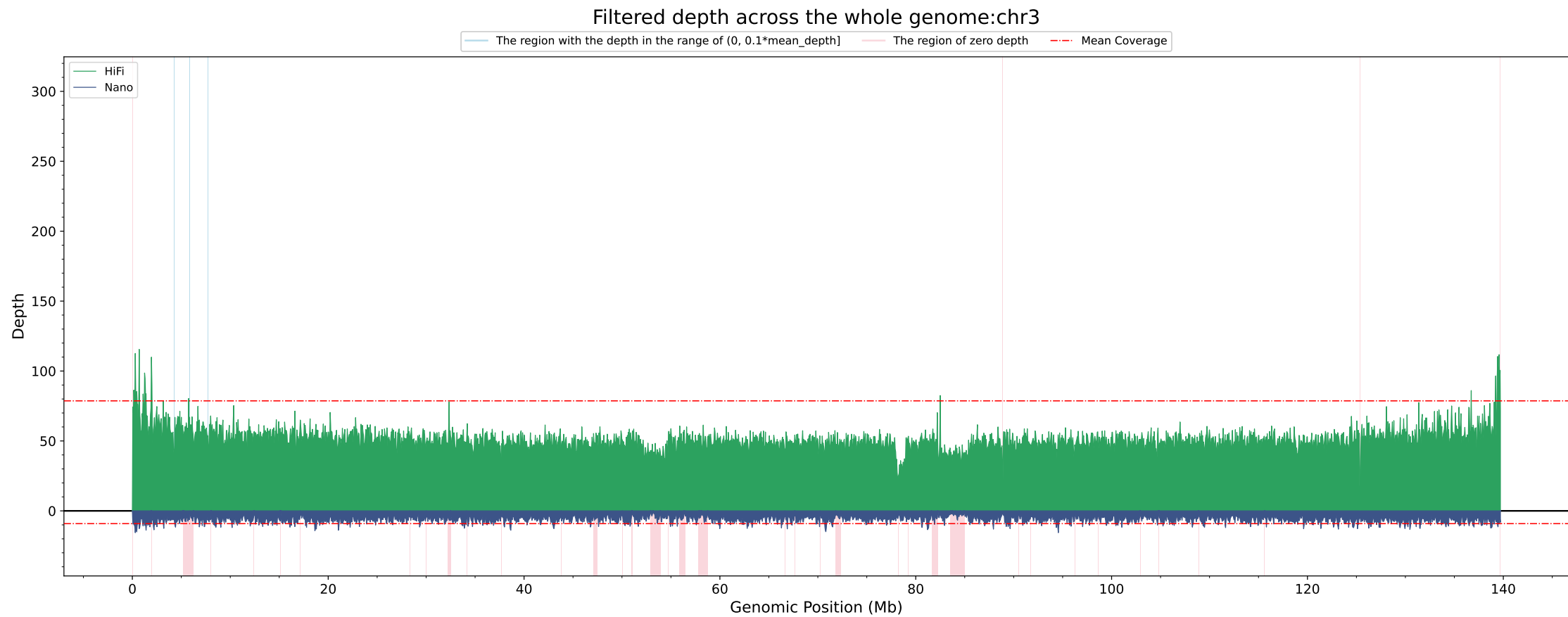


Figure S4. GCI assessment analysis of chromosome 3 of *S. guianensis* based on ONT and PacBio HiFi reads.

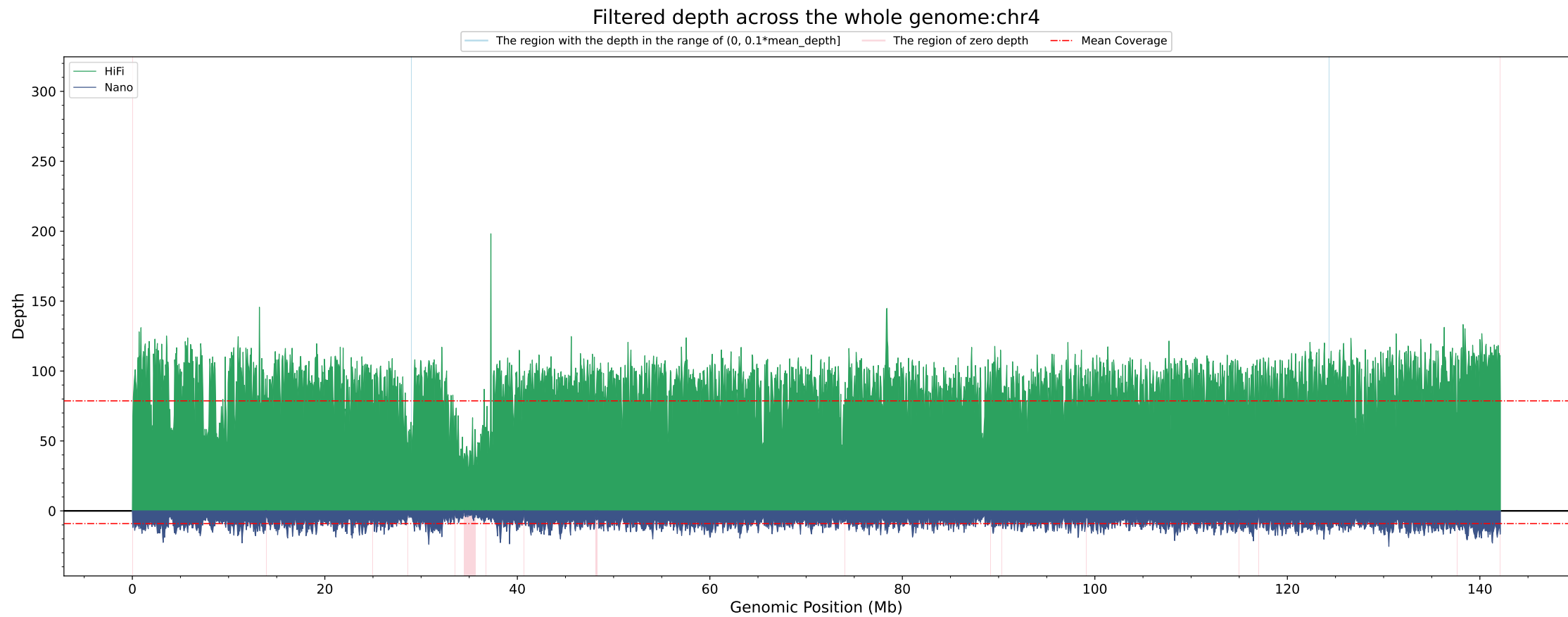


Figure S5. GCI assessment analysis of chromosome 4 of *S. guianensis* based on ONT and PacBio HiFi reads.

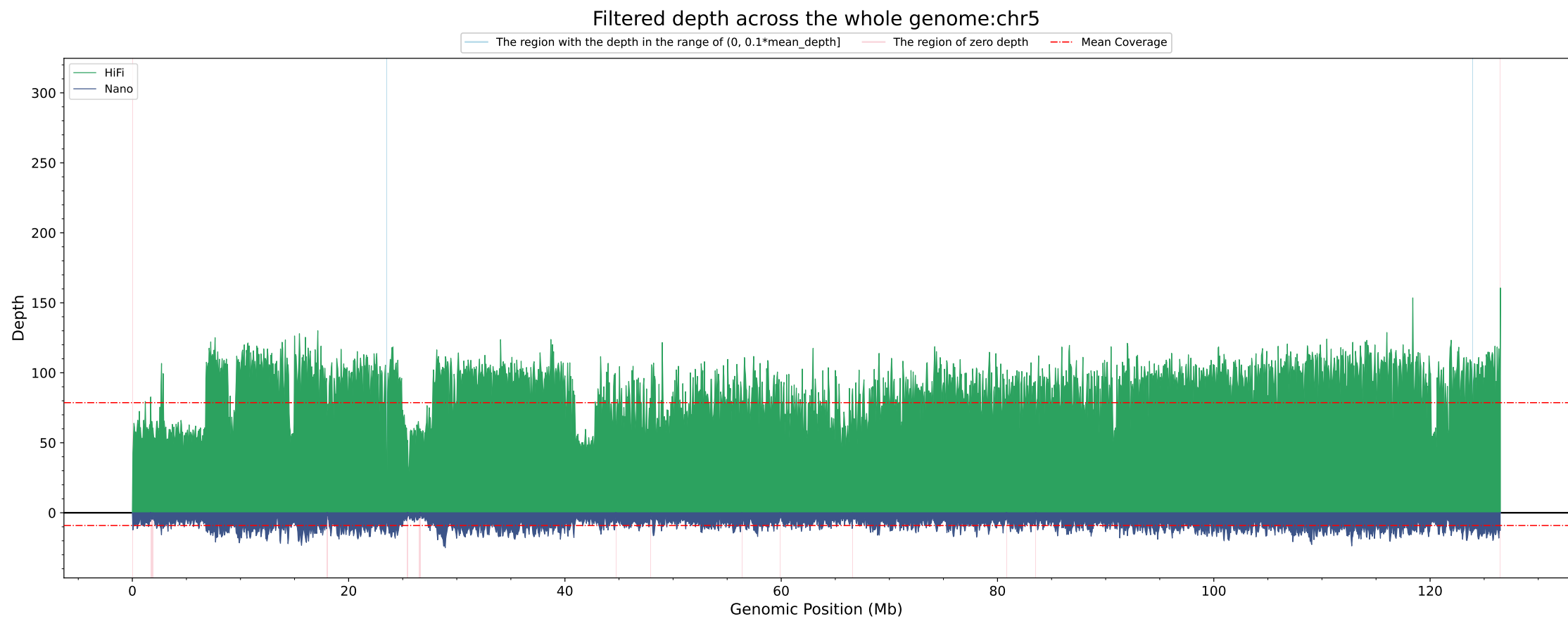


Figure S6. GCI assessment analysis of chromosome 5 of *S. guianensis* based on ONT and PacBio HiFi reads.

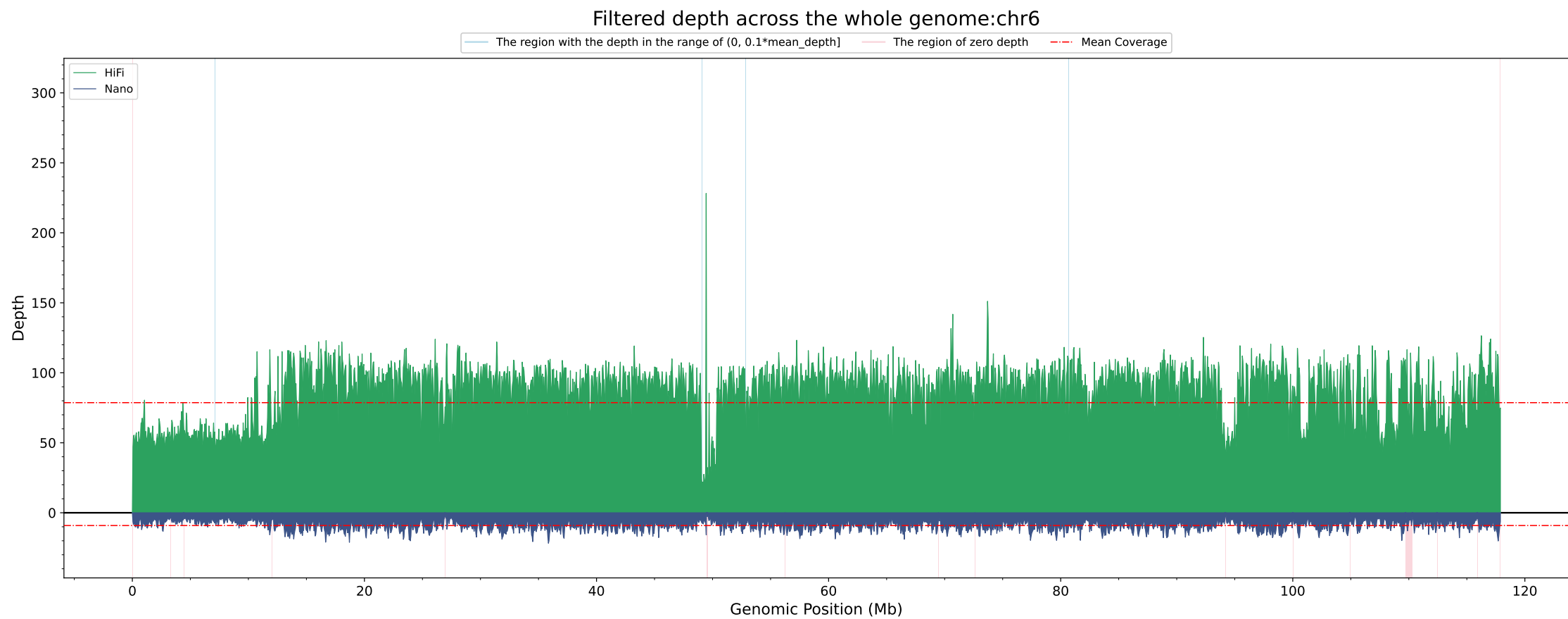


Figure S7. GCI assessment analysis of chromosome 6 of *S. guianensis* based on ONT and PacBio HiFi reads.

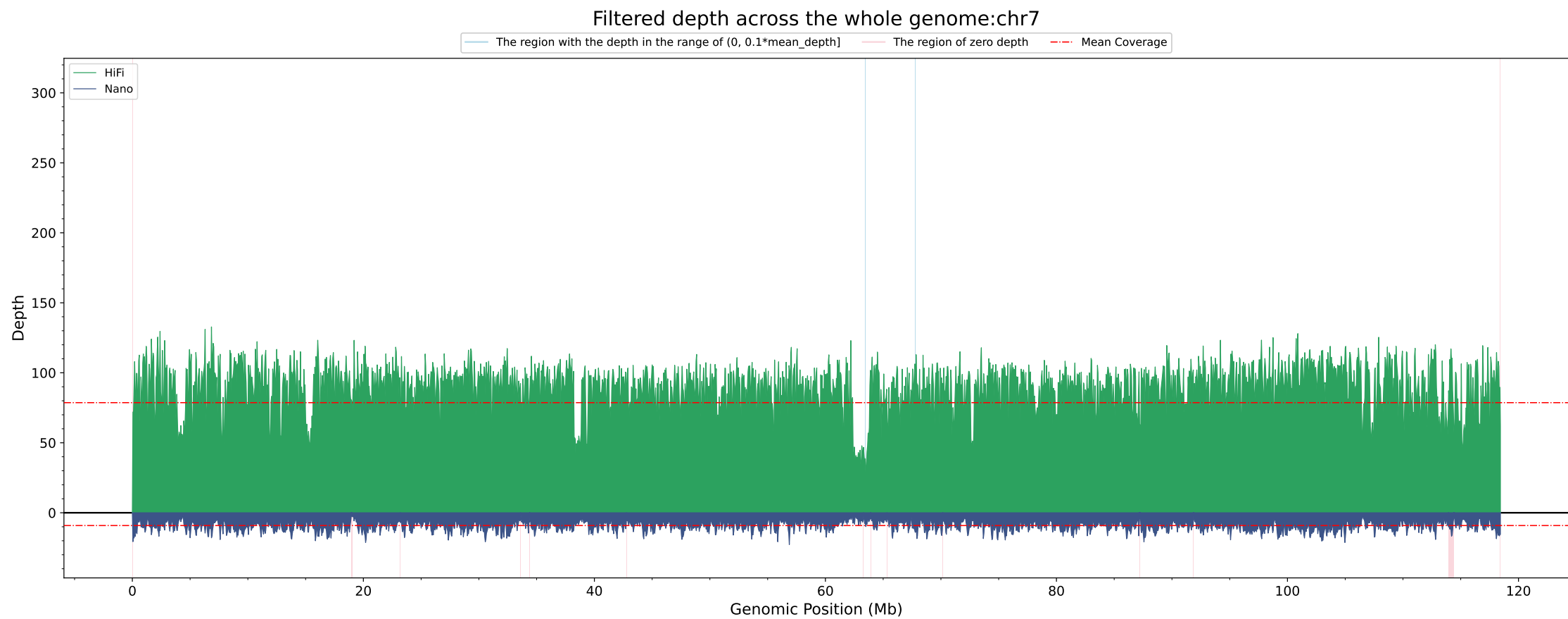


Figure S8. GCI assessment analysis of chromosome 7 of *S. guianensis* based on ONT and PacBio HiFi reads.

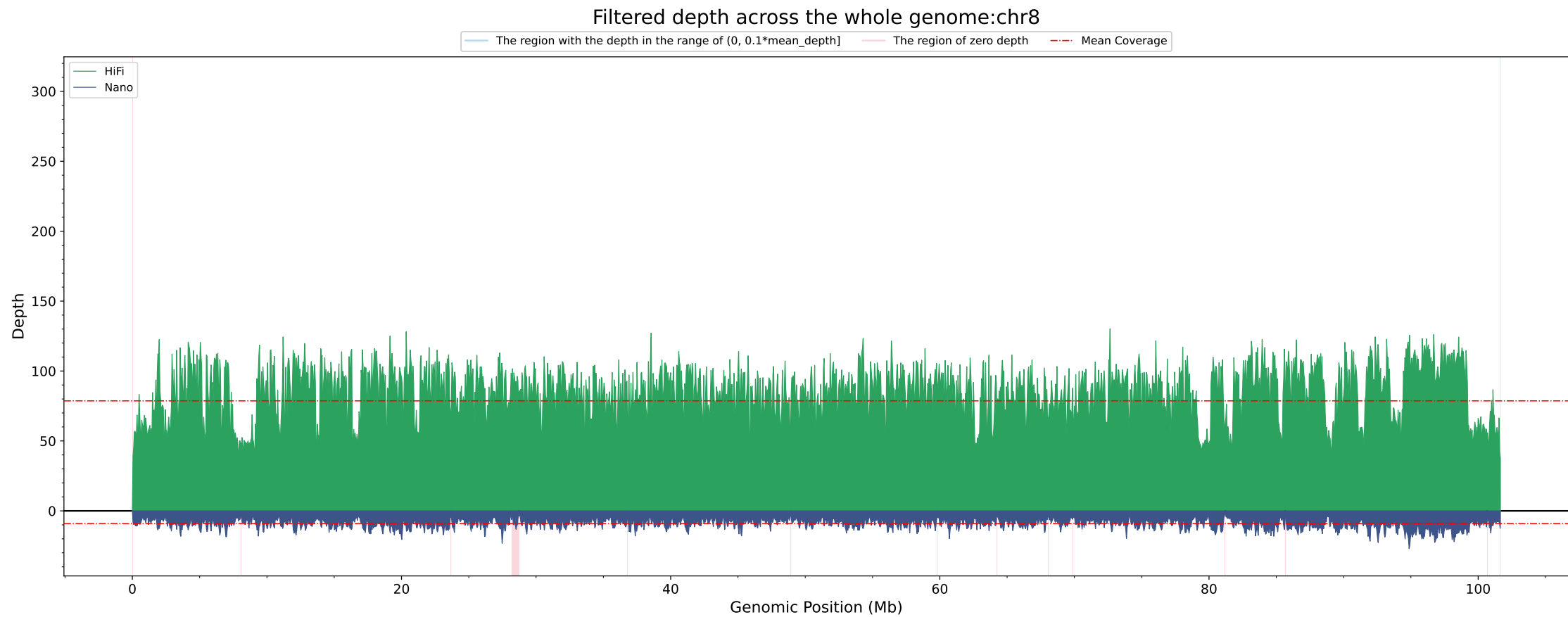


Figure S9. GCI assessment analysis of chromosome 8 of *S. guianensis* based on ONT and PacBio HiFi reads.

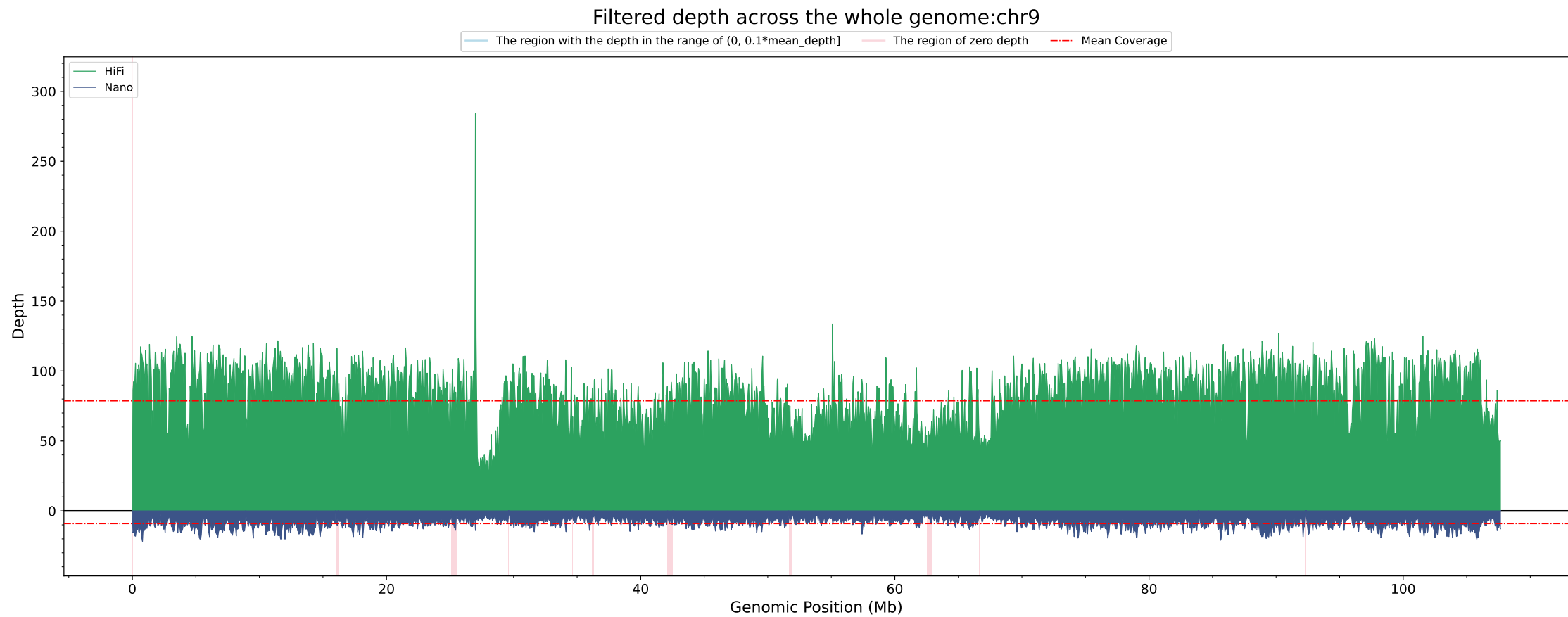


Figure S10. GCI assessment analysis of chromosome 9 of *S. guianensis* based on ONT and PacBio HiFi reads.

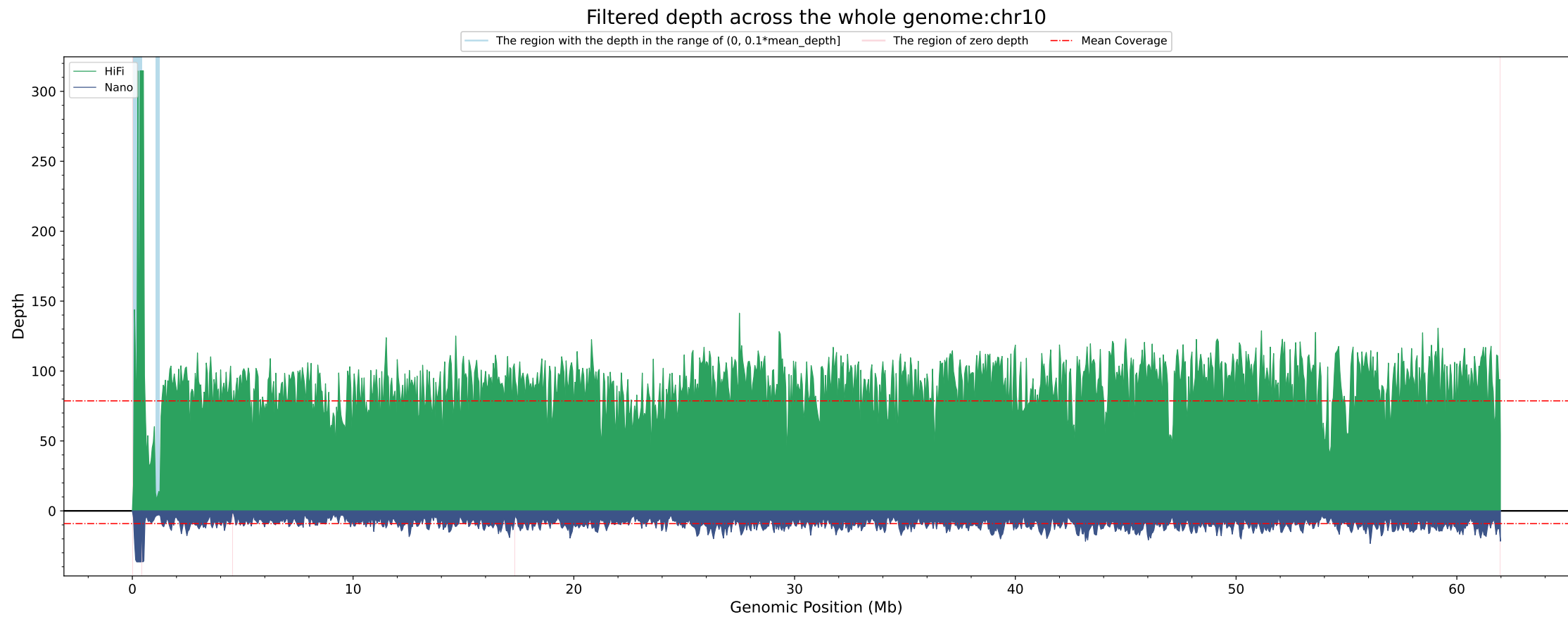


Figure S11. GCI assessment analysis of chromosome 10 of *S. guianensis* based on ONT and PacBio HiFi reads.

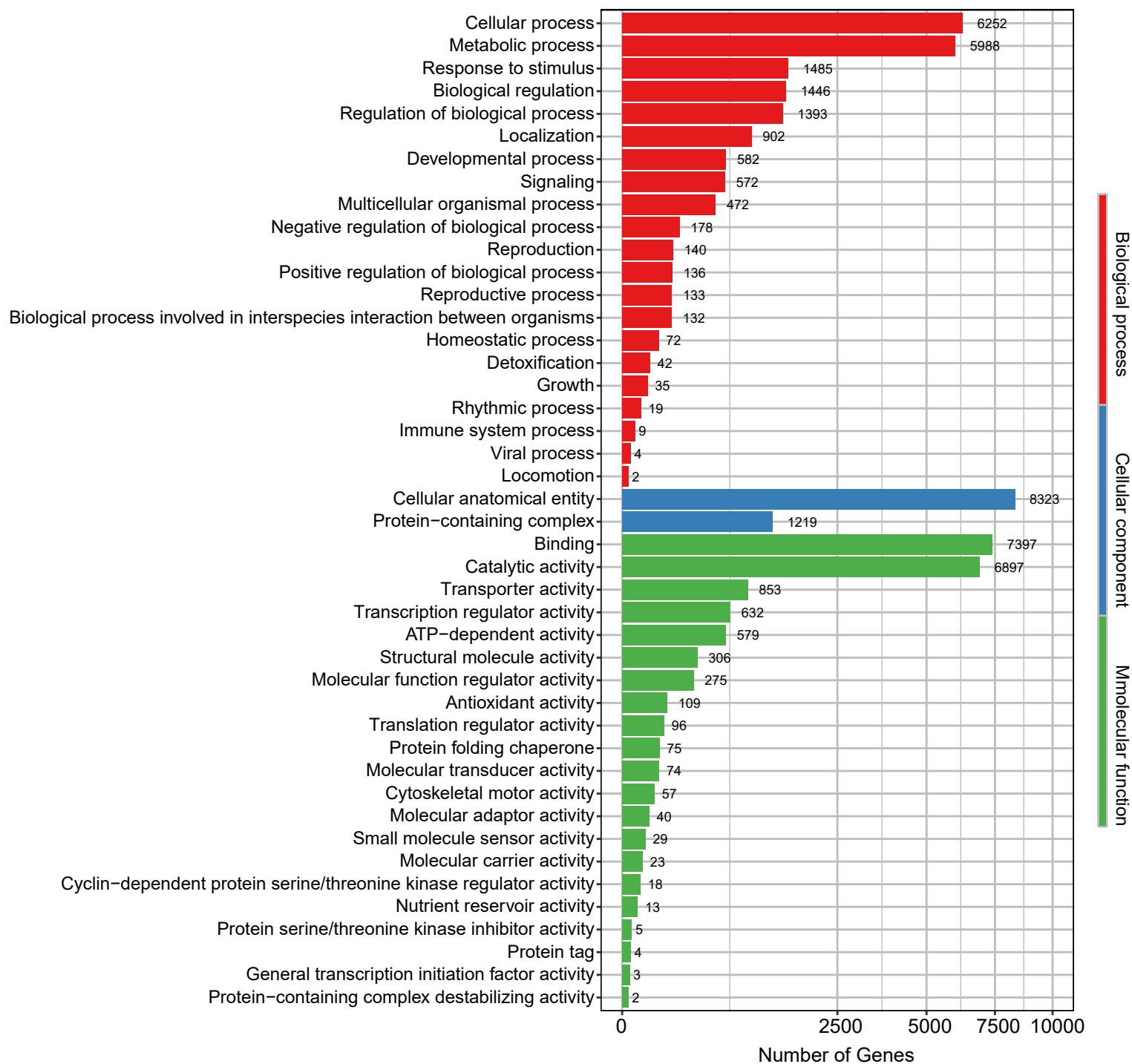


Figure S12. Gene Ontology (GO) classification of the *S. guianensis* gene set.

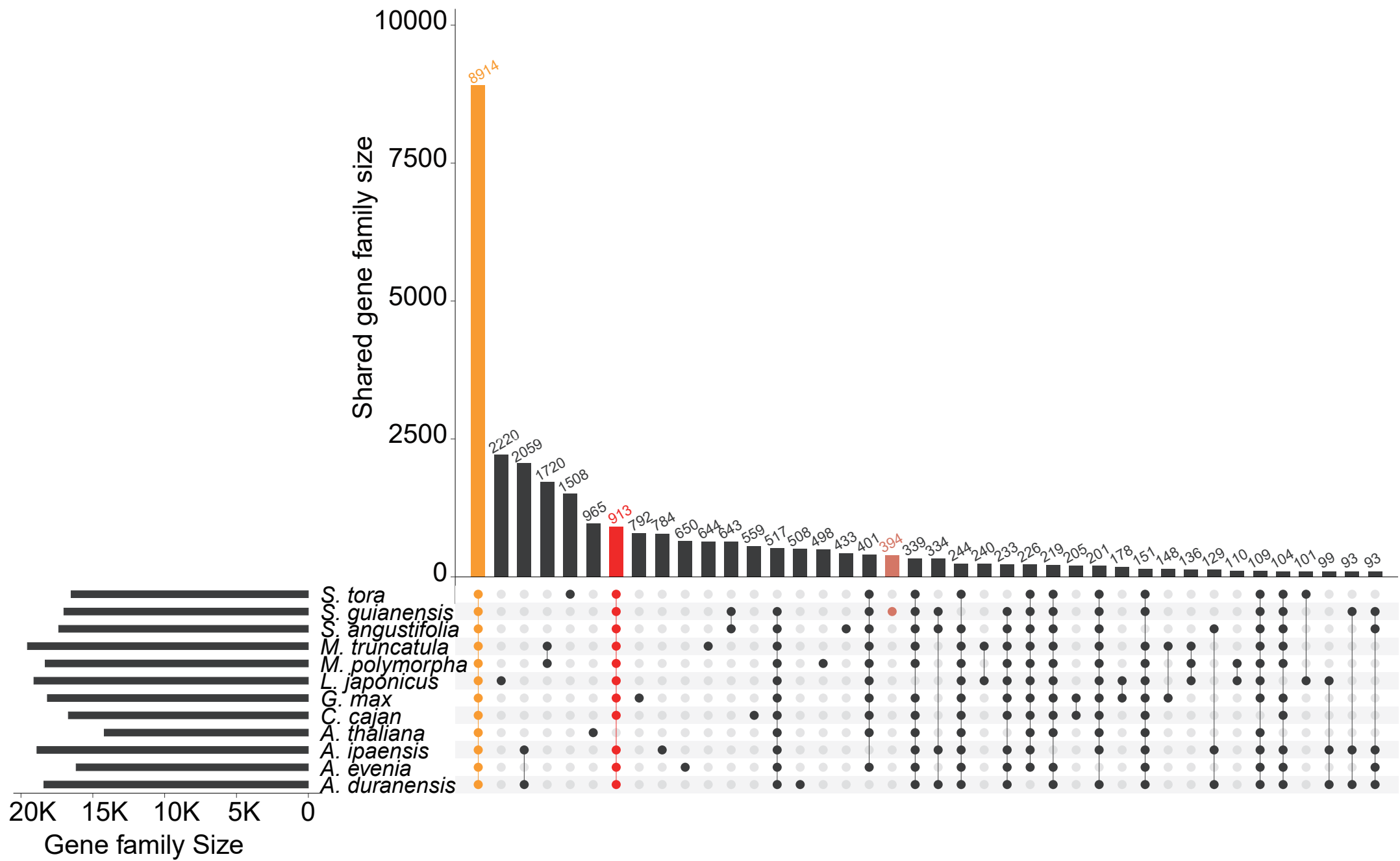


Figure S13. Upset plot illustrating the distribution of ortholog groups (OGs) among 11 legume plants and *A. thaliana*.

Tree scale: 0.1

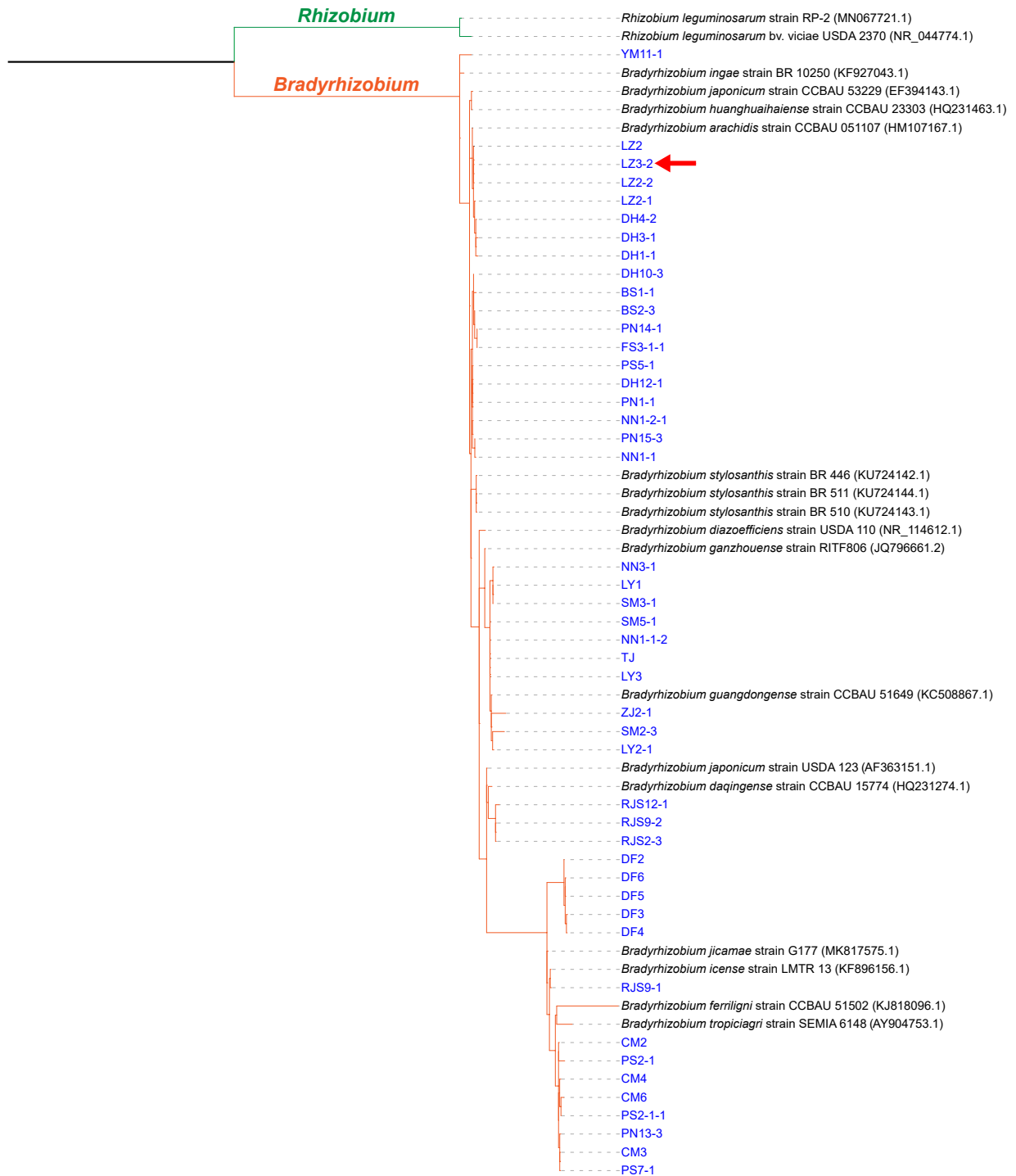


Figure S14. Phylogenetic tree analysis of bacteria isolated from the nodules of *S. guianensis* using 16S rRNA gene sequences. The red arrow indicates the *Bradyrhizobium* strain LZ3-2 used for inoculating *S. guianensis* in the field experiment.

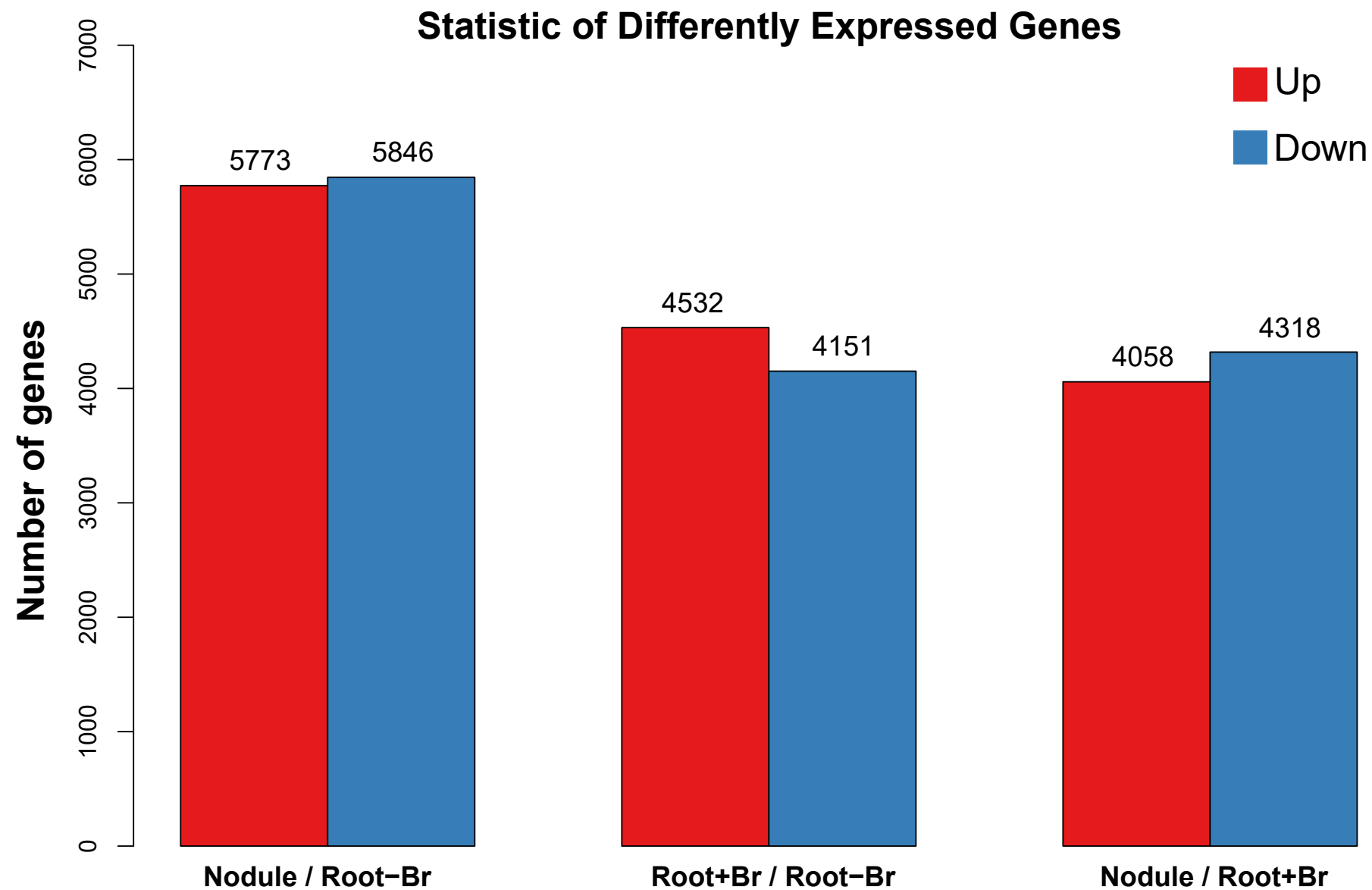


Figure S15. Number of DEGs in pairwise comparisons among nodules, root-Br, and root+Br groups of *S. guianensis*.

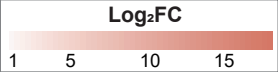
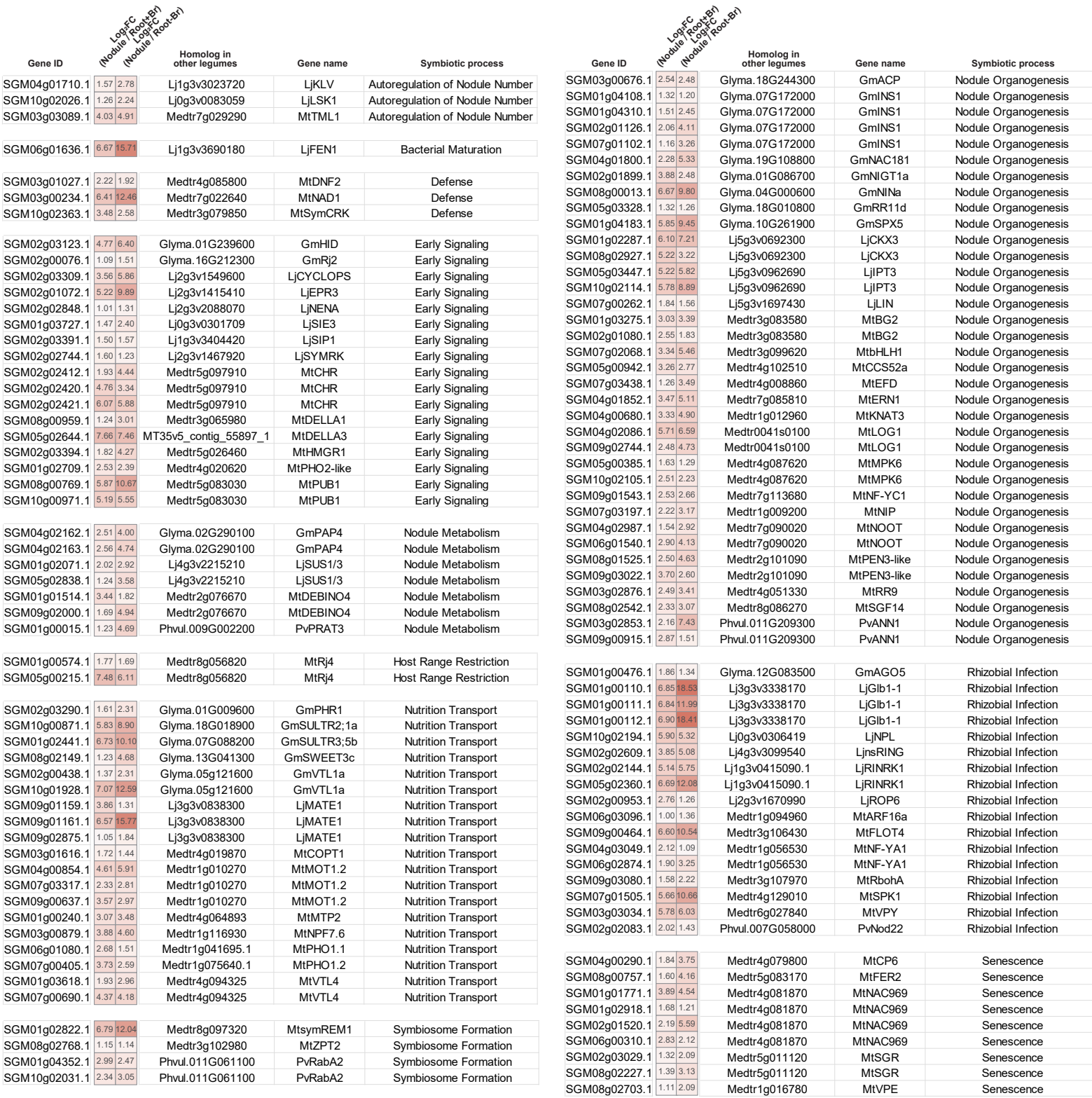


Figure S16. Heatmap of SNF genes upregulated in nodules relative to both root–Br and root+Br groups.

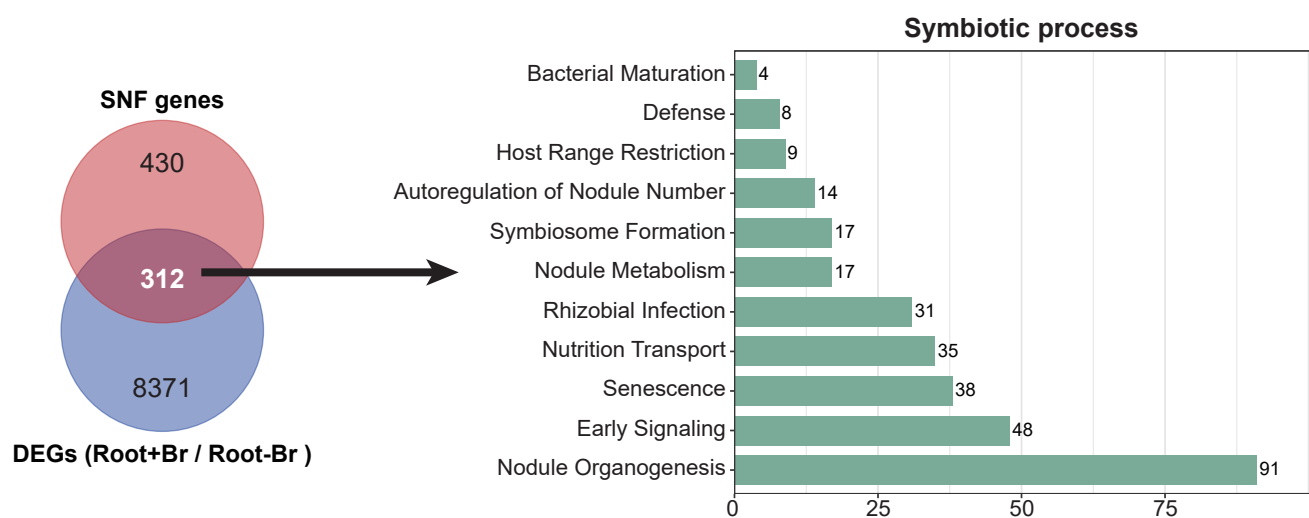


Figure S17. Venn diagram showing the overlap between SNF genes and DEGs in the root+Br group relative to the root–Br group.

Tree scale: 0.1

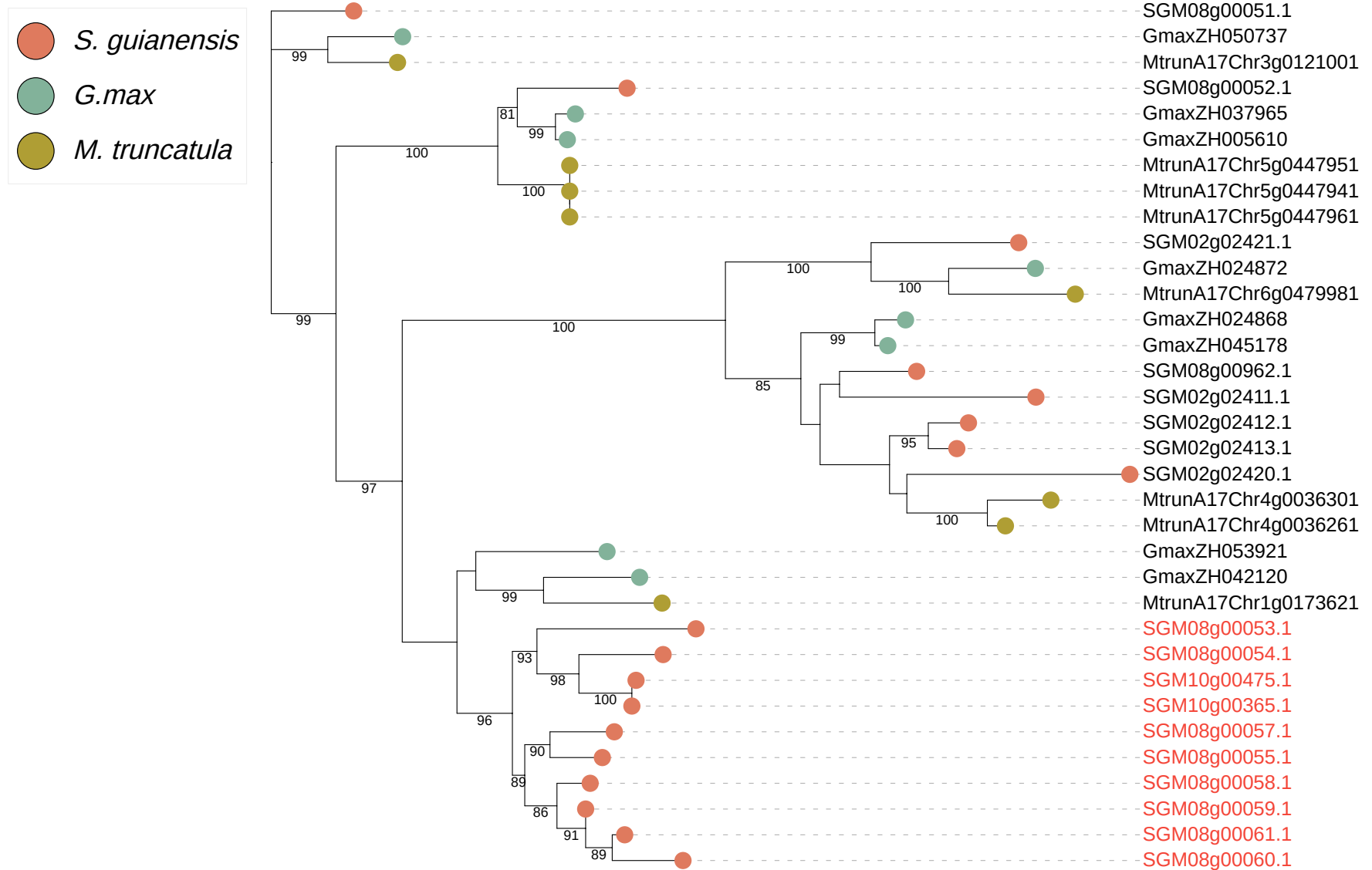


Figure S18. Phylogenetic tree of CHR family members from *S. guianensis*, *G. max*, and *M. truncatula*.

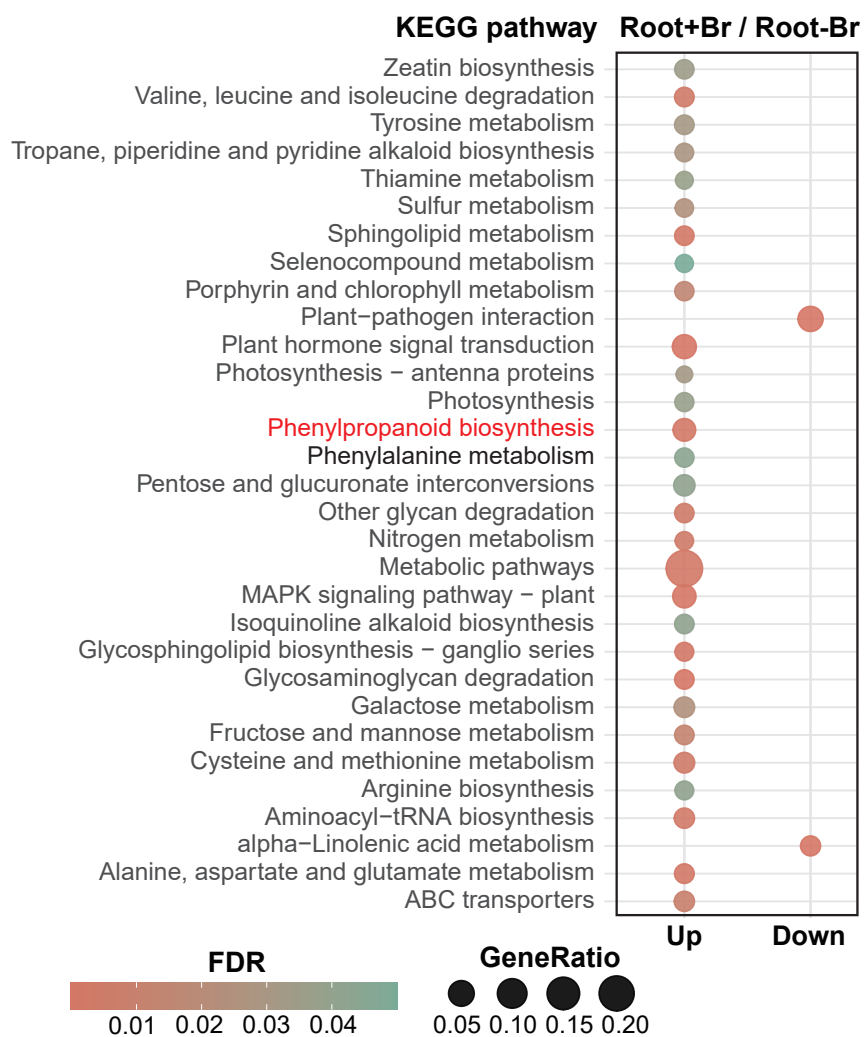


Figure S19. Significantly enriched KEGG pathways in DEGs between root+Br and root-Br groups.

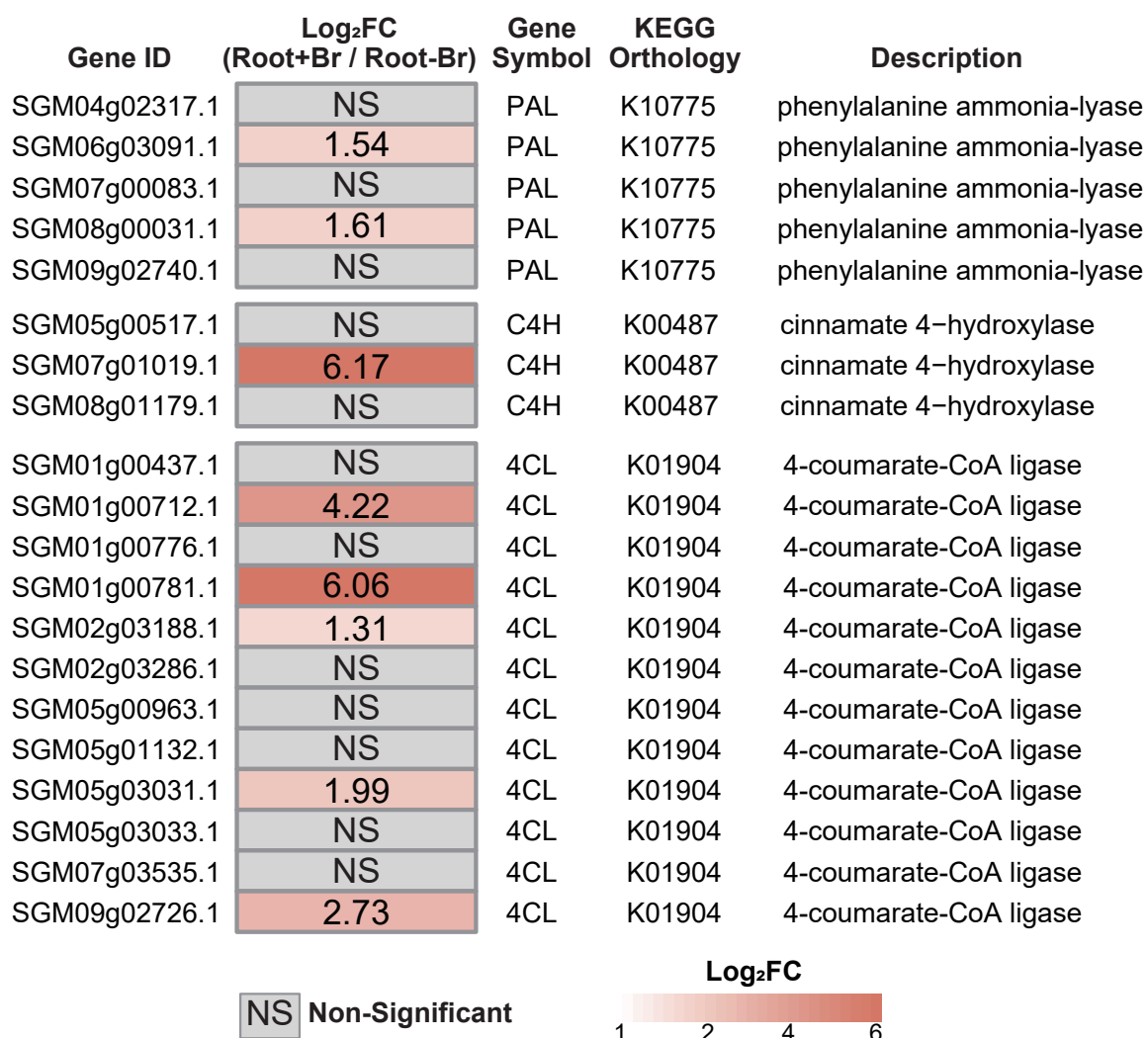


Figure S20. Heatmap of differentially expressed *PAL*, *C4H*, and *4CL* genes between the root+Br and root–Br groups.

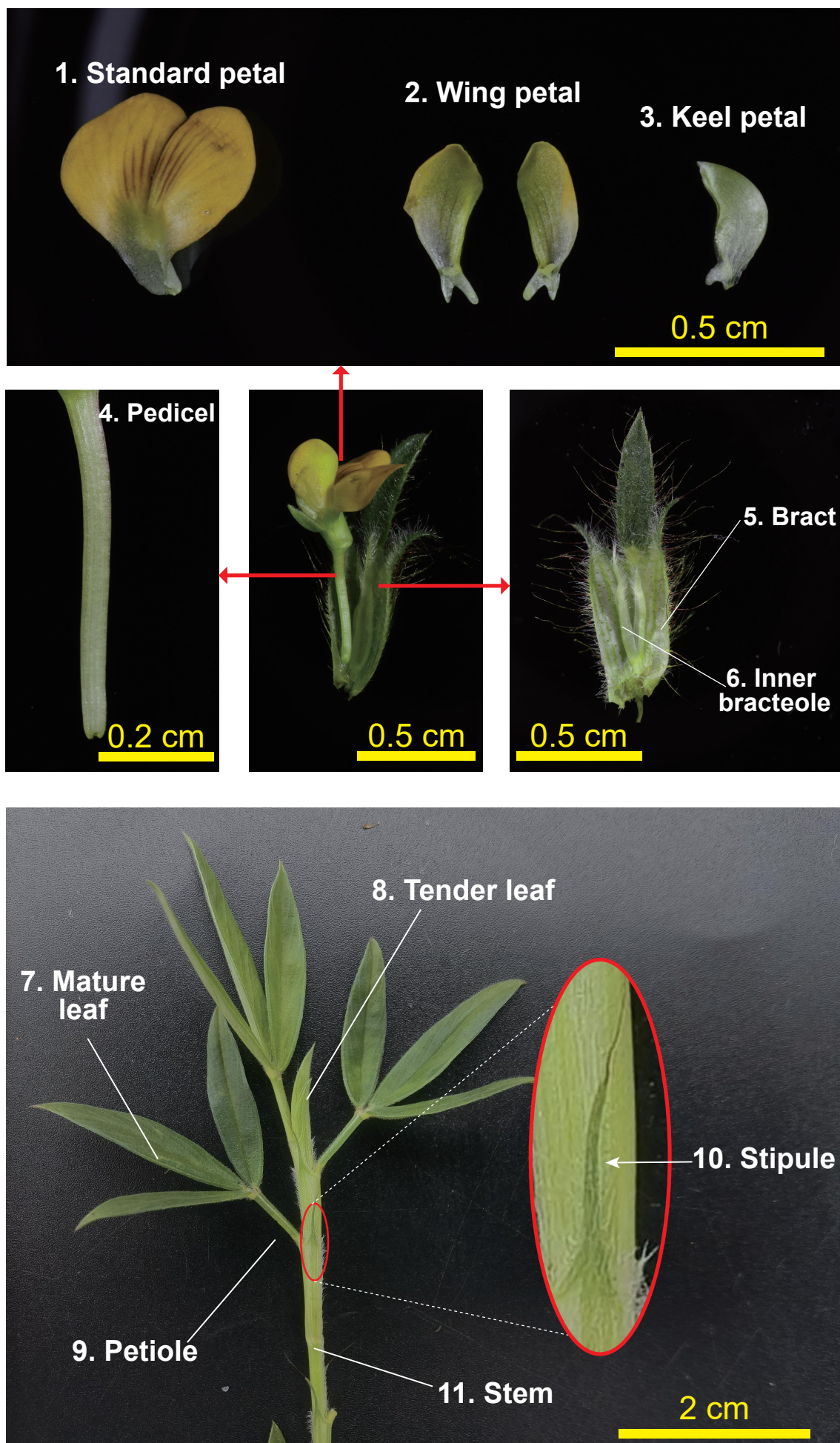


Figure S21. Photographs of different tissue parts of *S. guianensis* collected for transcriptome sequencing.

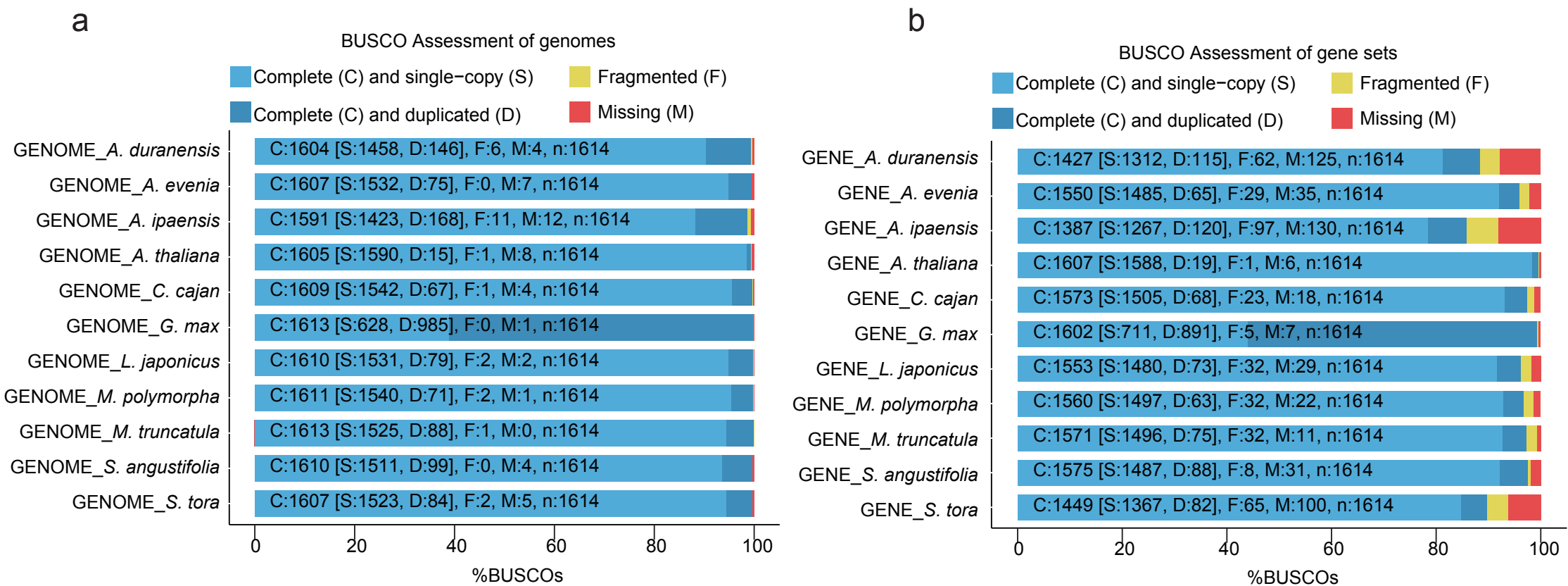


Figure S22. BUSCO completeness assessment of genome assemblies (a) and annotated gene sets (b) across eleven species in the comparative genomic analysis.