Chromosome-Scale Genome Assembly Provides Insights into the Molecular Mechanisms of Tissue Development of *Populus wilsonii*

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Chaofeng Li and Haitao Xing contributed equally to this work.

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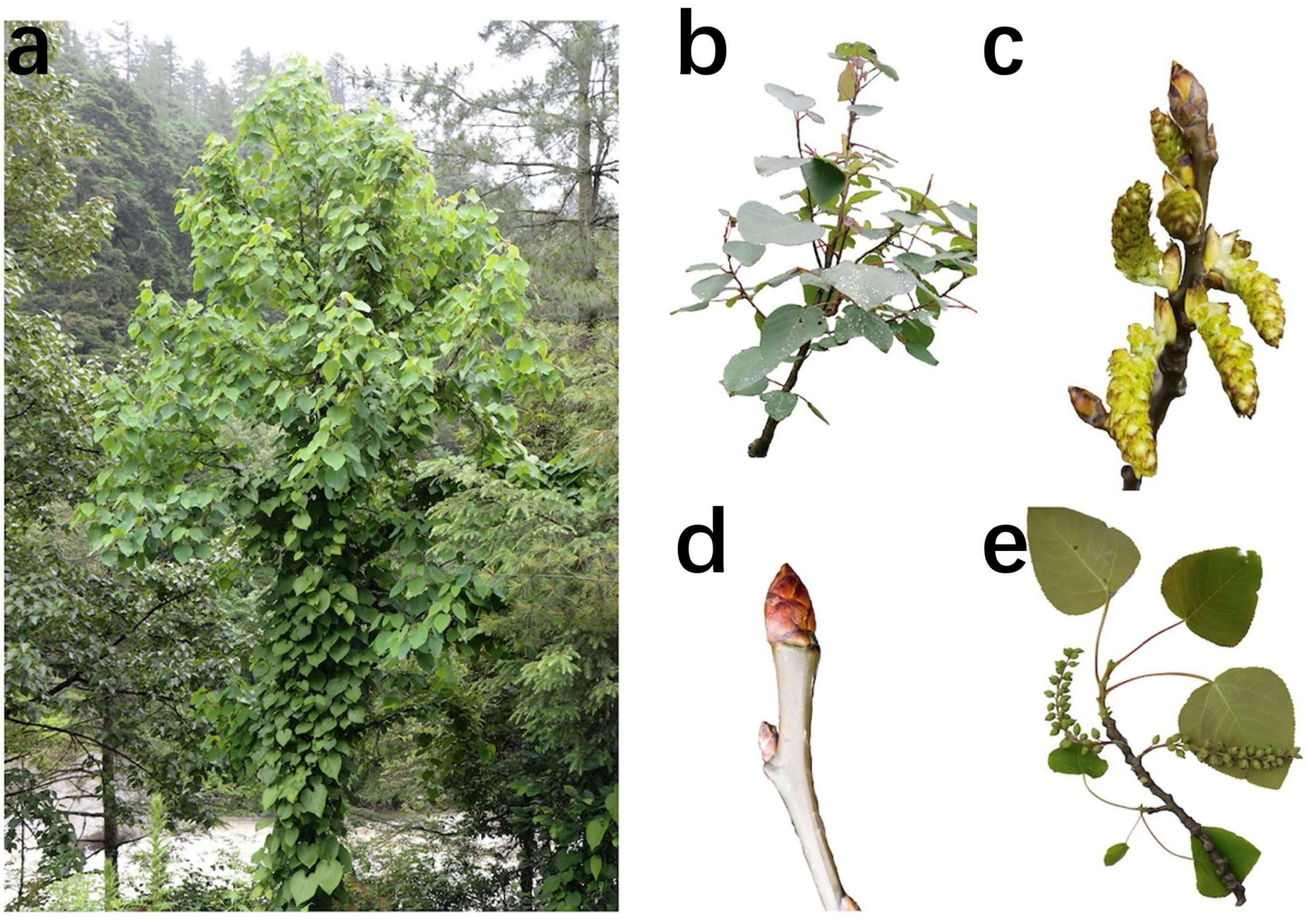
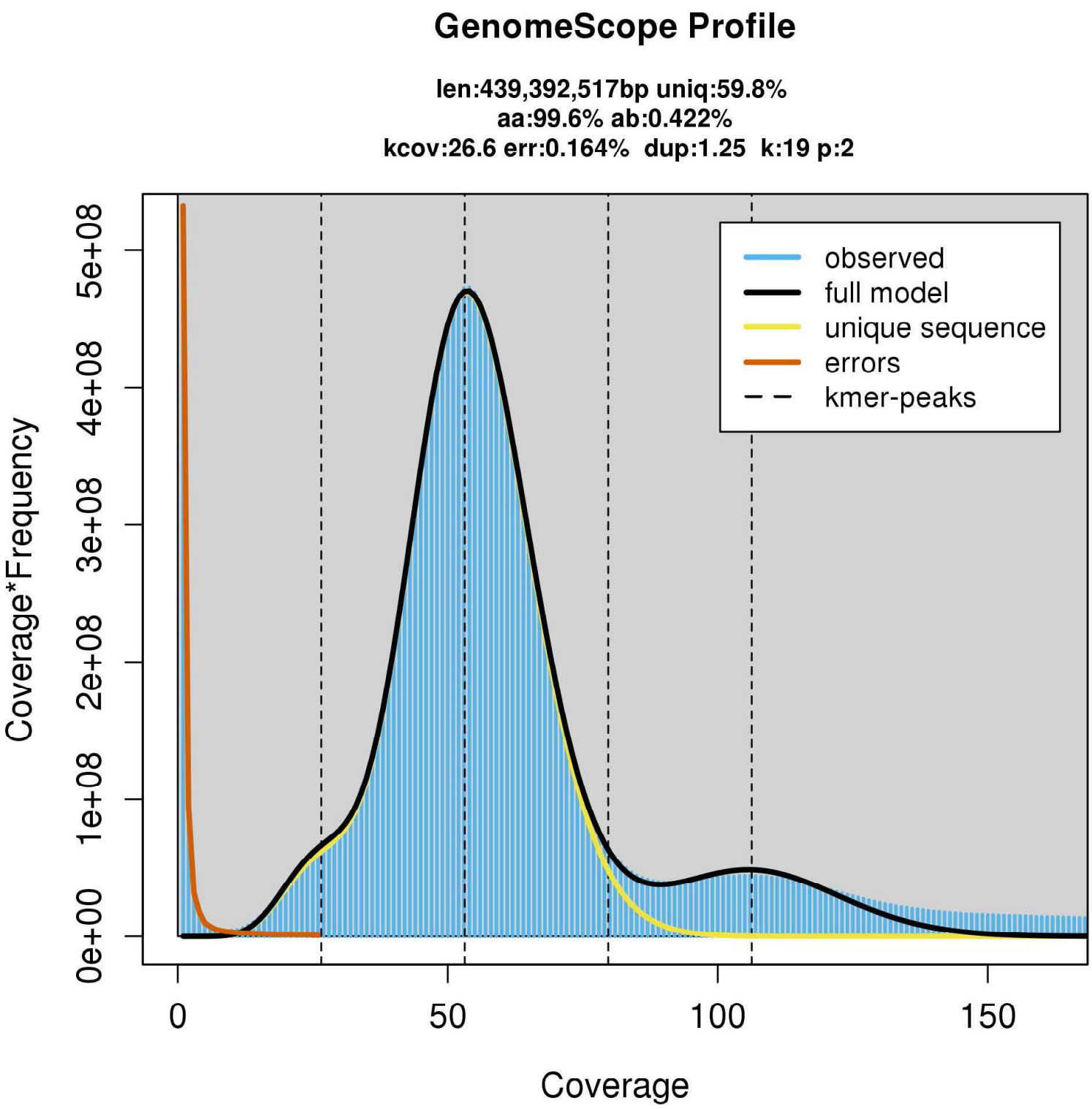
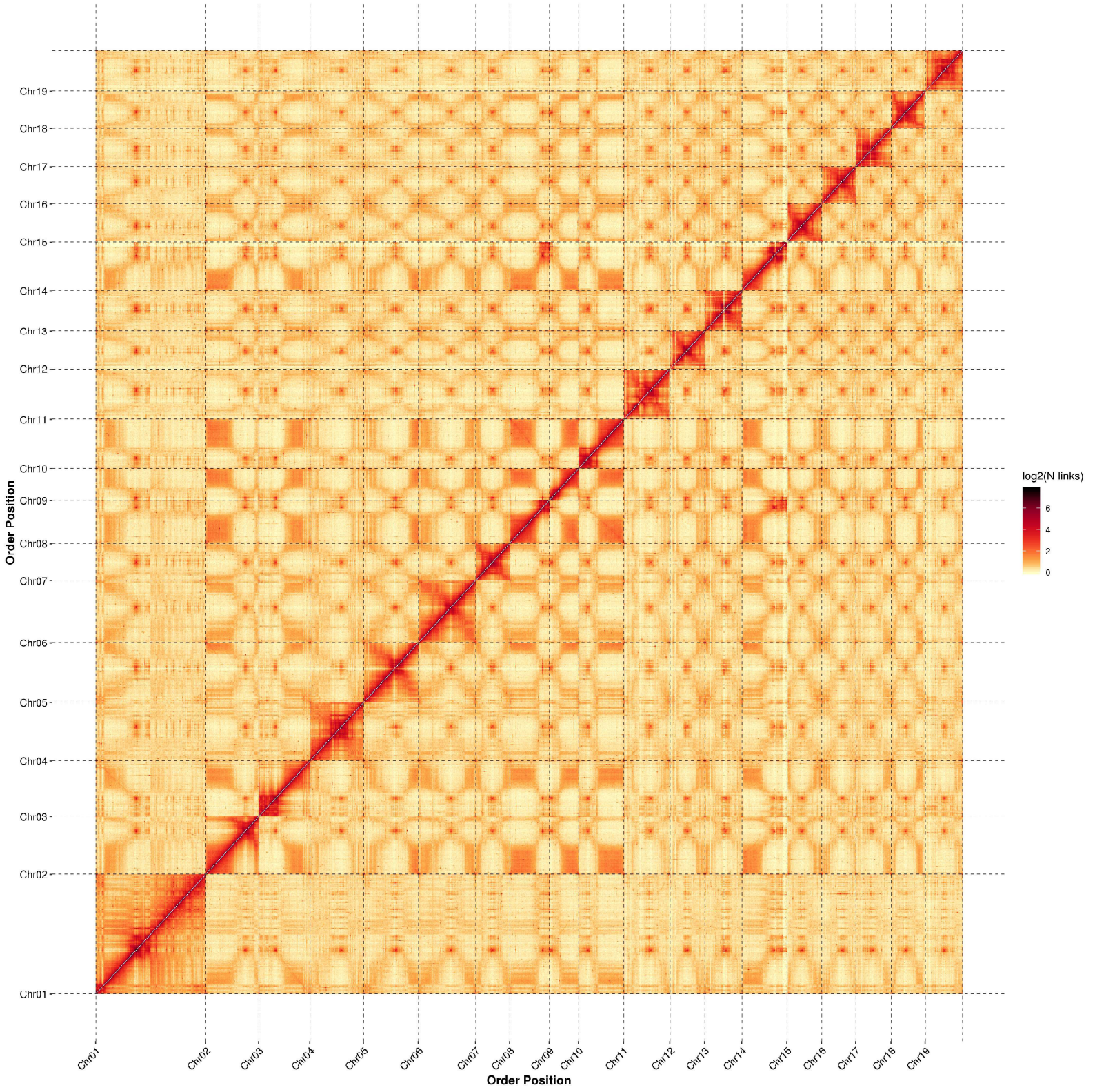

a
b
c
d
e

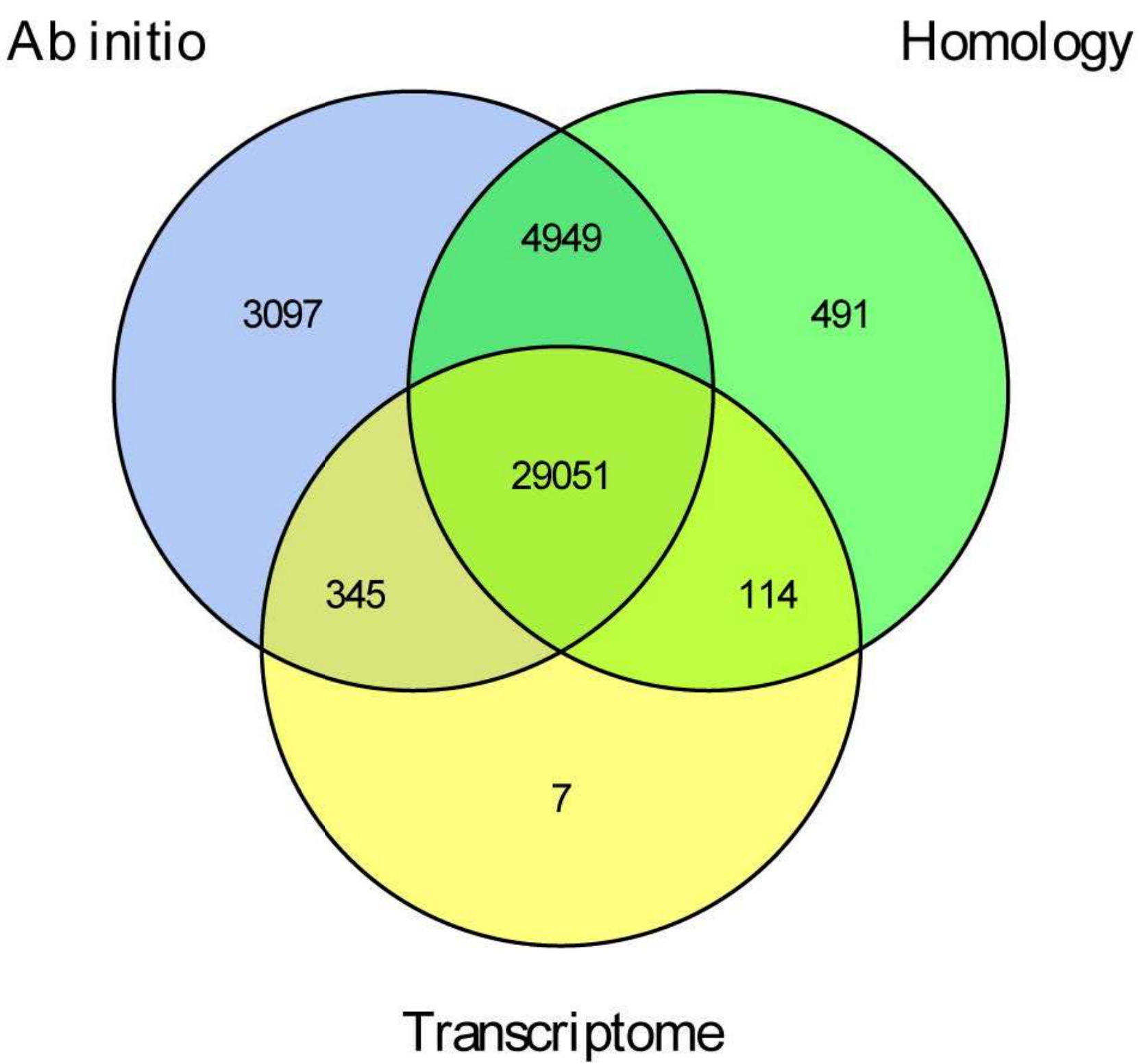
Supplementary Figure 1. Phenotype of the reference genome accession, "*Populus wilsonii*". (a) *Populus wilsonii* in their natural habitat. (b) Branches. (c) Male flowers. (d) Leaf bud. (e) Female flowers.


GenomeScope Profile
len:439,392,517bp uniq:59.8%
aa:99.6% ab:0.422%
kcov:26.6 err:0.164% dup:1.25 k:19 p:2
observed
full model
unique sequence
errors
kmer-peaks
Coverage*Frequency
0e+00
1e+08
2e+08
3e+08
4e+08
5e+08
0
50
100
150
Coverage

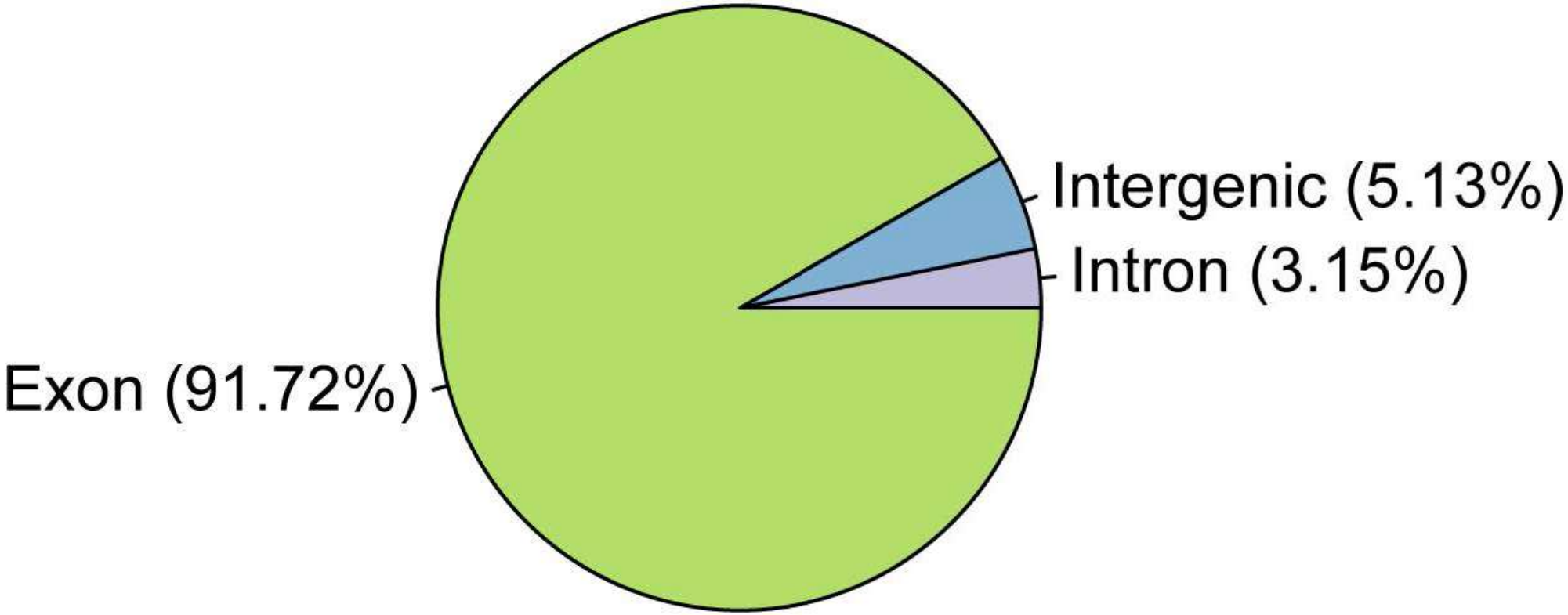
Supplementary Figure 2. The size estimation of the *Populus wilsonii* genome. The genome size was estimated by calculating the distribution of 19-mer frequency in the sequencing reads. The x-axis is the depth (X), and the y-axis is the proportion of sequences that represent the frequency at that depth divided by the total frequency of all depths.


Chr19
Chr18
Chr17
Chr16
Chr15
Chr14
Chr13
Chr12
Chr11
Chr10
Chr09
Chr08
Chr07
Chr06
Chr05
Chr04
Chr03
Chr02
Chr01
Order Position
Chr01
Chr02
Chr03
Chr04
Chr05
Chr06
Chr07
Chr08
Chr09
Chr10
Chr11
Chr12
Chr13
Chr14
Chr15
Chr16
Chr17
Chr18
Chr19
Order Position
log2(N links)
6
4
2
0

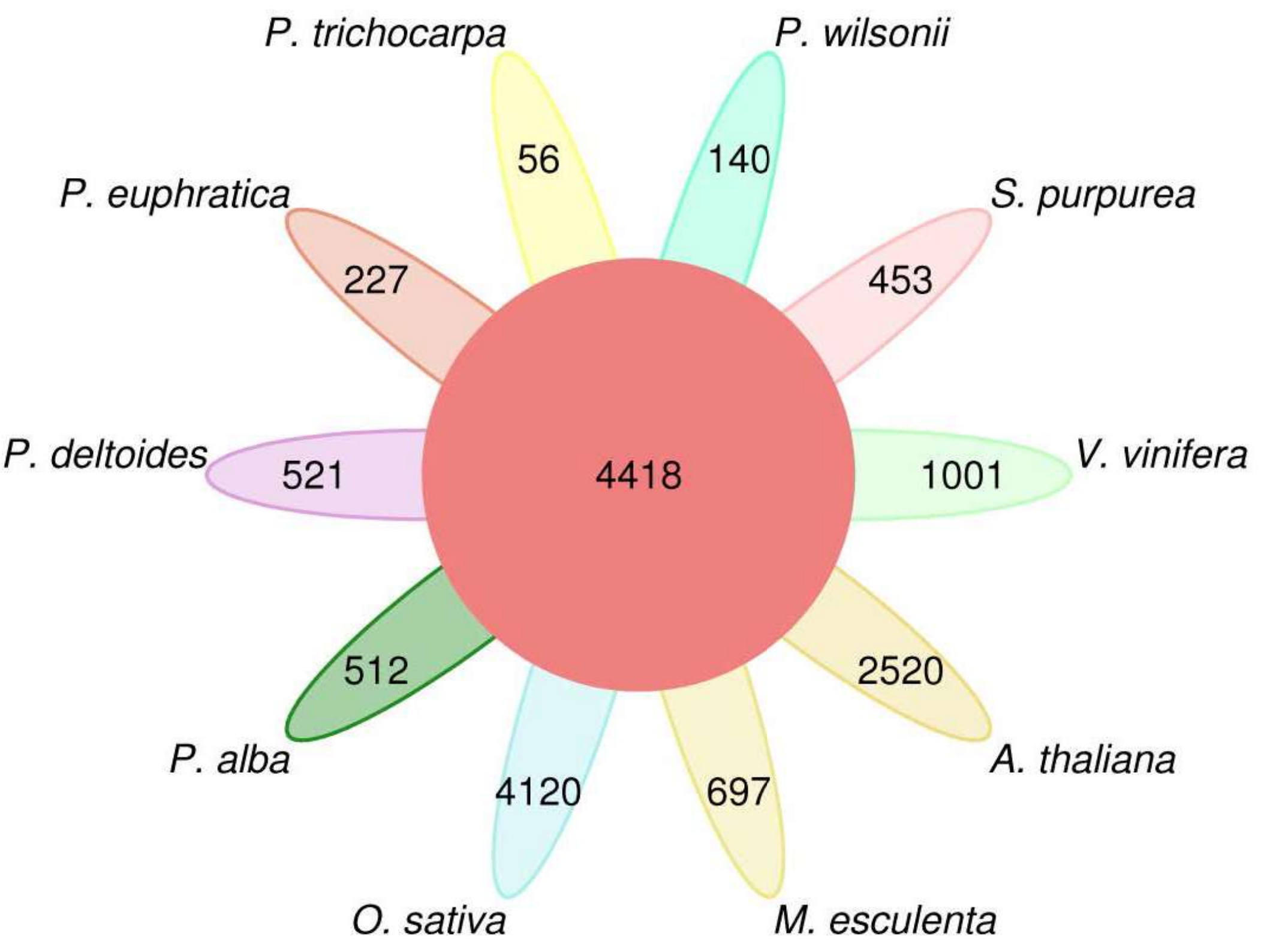
Supplementary Figure 3. The Hi-C chromatin interaction map for the 19 pseudomolecules of *Populus wilsonii* genome.


Ab initio
Homology
Transcriptome
3097
4949
491
29051
345
114
7

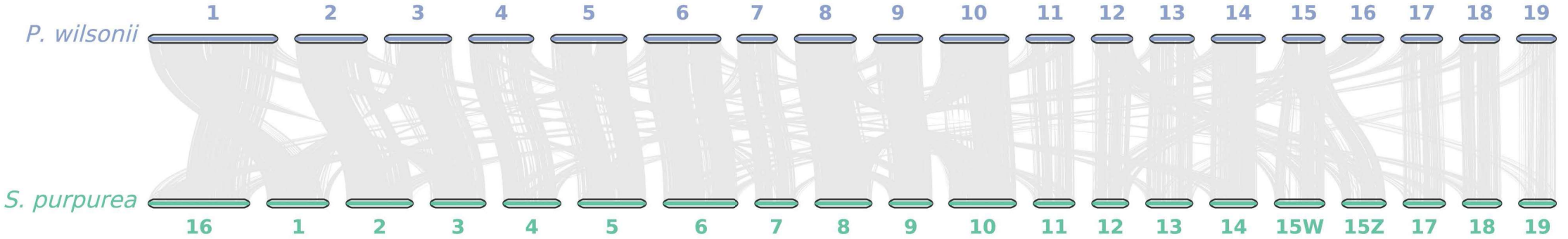
Supplementary Figure 4. The number of protein-coding gene models predicted by the homology-based, de novo and RNA-Seq based methods.


Intergenic (5.13%)
Intron (3.15%)
Exon (91.72%)

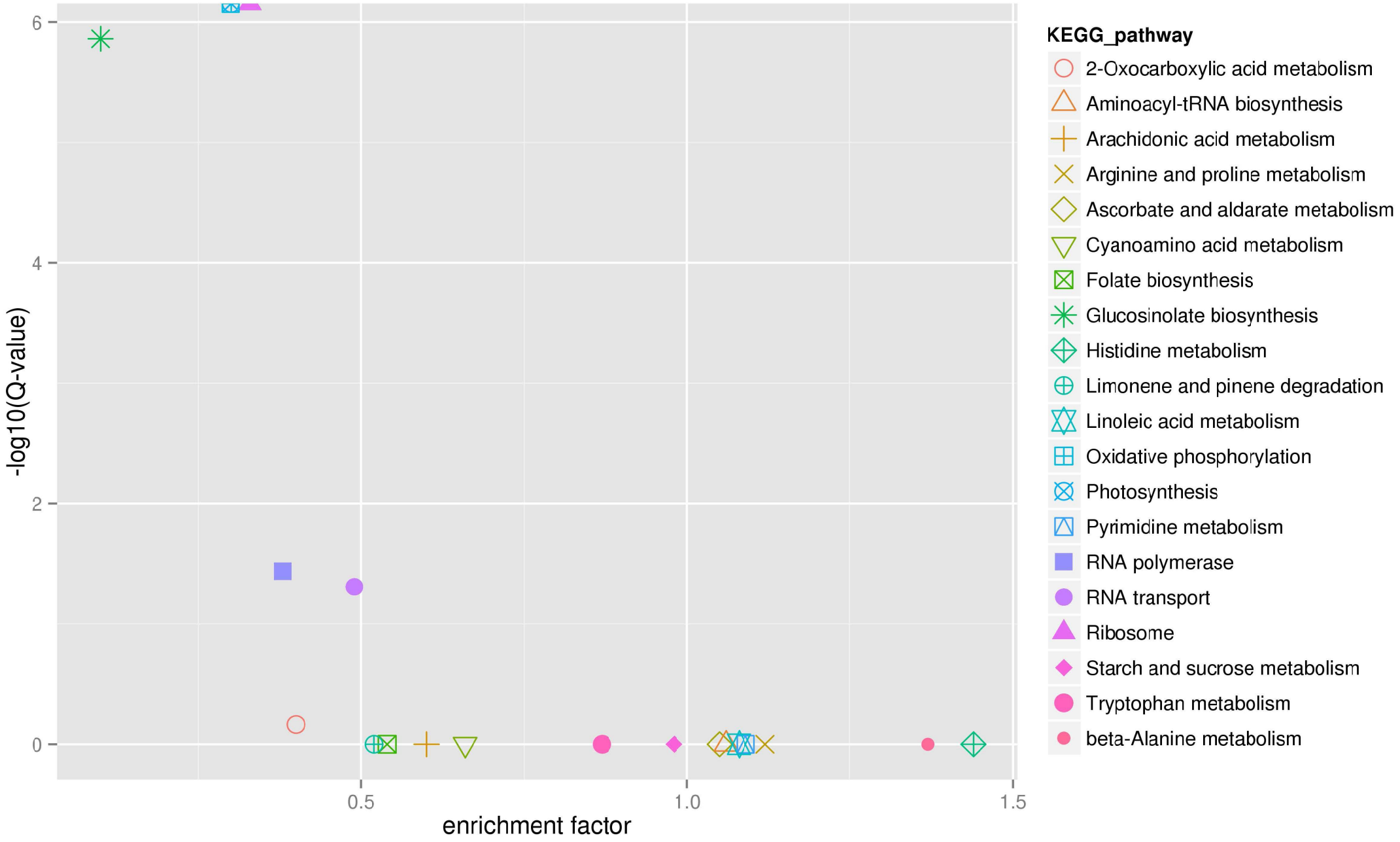
Supplementary Figure 5. Statistical results of RNA-seq clean data map to *Populus wilsonii* genome.


P. trichocarpa
P. wilsonii
56
140
P. euphratica
S. purpurea
227
453
P. deltoides
521
4418
1001
V. vinifera
512
2520
P. alba
A. thaliana
4120
697
O. sativa
M. esculenta

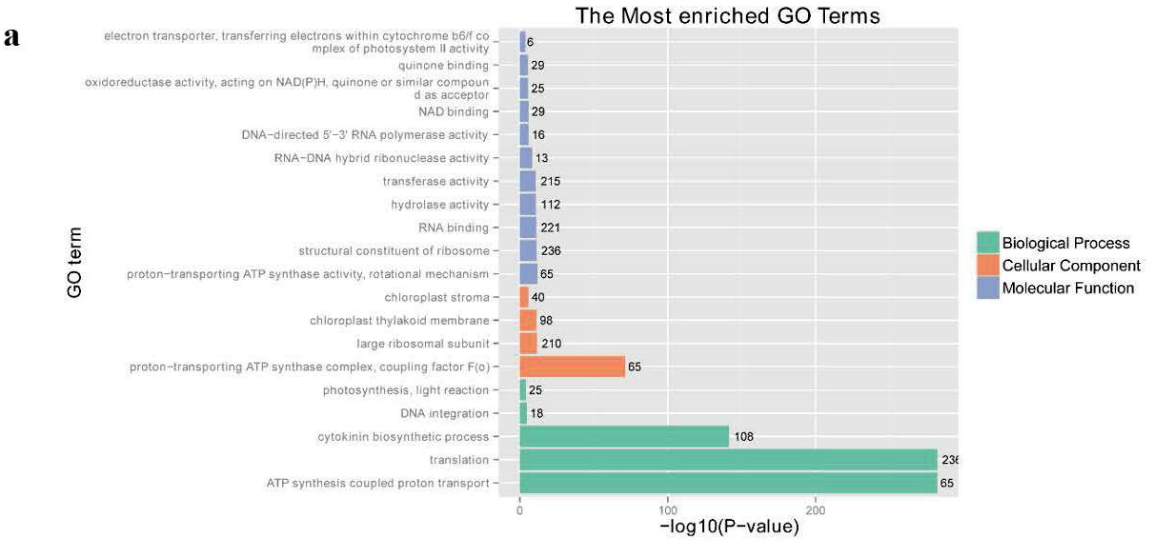
Supplementary Figure 6. Syntenic blocks between *Populus wilsonii* and *Salix purourea*.

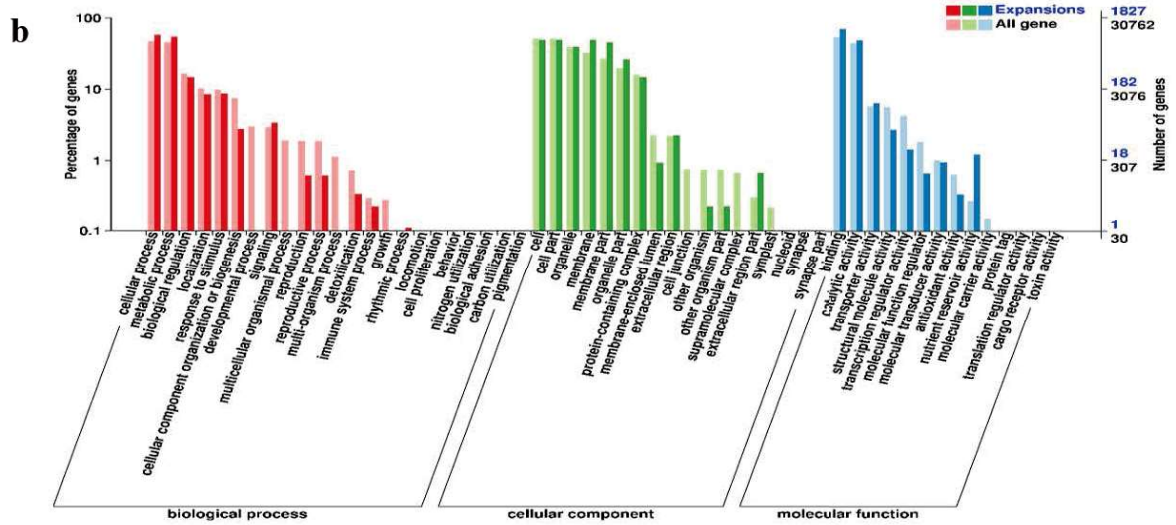

P. wilsonii
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19
S. purpurea
16 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15W 15Z 17 18 19

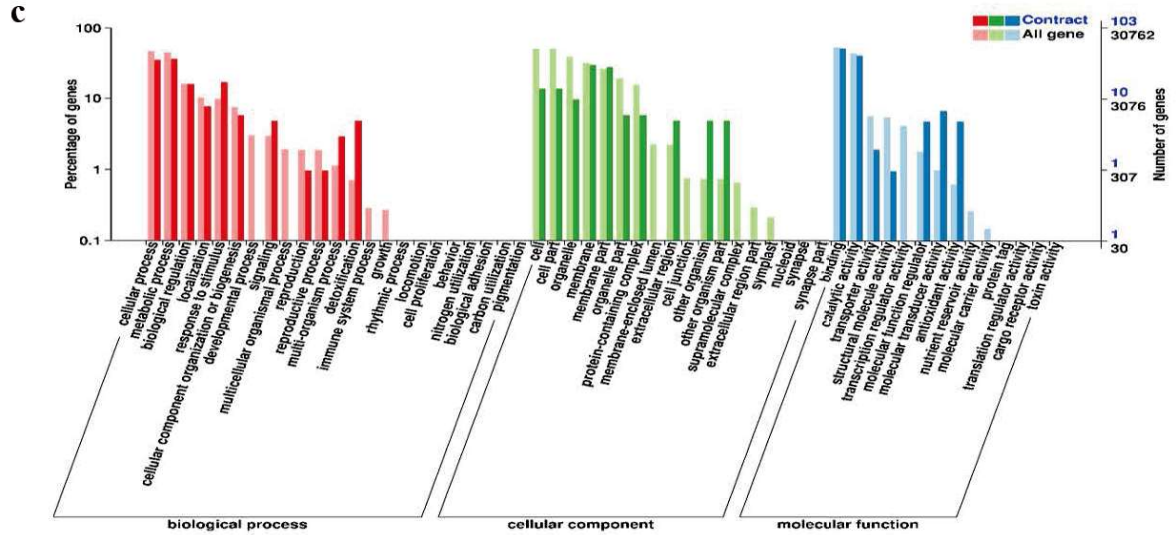
Supplementary Figure 7. The number of gene families shared among all species shown in Venn diagrams.

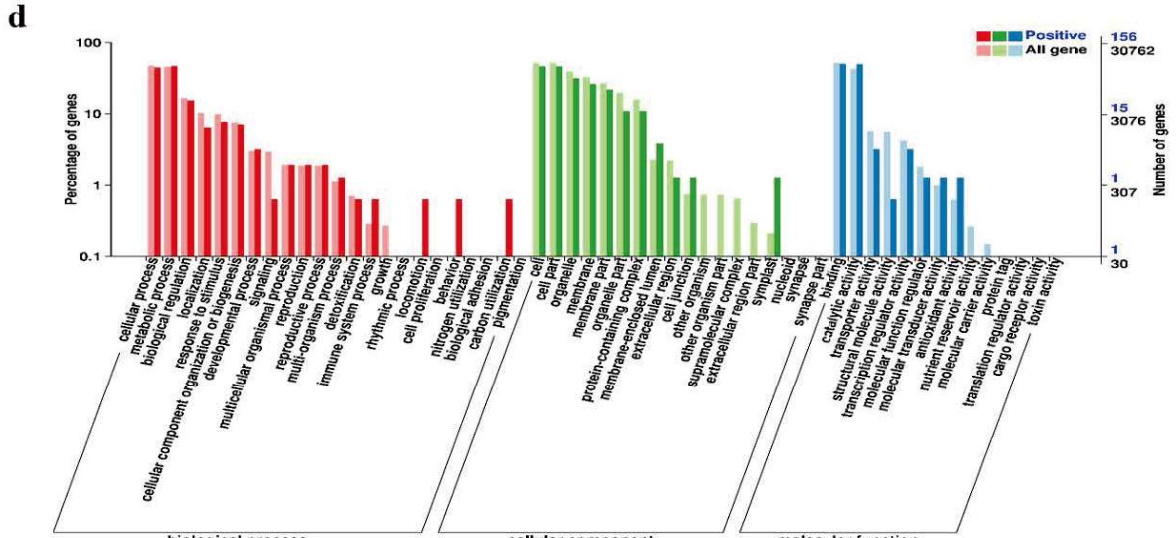

6
4
2
0
-log10(Q-value)
0.5
1.0
1.5
enrichment factor
KEGG_pathway
2-Oxocarboxylic acid metabolism
Aminoacyl-tRNA biosynthesis
Arachidonic acid metabolism
Arginine and proline metabolism
Ascorbate and aldarate metabolism
Cyanoamino acid metabolism
Folate biosynthesis
Glucosinolate biosynthesis
Histidine metabolism
Limonene and pinene degradation
Linoleic acid metabolism
Oxidative phosphorylation
Photosynthesis
Pyrimidine metabolism
RNA polymerase
RNA transport
Ribosome
Starch and sucrose metabolism
Tryptophan metabolism
beta-Alanine metabolism

Supplementary Figure 8. KEGG enrichment analysis of unique gene families in *Populus wilsonii*.


a
The Most enriched GO Terms
electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity
quinone binding
oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
NAD binding
DNA−directed 5'−3' RNA polymerase activity
RNA−DNA hybrid ribonuclease activity
transferase activity
hydrolase activity
RNA binding
structural constituent of ribosome
proton−transporting ATP synthase activity, rotational mechanism
chloroplast stroma
chloroplast thylakoid membrane
large ribosomal subunit
proton−transporting ATP synthase complex, coupling factor F(o)
photosynthesis, light reaction
DNA integration
cytokinin biosynthetic process
translation
ATP synthesis coupled proton transport
6
29
25
29
16
13
215
112
221
236
65
40
98
210
65
25
18
108
65
GO term
0
100
200
−log10(P−value)
Biological Process
Cellular Component
Molecular Function

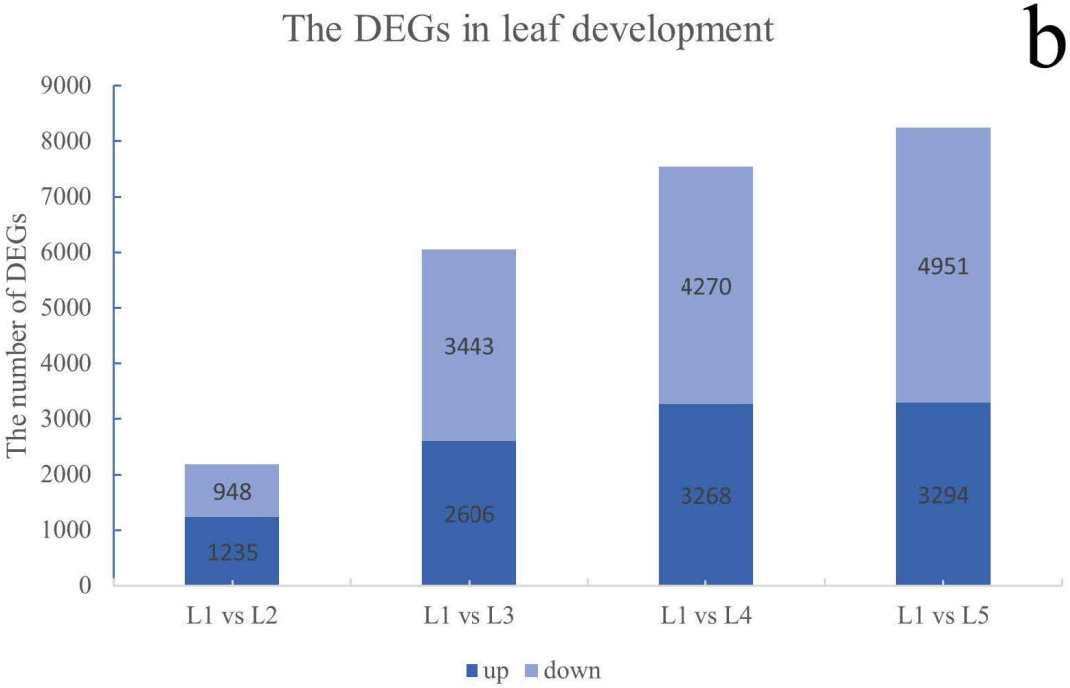

b
Expansions
All gene
1827
30762
182
3076
18
307
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function


c
Contract
All gene
103
30762
10
3076
1
307
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function

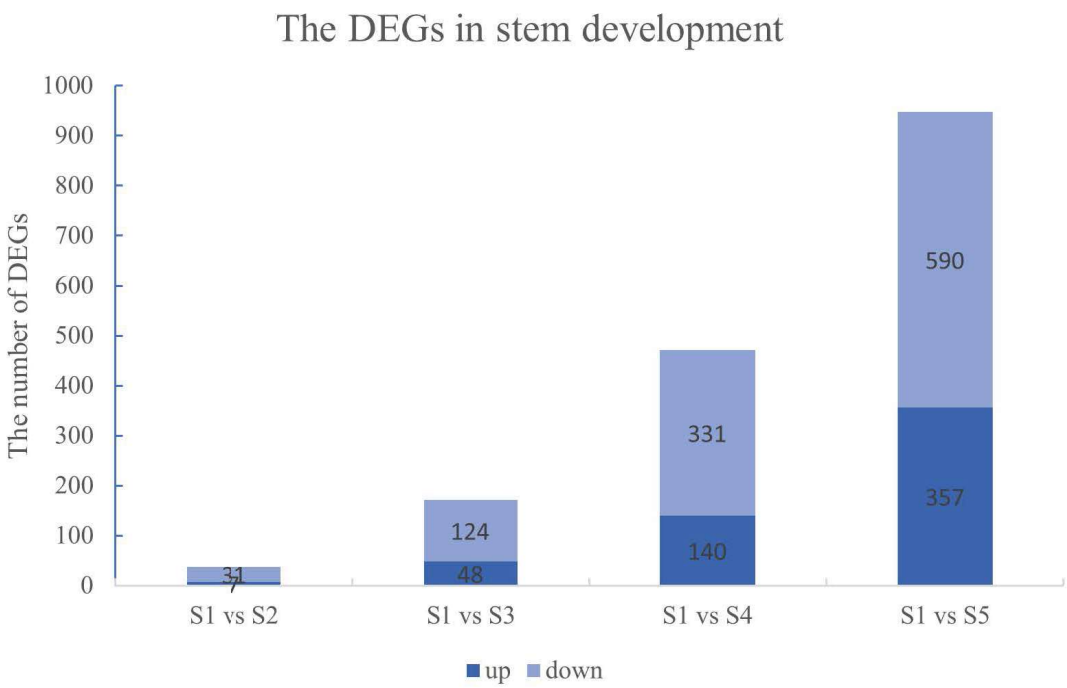

d
Positive
All gene
156
30762
15
3076
1
307
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function

Supplementary Figure 9. GO enrichment analysis of unique gene families(a), expansion gene families(b), contraction gene families(c) and positive selected gene families(d) in *Populus wilsonii*.

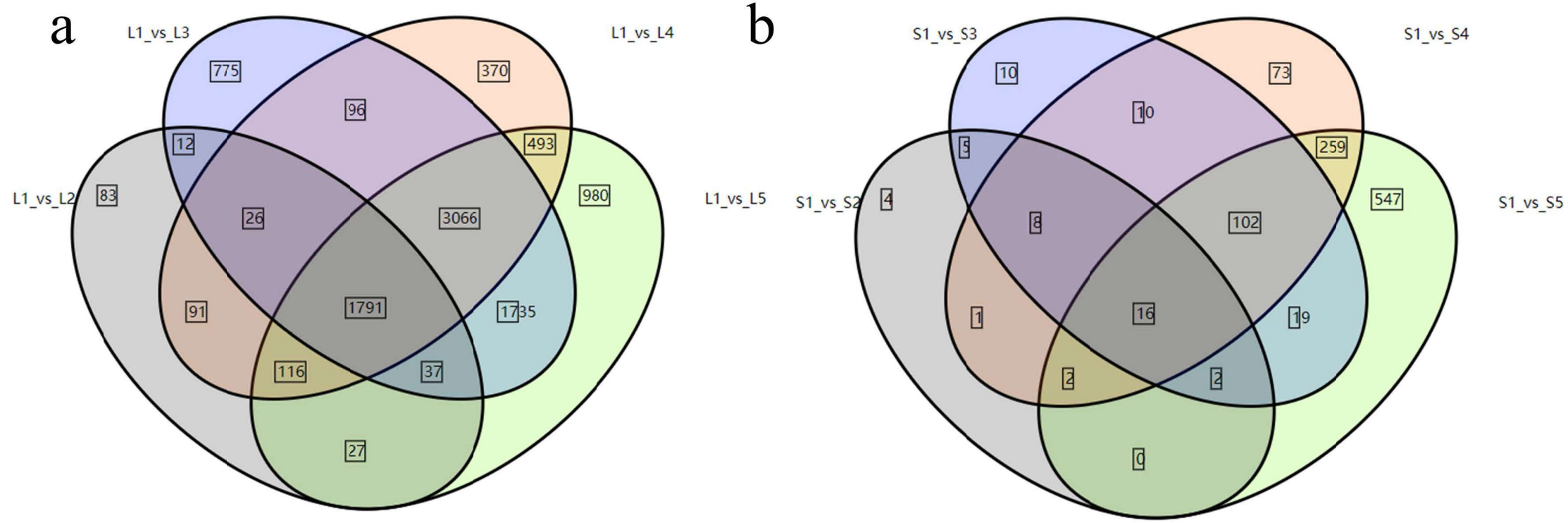
a


The DEGs in leaf development
The number of DEGs
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
948
1235
3443
2606
4270
3268
4951
3294
L1 vs L2
L1 vs L3
L1 vs L4
L1 vs L5
up
down

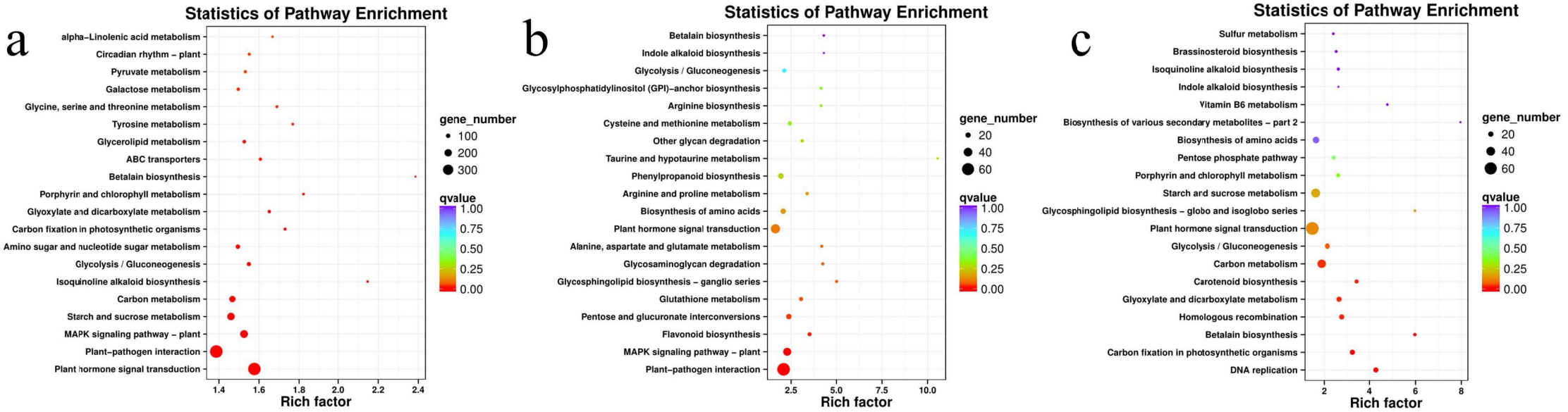
b


The DEGs in stem development
The number of DEGs
1000
900
800
700
600
500
400
300
200
100
0
31
7
124
48
331
140
590
357
S1 vs S2
S1 vs S3
S1 vs S4
S1 vs S5
up
down

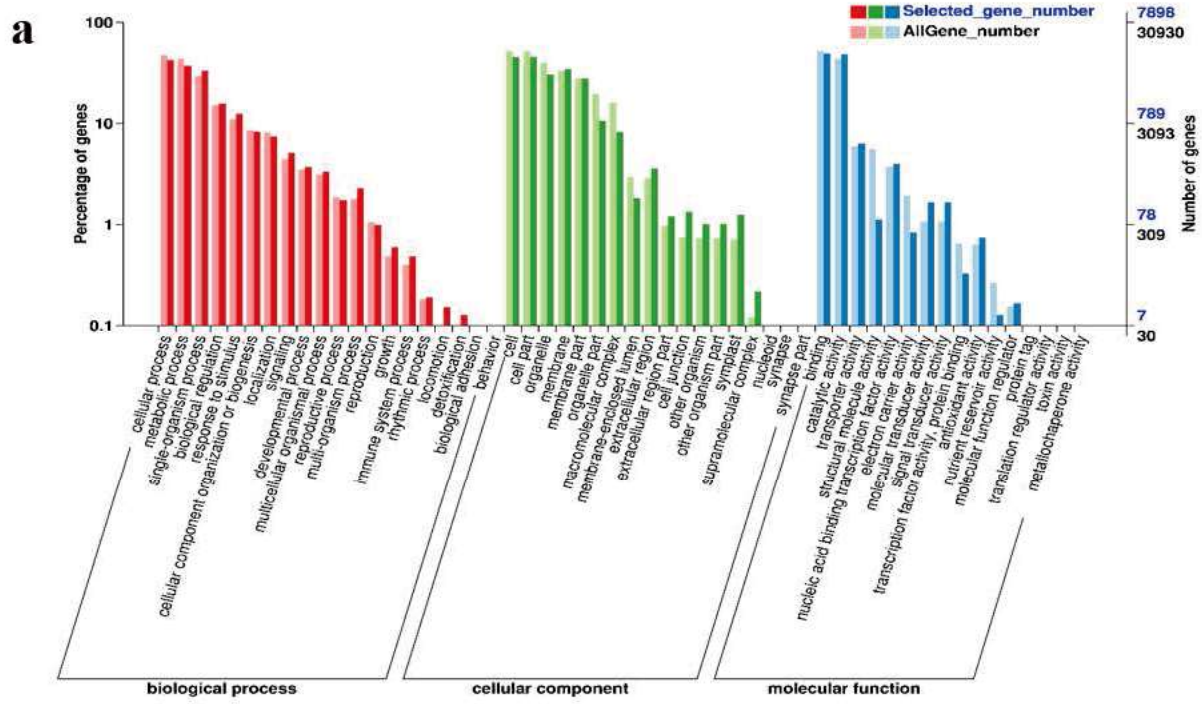
Supplementary Figure 10. The DEGs in leaf(a) and stem (b) development.

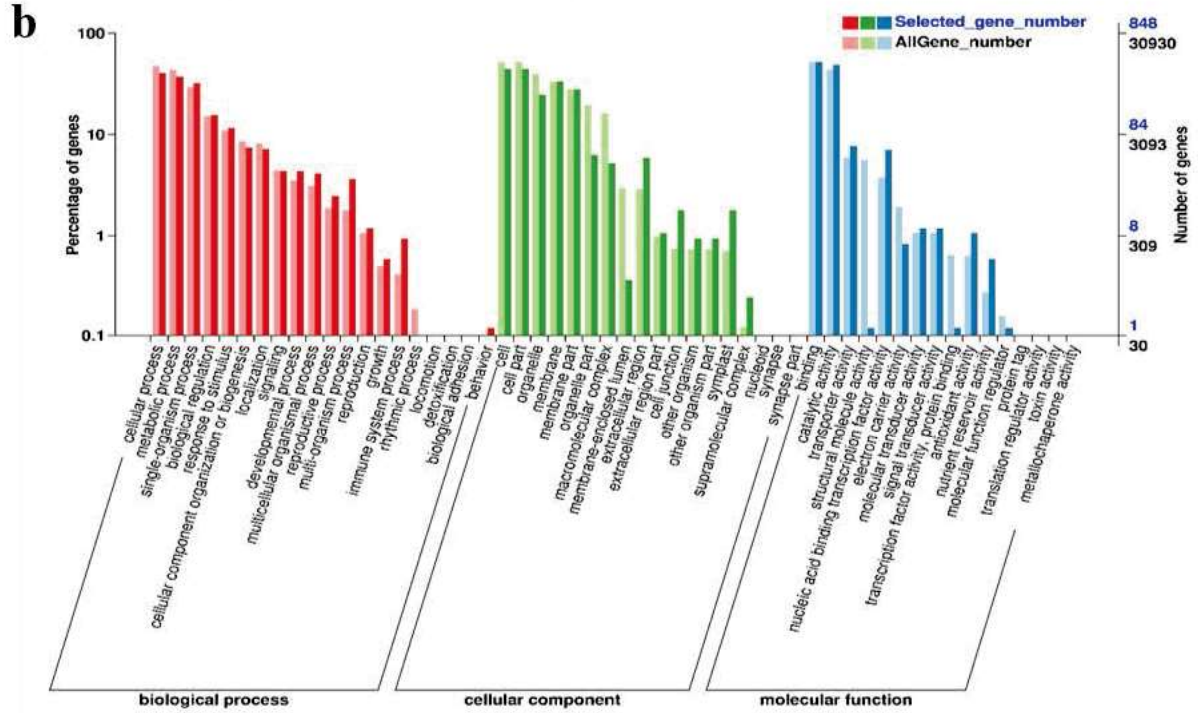

a
L1_vs_L3
L1_vs_L4
L1_vs_L2
L1_vs_L5
775
370
96
12
493
83
980
26
3066
91
1791
1735
116
37
27
b
S1_vs_S3
S1_vs_S4
S1_vs_S2
S1_vs_S5
10
73
10
5
259
4
547
8
102
1
16
19
2
2
0

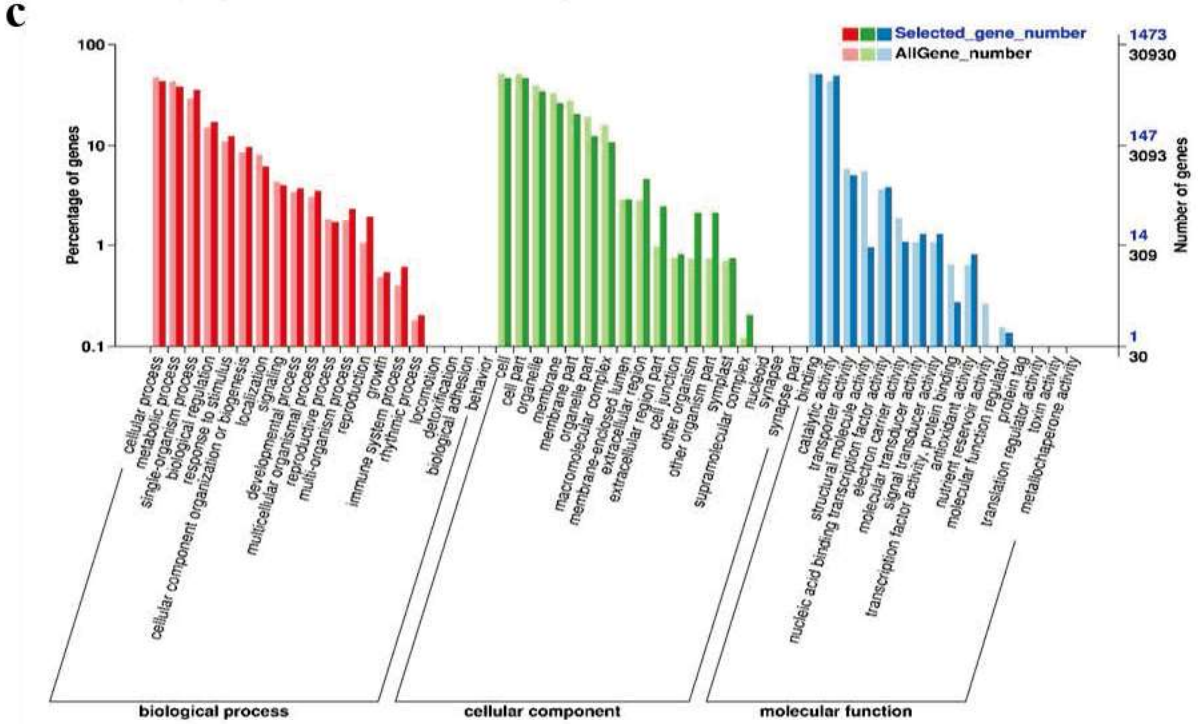
Supplementary Figure 11. The shared and unique DEGs between the five adjacent stages in leaf(a) and stem (b) development.


a
Statistics of Pathway Enrichment
alpha−Linolenic acid metabolism
Circadian rhythm − plant
Pyruvate metabolism
Galactose metabolism
Glycine, serine and threonine metabolism
Tyrosine metabolism
Glycerolipid metabolism
ABC transporters
Betalain biosynthesis
Porphyrin and chlorophyll metabolism
Glyoxylate and dicarboxylate metabolism
Carbon fixation in photosynthetic organisms
Amino sugar and nucleotide sugar metabolism
Glycolysis / Gluconeogenesis
Isoquinoline alkaloid biosynthesis
Carbon metabolism
Starch and sucrose metabolism
MAPK signaling pathway − plant
Plant−pathogen interaction
Plant hormone signal transduction
1.4
1.6
1.8
2.0
2.2
2.4
Rich factor
gene_number
100
200
300
qvalue
1.00
0.75
0.50
0.25
0.00
b
Statistics of Pathway Enrichment
Betalain biosynthesis
Indole alkaloid biosynthesis
Glycolysis / Gluconeogenesis
Glycosylphosphatidylinositol (GPI)−anchor biosynthesis
Arginine biosynthesis
Cysteine and methionine metabolism
Other glycan degradation
Taurine and hypotaurine metabolism
Phenylpropanoid biosynthesis
Arginine and proline metabolism
Biosynthesis of amino acids
Plant hormone signal transduction
Alanine, aspartate and glutamate metabolism
Glycosaminoglycan degradation
Glycosphingolipid biosynthesis − ganglio series
Glutathione metabolism
Pentose and glucuronate interconversions
Flavonoid biosynthesis
MAPK signaling pathway − plant
Plant−pathogen interaction
2.5
5.0
7.5
10.0
Rich factor
gene_number
20
40
60
qvalue
1.00
0.75
0.50
0.25
0.00
c
Statistics of Pathway Enrichment
Sulfur metabolism
Brassinosteroid biosynthesis
Isoquinoline alkaloid biosynthesis
Indole alkaloid biosynthesis
Vitamin B6 metabolism
Biosynthesis of various secondary metabolites − part 2
Biosynthesis of amino acids
Pentose phosphate pathway
Porphyrin and chlorophyll metabolism
Starch and sucrose metabolism
Glycosphingolipid biosynthesis − globo and isoglobo series
Plant hormone signal transduction
Glycolysis / Gluconeogenesis
Carbon metabolism
Carotenoid biosynthesis
Glyoxylate and dicarboxylate metabolism
Homologous recombination
Betalain biosynthesis
Carbon fixation in photosynthetic organisms
DNA replication
2
4
6
8
Rich factor
gene_number
20
40
60
qvalue
1.00
0.75
0.50
0.25
0.00

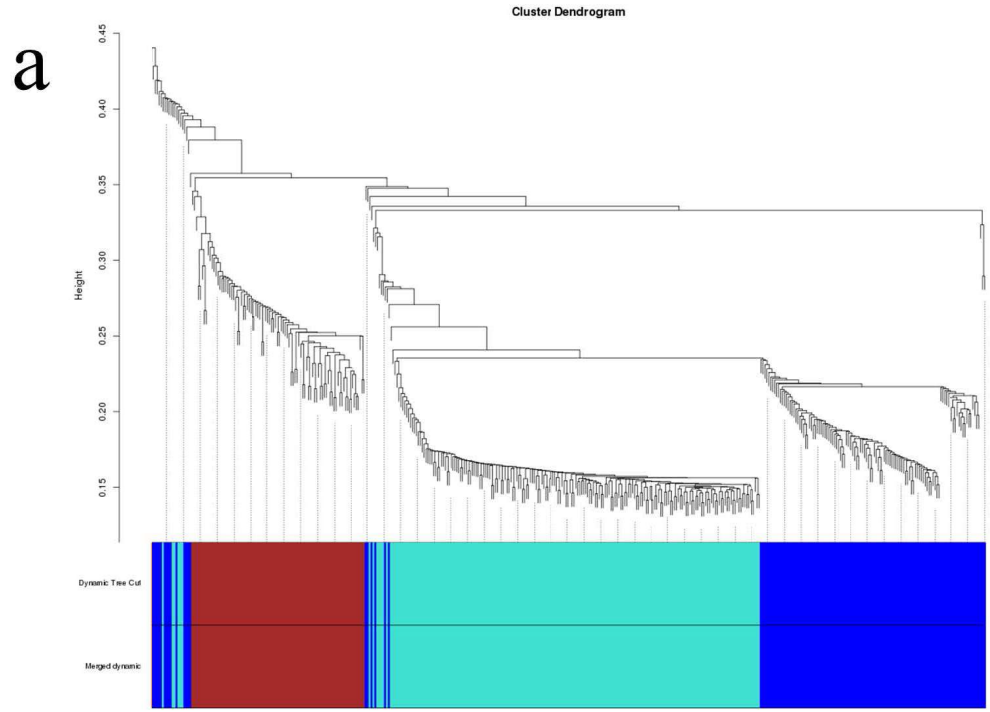
Supplementary Figure 12. KEGG enrichment analysis of all DEGs in leaf(a) and stem(b) development, and shared DEGs in leaf development(c).

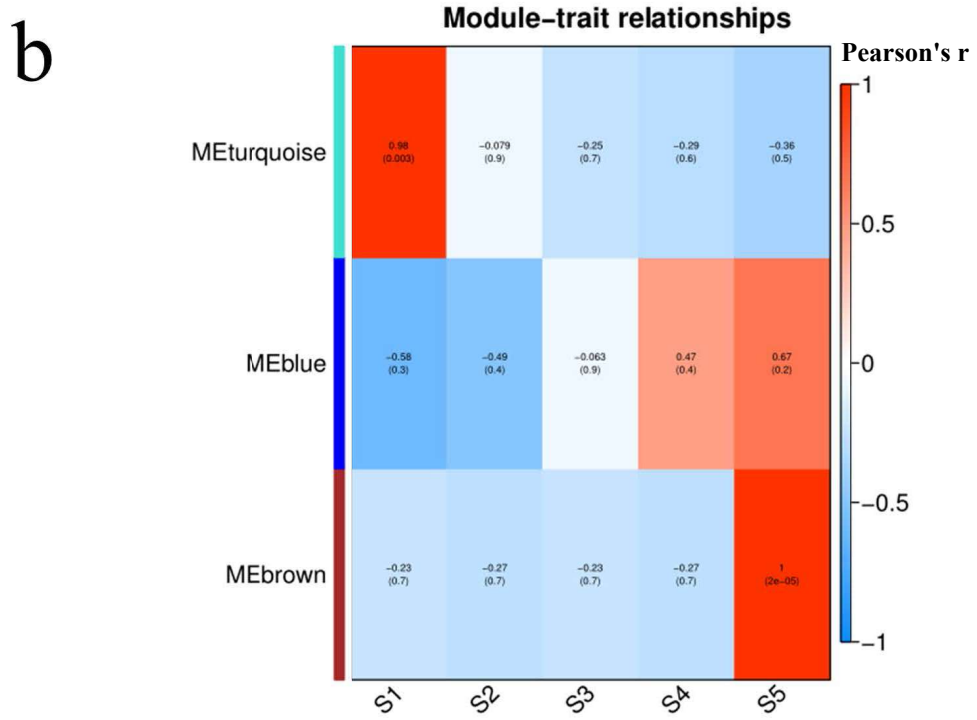

a
Selected_gene_number
AllGene_number
7898
30930
789
3093
78
309
7
30
Percentage of genes
Number of genes
100
10
1
0.1
cellular process
metabolic process
single-organism process
biological regulation
response to stimulus
cellular component organization or biogenesis
localization
signaling
developmental process
multicellular organismal process
reproductive process
multi-organism process
reproduction
growth
immune system process
rhythmic process
locomotion
detoxification
biological adhesion
behavior
cell
cell part
organelle
membrane
membrane part
organelle part
macromolecular complex
membrane-enclosed lumen
extracellular region
extracellular region part
cell junction
other organism
other organism part
symplast
supramolecular complex
nucleoid
synapse
synapse part
binding
catalytic activity
transporter activity
structural molecule activity
nucleic acid binding transcription factor activity
electron carrier activity
molecular transducer activity
signal transducer activity
transcription factor activity, protein binding
antioxidant activity
nutrient reservoir activity
molecular function regulator
translation regulator activity
protein tag
toxin activity
metallochaperone activity
biological process
cellular component
molecular function

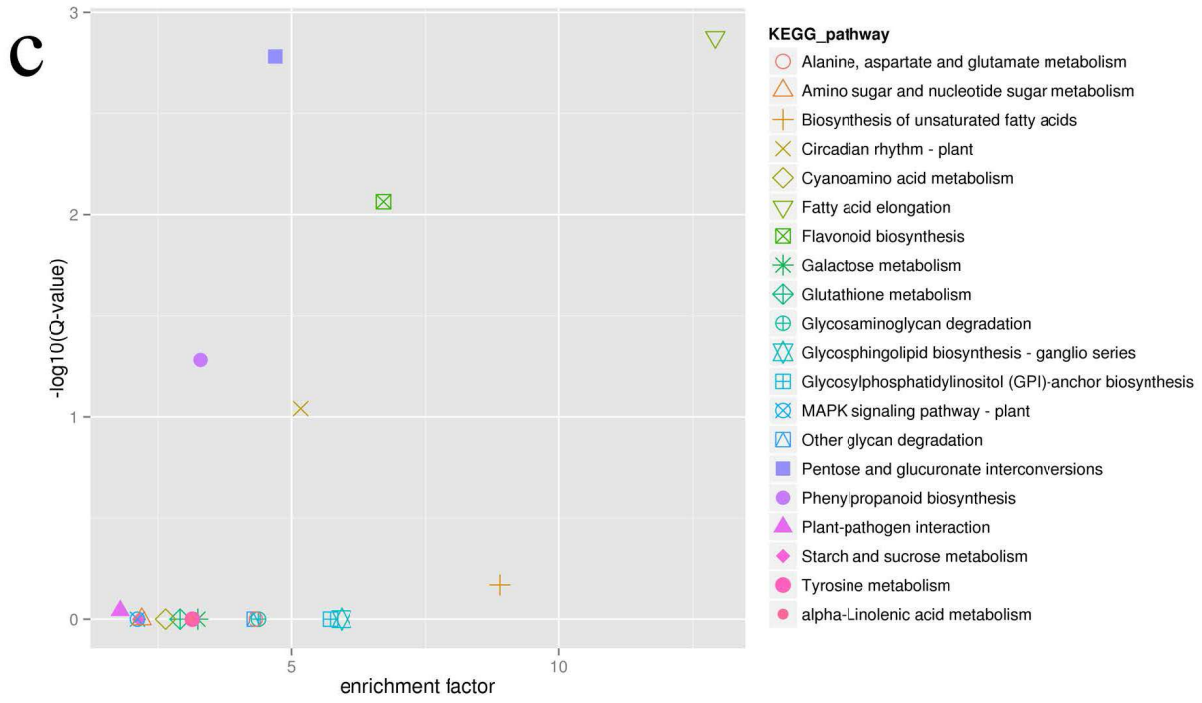

b
Selected_gene_number
AllGene_number
848
30930
84
3093
8
309
1
30
Percentage of genes
Number of genes
100
10
1
0.1
cellular process
metabolic process
single-organism process
biological regulation
response to stimulus
cellular component organization or biogenesis
localization
signaling
developmental process
multicellular organismal process
reproductive process
multi-organism process
reproduction
growth
immune system process
rhythmic process
locomotion
detoxification
biological adhesion
behavior
cell
cell part
organelle
membrane
membrane part
organelle part
macromolecular complex
membrane-enclosed lumen
extracellular region
extracellular region part
cell junction
other organism
other organism part
symplast
supramolecular complex
nucleoid
synapse
synapse part
binding
catalytic activity
transporter activity
structural molecule activity
nucleic acid binding transcription factor activity
electron carrier activity
molecular transducer activity
signal transducer activity
transcription factor activity, protein binding
antioxidant activity
nutrient reservoir activity
molecular function regulator
translation regulator activity
protein tag
toxin activity
metallochaperone activity
biological process
cellular component
molecular function

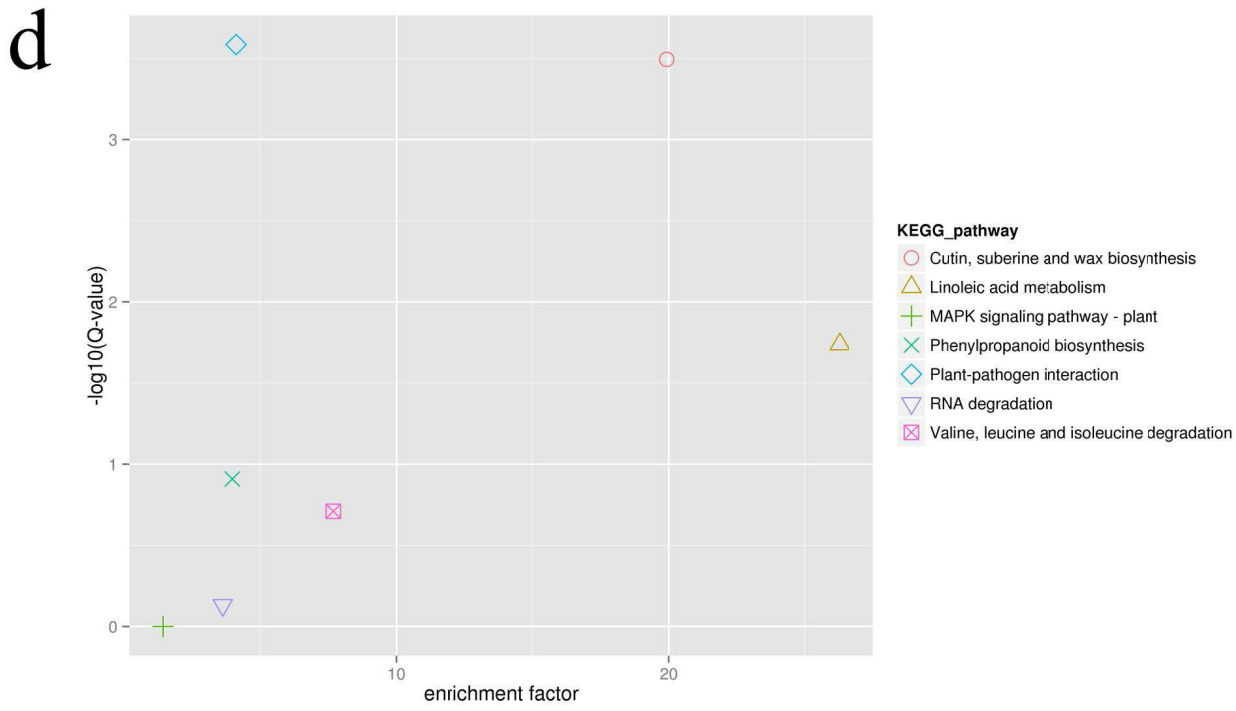

c
Selected_gene_number
AllGene_number
1473
30930
147
3093
14
309
1
30
Percentage of genes
Number of genes
100
10
1
0.1
cellular process
metabolic process
single-organism process
biological regulation
response to stimulus
cellular component organization or biogenesis
localization
signaling
developmental process
multicellular organismal process
reproductive process
multi-organism process
reproduction
growth
immune system process
rhythmic process
locomotion
detoxification
biological adhesion
behavior
cell
cell part
organelle
membrane
membrane part
organelle part
macromolecular complex
membrane-enclosed lumen
extracellular region
extracellular region part
cell junction
other organism
other organism part
symplast
supramolecular complex
nucleoid
synapse
synapse part
binding
catalytic activity
transporter activity
structural molecule activity
nucleic acid binding transcription factor activity
electron carrier activity
molecular transducer activity
signal transducer activity
transcription factor activity, protein binding
antioxidant activity
nutrient reservoir activity
molecular function regulator
translation regulator activity
protein tag
toxin activity
metallochaperone activity
biological process
cellular component
molecular function

Supplementary Figure 13. GO enrichment analysis of all DEGs in leaf(a) and stem(b) development, and shared DEGs in leaf development(c).

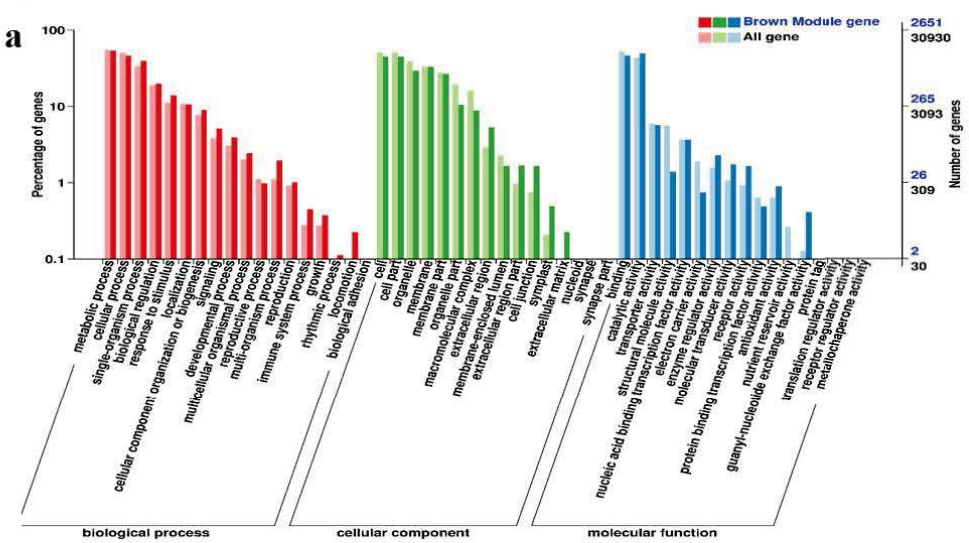

a
Cluster Dendrogram
Height
0.45
0.40
0.35
0.30
0.25
0.20
0.15
Dynamic Tree Cut
Merged dynamic

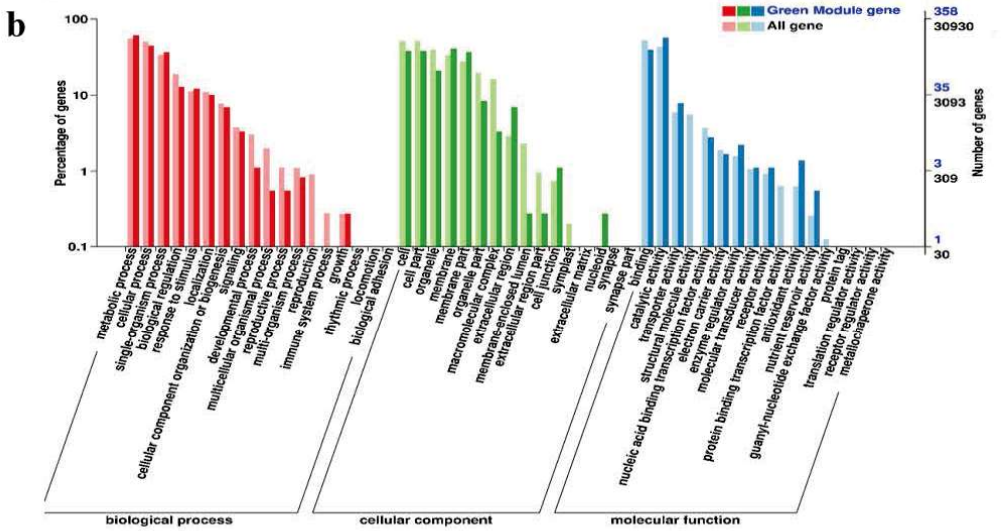

b
Module−trait relationships
Pearson's r
1
0.5
0
−0.5
−1
MEturquoise
MEblue
MEbrown
0.98
(0.003)
−0.079
(0.9)
−0.25
(0.7)
−0.29
(0.6)
−0.36
(0.5)
−0.58
(0.3)
−0.49
(0.4)
−0.063
(0.9)
0.47
(0.4)
0.67
(0.2)
−0.23
(0.7)
−0.27
(0.7)
−0.23
(0.7)
−0.27
(0.7)
1
(2e−05)
S1
S2
S3
S4
S5

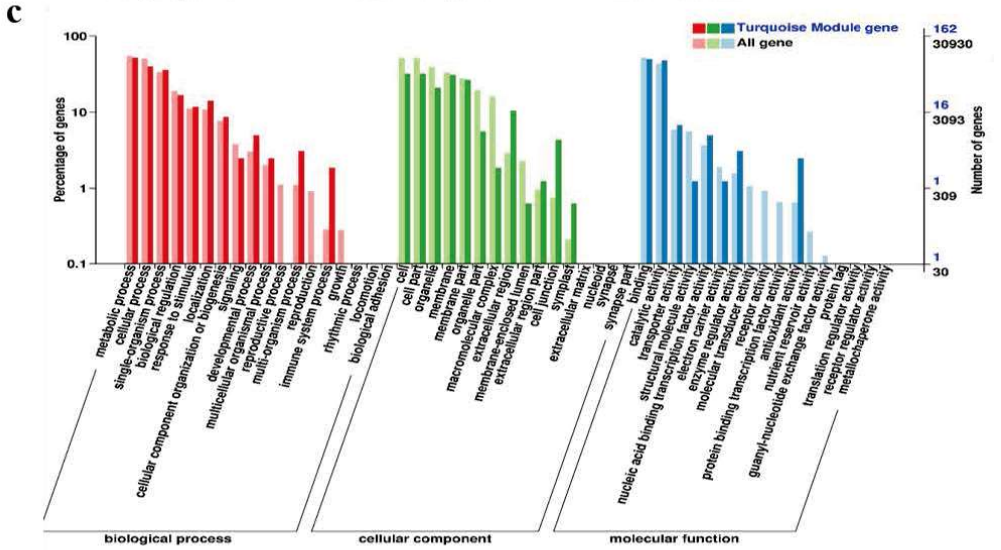

c
-log10(Q-value)
enrichment factor
KEGG_pathway
Alanine, aspartate and glutamate metabolism
Amino sugar and nucleotide sugar metabolism
Biosynthesis of unsaturated fatty acids
Circadian rhythm - plant
Cyanoamino acid metabolism
Fatty acid elongation
Flavonoid biosynthesis
Galactose metabolism
Glutathione metabolism
Glycosaminoglycan degradation
Glycosphingolipid biosynthesis - ganglio series
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
MAPK signaling pathway - plant
Other glycan degradation
Pentose and glucuronate interconversions
Phenylpropanoid biosynthesis
Plant-pathogen interaction
Starch and sucrose metabolism
Tyrosine metabolism
alpha-Linolenic acid metabolism

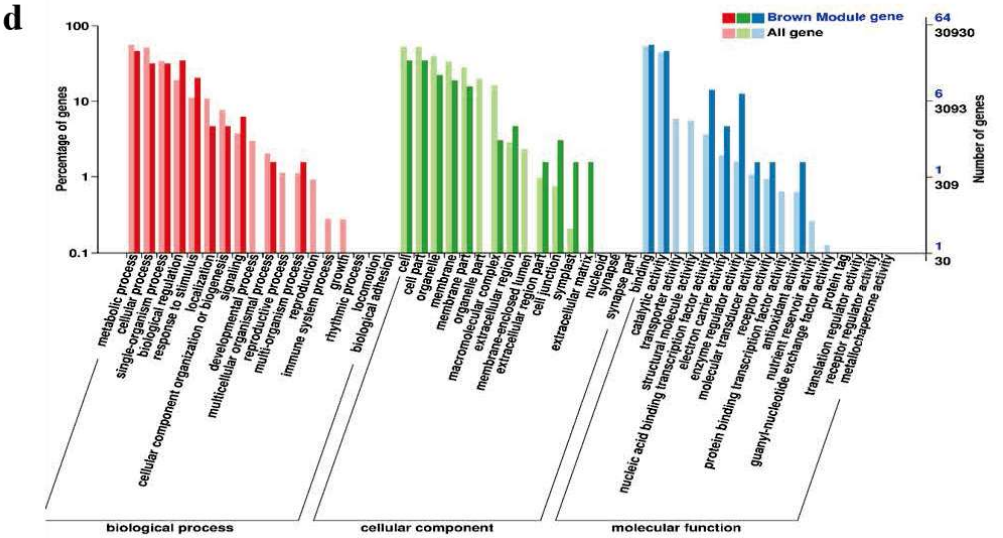

d
-log10(Q-value)
enrichment factor
KEGG_pathway
Cutin, suberine and wax biosynthesis
Linoleic acid metabolism
MAPK signaling pathway - plant
Phenylpropanoid biosynthesis
Plant-pathogen interaction
RNA degradation
Valine, leucine and isoleucine degradation

Supplementary Figure 14. Weighted gene co-expression network analysis (WGCNA) of genes during the stem development. a, hierarchical cluster tree showing co-expression modules identified by WGCNA. b, module-stage association (each row corresponds to a module, and each column represents a specific stage. The color of each cell at the row column intersection indicates the Pearson correlation coefficient (Pearson's r) between a module and the stage), positive and negative correlations are shown in red and blue, respectively. c, KEGG enrichment analysis of genes in turquoise module. d, KEGG enrichment analysis of genes in brown module. Each sample for WGCNA had three biological replicates.

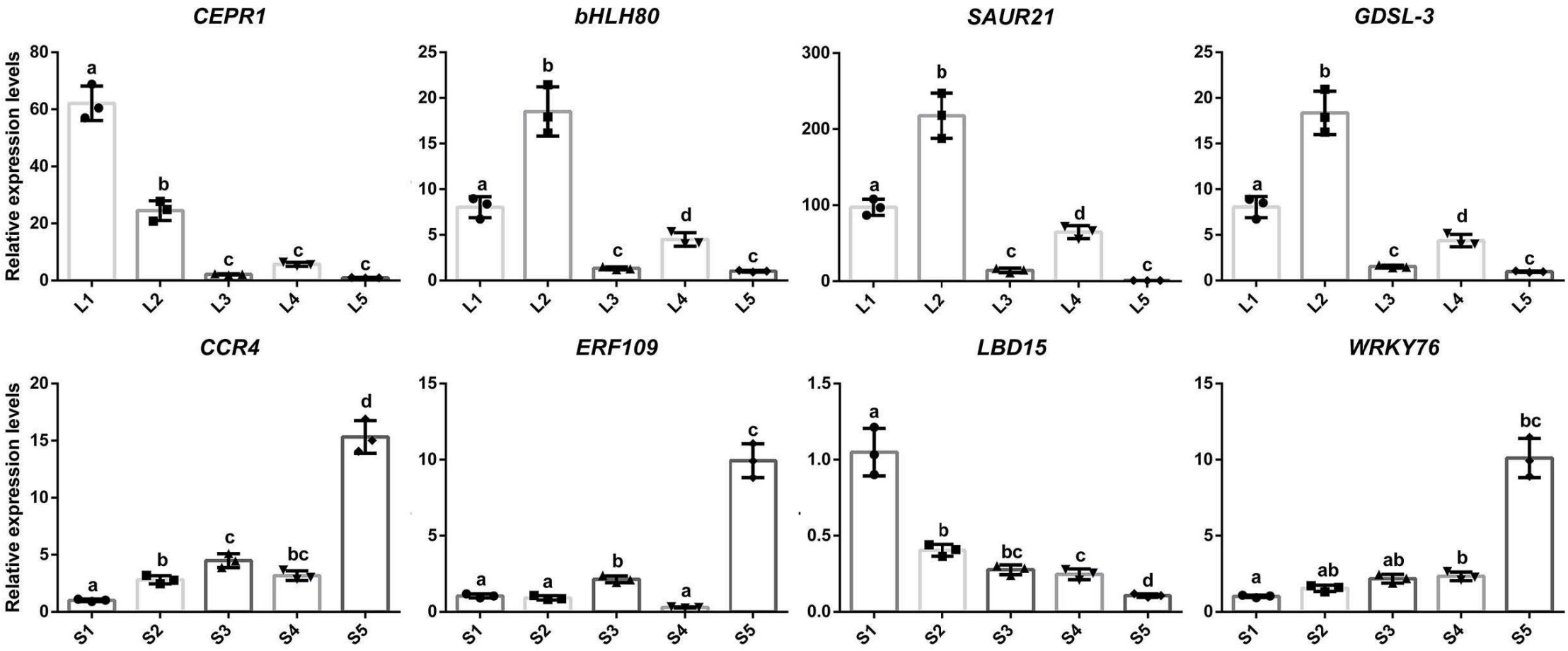

a
Brown Module gene
All gene
2651
30930
265
3093
26
309
2
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function


b
Green Module gene
All gene
358
30930
35
3093
3
309
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function

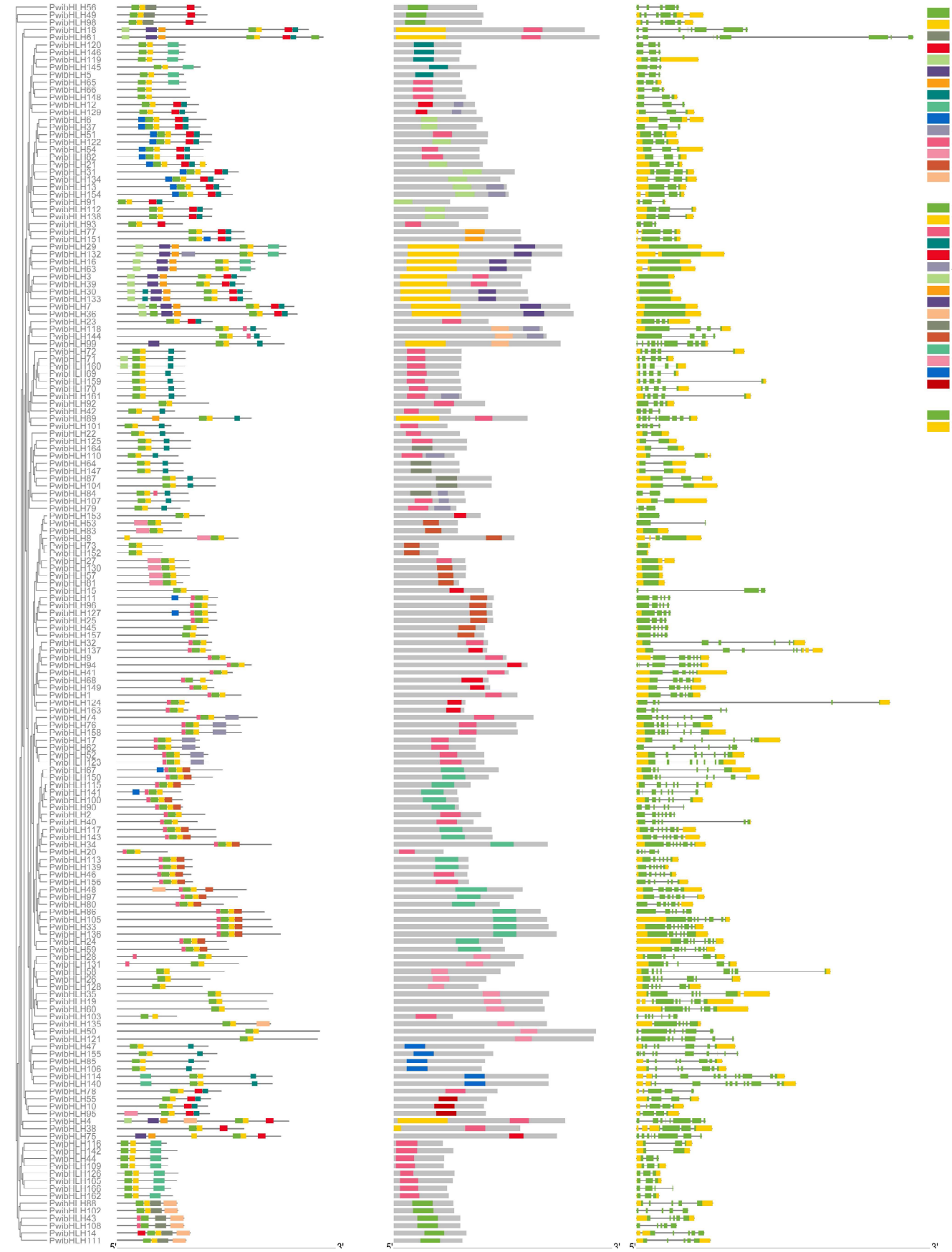

c
Turquoise Module gene
All gene
162
30930
16
3093
1
309
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function


d
Brown Module gene
All gene
64
30930
6
3093
1
309
1
30
Percentage of genes
Number of genes
biological process
cellular component
molecular function

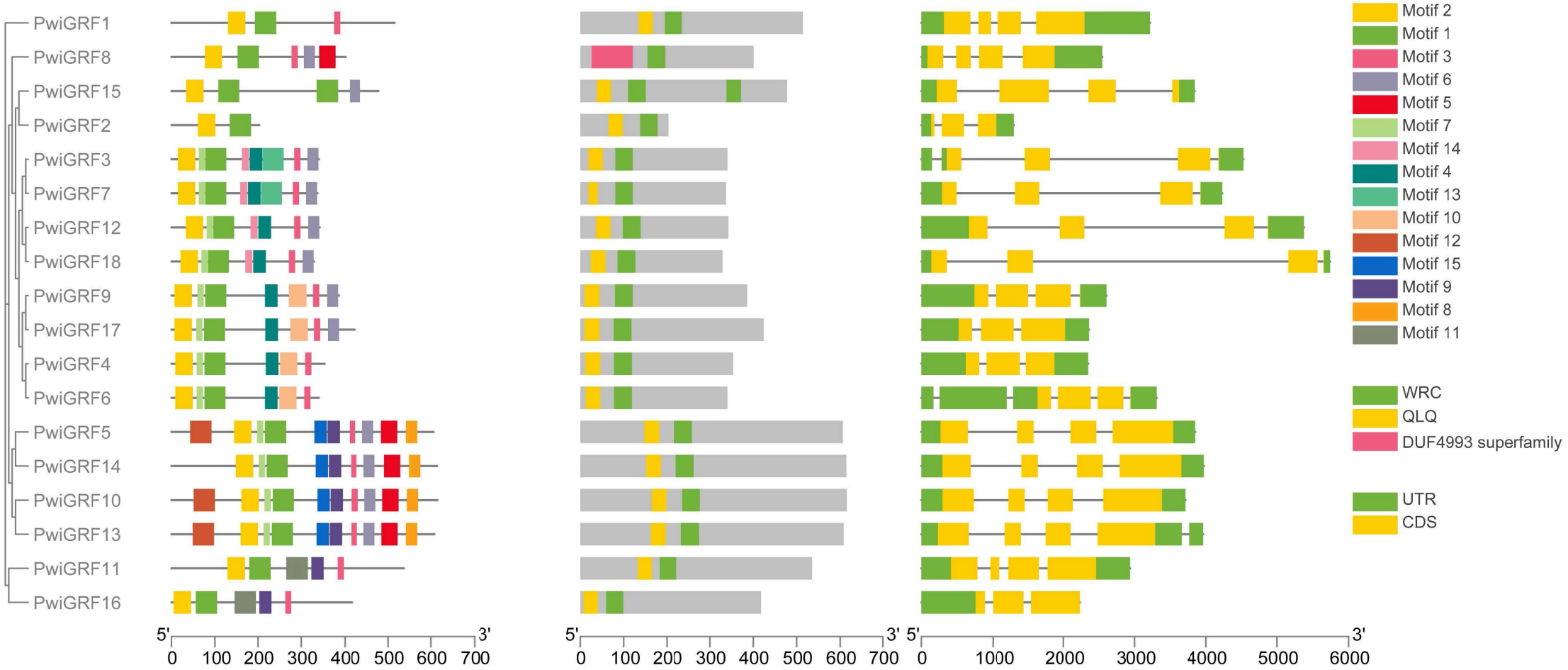
Supplementary Figure 15. GO enrichment analysis of the genes in brown(a) and green(b) module during the leaf development; and the genes in turquoise(c) and brown(d) module during the stem development.


CEPR1
bHLH80
SAUR21
GDSL-3
CCR4
ERF109
LBD15
WRKY76
Relative expression levels
L1
L2
L3
L4
L5
S1
S2
S3
S4
S5

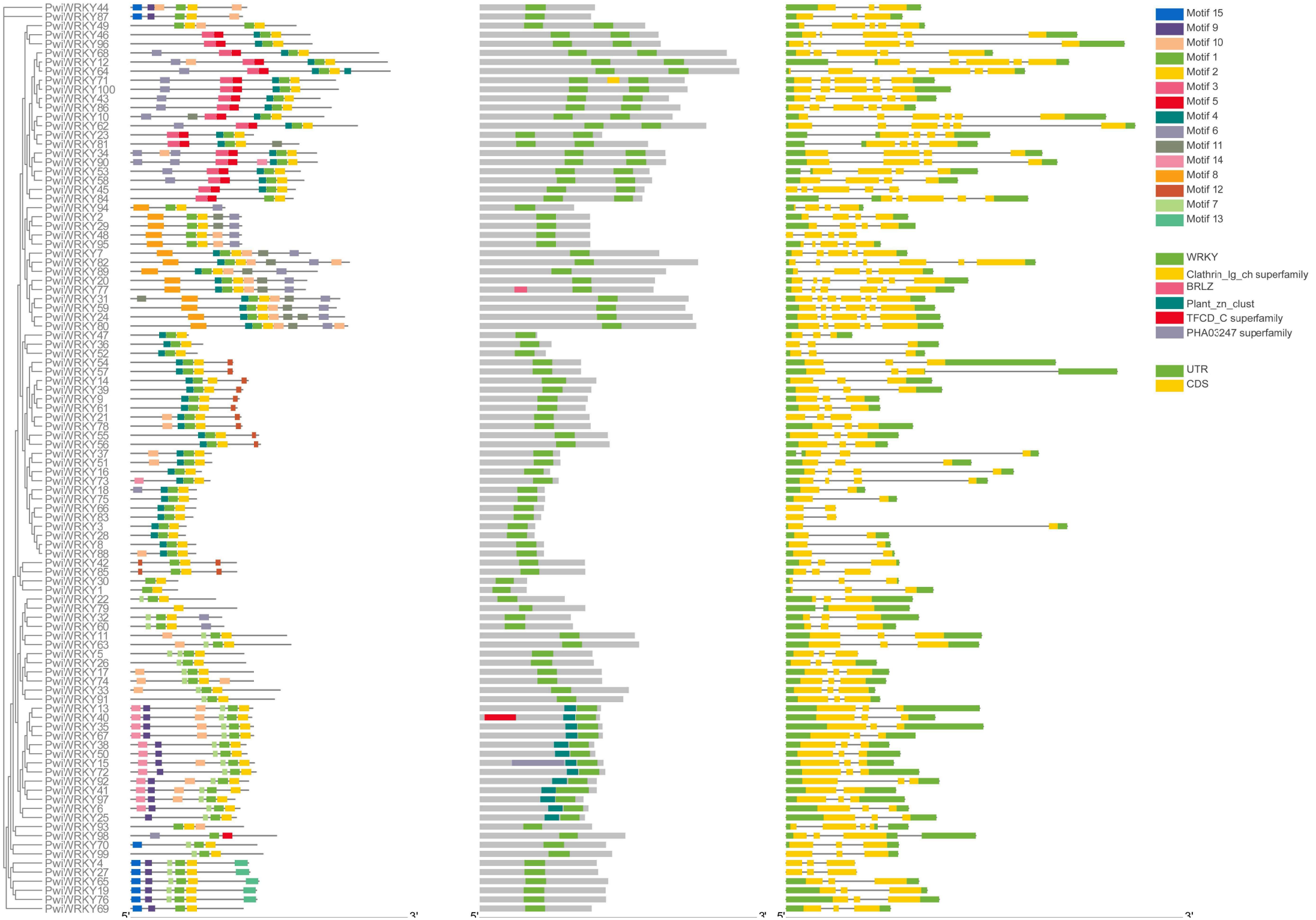
Supplementary Figure 16. Relative expression levels of some identified genes of WCGNA in different development stages of leaf (L1-L5) or stem (S1-S5). Expression profiles of these genes were analyzed using RT-qPCR analysis. The poplar *Ubiquitin* (*UBQ*) gene was used as an internal control and gene expression profiles were evaluated using the $2^{-\Delta\Delta Ct}$ method. Three biological replicates for each tissue were analyzed. Error bars represent the SD of the mean (n=3). Different letters above bars represent statistically significant differences between groups ($p < 0.05$) as determined by one-way ANOVA followed by Dunnett's test. In these groups, the same letter indicates that there is no significant difference between the two groups, different letters indicate that there is a significant difference between the two groups. For *CEPR1*, *bHLH80*, *SAUR1*, and *GDSL-3*, the relative expression level of L5 stage was set to be 1. For *CCR4*, *ERF109*, *LBD15*, and *WRKY76*, the relative expression level of S1 stage was set to be 1.


Motif 1
Motif 2
Motif 11
Motif 5
Motif 7
Motif 9
Motif 8
Motif 4
Motif 13
Motif 15
Motif 6
Motif 3
Motif 14
Motif 12
Motif 10
bHLH_AtILR3_like
bHLH-MYC_N
bHLH_SF superfamily
bHLH_AtORG2_like
bHLH_AtbHLH_like
ACT_UUR-ACR-like
bHLH_AtFAMA_like
bHLH_AtMYC1_like
bHLH_AtAIB_like
bHLH_AtAMS_like
bHLH_AtAIG1_like
bHLH_AtINDL_like
bHLH_AtBPE_like
bHLH_AtPIF_like
bHLH_AtBIM_like
bHLH_AtNAI1_like
CDS
UTR
5'
3'

Supplementary Figure 17. The gene structures and conserved motifs of *Populus wilsonii* bHLH family members. From left to right of this panel are phylogenetic trees, conserved motifs, conserved domains, and gene structures of the PwibHLH members.


PwiGRF1
PwiGRF8
PwiGRF15
PwiGRF2
PwiGRF3
PwiGRF7
PwiGRF12
PwiGRF18
PwiGRF9
PwiGRF17
PwiGRF4
PwiGRF6
PwiGRF5
PwiGRF14
PwiGRF10
PwiGRF13
PwiGRF11
PwiGRF16
5'
3'
0 100 200 300 400 500 600 700
5'
3'
0 100 200 300 400 500 600 700
5'
3'
0 1000 2000 3000 4000 5000 6000
Motif 2
Motif 1
Motif 3
Motif 6
Motif 5
Motif 7
Motif 14
Motif 4
Motif 13
Motif 10
Motif 12
Motif 15
Motif 9
Motif 8
Motif 11
WRC
QLQ
DUF4993 superfamily
UTR
CDS

Supplementary Figure 18. The gene structures and conserved motifs of *Populus wilsonii* GRF family members. From left to right of this panel are phylogenetic trees, conserved motifs, conserved domains, and gene structures of the PwiGRF members.


PwiWRKY44
PwiWRKY87
PwiWRKY49
PwiWRKY46
PwiWRKY96
PwiWRKY68
PwiWRKY12
PwiWRKY64
PwiWRKY71
PwiWRKY100
PwiWRKY43
PwiWRKY86
PwiWRKY10
PwiWRKY62
PwiWRKY23
PwiWRKY81
PwiWRKY34
PwiWRKY90
PwiWRKY53
PwiWRKY58
PwiWRKY45
PwiWRKY84
PwiWRKY94
PwiWRKY2
PwiWRKY29
PwiWRKY48
PwiWRKY95
PwiWRKY7
PwiWRKY82
PwiWRKY89
PwiWRKY20
PwiWRKY77
PwiWRKY31
PwiWRKY59
PwiWRKY24
PwiWRKY80
PwiWRKY47
PwiWRKY36
PwiWRKY52
PwiWRKY54
PwiWRKY57
PwiWRKY14
PwiWRKY39
PwiWRKY9
PwiWRKY61
PwiWRKY21
PwiWRKY78
PwiWRKY55
PwiWRKY56
PwiWRKY37
PwiWRKY51
PwiWRKY16
PwiWRKY73
PwiWRKY18
PwiWRKY75
PwiWRKY66
PwiWRKY83
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PwiWRKY28
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PwiWRKY33
PwiWRKY91
PwiWRKY13
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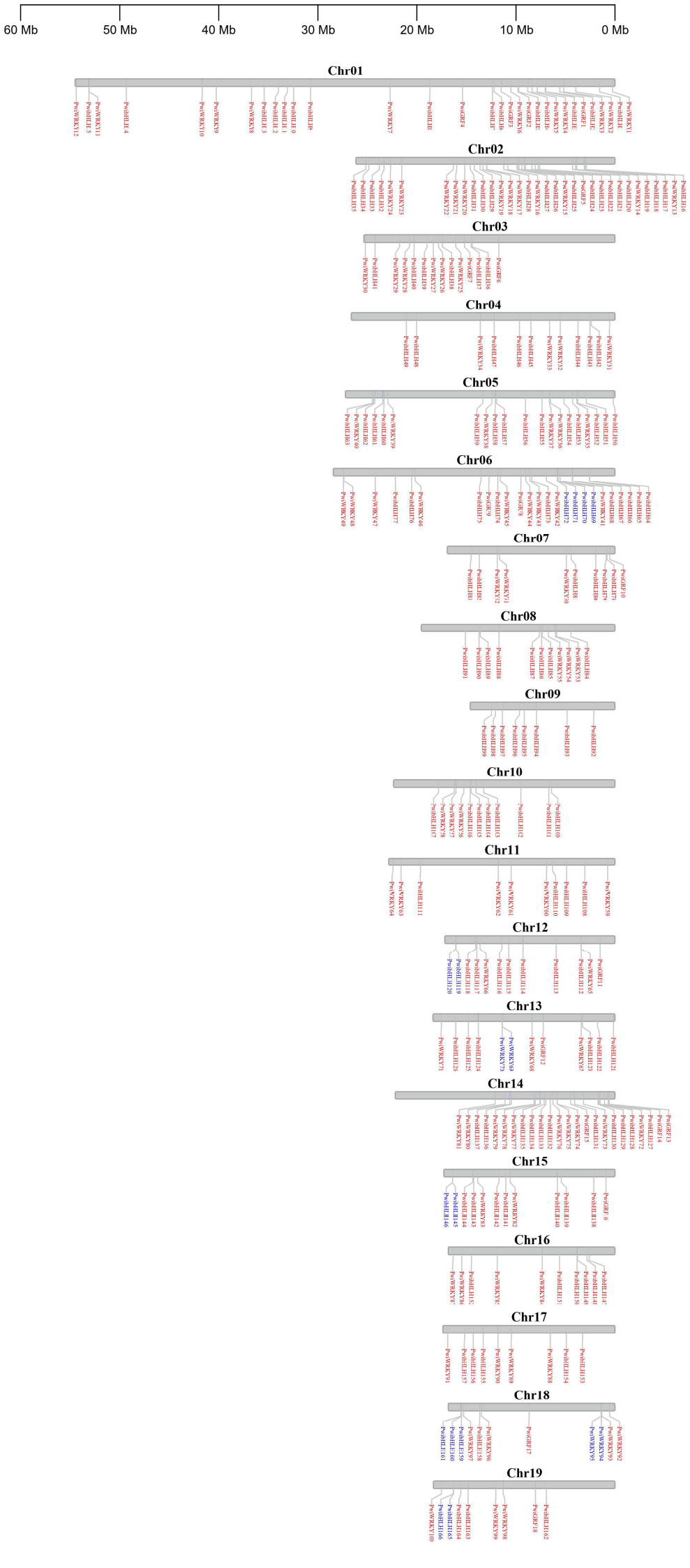
PwiWRKY35
PwiWRKY67
PwiWRKY38
PwiWRKY50
PwiWRKY15
PwiWRKY72
PwiWRKY92
PwiWRKY41
PwiWRKY97
PwiWRKY6
PwiWRKY25
PwiWRKY93
PwiWRKY98
PwiWRKY70
PwiWRKY99
PwiWRKY4
PwiWRKY27
PwiWRKY65
PwiWRKY19
PwiWRKY76
PwiWRKY69
5'
3'
5'
3'
5'
3'
Motif 15
Motif 9
Motif 10
Motif 1
Motif 2
Motif 3
Motif 5
Motif 4
Motif 6
Motif 11
Motif 14
Motif 8
Motif 12
Motif 7
Motif 13
WRKY
Clathrin_lg_ch superfamily
BRLZ
Plant_zn_clust
TFCD_C superfamily
PHA03247 superfamily
UTR
CDS

Supplementary Figure 19. The gene structures and conserved motifs of *Populus wilsonii* WRKY family members. From left to right of this panel are phylogenetic trees, conserved motifs, conserved domains, and gene structures of the PwiGRF members.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Chr01
Chr02
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Chr08
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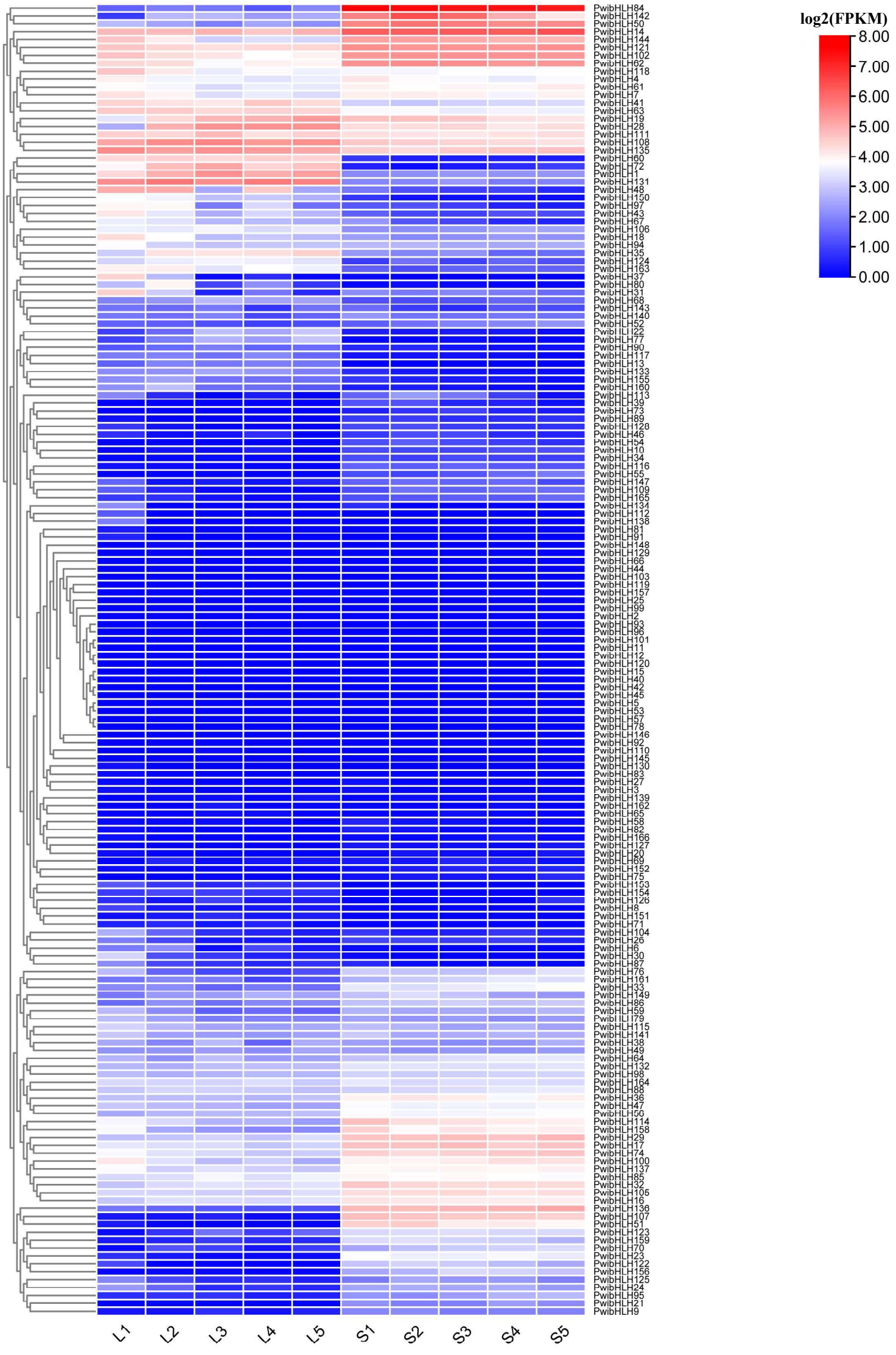
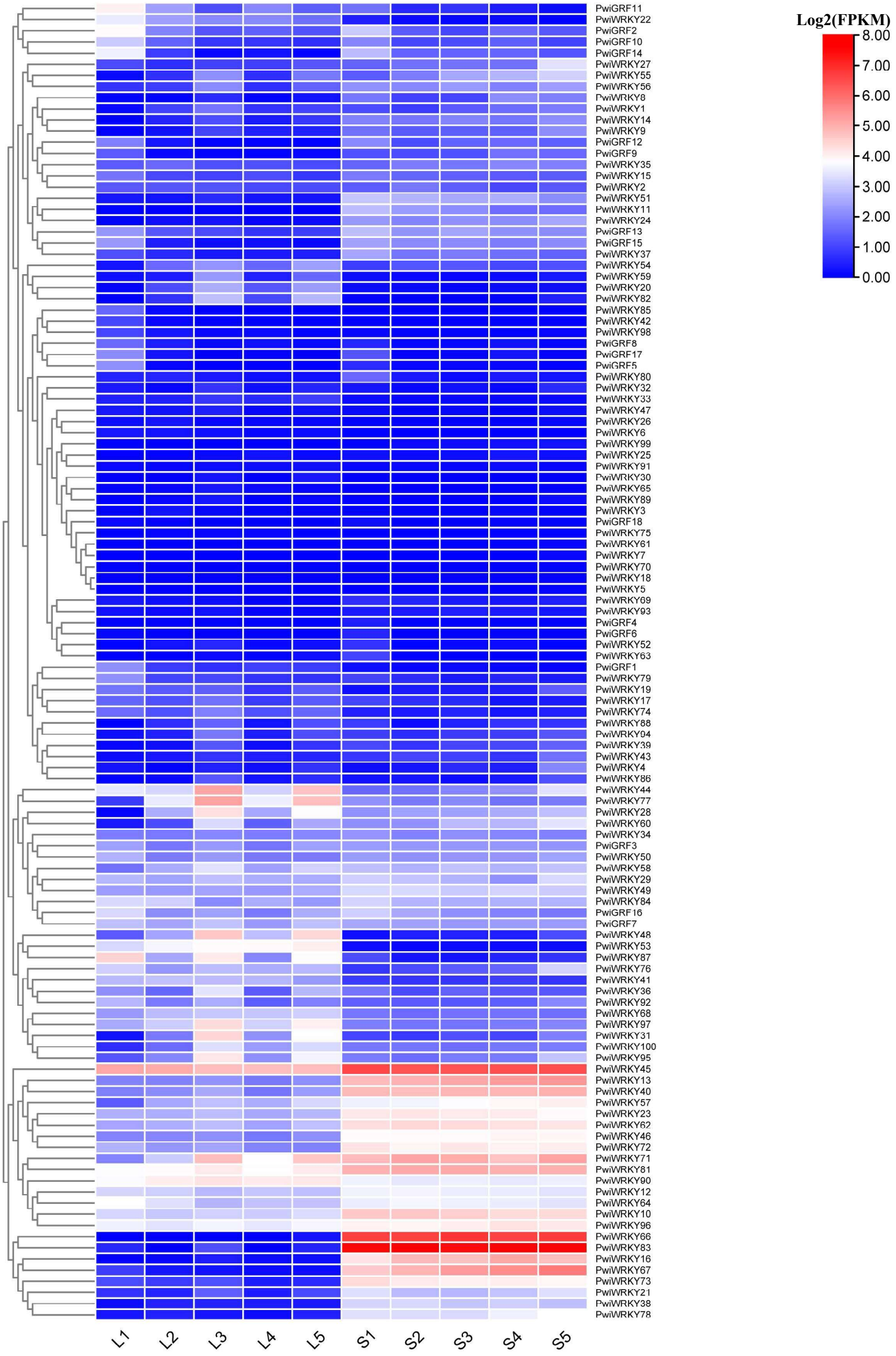
Chr10
Chr11
Chr12
Chr13
Chr14
Chr15
Chr16
Chr17
Chr18
Chr19

Supplementary Figure 20. Chromosomal locations of *Populus wilsonii* bHLH (PwibHLH), GRF (PwiGRF) and WRKY (PwiWRKY) gene families. Tandem duplicates are represented by blue font.


log2(FPKM)
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
L1
L2
L3
L4
L5
S1
S2
S3
S4
S5

Supplementary Figure 21. Heatmap showing the expression level of bHLH gene members in different development stages of leaf and stem in *Populus wilsonii*. The FPKM values are log2-based. Red and blue indicate high and low expression levels, respectively. Each sample for every development stage had three biological replicates.


Log2(FPKM)
8.00
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
PwiGRF11
PwiWRKY22
PwiGRF2
PwiGRF10
PwiGRF14
PwiWRKY27
PwiWRKY55
PwiWRKY56
PwiWRKY8
PwiWRKY1
PwiWRKY14
PwiWRKY9
PwiGRF12
PwiGRF9
PwiWRKY35
PwiWRKY15
PwiWRKY2
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PwiGRF13
PwiGRF15
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PwiWRKY5
PwiWRKY69
PwiWRKY93
PwiGRF4
PwiGRF6
PwiWRKY52
PwiWRKY63
PwiGRF1
PwiWRKY79
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PwiWRKY17
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PwiWRKY39
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PwiWRKY4
PwiWRKY86
PwiWRKY44
PwiWRKY77
PwiWRKY28
PwiWRKY60
PwiWRKY34
PwiGRF3
PwiWRKY50
PwiWRKY58
PwiWRKY29
PwiWRKY49
PwiWRKY84
PwiGRF16
PwiGRF7
PwiWRKY48
PwiWRKY53
PwiWRKY87
PwiWRKY76
PwiWRKY41
PwiWRKY36
PwiWRKY92
PwiWRKY68
PwiWRKY97
PwiWRKY31
PwiWRKY100
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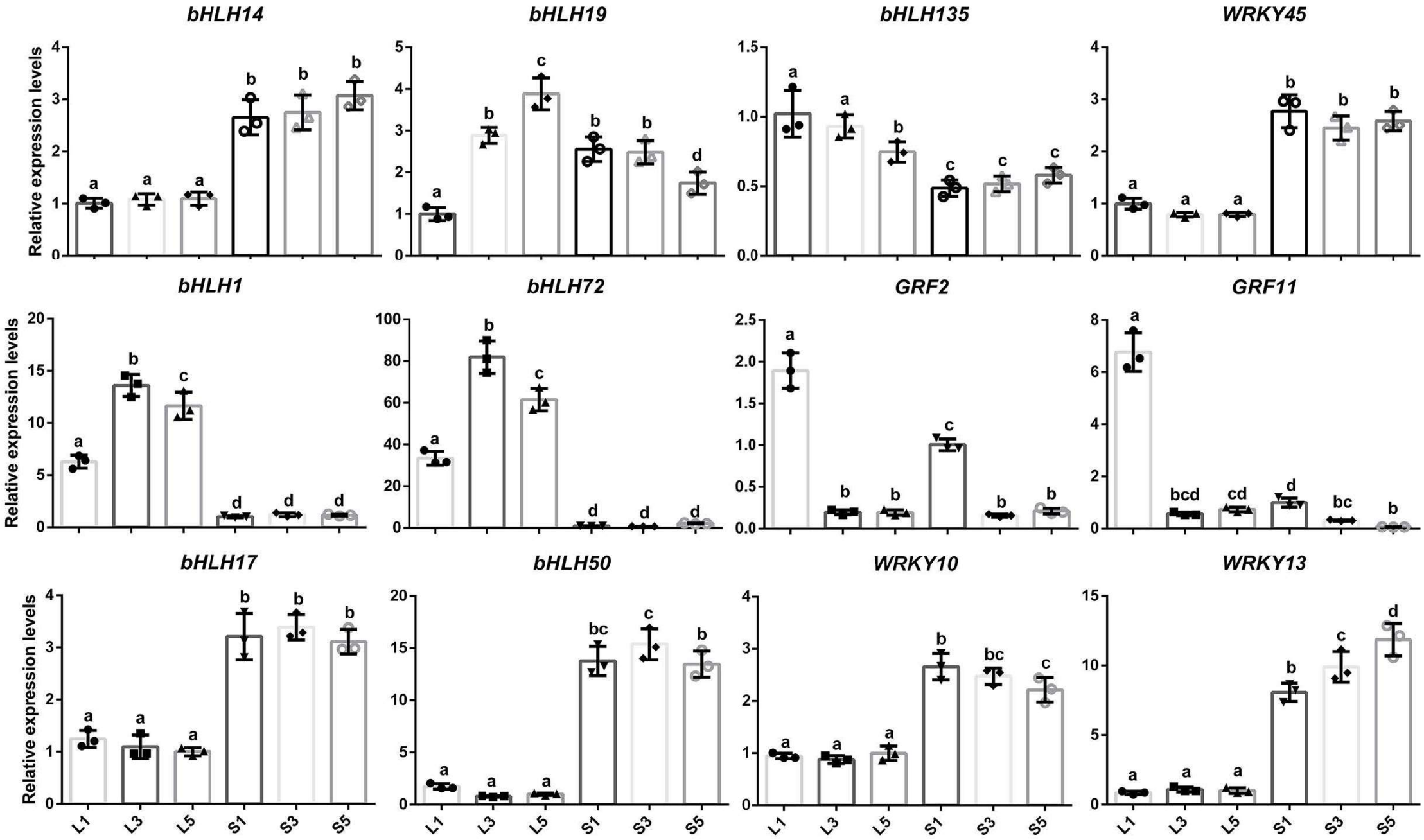
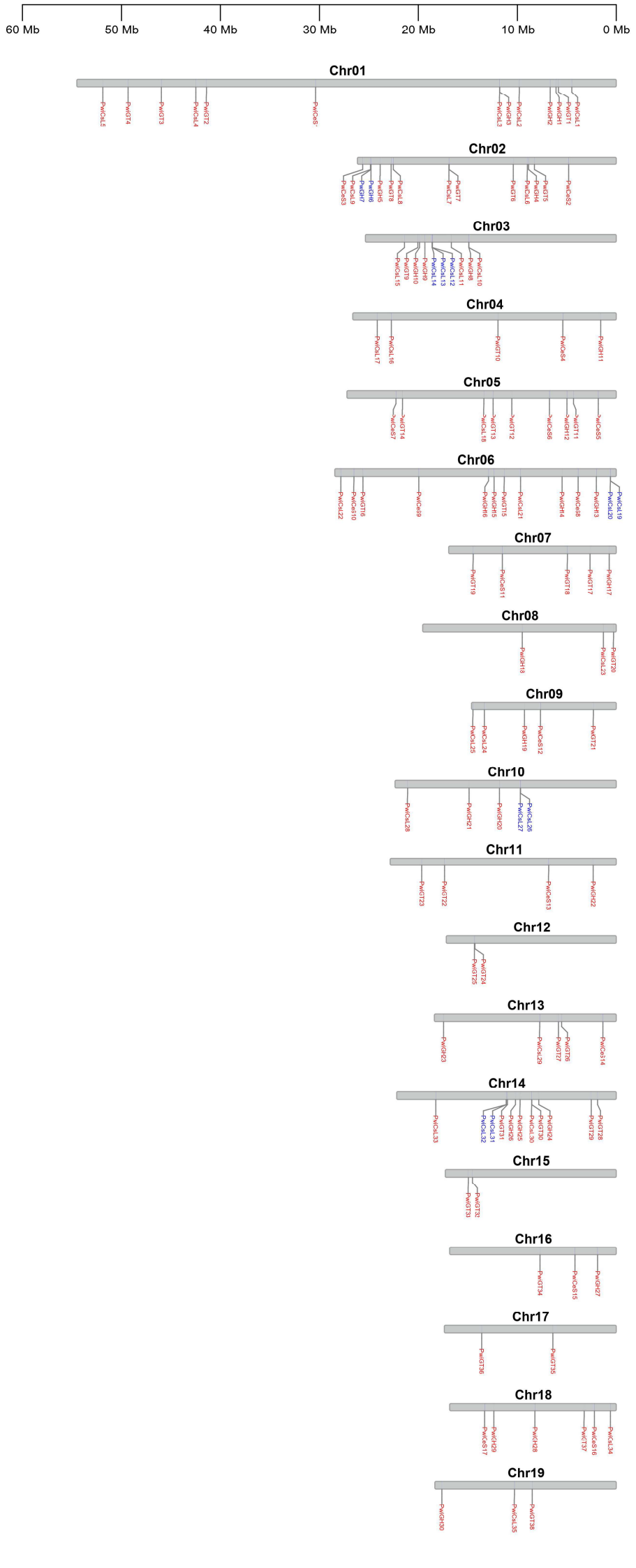
PwiWRKY45
PwiWRKY13
PwiWRKY40
PwiWRKY57
PwiWRKY23
PwiWRKY62
PwiWRKY46
PwiWRKY72
PwiWRKY71
PwiWRKY81
PwiWRKY90
PwiWRKY12
PwiWRKY64
PwiWRKY10
PwiWRKY96
PwiWRKY66
PwiWRKY83
PwiWRKY16
PwiWRKY67
PwiWRKY73
PwiWRKY21
PwiWRKY38
PwiWRKY78
L1
L2
L3
L4
L5
S1
S2
S3
S4
S5

Supplementary Figure 22. Heatmap showing the expression level of GRF and WRKY gene members in different development stages of leaf and stem in *Populus wilsonii*. The FPKM values are log2-based. Red and blue indicate high and low expression levels, respectively. Each sample for every development stage had three biological replicates.


bHLH14
bHLH19
bHLH135
WRKY45
bHLH1
bHLH72
GRF2
GRF11
bHLH17
bHLH50
WRKY10
WRKY13
Relative expression levels
L1
L3
L5
S1
S3
S5

Supplementary Figure 23. Relative expression levels of some bHLH, WRKY and GRF transcription factors in different development stage of leaf (L1, L3 and L5) or stem (S1, S3 and S5). Expression profiles of these genes were analyzed using RT-qPCR analysis. The poplar *Ubiquitin* (*UBQ*) gene was used as an internal control and gene expression profiles were evaluated using the $2^{-\Delta\Delta Ct}$ method. Three biological replicates for each tissue were analyzed. Error bars represent the SD of the mean (n=3). Different letters above bars represent statistically significant differences between groups ($p < 0.05$) as determined by one-way ANOVA followed by Dunnett's test. In these groups, the same letter indicates that there is no significant difference between the two groups, different letters indicate that there is a significant difference between the two groups. For *bHLH14*, *bHLH19*, *bHLH135*, and *WRKY45*, the relative expression level of L1 stage was set to be 1. For *bHLH1*, *bHLH72*, *GRF2*, and *GRF11*, the relative expression level of S1 stage was set to be 1. For *bHLH17*, *bHLH50*, *WRKY10*, and *WRKY13*, the relative expression level of L5 stage was set to be 1.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Chr01
Chr02
Chr03
Chr04
Chr05
Chr06
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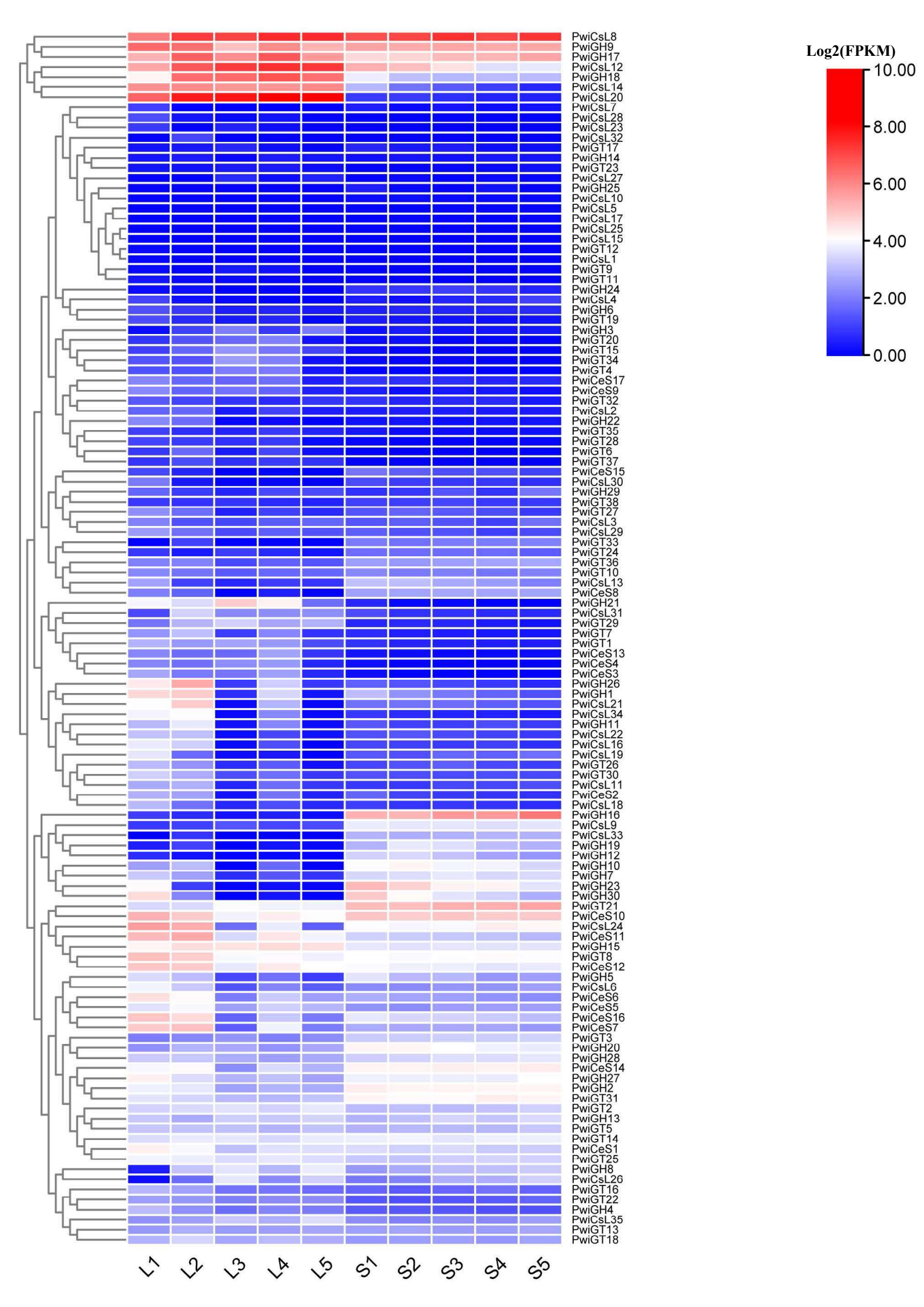
Chr08
Chr09
Chr10
Chr11
Chr12
Chr13
Chr14
Chr15
Chr16
Chr17
Chr18
Chr19

Supplementary Figure 24. Chromosomal locations of *Populus wilsonii* Ces (Pwi Ces), Csl (PwiCsl), GH (PwiGH) and GT (PwiGT) gene families. Tandem duplicates are represented by blue font.


Log2(FPKM)
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8.00
6.00
4.00
2.00
0.00
PwiCsL8
PwiGH9
PwiGH17
PwiCsL12
PwiGH18
PwiCsL14
PwiCsL20
PwiCsL7
PwiCsL28
PwiCsL23
PwiCsL32
PwiGT17
PwiGH14
PwiGT23
PwiCsL27
PwiGH25
PwiCsL10
PwiCsL5
PwiCsL17
PwiCsL25
PwiCsL15
PwiGT12
PwiCsL1
PwiGT9
PwiGT11
PwiGH24
PwiCsL4
PwiGH6
PwiGT19
PwiGH3
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PwiCeS9
PwiGT32
PwiCsL2
PwiGH22
PwiGT35
PwiGT28
PwiGT6
PwiGT37
PwiCeS15
PwiCsL30
PwiGH29
PwiGT38
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PwiGH10
PwiGH7
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PwiGT21
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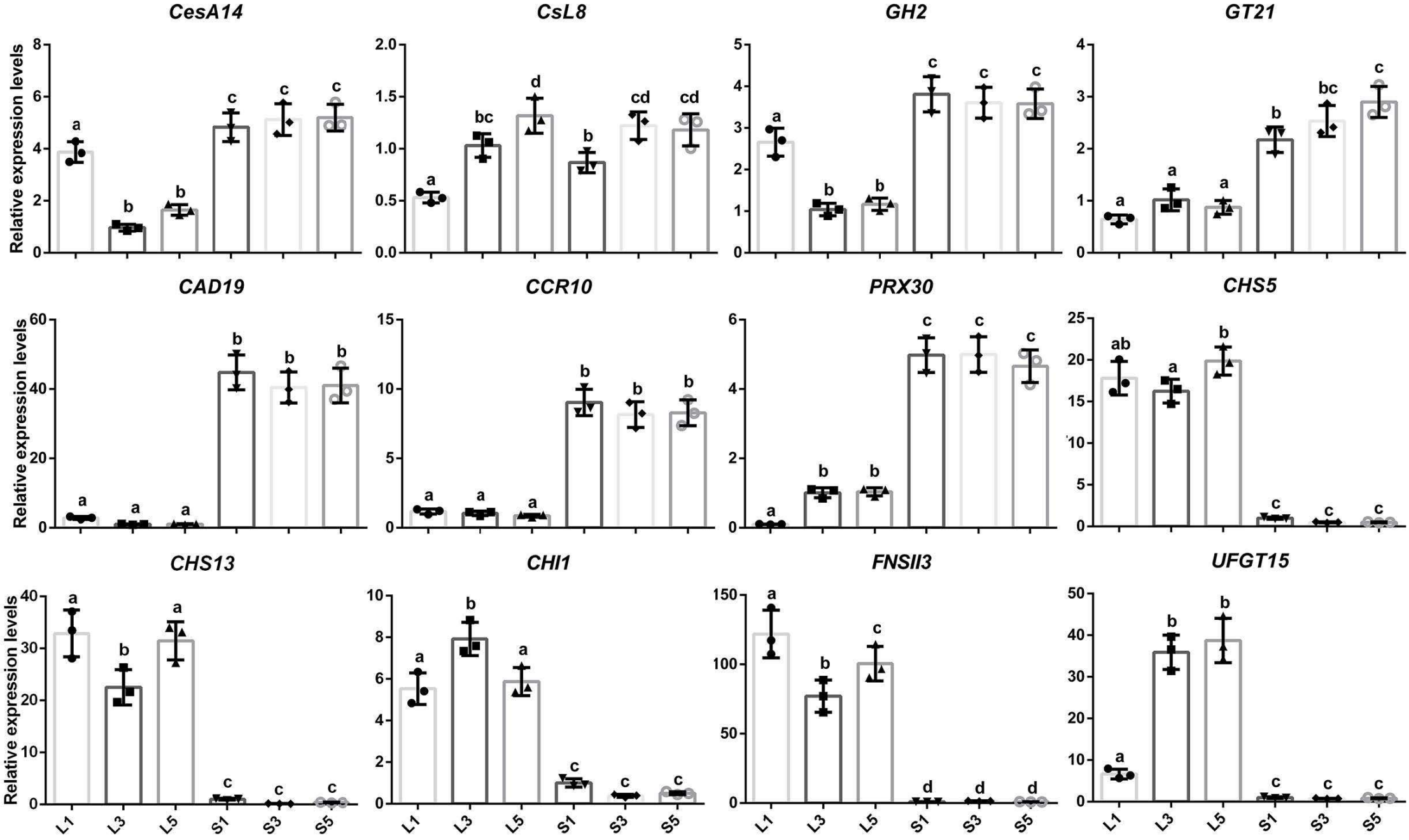
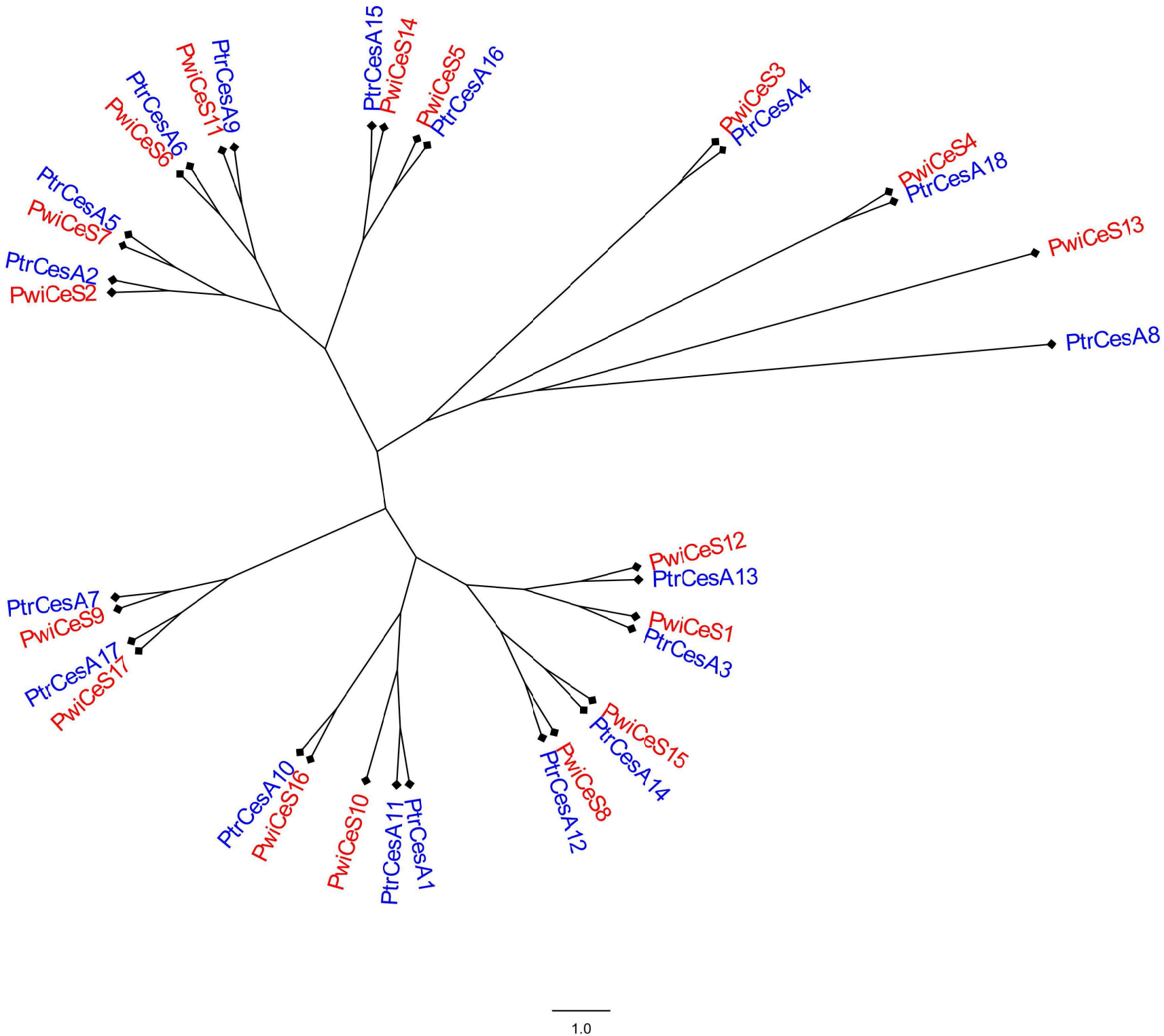
PwiCsL24
PwiCeS11
PwiGH15
PwiGT8
PwiCeS12
PwiGH5
PwiCsL6
PwiCeS6
PwiCeS5
PwiCeS16
PwiCeS7
PwiGT3
PwiGH20
PwiGH28
PwiCeS14
PwiGH27
PwiGH2
PwiGT31
PwiGT2
PwiGH13
PwiGT5
PwiGT14
PwiCeS1
PwiGT25
PwiGH8
PwiCsL26
PwiGT16
PwiGT22
PwiGH4
PwiCsL35
PwiGT13
PwiGT18
L1
L2
L3
L4
L5
S1
S2
S3
S4
S5

Supplementary Figure 25. Heatmap showing the expression level of four Cellulose synthesis gene in different development stages of leaf and stem in *Populus wilsonii*. The FPKM values are log2-based. Red and blue indicate high and low expression levels, respectively. Each sample for every development stage had three biological replicates.


CesA14
CsL8
GH2
GT21
CAD19
CCR10
PRX30
CHS5
CHS13
CHI1
FNSII3
UFGT15
Relative expression levels
L1
L3
L5
S1
S3
S5

Supplementary Figure 26. Relative expression levels of some key enzyme genes involved in cellulose, hemicellulose, lignin and flavonoid biosynthesis in different development stage of leaf (L1, L3 and L5) or stem (S1, S3 and S5). Expression profiles of these genes were analyzed using RT-qPCR analysis. The poplar *Ubiquitin* (*UBQ*) gene was used as an internal control and gene expression profiles were evaluated using the $2^{-\Delta\Delta Ct}$ method. Three biological replicates for each tissue were analyzed. Error bars represent the SD of the mean (n=3). Different letters above bars represent statistically significant differences between groups ($p < 0.05$) as determined by one-way ANOVA followed by Dunnett's test. In these groups, the same letter indicates that there is no significant difference between the two groups, different letters indicate that there is a significant difference between the two groups. For *CesA14*, *CsL8*, *GH2*, and *GT21*, the relative expression level of L3 stage was set to be 1. For *CAD19*, *CCR10*, and *PRX30*, the relative expression level of L3 stage was set to be 1. For *CHS5*, *CHS13*, *CHI1*, *FNSII3*, and *UFGT15*, the relative expression level of S1 stage was set to be 1.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PwiCeS17
PtrCesA10
PwiCeS16
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PtrCesA11
PtrCesA1
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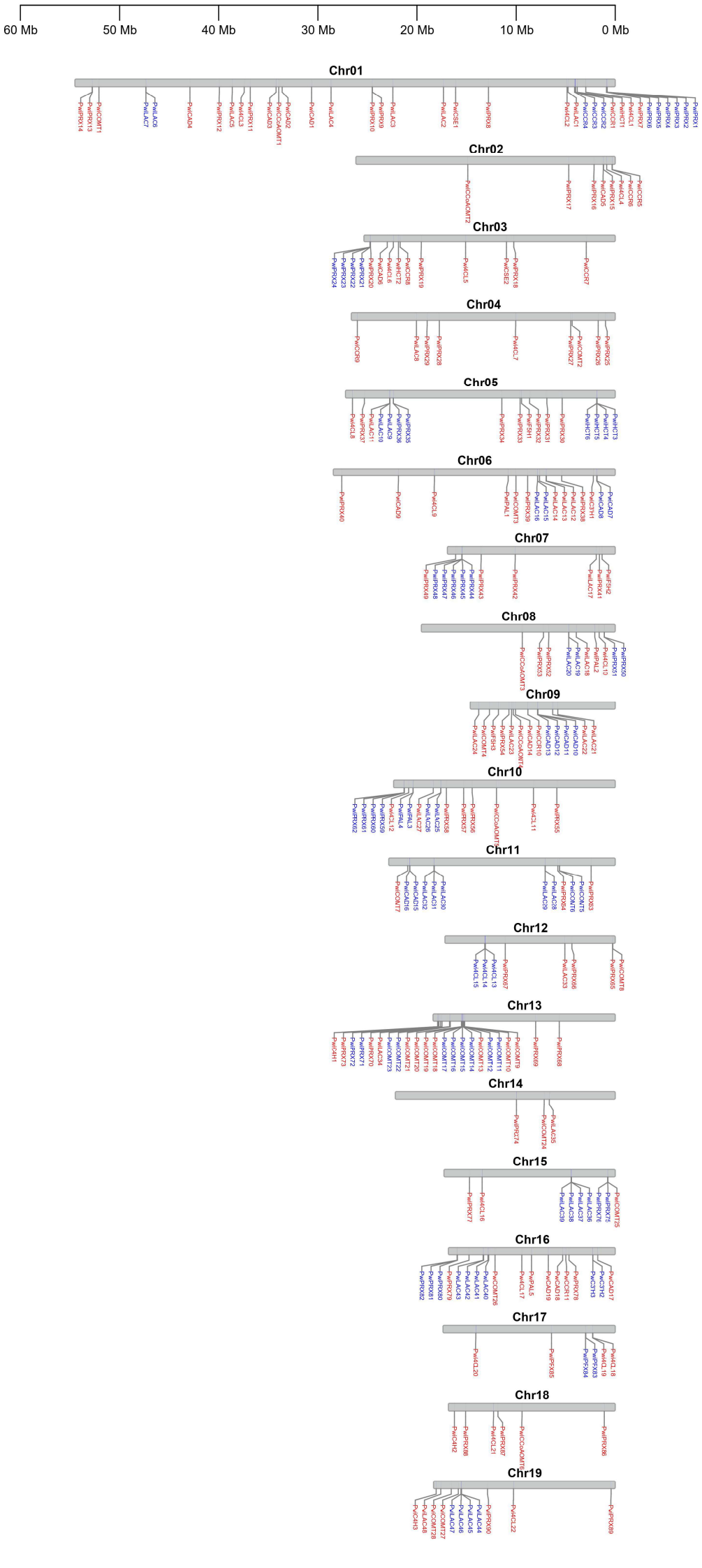
Supplementary Figure 27. Phylogenetic analysis of Cellulose genes in *Populus wilsonii* (red) and *Populus trichocarpa* (blue).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PwCCR2
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PwCCR4
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PwC4CL2
PwPRX8
PwCSE1
PwLAC2
PwPRX9
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PwLAC4
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PwCAD2
PwCCoAOMT1
PwCAD3
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PwCCR8
PwHCT2
PwC4CL6
PwCAD6
PwPRX20
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PwLAC46
PwLAC47
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PwLAC48
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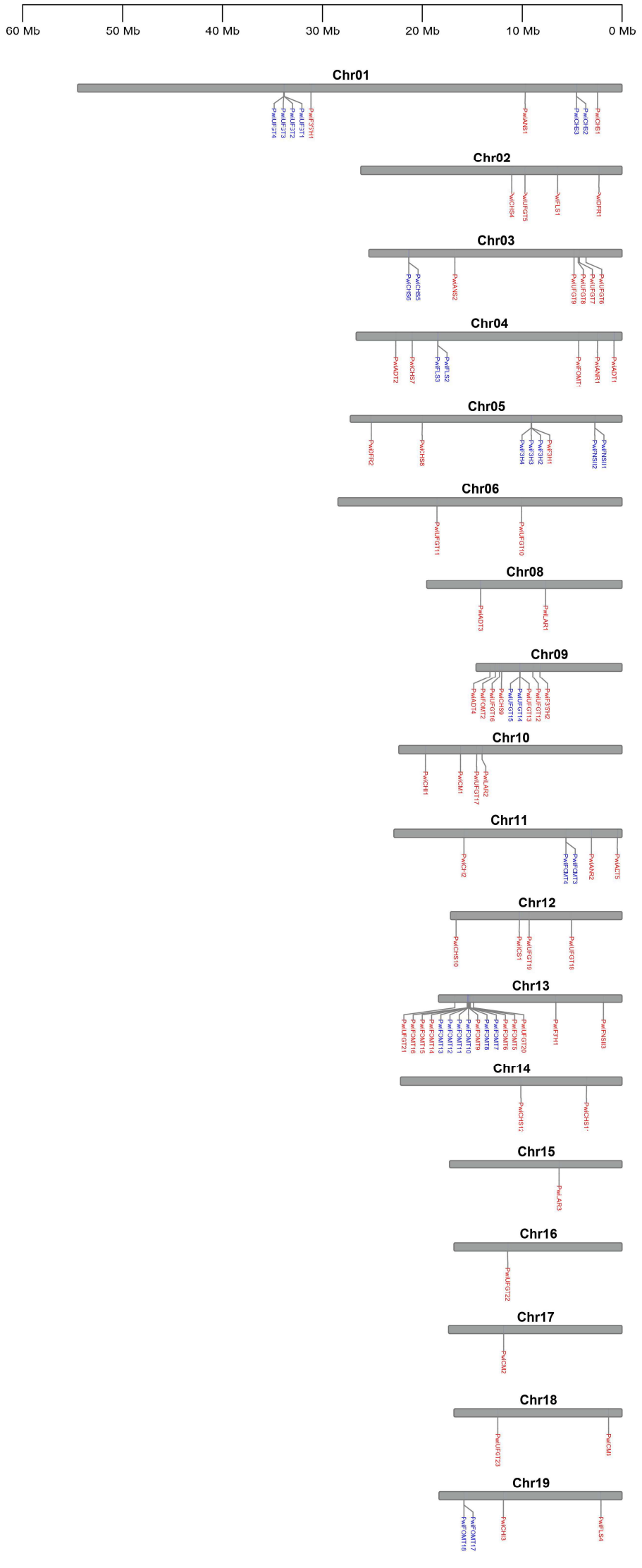
Supplementary Figure 28. Chromosomal locations of Lignin synthesis gene families in *Populus wilsonii*. Tandem duplicates are represented by blue font.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Chr02
PwCHS4
PwFLS1
PwDFR1
Chr03
PwANS2
PwCHS5
PwCHS6
PwCHS7
PwCHS8
Chr04
PwADT2
PwFLS2
PwFLS3
PwANR1
PwADT1
Chr05
PwDFR2
PwF3H1
PwF3H2
PwF3H3
PwF3H4
PwFNSII1
PwFNSII2
Chr06
PwUFGT11
PwUFGT10
Chr08
PwADT3
PwLAR1
Chr09
PwADT4
PwUFGT16
PwUFGT15
PwUFGT14
PwUFGT13
PwUFGT12
PwF3'5'H2
Chr10
PwCHI1
PwCCM1
PwUFGT17
PwLAR2
Chr11
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PwANR2
PwADT5
Chr12
PwCHS10
PwICS1
PwUFGT19
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Chr13
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PwFOMT14
PwFOMT13
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PwFOMT11
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PwFOMT9
PwFOMT8
PwFOMT7
PwFOMT6
PwFOMT5
PwUFGT20
PwF3'H1
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Chr14
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Chr15
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Chr16
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Chr18
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Chr19
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PwFOMT18
PwCHI3
PwFLS4

Supplementary Figure 29. Chromosomal locations of flavonoids synthesis gene families in *Populus wilsonii*. Tandem duplicates are represented by blue font.

Supplementary Tables

Supplementary Table 1. Overview of sequencing data in *Populus wilsonii*.

Reads Type	Total bases (Gb)	Total reads	Reads N50 (Bp)	Mean Length (bp)	Longest Read (bp)	Function
Subreads	475.88	33,348,682	15,645	14,270	387,426	Assembly
CCS read	30.4	2,019,886	15,075	15,049	36,256	
Read length (bp)	**Clean data (Gb)**	**Total Read Pairs**	**Mapped Reads**	**Unique Mapped Read Pairs**	**Q30(%)**	**Function**
150_150	54.30	181,253,818	320,850,736.00	148,575,876	93.24	Assembly
Read length (bp)	**Library**	**Data (Gb)**	**Filtered data (Gb)**	**Depth (×)**	**Q30 (%)**	**Function**
150_150	350 bp	32.10	27.37	62.28	93.08	Survey

Note: Assuming the genome size of *Populus wilsonii* is 440 Mb.

Supplementary Table 2. Estimation of *Populus wilsonii* genome size based on 19 K-mer statistics.

Clean data	Q30 (%)	Sequencing depth（X）	GC content (%)
27.37Gb	93.08	62.28	35.14
k-mer	**Main peak depth of k-mer**	**Estimated genome Size**	**Heterozygote frequencies**
19	26	439.39 Mb	0.42%

Supplementary Table 3. Overview of the type of Hi-C date.

Type	Number	Ratio (%)
Total Read Pairs	181,253,818	100
Mapped Reads	160,425,368	88.5
Unique Paired Alignments	148,575,876	100
Valid Interaction Pairs	83,433,287	56
Dangling End Pairs	50456221	34
Re-ligation Pairs	3,318,277	2
Self-cycle Pairs	992,030	1
Dumped Pairs	10,376,061	6.98

Supplementary Table 4. Evaluation of Benchmarking Universal Single-Copy Orthologs (BUSCO) and Gene Space Coverage Using Core Eukaryotic Gene Mapping Approach (CEGMA) in *Populus wilsonii* genome.

Type	Number	Percent (%)
Complete BUSCOs (C)	1,591	98.57
Complete and single-copy BUSCOs (S)	1338	82.9
Complete and duplicated BUSCOs (D)	253	15.68
Fragmented BUSCOs (F)	4	0.25
Missing BUSCOs (M)	19	1.18
Total BUSCO groups searched	1,614	-
Number of 458 CEG present in assembly	452	98.69
Number of 248 highly conserved CEGs present	233	93.95

Supplementary Table 5. The clean data of NovaSeq6000 and PacBio mapped to reference genome.

Data Type	Total Reads	Map Reads	Map Rate (%)	Coverage at least 10X (%)	Coverage at least 20X (%)	Coverage at least 30X (%)
NovaSeq 6000	214,444,004	213,643,498	99.63	99.32	99.02	98.63
PacBio CCS	2,019,886	2,018,736	99.94	99.76	99.64	99.43

Supplementary Table 6. Statistics of samples used for RNA-Seq sequencing.

Samples	Organ	Clean reads pair	Clean bases(bp)	Mapped Reads	Rate	Q30(%)
bud	Leaf bud	25782466	7702341298	48,095,328	93.27%	0.9471
flowers	Flowers	23045560	6891330014	43,569,328	94.53%	0.9409
flower_bud	Flower bud	25916157	7748961270	49,085,581	94.70%	0.936
leaf	Leaf	24515553	7312556460	46,805,278	95.46%	0.9416
phloem	Phloem	36645427	10965845302	56,998,075	77.77%	0.9428
root	Root	24735027	7387490240	44,133,181	89.21%	0.942
xylem	Xylem	34560191	10286616988	61,182,923	88.52%	0.9347
L1-1	Leaf	21575061	6441369768	40,721,905	94.37%	0.9411
L1-2	Leaf	24247276	7237877412	45,436,030	93.69%	0.9395
L1-3	Leaf	22712343	6778821166	41,167,377	90.63%	0.9459
L2-1	Leaf	27146929	8097157696	51,268,633	94.43%	0.9427
L2-2	Leaf	23155374	6915249116	43,694,345	94.35%	0.9384
L2-3	Leaf	19902165	5947708884	37,704,181	94.72%	0.9423
L3-1	Leaf	24424927	7296339670	45,941,555	94.05%	0.9418
L3-2	Leaf	19758603	5910762376	37,453,786	94.78%	0.9404
L3-3	Leaf	19639126	5862503642	37,025,030	94.26%	0.9348
L4-1	Leaf	24120701	7194014772	45,692,780	94.72%	0.9429
L4-2	Leaf	25240674	7538611890	47,583,169	94.26%	0.9408
L4-3	Leaf	25578929	7634602964	48,485,165	94.78%	0.944
L5-1	Leaf	23520561	7019809848	44,475,965	94.55%	0.9414
L5-2	Leaf	25735037	7672017466	48,427,848	94.09%	0.942
L5-3	Leaf	20405526	6095447932	38,349,309	93.97%	0.9448
S1-1	Stem	22800715	6812742042	42,980,243	94.25%	0.9106
S1-2	Stem	22836218	6828492916	42,832,487	93.78%	0.9087
S1-3	Stem	22735787	6802845532	43,103,569	94.79%	0.921
S2-1	Stem	19265879	5762734554	35,745,131	92.77%	0.9195
S2-2	Stem	20989232	6280314128	39,433,787	93.94%	0.9196
S2-3	Stem	22355168	6687921290	41,716,552	93.30%	0.9119
S3-1	Stem	22815587	6826112342	43,028,897	94.30%	0.9139
S3-2	Stem	22348949	6673546576	41,673,496	93.23%	0.9125
S3-3	Stem	22312298	6672517446	41,339,946	92.64%	0.911
S4-1	Stem	22410173	6701281464	41,481,410	92.55%	0.9154
S4-2	Stem	23031748	6888293788	43,192,485	93.77%	0.9225
S4-3	Stem	22370476	6686367792	41,527,114	92.82%	0.9142
S5-1	Stem	19240953	5757499444	34,723,306	90.23%	0.9194
S5-2	Stem	19540603	5844492582	36,650,703	93.78%	0.9177
S5-3	Stem	22383929	6696077498	41,118,786	91.85%	0.9144

Supplementary Table 7. Statistics of repeat contents in *Populus wilsonii* genome.

Type	Number	Length(bp)	Rate (%)
Retroelement	213,466	122,441,381	25.65
LTR/Gypsy	91,583	61,579,392	12.9
LTR/Copia	46,293	36,611,814	7.67
LTR/others	50624	18,528,103	3.89
LINE	23,221	5,536,069	1.16
SINE	1,745	186,003	0.04
DNA transposon	176,705	59,967,949	12.56
tandem repeat	318,075	56,056,995	11.74
Total	708,246	238,466,325	49.96

Supplementary Table 8. Statistics on gene information of different species.

	Species	*P. trichocarpa*	*P. wilsonii*	*A. thaliana*	*P. deltoides*	*P. euphratica*
Gene	Number	34,699	38,054	27,628	44,853	36,426
	Length(bp)	126,544,386	133,688,470	65,552,768	136,044,577	126,214,227
	Average Length(bp)	3646.92	3513.13	2372.69	3033.12	3464.95
Exon	Number	177,938	198,300	141,285	212,920	201,601
	Average Number	5.13	5.21	5.11	4.75	5.53
	Length(bp)	43,737,174	68,941,684	33,622,504	48,528,846	54,848,341
	Average Length(bp)	1260.47	1811.68	1216.97	1081.95	1505.75
CDS	Number	177,938	190,693	141,285	212,920	193,128
	Average Number	5.13	5.01	5.11	4.75	5.3
	Length(bp)	43,737,174	50,284,380	33,622,504	48,528,846	41,373,495
	Average Length(bp)	1260.47	1321.4	1216.97	1081.95	1135.82
Intron	Number	143,239	160,246	113,657	168,067	165,175
	Average Number	4.13	4.21	4.11	3.75	4.53
	Length(bp)	82,807,212	64,746,786	31,930,264	87,515,731	71,365,886
	Average Length(bp)	2386.44	1701.44	1155.72	1951.17	1959.2

Supplementary Table 9. Evaluation the Gene Completeness by Benchmarking Universal Single-Copy Orthologs (BUSCO) in *Populus wilsonii* genome.

Type	Number	Percent
Complete BUSCOs(C)	1,558	96.53%
Complete and single-copy BUSCOs(S)	1,317	81.60%
Complete and duplicated BUSCOs(D)	241	14.93%
Fragmented BUSCOs(F)	37	2.29%
Missing BUSCOs(M)	19	1.18%
Total Lineage BUSCOs	1,614	

Supplementary Table 10. Statistical information of gene function annotation

Annotation Database	Annotated Number	Annotated Ratio (%)
GO Annotation	30,762	80.84
KEGG Annotation	27,948	73.44
KOG Annotation	20,082	52.77
Pfam Annotation	31,963	83.99
Swissprot Annotation	30,446	80.01
TrEMBL Annotation	37,391	98.26
eggNOG Annotation	31,448	82.64
nr Annotation	37,435	98.37
All Annotated	37,547	98.67

Supplementary Table 11. Statistical information of non-coding RNA in *P. wilsonii* genome

Type	Number	Length(bp)
rRNA	8,186	11,428,311
tRNA	5,066	381,283
miRNA	126	14,650
snRNA	101	14,963
snoRNA	474	51,055
Total	13,953	11,890,262

Supplementary Table 12. Species and gene sets used in this study

Species	Abbreviations	Database	Version
Populus euphratica	*P. euphratica*	BIG Submission	V3.1
Populus alba	*P. alba*	BIG Submission	V3.1.1
Populus deltoides	*P. deltoides*	phytozome	v2.1
Populus trichocarpa	*P. trichocarpa*	phytozome	v4.1
Arabidopsis thaliana	*A. thaliana*	phytozome	Araport11
Oryza sativa	*O. sativa*	phytozome	V7_JGI
Manihot esculenta	*M. esculenta*	phytozome	v7.1
Vitis vinifera	*V. vinifera*	phytozome	V2.1
Salix purpurea	*S. purpurea*	phytozome	v5_1

Supplementary Table 13. Orthologous Groups in *P. wilso*nii and other plant species

Item	*A. thaliana*	*M. esculenta*	*O. sativa*	*P. alba*	*P. deltoides*	*P. euphratica*	*P. trichocarpa*	*P. wilsonii*	*S. purpurea*	*V. vinifera*
Number of genes	27,628	33,849	39,049	40,213	44,853	36,426	34,699	38,054	35,125	31,845
Number of genes in orthogroups	18,385	30,635	21,136	32,537	39,386	30,433	32,862	35,618	33,268	23,665
Number of unassigned genes	9,243	3,214	17,913	7,676	5,467	5,993	1,837	2,436	1,857	8,180
Percentage of genes in orthogroups	66.5	90.5	54.1	80.9	87.8	83.5	94.7	93.6	94.7	74.3
Percentage of unassigned genes	33.5	9.5	45.9	19.1	12.2	16.5	5.3	6.4	5.3	25.7
Number of orthogroups containing species	12,663	18,195	12,589	20,107	22,715	20,499	20,630	21,338	19,011	16,934
Percentage of orthogroups containing species	33.6	48.2	33.4	53.3	60.2	54.3	54.7	56.6	50.4	44.9
Number of species-specific orthogroups	2,520	697	4,120	512	521	227	56	140	453	1,001
Number of genes in species-specific orthogroups	6,823	2,669	11,486	1,211	1,306	504	156	1,072	2,531	3,448
Percentage of genes in species-specific orthogroups	24.7	7.9	29.4	3	2.9	1.4	0.4	2.8	7.2	10.8

Supplementary Table 14. Gene copy number of key genes involved in cellulose synthesis in *Populus wilsonii* and 4 other *Salicaceae* species.

Gene	*S. purpurea*	*P. alba*	*P. deltoides*	*P. euphratica*	*P. trichocarpa*	*P. wilsonii*
CES	16	21	17	23	18	17
CsL	27	41	36	37	36	35
GH	34	36	35	33	33	30
GT	38	42	47	35	40	38

Supplementary Table 15. Gene copy number of key genes involved in lignin and flavonoids synthesis in *Populus wilsonii* and 4 other *Salicaceae* species.

Type	Gene	*S. purpurea*	*P. alba*	*P. deltoides*	*P. euphratica*	*P. trichocarpa*	*P. wilsonii*
Commom	CM	4	5	3	3	3	3
	ADT	8	6	8	5	5	5
	PAL	5	6	6	6	5	5
	C4H	4	4	4	3	4	3
	4CL	16	16	23	21	19	22
Lignin	HCT	3	5	9	4	5	6
	LAC	44	43	45	40	49	48
	PRX	95	98	113	81	97	90
	CCoCAMT	4	6	6	5	6	6
	CCR	15	8	22	12	13	11
	COMT	15	33	42	30	33	28
	CSE	2	2	2	2	2	2
	F5H	4	4	3	2	3	3
	C3H	4	3	3	1	3	3
	CAD	16	18	18	15	18	19
Flavonoids	ANR	1	1	2	2	2	2
	ANS	2	3	2	2	2	2
	CHI	3	5	3	4	4	3
	CHS	10	15	17	10	13	12
	DFR	2	2	4	2	2	2
	FLS	4	5	3	4	4	4
	F3'H	1	1	1	1	1	1
	F3'5'H	1	3	2	1	2	2
	FNS II	2	1	1	0	3	3
	FOMT	12	20	19	16	18	18
	ICS	1	1	1	2	1	1
	LAR	2	3	3	4	3	3
	F3H	3	2	4	1	2	4
	UFGT	22	28	16	25	26	23

Supplementary Table 16. Primers used in this study for qRT-PCR analysis.

Gene Name	Gene ID	Forward Primer sequence (5´-3´)	Reverse primer sequence (5´-3´)
bHLH1	Pwi01G001590	ACGAATTTGAACCAAAACCCACT	TATGCATGCACACCTTGCAC
GH2	Pwi01G006950	ACAGGCATGATGGTTTCCGT	CCTGACAAAGCCACAAGTGC
GRF2	Pwi01G010250	TGGAACGGAACATGAGCCAG	GCACTACCGATTCCAGGGAG
GDSL-3	Pwi01G017170	CGGGGAGCAGTGACTTTCTT	GGCATCAGCGTTGATCCTTG
WRKY10	Pwi01G032650	CATGCAACCCCAATTACGGC	GCCTGAGATGGATGAACGCT
bHLH14	Pwi01G037250	TCGGTGCGGAAATTGATGGA	AGGCTCCAAGATAGAGCCCA
WRKY13	Pwi02G004060	AGCTGCACACCTACAATGTCA	GAACTCTGATCCGAGGAGCG
bHLH17	Pwi02G004200	AAATGTTGGTGCTGCCATGC	GACGGATCTTCCAAGCACCT
bHLH19	Pwi02G005150	GTGGCAAGATGGGTAAGCCT	ATTGTGCTGGAATCCTCGGG
CsL8	Pwi02G020210	GGTTCATGTCCCCGTGATGTAA	CAACCCACCTCTTGACCCC
CHS5	Pwi03G016840	AGCCTAACCGAGGCATTCAA	TTCTCTGGTTTCAGCGCCAA
CEPR1	Pwi04G000150	TATCGGGTGGAGTCCCATCA	GCCTCCATACACGCTCTTCA
SAUR21	Pwi04G014630	TGGCCATCCTTCTTAAGGGTA	AAGGAAGTGTAAGACCGCCC
bHLH50	Pwi05G000190	GCTACGGCCTGTAGTTCACA	TTGCAAATGCTCACCAGCCT
PRX30	Pwi05G006230	GTTTGTCCAGGCACGGTTTC	GTGACCCTGAAAGGGCTACC
bHLH72	Pwi06G006550	CGTGGTCCCCAACATTACCA	TCAGCTTGAATTCTTCTCTCTTGC
WRKY45	Pwi06G011910	GAACCAGGAGGAGGATCCAA	ACCTTCTTTTTCACTGGACAACT
bHLH80	Pwi07G002170	TGGCAGGTGAAGATGTGACC	TGCCCGCACATGAATGTAGT
GT21	Pwi09G001110	AGGAACTCTACTCGACCAGG	TTGGAAGCCTCACGGTTCTG
CCR10	Pwi09G007320	TACTAACGGCGGCAAAGGAG	CTGTACCCGGATTCACCACC
UFGT15	Pwi09G009350	AGCTTTATTGGGCGGGGA	CCCCCTTCTTCAACTGCCTTC
ERF109	Pwi09G009600	TTAACACTGCAGAGGAGGCG	AGAACGCATTGTCTTTCCCCA
LBD15	Pwi10G015830	GAGGCAAGGCTCAGAGATCC	GGAGGAGAATTGGCAGCGTA
CHI1	Pwi10G018290	TGGCGCAGGGGCGAG	CCGAATATTGGAGGCCCGT
GRF11	Pwi12G001090	AACACCAGCAGCACCCCAG	TGGCAAGAGTTGGACTGCTATT
CesA14	Pwi13G001780	CTTTGCCCCAAGTCCCTCTC	CCACTGCCACCAATAGGAGC
FNSII3	Pwi13G002490	ACGAAGAAAGGAACTGCGCC	GTTATCAGTCCCTGAACACCTGA
WRKY76	Pwi14G007110	GGACTTGGGCTCTAAGGACG	TGGGGTCTGCACATTTTGGT
bHLH135	Pwi14G008540	TGCAACAAGACCAACAAGCG	AGGAACTATCTGACTTGCCGA
CHS13	Pwi14G011620	TCAGCTGCACAAACCATCCT	ACCAGGGTGTGCAATCCAAA
CAD19	Pwi16G007310	AAGCCTCTTGAGCTTCCTGC	CCAAACGTTCCATTGCCGTA
CCR4	Pwi19G008730	ATGTCACACCTCTCACTCCAC	TCAACGACATTCCTCGGCAC
UBQ	Pwi01G037400	GTTGATTTTTGCTGGGAAGC	GATCTTGGCCTTCACGTTGT