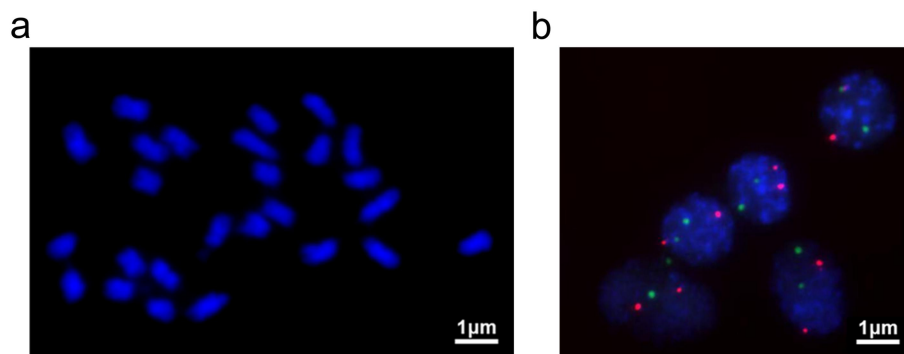
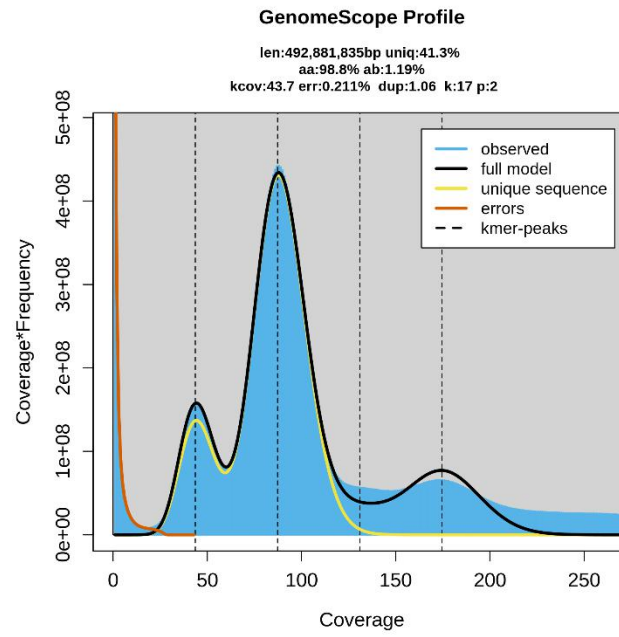
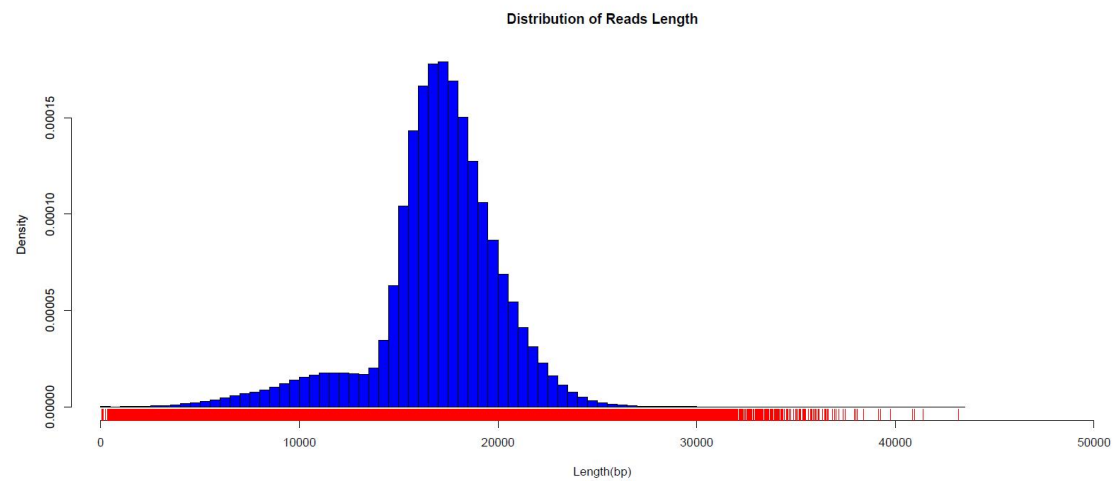




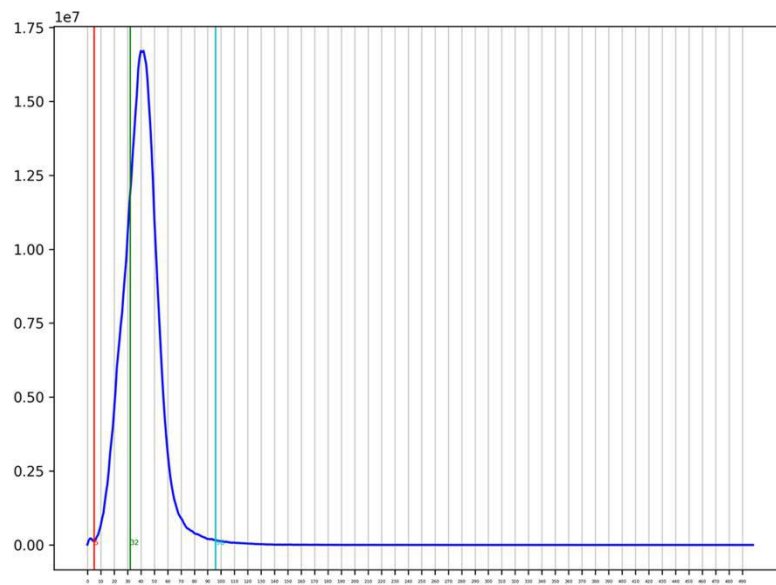
Supplementary Figure 1. Cytological analysis of “Hutou” jasmine chromosomes in root tip cells. **a** The karyotype analysis of chromosomes. **b** The karyotyping based on 5S and 45S rDNA fluorescence in situ hybridization (FISH). The 5S (in red) and 45S rDNA (in green) probes were detected on chromatids of interphase nucleus. The chromosomes were counterstained with DAPI (blue). Scale bar, 1 μm .



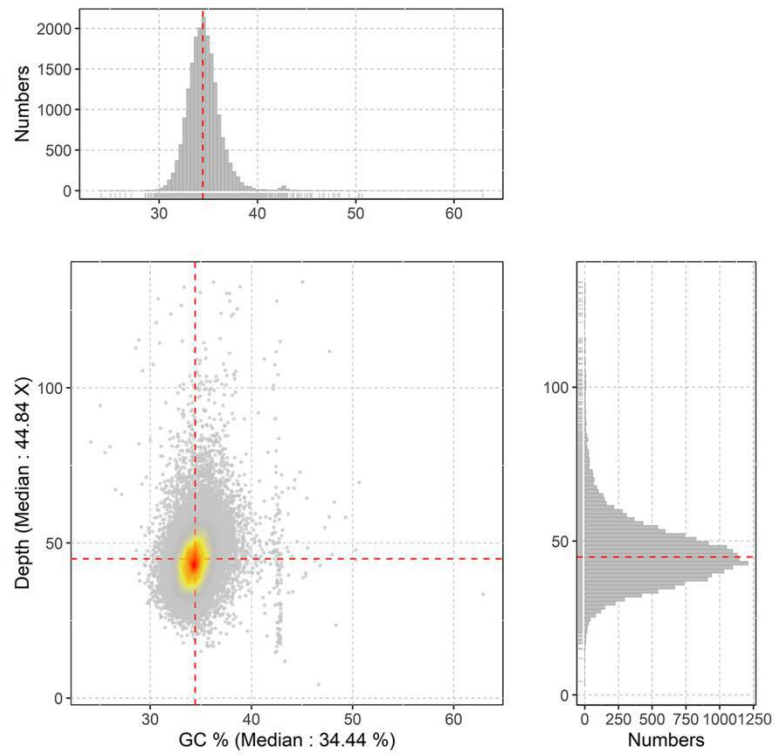
Supplementary Figure 2. Evaluation of the genome size of “Hutou” jasmine by 17-mer analyses based on Illumina short reads. The x-axis represents the sequencing depth and the y-axis represents the frequency of the 17-mer at a given sequencing depth.



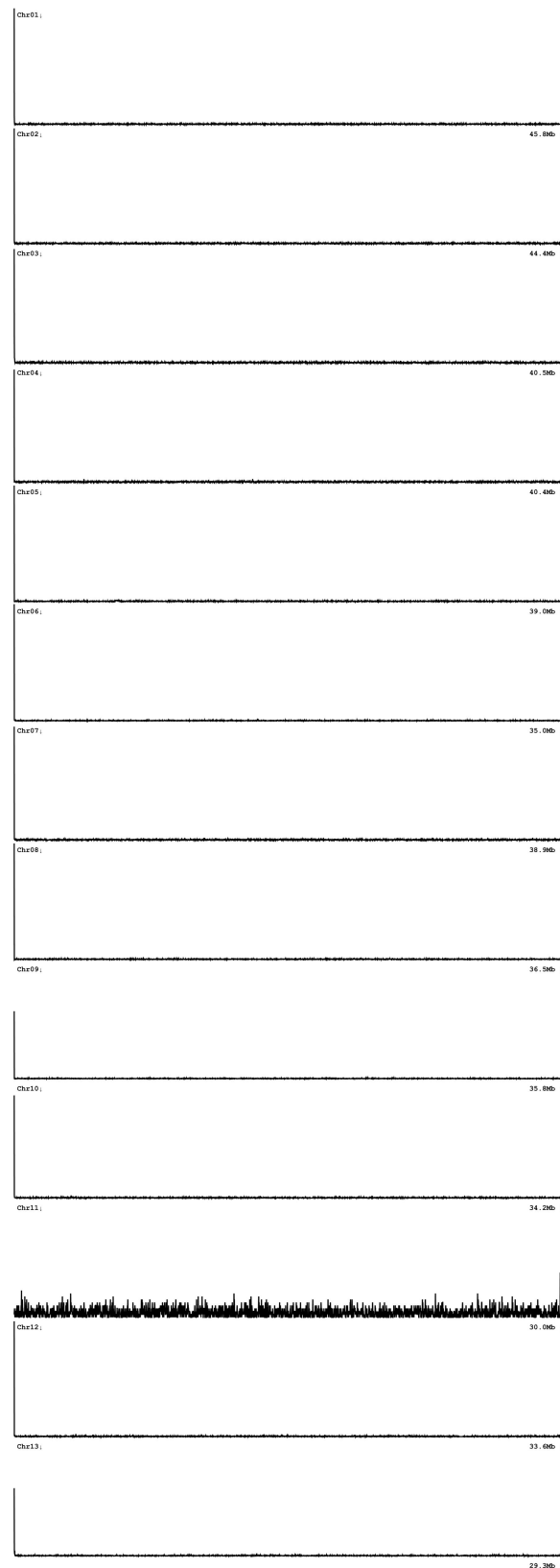
Supplementary Figure 3. The frequency plot of the distribution of HiFi reads. The x-axis and y-axis indicate the frequency distribution of sequence length and number, respectively.



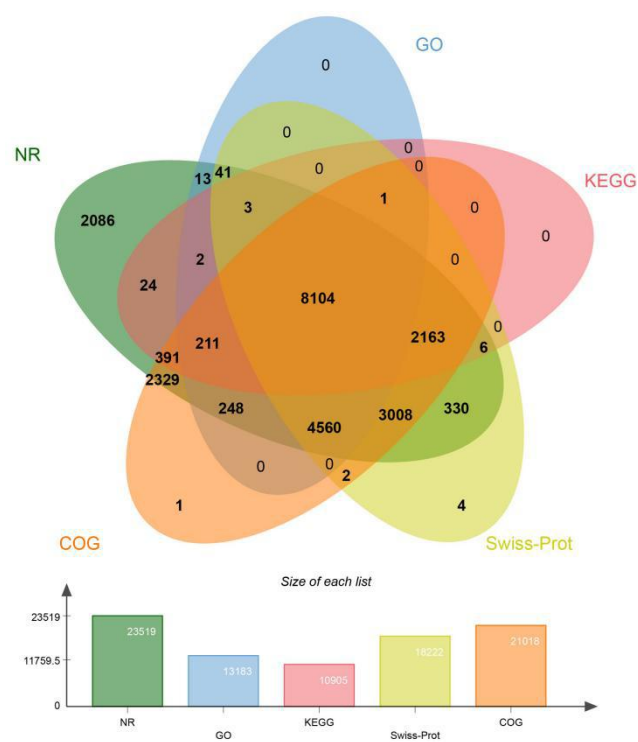
Supplementary Figure 4. The read depths on the final contig assembly that was de-dupped by purge-dups.



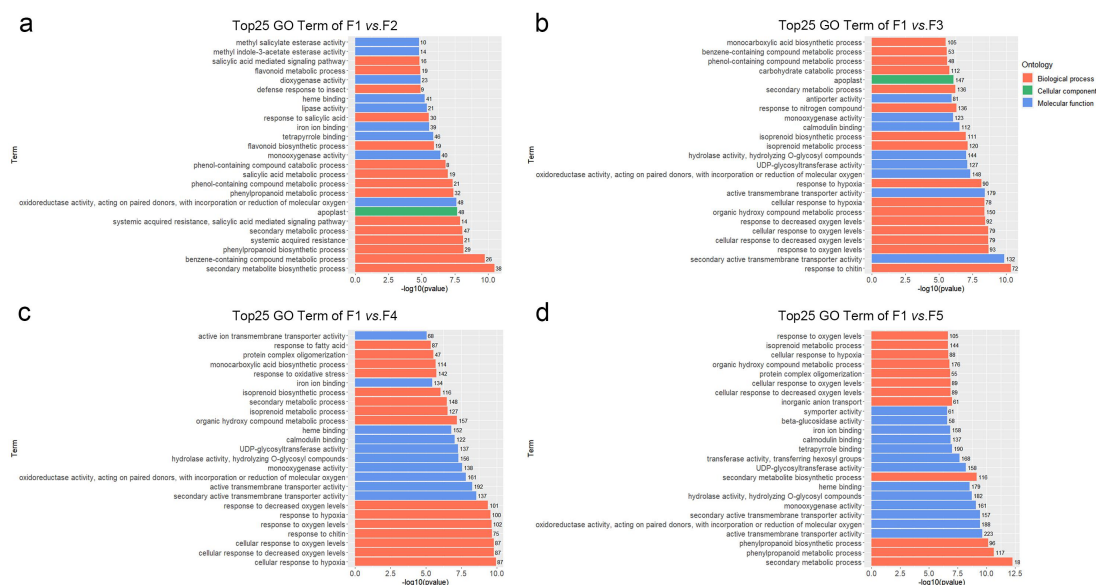
Supplementary Figure 5. The GC depth distribution of “Hutou” genome. The horizontal axis represents GC content (%), and the vertical axis represents depth.



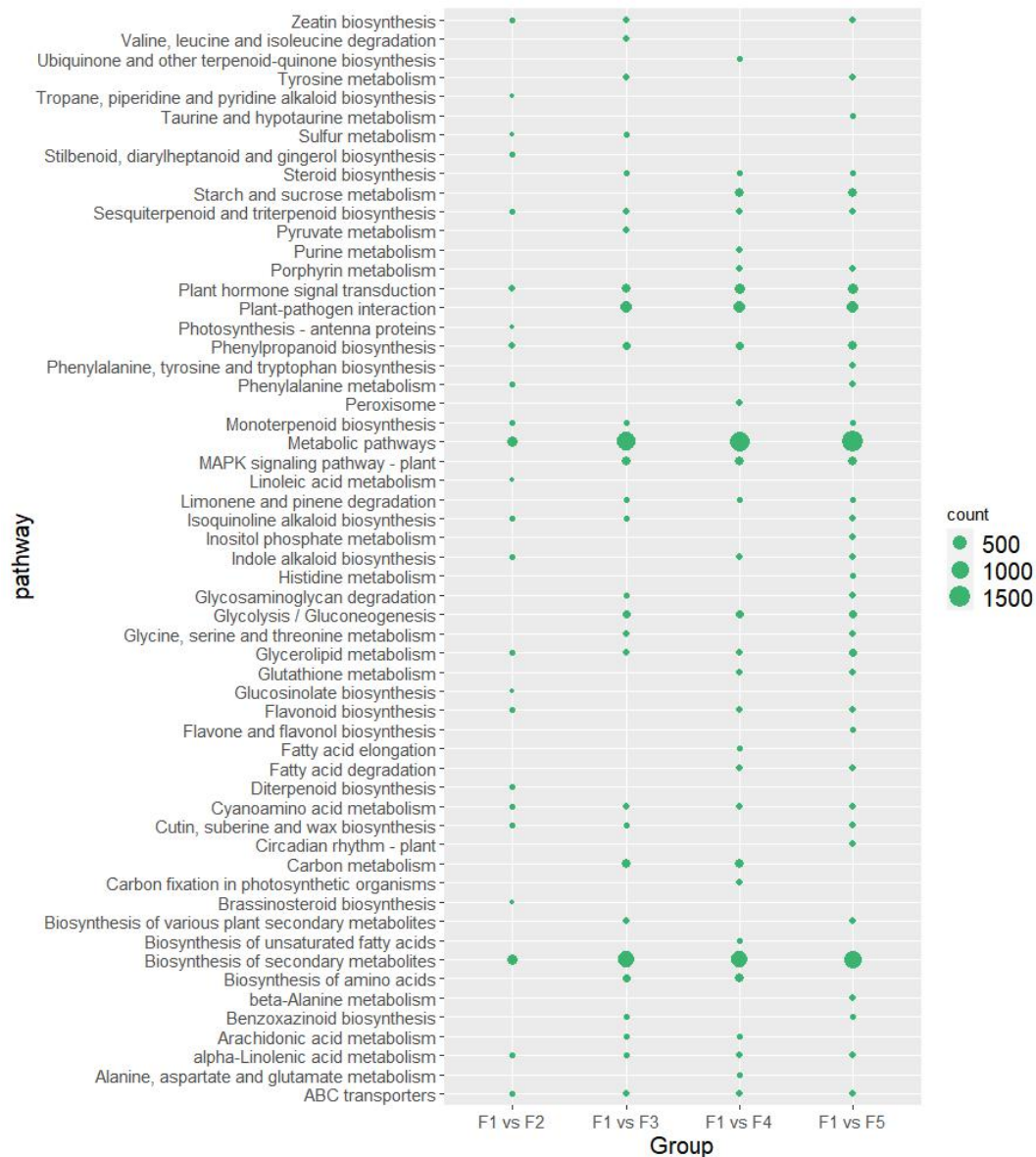
Supplementary Figure 6. The telomere repeats of chromosomes (11/13) in “Hutou” jasmine genome plotted by TIDK.



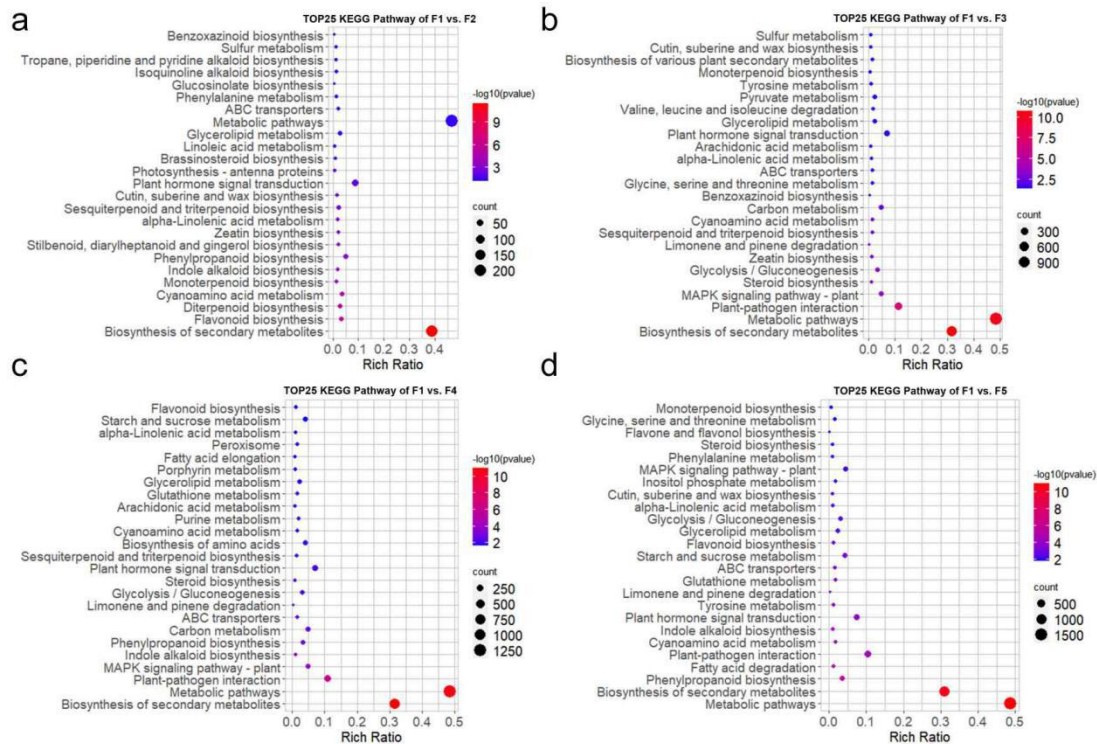
Supplementary Figure 7. The Venn diagram of gene functional annotation for each database of “Hutou” jasmine.



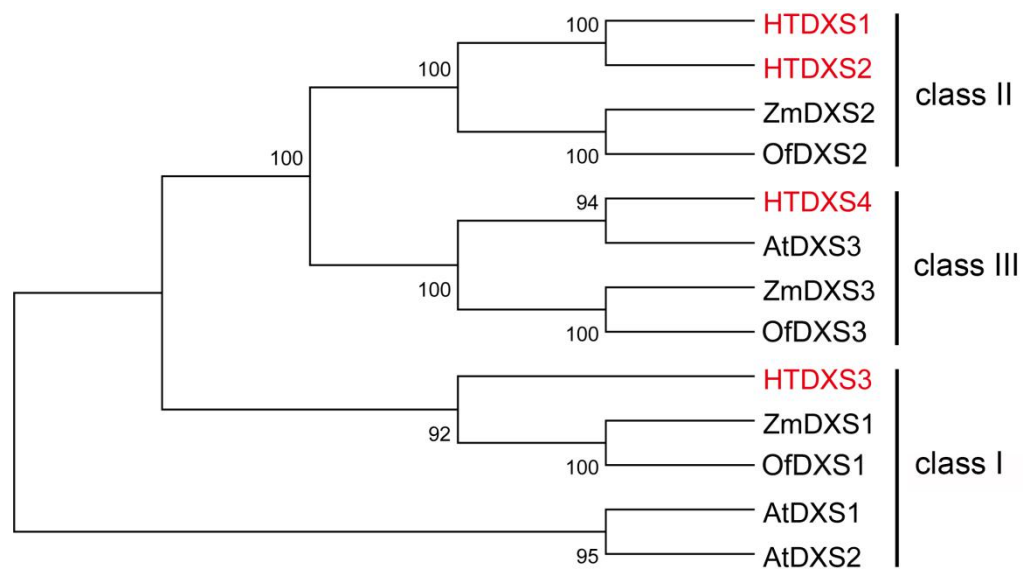
Supplementary Figure 9. The GO enrichment of differentially expressed genes (DEGs) between different pairs of groups. a F1 vs. F2, **b** F1 vs. F3, **c** F1 vs. F4, and **d** F1 vs. F5. F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. The red, green, and blue represent the three major GO categories: biological process, cellular component, and molecular function, respectively. The horizontal axis represents the significance, while the vertical axis represents secondary GO terms. The numbers indicate the count of DEGs associated with each GO term.



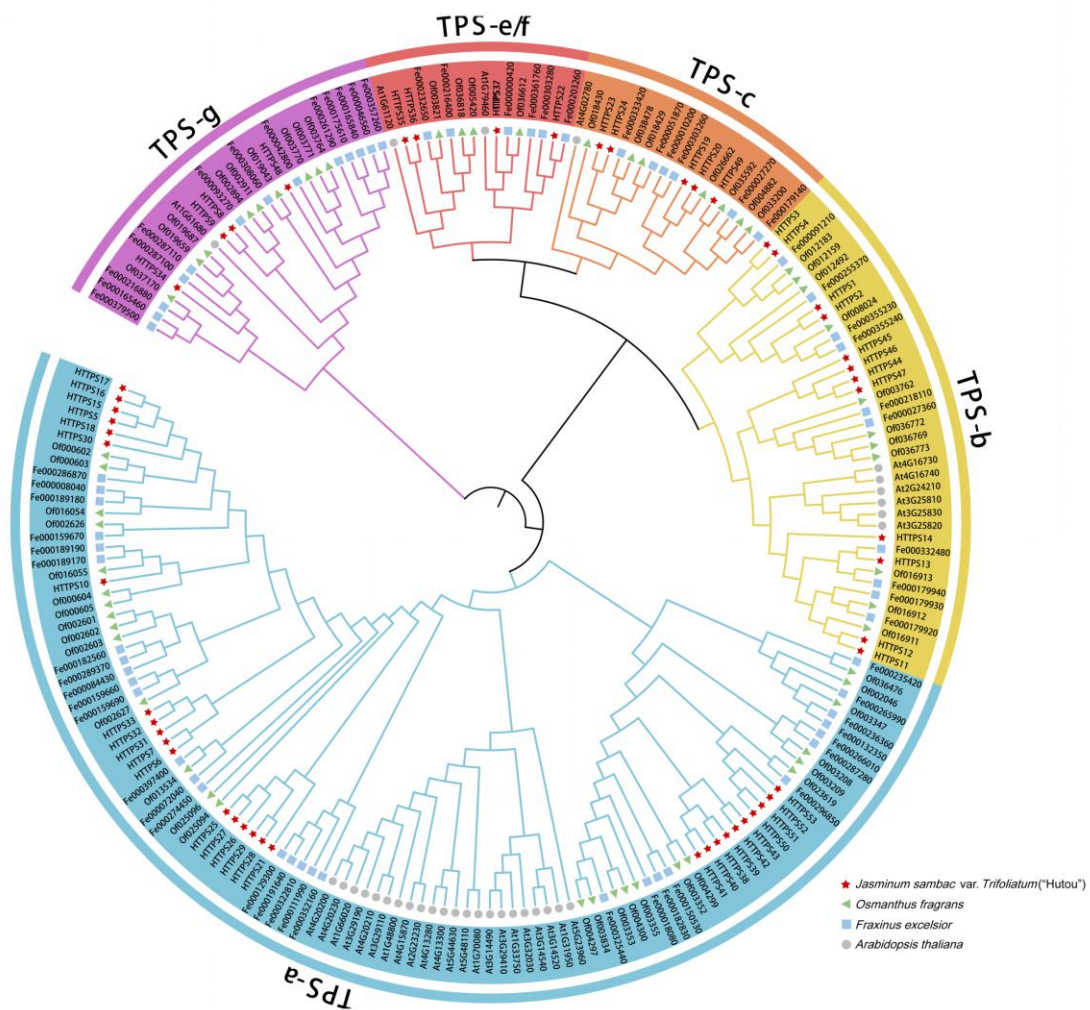
Supplementary Figure 10. The KEGG enrichment analysis of differentially expressed genes (DEGs) in four comparison sets. F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. A total of 57 significantly different metabolic pathways ($P < 0.05$) are shown in the diagram. The size of the bubble represents the number of DEGs in the pathway.



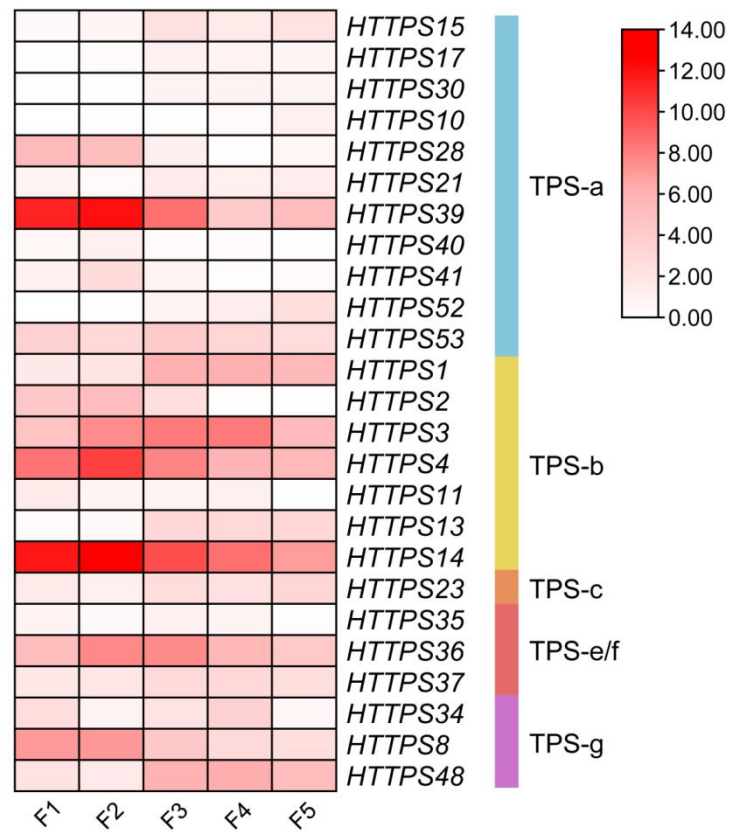
Supplementary Figure 11. The top 25 KEGG pathways of differentially expressed genes (DEGs) in four different comparison groups. a F1 vs. F2, b F1 vs. F3, c F1 vs. F4, and d F1 vs. F5. F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. The y-axis represents KEGG pathways and the x-axis indicates the rich ratio. The rich ratio is the ratio of the number of genes associated with the pathway in the DEGs to the number of genes linked to the pathway in the whole genome. Bubble size represents the number of DEGs in the pathway and color indicates the significance of pathway enrichment.



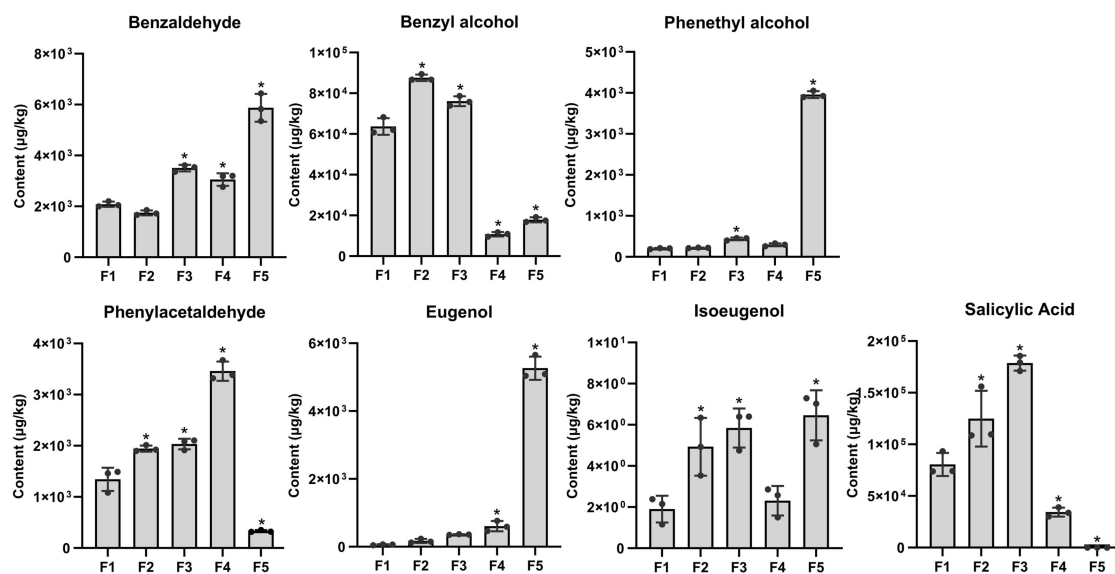
Supplementary Figure 12. The phylogenetic relationship of “Hutou” jasmine DXS protein sequences (HTDXSs), *Arabidopsis thaliana* DXSs (AtDXSs), *Zea mays* (ZmDXSs), and *Osmanthus fragrans* (OfDXSs). All DXS protein sequences are divided into three classes (class I, II, and III).



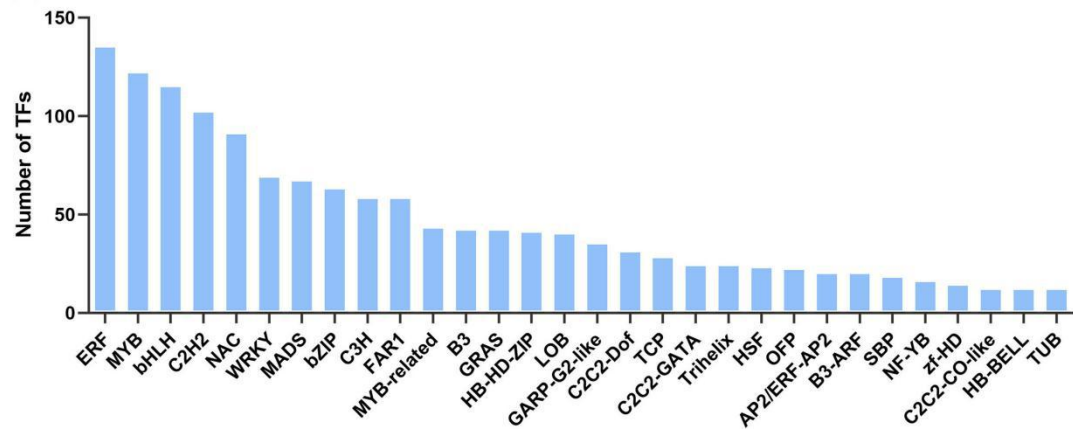
Supplementary Figure 13. Phylogenetic analysis of TPS protein sequences in “Hutou” jasmine and three other Oleaceae species. The full-length amino acid sequences of “Hutou” jasmine (*Jasminum sambac* var. *Trifoliatum*) (53), *Arabidopsis thaliana* (32), *Osmanthus fragrans* (62), and *Fraxinus excelsior* (65) TPS protein sequences were compared using RAxML software to generate the ML phylogenetic tree with 1,000 bootstrap values. The iTOL was used to visualize the tree. Red stars, green triangles, blue squares and grey circles represent TPS proteins of four species, respectively. All TPS proteins are divided into five subgroups (TPS-a, b, c, e/f, and g).



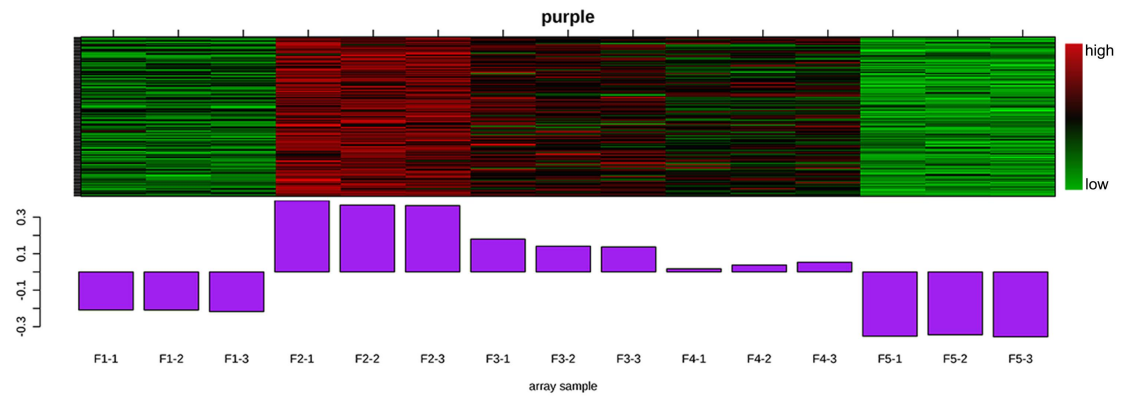
Supplementary Figure 14. The expression of *TPS* genes at five different flowering stages. F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. These genes were expressed in at least one of the five flowering stages. The different colors indicate different subfamilies. The gradient color for each gene represents the gene expression levels.



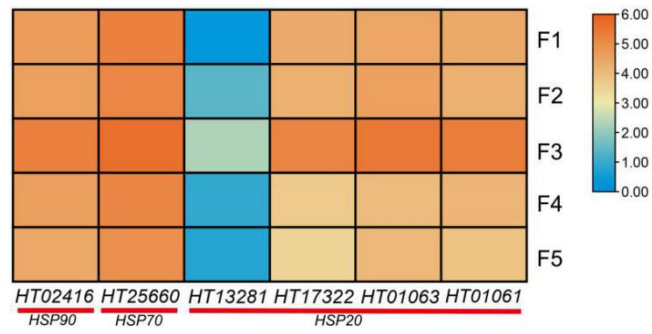
Supplementary Figure 15. The histogram of other seven phenylpropanoids identified in “Hutou” jasmine flowers at five flowering stages. The x-axis represents different flowering periods and the y-axis indicates the relative content (μg/kg) of phenylpropanoid compounds. F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. Data are represented as means±standard deviations (SD), and “*” indicates significant difference (P -value≤0.05) compared to F1.



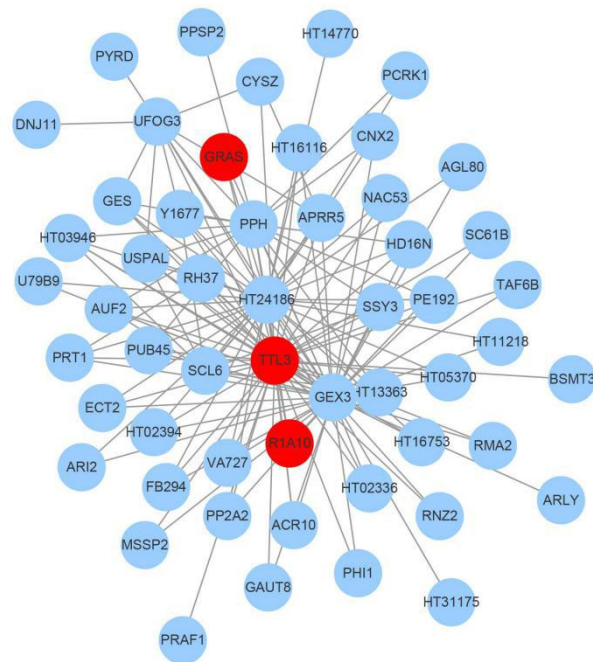
Supplementary Figure 16. Statistics of transcription factor (TF) families identified in the “Hutou” jasmine genome. The x-axis represents different TF families and the y-axis indicates the number of TFs.



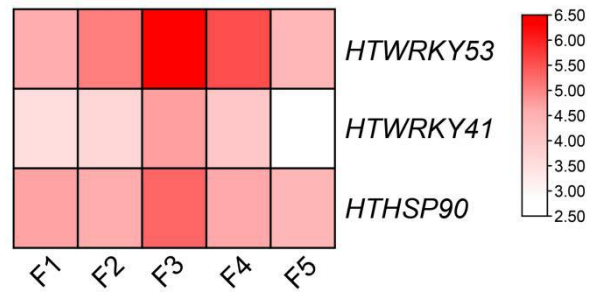
Supplementary Figure 17. Expression heatmap and consensus profile of co-expressed genes in the MEpurple module. The upper section displays a clustered heatmap of genes within the module (red and green represent high and low expression, respectively), while the lower section represents the expression pattern of the module eigengene across different samples.



Supplementary Figure 18. The expression pattern of six HSP family genes in magenta module across different flowering stages (F1-F5). F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. The expression levels ranging from low to high are represented by colors from blue to orange.



Supplementary Figure 19. The hub genes subnetwork (top 150 genes) in the MEpurple module visualized by Cytoscape (v 3.10.2). The red solid points indicate the key hub genes.



Supplementary Figure 20. The expression of hub genes in magenta module across different flowering stages (F1-F5). F1, flower at the closed bud stage; F2, flower starts opening; F3, flower fully opening; F4, flower starts senescence; F5, withered flower stage. The gradient color for each gene represents the gene expression levels.

Supplementary Table 1. Sequencing data statistics of "Hutou" jasmine

Library	Tissue	Read number	Base (Gbp)	Depth	Q20 (%)	Q30 (%)
Hi-C	Leaf	354,823,470	53.13	109	97.83	93.49
DNA-seq	Leaf	345,331,888	51.80	106	96.78	91.53
HIFI	Leaf	1,273,938	21.68	44.49	97.86	95.09
RNA-seq	Flower	47,654,142	7.15		96.42	91.04
RNA-seq	Flower	51,101,704	7.70		96.49	91.15
RNA-seq	Flower	43,599,312	6.54		96.74	91.66
RNA-seq	Leaf	81,934,930	12.29		96.89	92.02
RNA-seq	Leaf	54,254,488	8.14		97.96	94.23
RNA-seq	Leaf	64,063,614	9.61		96.11	90.42

Supplementary Table 2. Genome assembly statistics of "Hutou" jasmine

Genomic feature	"Hutou" jasmine		
	initial	purged	chromosome
Total length of contigs	514,718,268	487,993,457	487,454,167
Total scaffolds	480	62	26
Number of contigs (>2 kb)	480	62	26
N90 (bp)	5,439,924	12,941,550	29,979,644
N80 (bp)	17,735,402	18,035,256	34,237,086
N70 (bp)	19,267,972	19,151,207	34,955,313
N60 (bp)	22,454,255	24,880,278	35,778,844
N50 (bp)	26,902,803	28,290,690	38,933,210
Average length (bp)	1,072,329	4,821,468	18,748,237
Maximum length (bp)	44,446,983	29,243,321	45,819,973
Minimum length (bp)	2,769	2,769	2,769
GC (%)	34.95	34.60	34.56

Supplementary Table 3. The results of high-throughput chromosomal conformation capture (Hi-C) assisted assembly for "Hutou" jasmine genome

Chromosome	Contig number	Size (bp)
Chr01	3	45,819,973
Chr02	2	44,446,983
Chr03	2	40,520,013
Chr04	2	40,414,263
Chr05	5	38,983,048
Chr06	2	34,955,313
Chr07	1	38,933,210
Chr08	2	36,506,272
Chr09	2	35,778,844
Chr10	3	34,237,086
Chr11	1	29,979,644
Chr12	2	33,551,896
Chr13	1	29,320,500
Total length of chromosome level assembly	28	483,447,045
Other	13	4,007,122
Total	41	487,454,167

Supplementary Table 4. Statistics of genome alignment of "Hutou" jasmine

Library type	Tissue	Total Reads (bp)	Map Rate (%)
DNA-seq	Leaf	349,184,538	98.65
HIFI reads	Leaf	2,614,116	99.68
RNA-seq	Flower	23,827,071	92.06
RNA-seq	Flower	25,550,852	91.58
RNA-seq	Flower	21,799,656	92.46
RNA-seq	Leaf	31,379,252	88.35
RNA-seq	Leaf	27,127,244	89.05
RNA-seq	Leaf	32,031,807	86.75

Supplementary Table 5. Genome indices of "Hutou" jasmine genome

Item	"Hutou" jasmine
Contig assembly size (Mb)	487.99
Contig N50 (Mb)	26.90
Chromosome-level assembly size (Mb)	483.45
Anchor rate (%)	99.18
No. of genes	23,968
Complete BUSCO ratio (%)	98.50
LAI	21.81
Quality value (QV)	63.40
Average gene length (bp)	4,217
Average CDS length (bp)	1,304
Average exon length (bp)	318
Average exon number per gene	5.90
Exon GC content (%)	42.46
Average intron length (bp)	521
Intron GC content (%)	34.33

Supplementary Table 6. The BUSCO evaluation of gene annotation in "Hutou" jasmine

Type	Number	Percentage (%)
Complete BUSCOs (C)	1,535	95.2
Complete and single-copy BUSCOs (S)	1,497	92.8
Complete and duplicated BUSCOs (D)	38	2.4
Fragmented BUSCOs (F)	28	1.7
Missing BUSCOs (M)	51	3.1
Total BUSCO groups searched	1,614	100

Supplementary Table 7. Gene functional annotation with different protein databases

Type	Number	Percentage (%)
NR	23,519	98.13
EGGNOG	22,359	93.29
Swissprot	18,222	76.03
GO	13,183	55.00
KEGG	10,905	45.50
COG	21,018	87.69
PFAM	16,559	69.09
Total	23,527	98.16

Supplementary Table 8. Transposable elements (TE) annotation in "Hutou" jasmine genome

	Count	Length (Mb)	% of genome
Total repeat fraction	826,005	303.77	62.32
Class I: Retroelement	333,527	169.09	34.69
LTR retrotransposon	143,046	116.6	23.92
Ty1/Copia	31,285	28.61	5.87
Ty3/Gypsy	41,282	48.28	9.90
Other	70,479	39.71	8.15
Non-LTR retrotransposon	111,731	36.02	7.39
LINE	89,189	33.49	6.87
SINE	22,542	2.53	0.52
Unclassified retroelement	78,750	16.47	3.38
Class II: DNA transposon	221,952	88.37	18.13
TIR			
CMC[DTC]	10,696	7.57	1.55
hAT	9,473	3.45	0.71
Mutator	8,339	5.22	1.07
Tc1/Mariner	1,167	0.27	0.05
PIF/Harbinger	1,711	0.97	0.20
Other	189,399	70.62	14.49
Helitron	22,030	11.44	2.35
Tandem repeats	191,258	34.82	7.14
Unknown	34,859	10.3	2.11

Supplementary Table 9. Annotation of Non-coding genes in the "Hutou" jasmine genome

Type	Copy number
tRNA	653
miRNA	145
snRNA	2,085
rRNA	5,822
sRNA	1
Total	8,706

Supplementary Table 10. Statistics on the type and number of volatile compounds of "Hutou" jasmine flowers

Type	Number	Percentage (%)
Terpenoids	198	21.71
Esters	170	18.64
Heterocyclic compounds	125	13.71
Hydrocarbons	75	8.22
Ketones	73	8.00
Alcohols	65	7.13
Aromatics	48	5.26
Aldehydes	46	5.04
Acids	33	3.62
Phenols	27	2.96
Amines	22	2.41
Nitrogen compounds	8	0.88
Sulfur compounds	8	0.88
Halogenated hydrocarbons	7	0.77
Ethers	1	0.11
Others	6	0.66
Total	912	100

Supplementary Table 11. Statistical results of sequencing data and alignment between “Hutou” jasmine genome

Sample	Total Reads	Reads mapped	Mapped	Unique mapped	Multi mapped	Exon Mapped
F1-1	61,681,208	56,074,094	90.91%	54,532,061(88.41%)	1,542,033(2.50%)	90.76%
F1-2	64,816,752	58,995,523	91.02%	57,401,831(88.56%)	1,593,692(2.46%)	90.60%
F1-3	54,753,094	49,924,334	91.18%	48,578,953(88.72%)	1,345,381(2.46%)	90.29%
F2-1	63,088,572	58,260,531	92.35%	56,710,859(89.89%)	1,549,672(2.46%)	90.20%
F2-2	45,455,892	41,557,460	91.42%	40,469,356(89.03%)	1,088,104(2.39%)	89.30%
F2-3	47,559,528	44,136,876	92.80%	42,994,508(90.40%)	1,142,368(2.40%)	89.37%
F3-1	49,032,932	44,757,771	91.28%	43,469,572(88.65%)	1,288,199(2.63%)	88.10%
F3-2	42,108,604	38,576,596	91.61%	37,480,604(89.01%)	1,095,992(2.60%)	88.17%
F3-3	47,968,290	43,873,726	91.46%	42,621,523(88.85%)	1,252,203(2.61%)	88.66%
F4-1	53,795,732	49,022,061	91.13%	47,571,297(88.43%)	1,450,764(2.70%)	88.37%
F4-2	41,738,778	37,946,505	90.91%	36,829,857(88.24%)	1,116,648(2.68%)	87.82%
F4-3	50,888,910	46,433,311	91.24%	45,064,384(88.55%)	1,368,927(2.69%)	88.03%
F5-1	58,996,956	54,126,264	91.74%	52,224,577(88.52%)	1,901,687(3.22%)	87.91%
F5-2	52,620,054	47,824,985	90.89%	46,182,598(87.77%)	1,642,387(3.12%)	87.51%
F5-3	53,905,012	49,412,113	91.67%	47,777,876(88.63%)	1,634,237(3.03%)	87.82%

Supplementary Table 12. The statistics of gene expression abundance

Sample	FPKM<1	1≤FPKM<10	10≤FPKM<100	FPKM≥100
F1-1	8,369(31.36%)	8,378(31.40%)	8,831(33.09%)	1,107(4.15%)
F1-2	8,414(31.53%)	8,366(31.35%)	8,758(32.82%)	1,147(4.30%)
F1-3	8,246(30.90%)	8,428(31.58%)	8,875(33.26%)	1,136(4.26%)
F2-1	8,535(31.98%)	8,796(32.96%)	8,293(31.08%)	1,061(3.98%)
F2-2	8,336(31.24%)	8,901(33.36%)	8,343(31.26%)	1,105(4.14%)
F2-3	8,409(31.51%)	8,794(32.95%)	8,399(31.47%)	1,083(4.06%)
F3-1	7,364(27.60%)	8,904(33.37%)	9,299(34.85%)	1,118(4.19%)
F3-2	7,410(27.77%)	8,903(33.36%)	9,265(34.72%)	1,107(4.19%)
F3-3	7,408(27.76%)	8,896(33.34%)	9,268(34.73%)	1,113(4.17%)
F4-1	7,344(27.52%)	9,311(34.89%)	8,999(33.72%)	1,031(3.86%)
F4-2	7,276(27.27%)	9,345(35.02%)	9,031(33.81%)	1,033(3.87%)
F4-3	7,334(27.48%)	9,299(34.85%)	9,021(33.81%)	1,031(3.86%)
F5-1	7,780(29.15%)	9,076(34.01%)	8,855(33.18%)	974(3.65%)
F5-2	7,707(28.88%)	9,143(34.26%)	8,851(33.17%)	984(3.69%)
F5-3	7,728(28.96%)	9,073(34.00%)	8,899(33.35%)	985(3.69%)

Note: $FPKM < 1$, $1 \leq FPKM < 10$, $10 \leq FPKM < 100$, and $FPKM \geq 100$ represent gene non-expression, low expression, high expression, and very high expression, respectively.

Supplementary Table 13. Annotations of hub genes obtained from the coexpression network.

Module	Gene ID	Gene name	KEGG pathway	Description
purple	HT29050	<i>RIA10</i>	ko04626 Plant-pathogen interaction	disease resistance protein
	HT30595	<i>GRAS</i>	ko04075 Plant hormone signal transduction	DELLA protein
	HT19096	<i>TTL3</i>	-	DnaJ homolog subfamily C member 7
magenta	HT24808	<i>WRKY41</i>	ko04626 Plant-pathogen interaction	disease resistance protein RPS2
	HT00049	<i>WRKY53</i>	ko04626 Plant-pathogen interaction	disease resistance protein RPS2
	HT02416	<i>HSP90</i>	ko04141 Protein processing in endoplasmic reticulum	heat shock protein 90kDa beta

Supplementary Table 14. Quality detection results of total RNA of 15 flower samples in "Hutou" jasmine

Sample	RNA concentration (ng/μL)	RIN
F1-1	160.78	9.02
F1-2	440.69	9.17
F1-3	248.11	8.61
F2-1	554.60	8.60
F2-2	639.49	8.61
F2-3	382.18	8.86
F3-1	426.47	8.62
F3-2	284.46	8.94
F3-3	210.12	8.72
F4-1	241.69	8.79
F4-2	256.71	8.63
F4-3	186.36	8.72
F5-1	101.45	8.62
F5-2	298.12	8.61
F5-3	261.71	8.75

Supplementary Table 15. List of primer sequences used for PCR and qRT-PCR analysis in this study

Gene name	Purpose	Forward (5'-3')	Reverse (5'-3')
<i>HTWRKY53</i>	PCR	caattactatttacaattacggatccatggagaacacttcga catg	aacagctcctcgccttgetcaccatAGATCCTC CTCCAGATCCTCCTCCTgtgaaaaatccgt ggatgtg
<i>HTHMGs2</i>	qRT-PCR	GAAATCTACTTCCCTCCCACTT	TGTCTAGTACAGTCTCGCTTCC
<i>HTHMGR3</i>	qRT-PCR	CTGCCGTTTACATAGCGACTGG	TCCCACCTCCAAGTGTGCCAAC
<i>HTDxs3</i>	qRT-PCR	CGAGAAAGCTGCGGACAAGTAC	AGATTCAAACCCGTCCACCTC
<i>HTDxR</i>	qRT-PCR	CTGCTGATTCCGAACATTCTGCTA	TGTCATCATACTCGGCTCCAAAGA
<i>HTBSMT1</i>	qRT-PCR	AACAAATGGTCTCGGAGGGAT	AGGCAGCCCAGTTTATTTCAG
<i>HTBPBT3</i>	qRT-PCR	AGTGGCAGCGAGAAGTATTGAC	TTGGTGTcAGGTACTTGGTCGT
<i>JsActin</i>	qRT-PCR	TCTCTATGGTAACATTGTCCTG	ATCCAGACACTGTACTTCCTCT