

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: The volatile content at different stages of flowering (F1-F5).

File name: Supplementary Data 2

Description: The volatile profiles of “Hutou” jasmine at different flowering stages (F1-F5) analyzed using headspace solid-phase microextraction (HS-SPME) coupled with gas chromatography-mass spectrometry (GC-MS).

File name: Supplementary Data 3

Description: The statistics of significantly differential volatiles (SDVs) in F1 vs. F2 and F1 vs. F3 comparison groups.

File name: Supplementary Data 4

Description: The statistics of significantly differential volatiles (SDVs) in F1 vs. F2 and F1 vs. F3 comparison groups.

File name: Supplementary Data 5

Description: The 16 predominant SDVs during “Hutou” jasmine flowering.

File name: Supplementary Data 6

Description: The transcriptome data of 15 flower samples of “Hutou” jasmine.

File name: Supplementary Data 7

Description: The candidate genes involved in terpene biosynthesis (MVA and MEP pathways) in “Hutou” jasmine genome.

File name: Supplementary Data 8

Description: The candidate genes involved in terpene biosynthesis (MVA and MEP pathways) in “Hutou” jasmine genome.

File name: Supplementary Data 9

Description: The candidate genes involved in terpene biosynthesis (MVA and MEP pathways) in “Hutou” jasmine genome.

File name: Supplementary Data 10

Description: The candidate genes involved in the phenylpropanoids/benzenoids synthesis in “Hutou” jasmine genome.

File name: Supplementary Data 11

Description: The correlation between 20 terpenoids SDVs and 31 terpene biosynthesis-related genes in subclass 4, 6, and 9.

File name: Supplementary Data 12

Description: The correlation between terpene biosynthesis-related genes and 142 transcription factors in subclass 4, 6, and 9.

File name: Supplementary Data 13

Description: The annotation of 237 genes in magenta module in WGCNA analysis.