

# Survey of the genome of *Pogostemon cablin* provides insights into its evolutionary history and sesquiterpenoid biosynthesis

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1. Supplementary Tables S1-S7 were submitted as ‘Supplementary Dataset’ in the manuscript tracking system:

Table S1. Statistics of the sequencing data.

Table S2. Length of organelle genomes of selected species.

Table S3. Statistics of reads mapping to plastid sequences.

Table S4. Statistics of reads mapping to the NCBI NT database.

Table S5. Statistics of sub-categories of repetitive sequences in the patchouli genome.

Table S6. Sesquiterpenoid biosynthesis reference pathway.

Table S7. Genes annotated to the sesquiterpenoid biosynthesis reference pathway.

2. Supplementary files related to gene annotation, including gff3 file and fasta files of coding sequences and protein sequences were submitted to [https://github.com/brentcaodeng/patchouli\\_genome\\_survey/tree/master/01.Annotation](https://github.com/brentcaodeng/patchouli_genome_survey/tree/master/01.Annotation)