

# **Chromosome-Level Assembly and Comparative Genomic Analysis of *Suillus bovinus* Provides Insights into the Mechanism of Mycorrhizal Symbiosis**

Jinhua Zhang <sup>1,2</sup>, Mengya An <sup>1</sup>, Yanliu Chen <sup>1</sup>, Shengkun Wang <sup>1</sup>, Junfeng Liang <sup>1,\*</sup>

1 Research Institute of Tropical Forestry, Chinese Academy of Forestry,

Guangzhou 510520, China

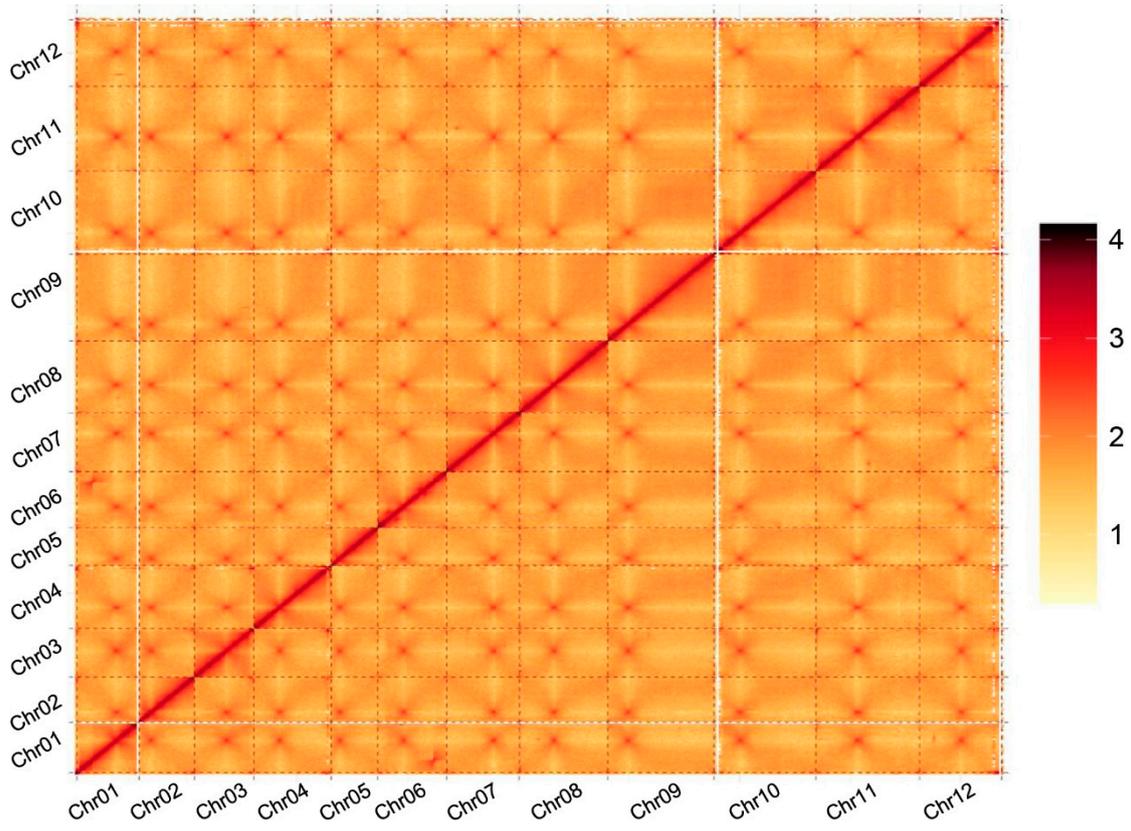
2 College of Forestry, Nanjing Forestry University, Nanjing 210037, China

\* Corresponding author:

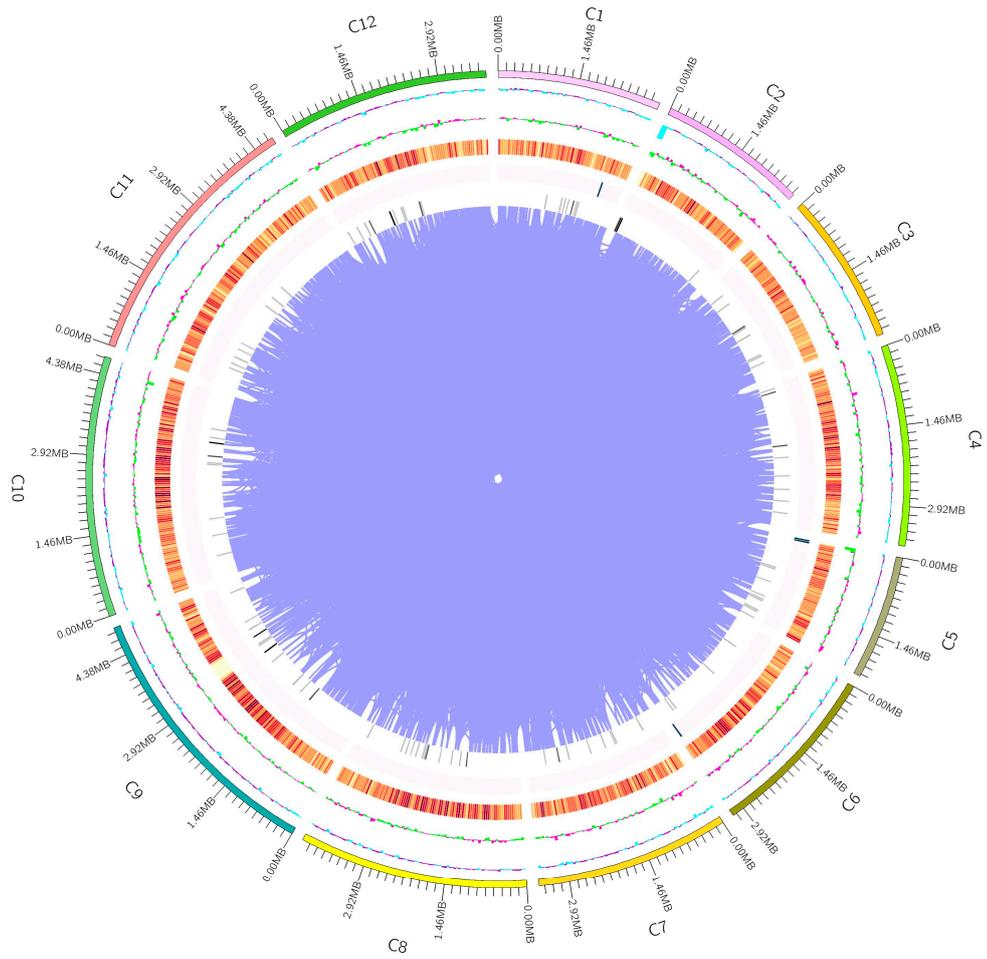
Junfeng Liang, E-mail: [jfliang2000@163.com](mailto:jfliang2000@163.com).

Mailing address: Research Institute of Tropical Forestry, Chinese Academy of Forestry,

Guangzhou 510520, China.

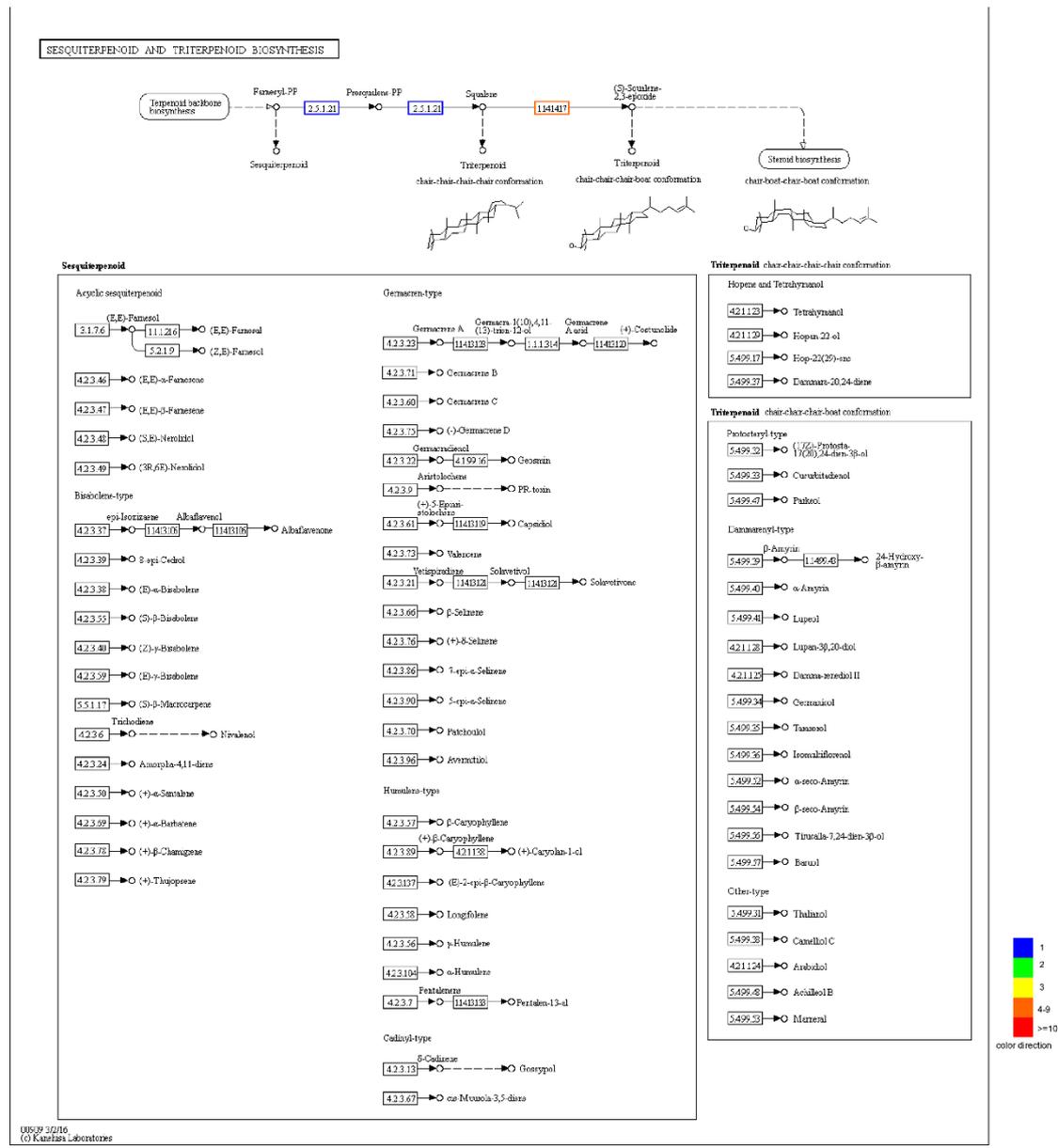


**Figure S1.** Hi-C contact heatmap for *S. bovinus*.



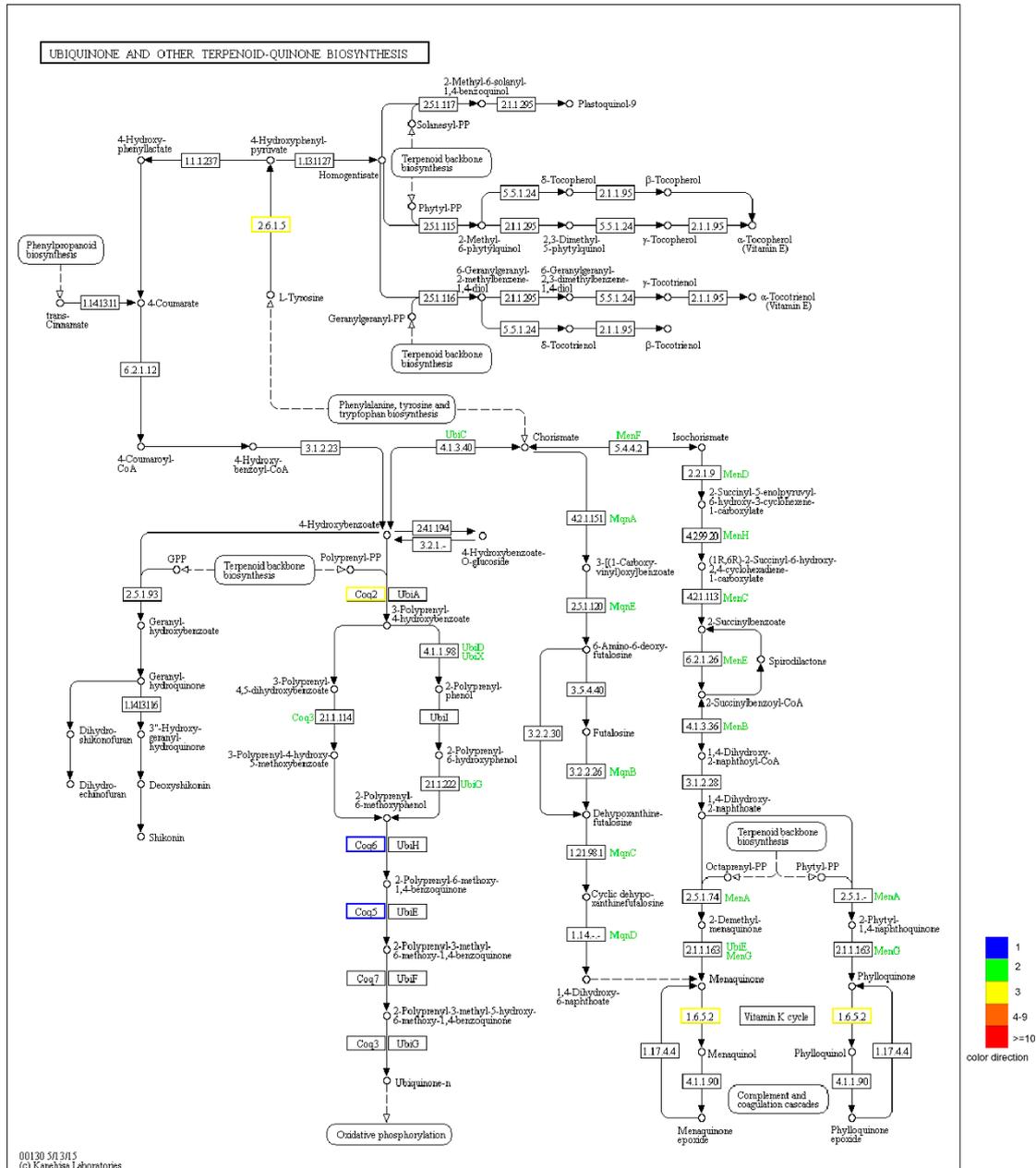
**Figure S2.** The circular genome diagram of *S. bovinus*.





**Figure S4.** Sesquiterpenoid and triterpenoid biosynthesis pathway of *S. bovinus*.

Note: The different colors of the boxes indicate the number of corresponding genes. Blue represents 1 gene, green represents 2 genes, yellow 4-9 genes, and red represents more than 10 genes, while white means not.



**Figure S5.** Ubiquinone and other terpenoid quinone biosynthesis pathway of *S. bovinus*.

Note: The different colors of the boxes indicate the number of corresponding genes. Blue represents 1 gene, green represents 2 genes, yellow 4-9 genes, and red represents more than 10 genes, while white means not.