

Supplementary Figures

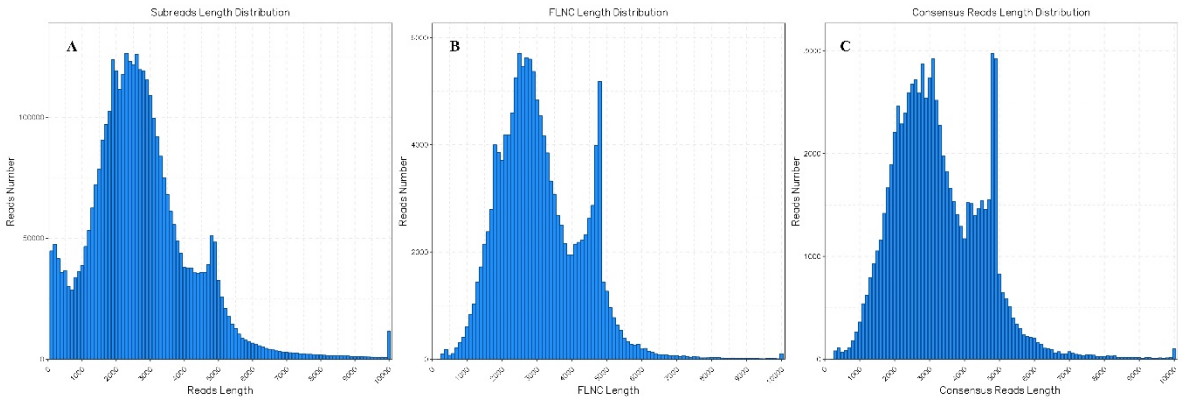


Figure S1. Length distribution of subreads (A), flnc (B) and consensus reads (C). x-axis represents the length, y-axis represents read numbers.

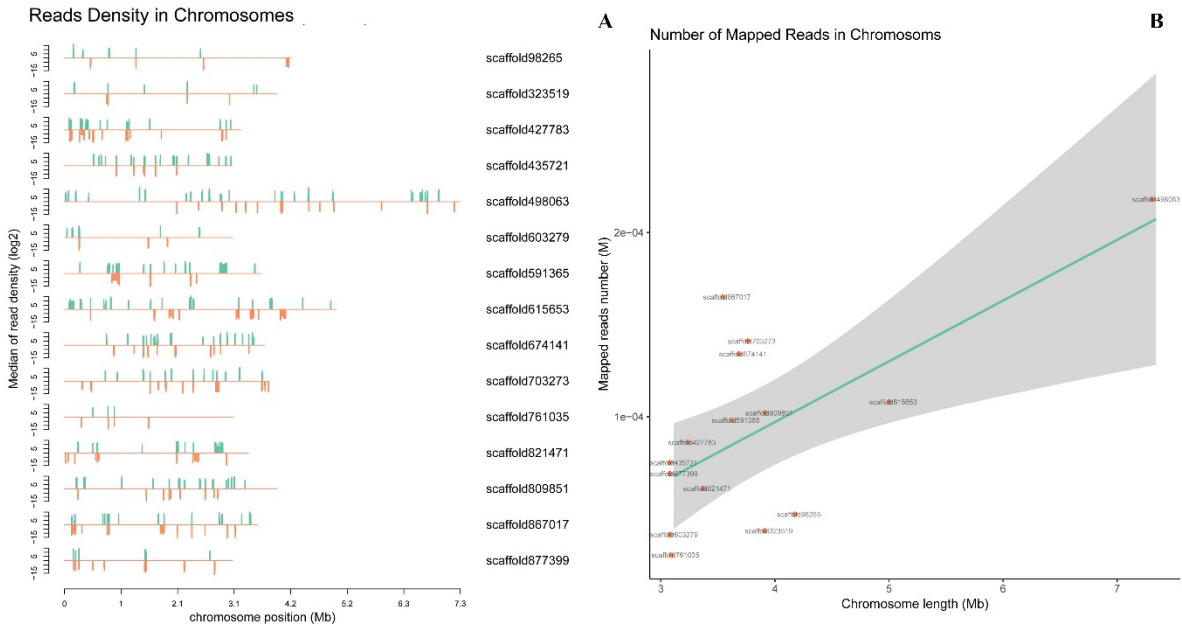


Figure S2. Number and density of mapped reads in several scaffolds. (A) Mapped reads density in scaffold, x-axis represents the scaffold position (Mb), y-axis represents the median of read density (log2), green and red vertical lines represent the positive strands and negative strands, respectively; (B) Number of mapped reads in several scaffolds, x-axis represents the scaffold position (Mb), y-axis represents numbers of mapped reads, the grey area shows the a confidence interval of 95%.

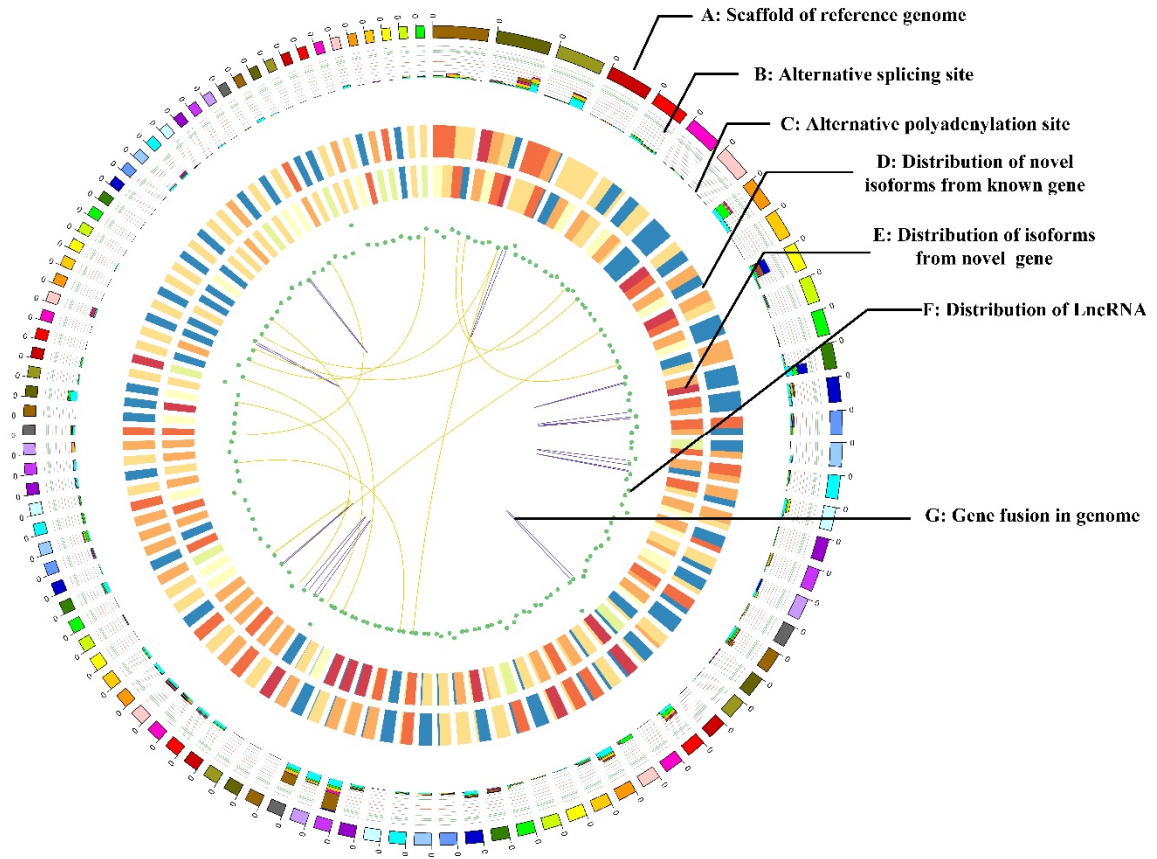


Figure S3. Visualization of Sequel sequencing data at the genome-wide level. (A) Scaffolds of the reference genome of *G. luofuense*, (B) Alternative splicing sites on the reference genome, different color represent varied types of alternative splicing events; (C) Alternative polyadenylation sites; (D) Distribution of novel isoforms from known genes, the red color represents the high density; (E) Distribution of isoforms from novel genes, the red color represents the high density; (F) Distribution of lncRNAs; (G) Gene fusion events detected on the reference genome.

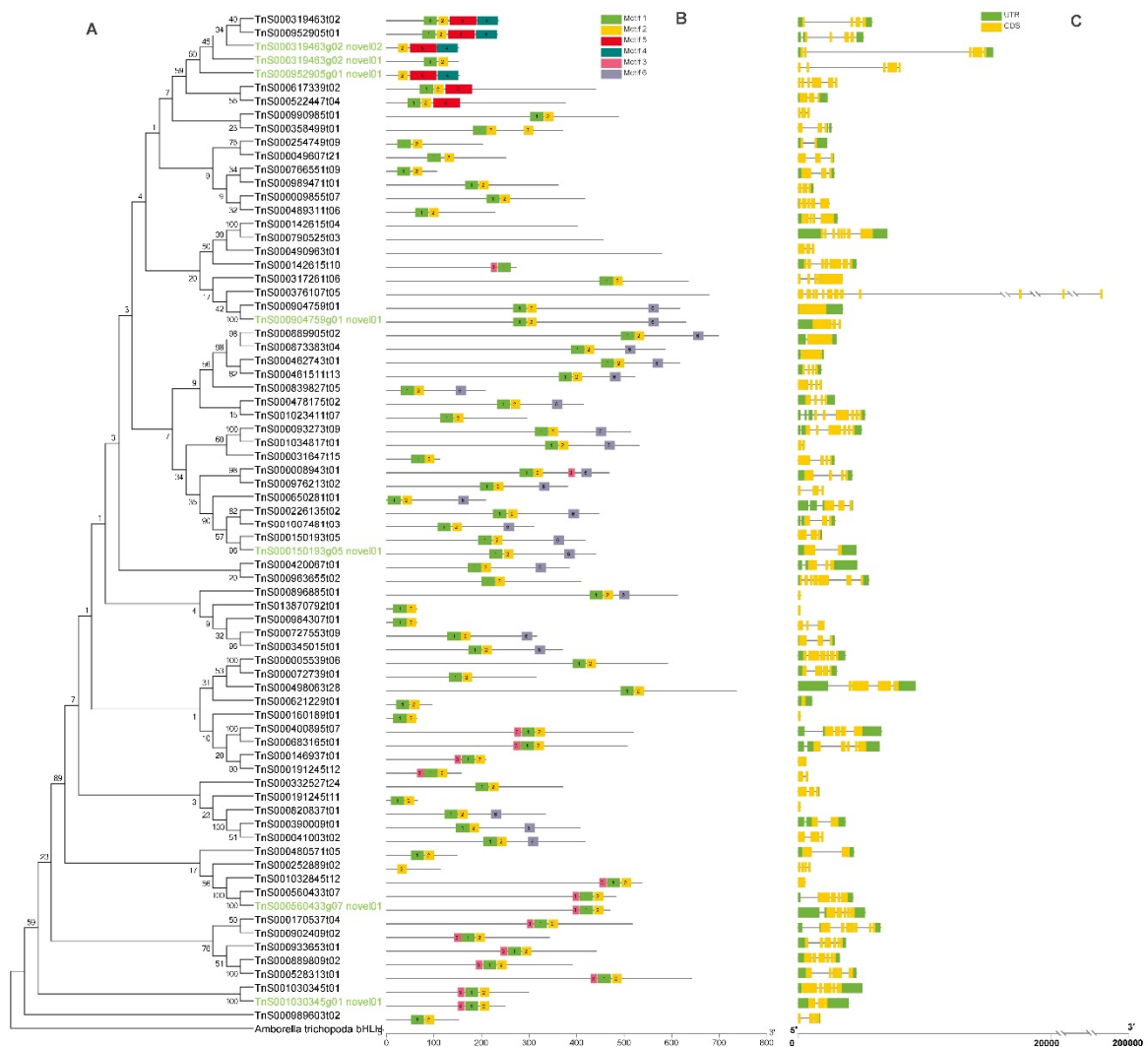


Figure S4. Gene structure, motif and phylogenetic analysis of *bHLH* genes. (A) The phylogenetic tree of the proteins constructed using the neighbour-joining method; (B) conserved motifs in *bHLH* gene; (C) Gene structures of *bHLH* genes.

Supplementary Files

File S1. List of isoforms from novel genes in *Gnetum* leaves.

File S2. List of the predicted lncRNAs.

File S3. Results of poly(A) prediction.

File S4. List of *bHLH* gene family identified in *Gnetum* genome and leaf transcriptome.