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Supplemental information

Chromosome-scale assembly reveals asymmetric paleo-subgenome evolution and targets for the acceleration of fungal resistance breeding in the nut crop, pecan

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Title: Chromosome-scale assembly reveals the asymmetric paleo-subgenomes evolution and targets for accelerating fungal resistance breeding in nut crop, pecan

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Running title: The chromosome-level genome of pecan

Short summary:

A high-quality chromosome-scale reference genome of pecan reveals two paleo-subgenomes with asymmetry in their features and evolution. Re-sequencing on pecan scab-associated core accessions identifies several key genes in chitin response pathway that may be important susceptibility factors for fungal diseases and valuable resources for pecan breeders. The study provides an example for production and quality improvement of tree nut crops.

Supplemental Information (SI)

Supplemental Figures and legends

Figure S1. Distribution of Nanopore reads.

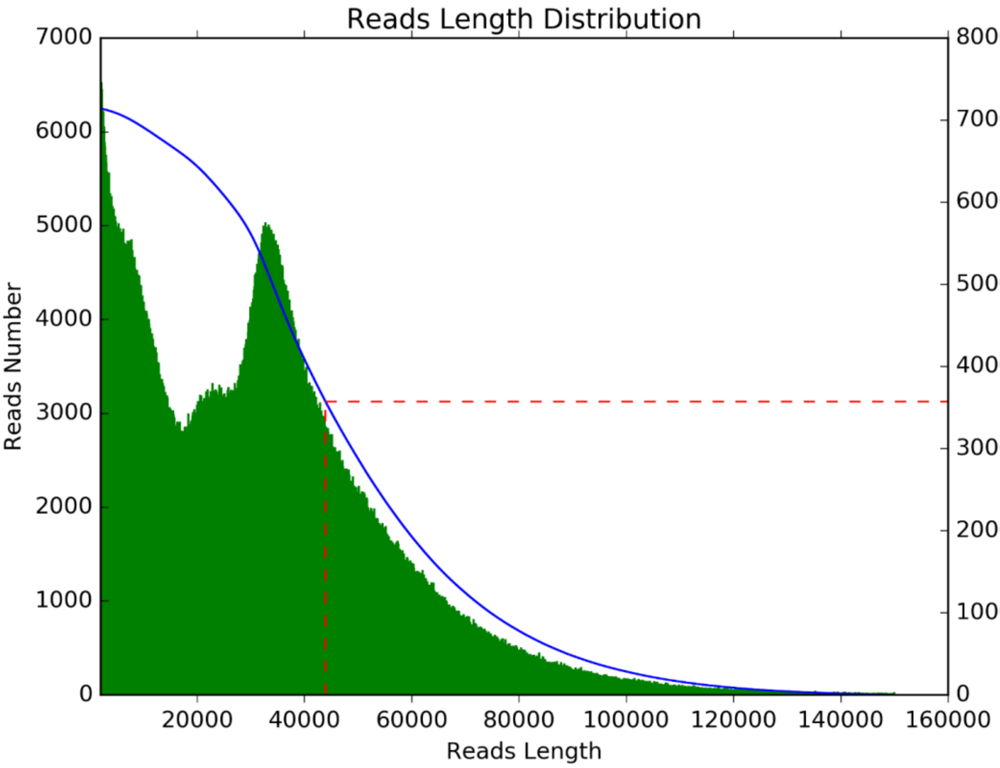


Figure S2. Genome survey by K-mer analysis.

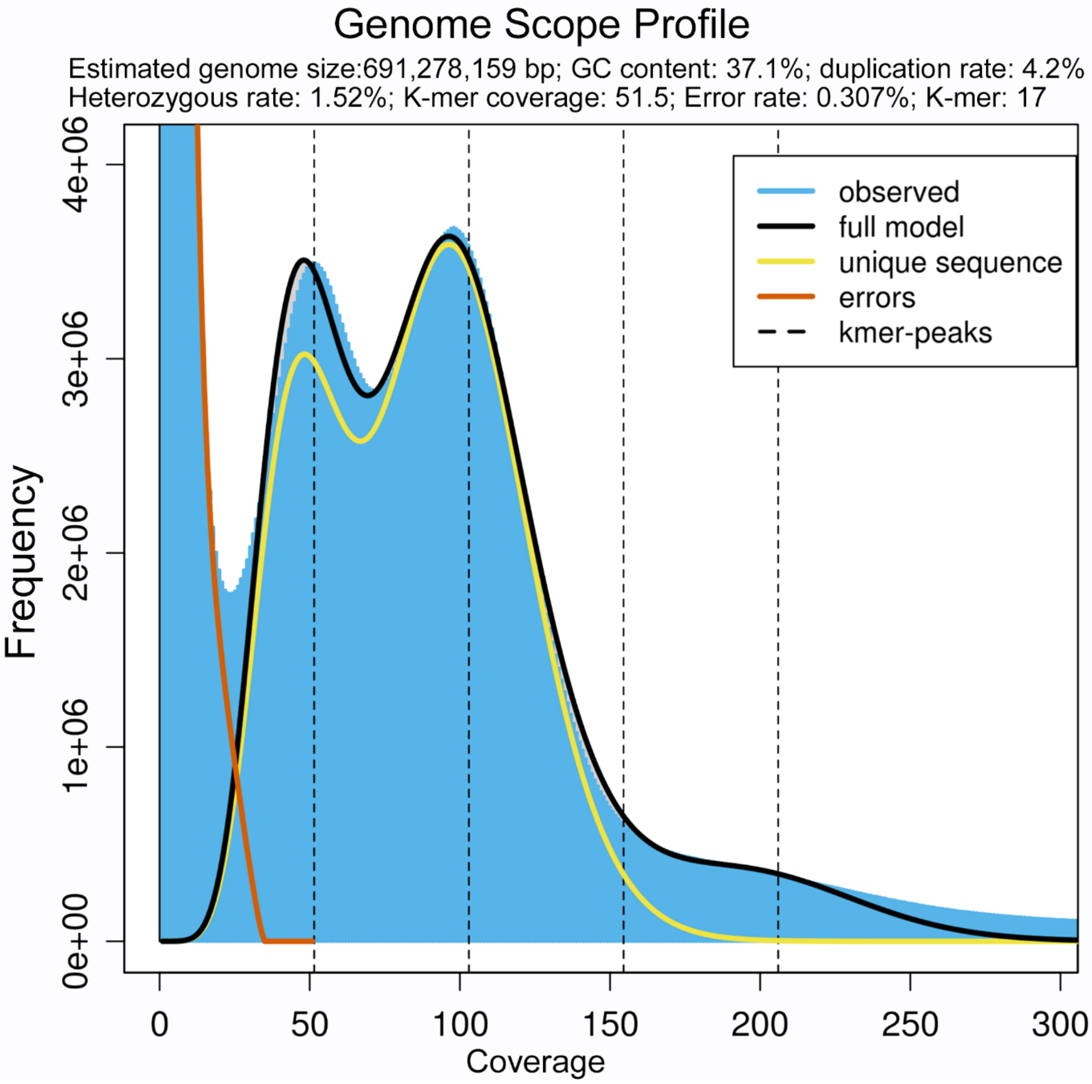


Figure S3. Heatmap of Hi-C assembly.

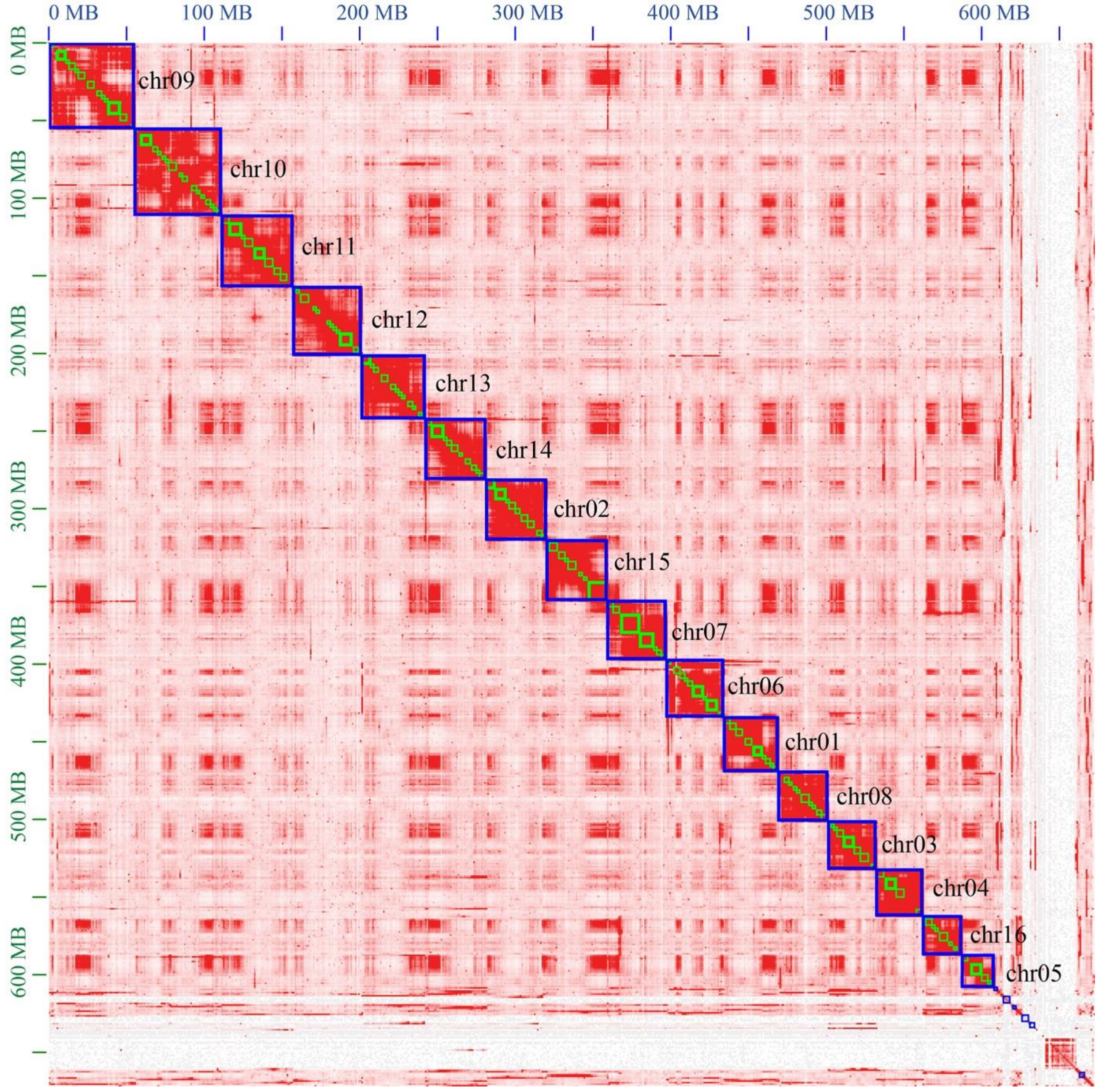


Figure S4. The distribution of GC content.

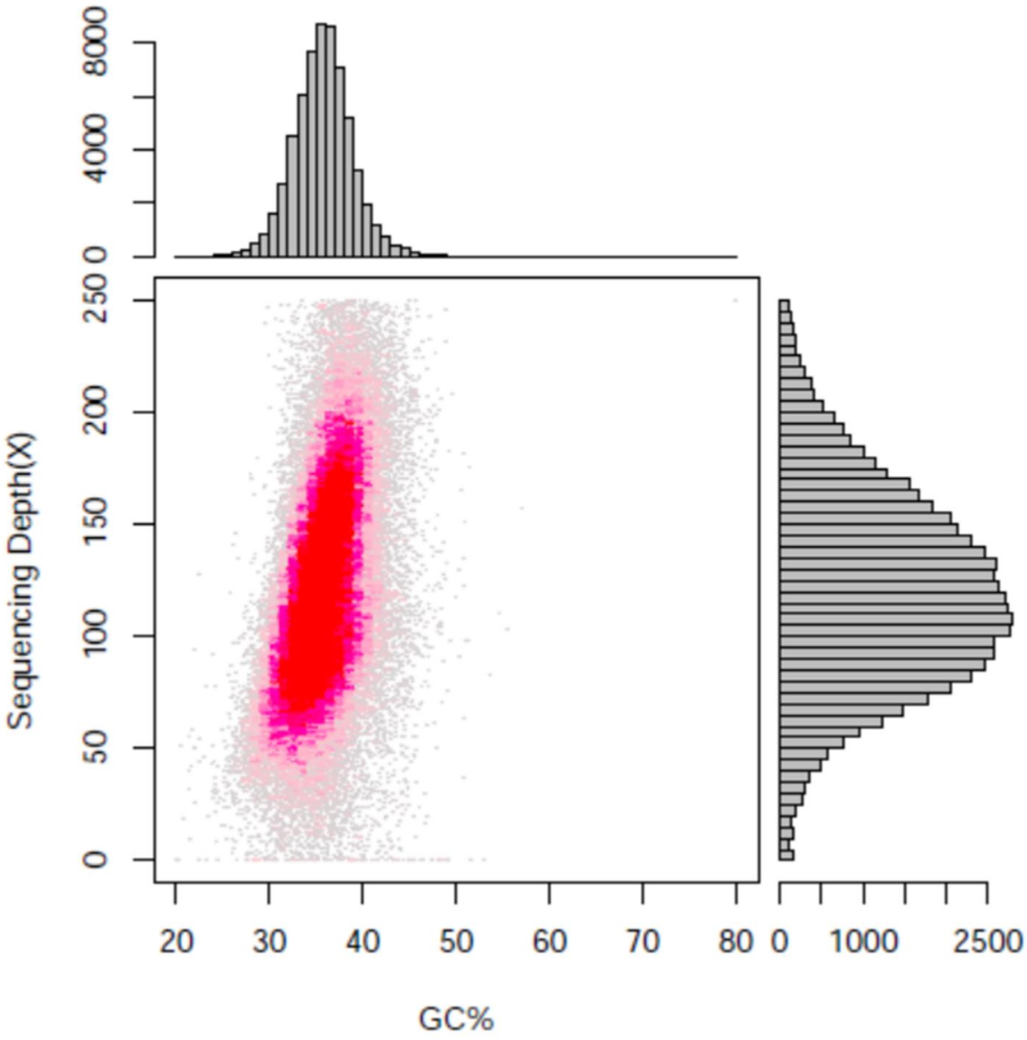


Figure S5. The contigs distribution of version 1.0 assembly on the chromosomes of version 2.0 assembly.

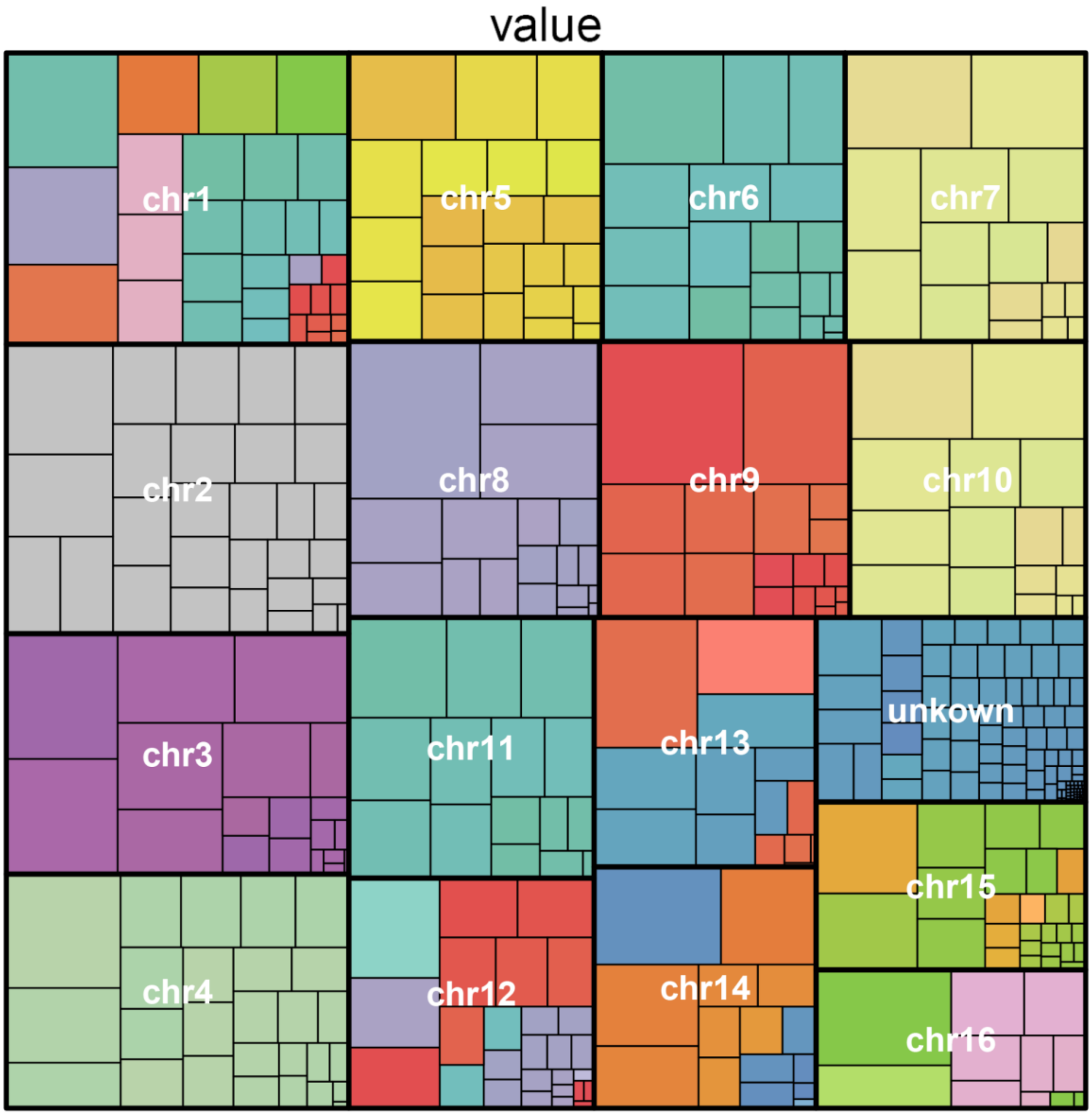


Figure S6. Global synteny between the gap-free ‘Pawnee’ assembly by Lovell et al. (2021) (chr1 – chr16) and Cil_V. 2.0 (CHR01 – CHR16).

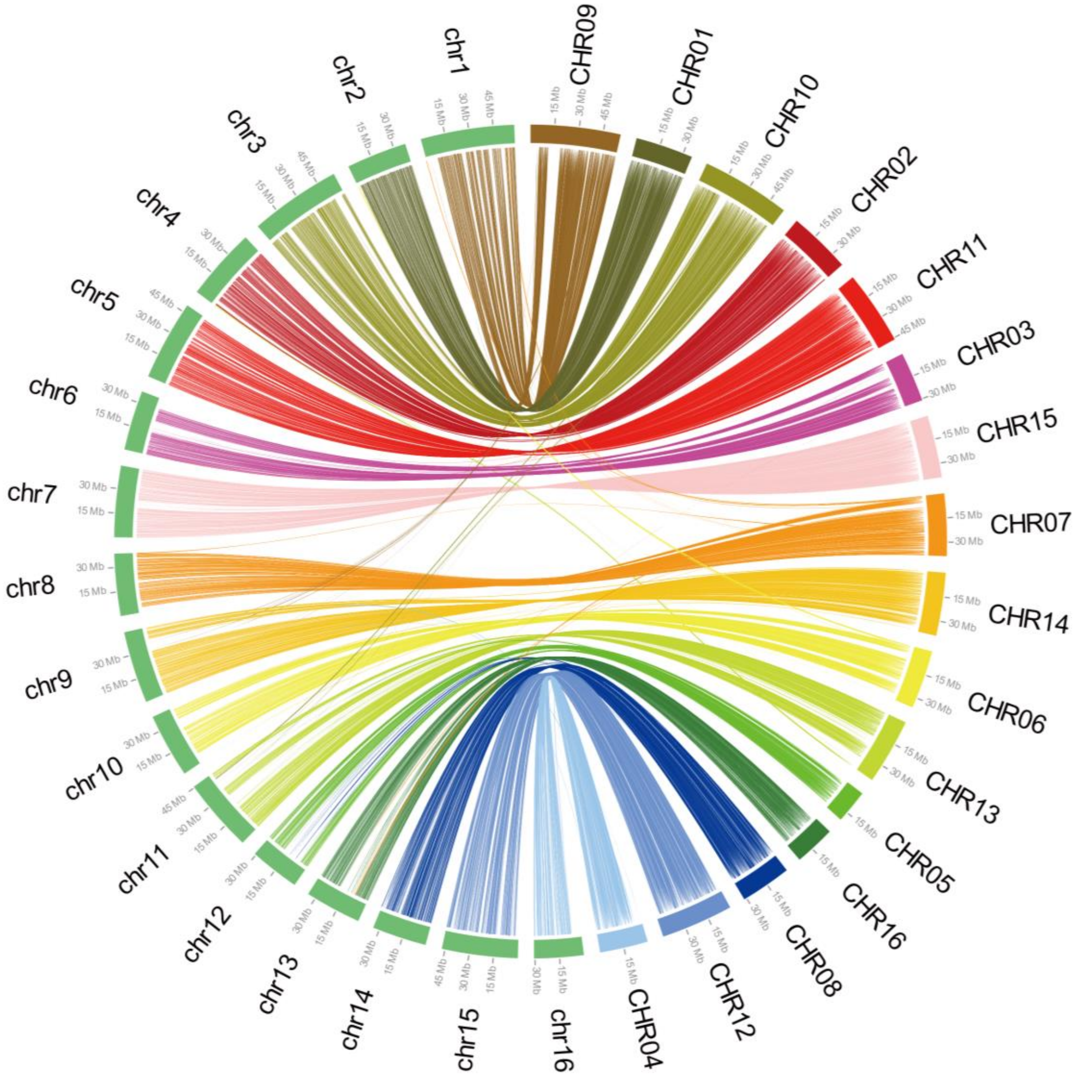


Figure S7. The details of syntenic relationship between the gap-free ‘Pawnee’ assembly by Lovell et al. (2021) (chr1 – chr16) and Cil_V. 2.0 (CHR01 – CHR16).

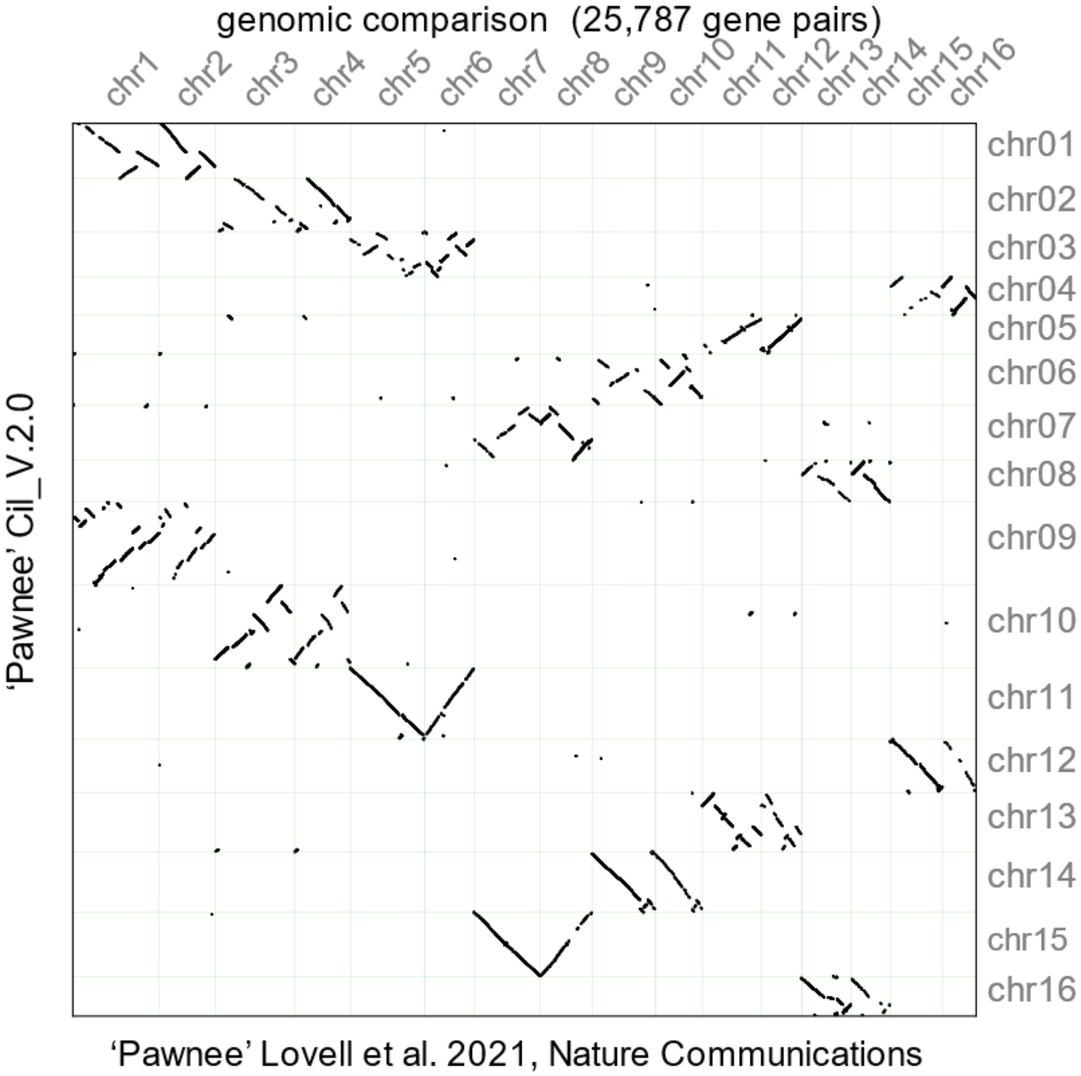


Figure S8. Evolutionary relationships of chromosomes among pecan, walnut and bayberry.

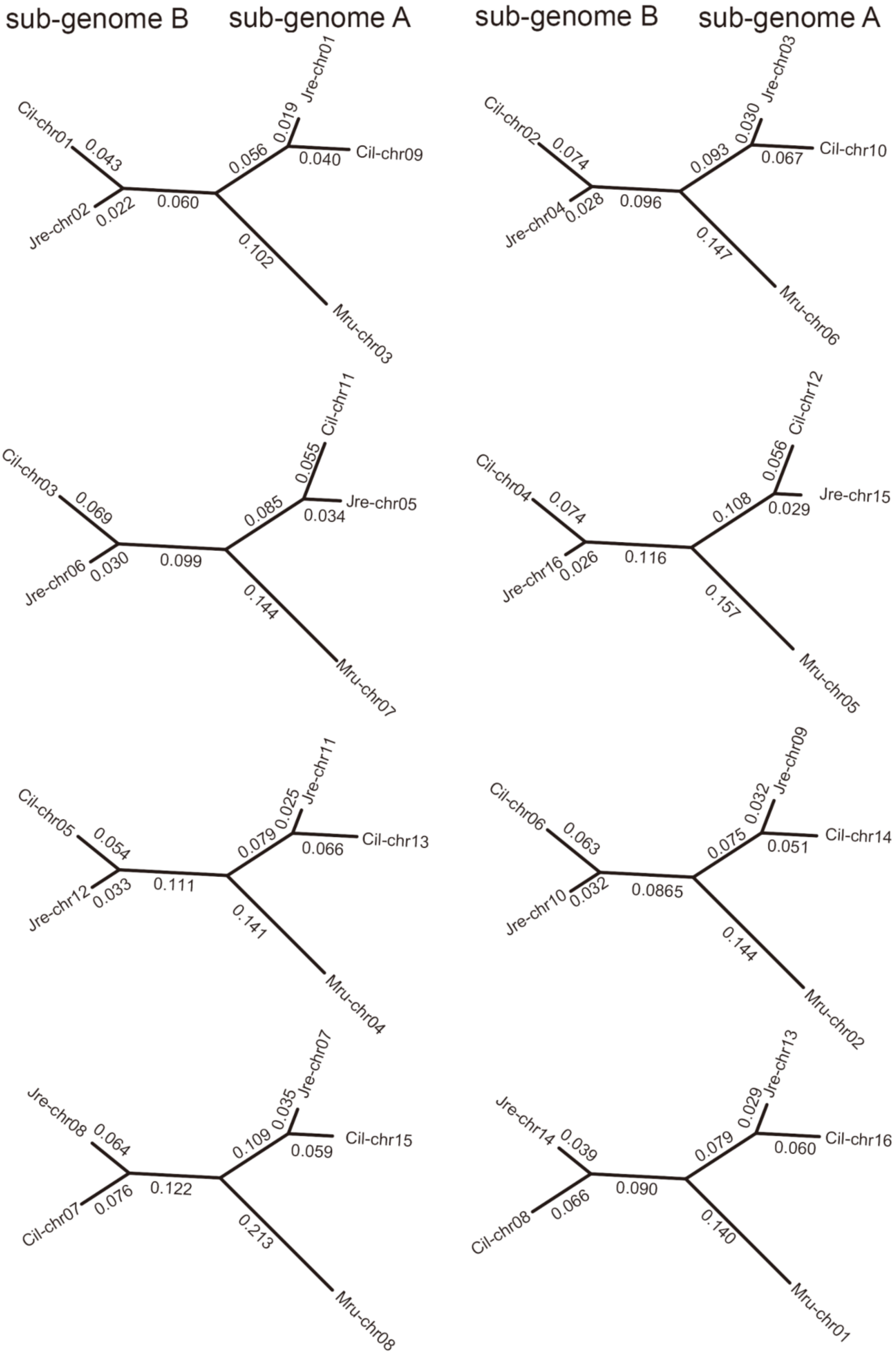
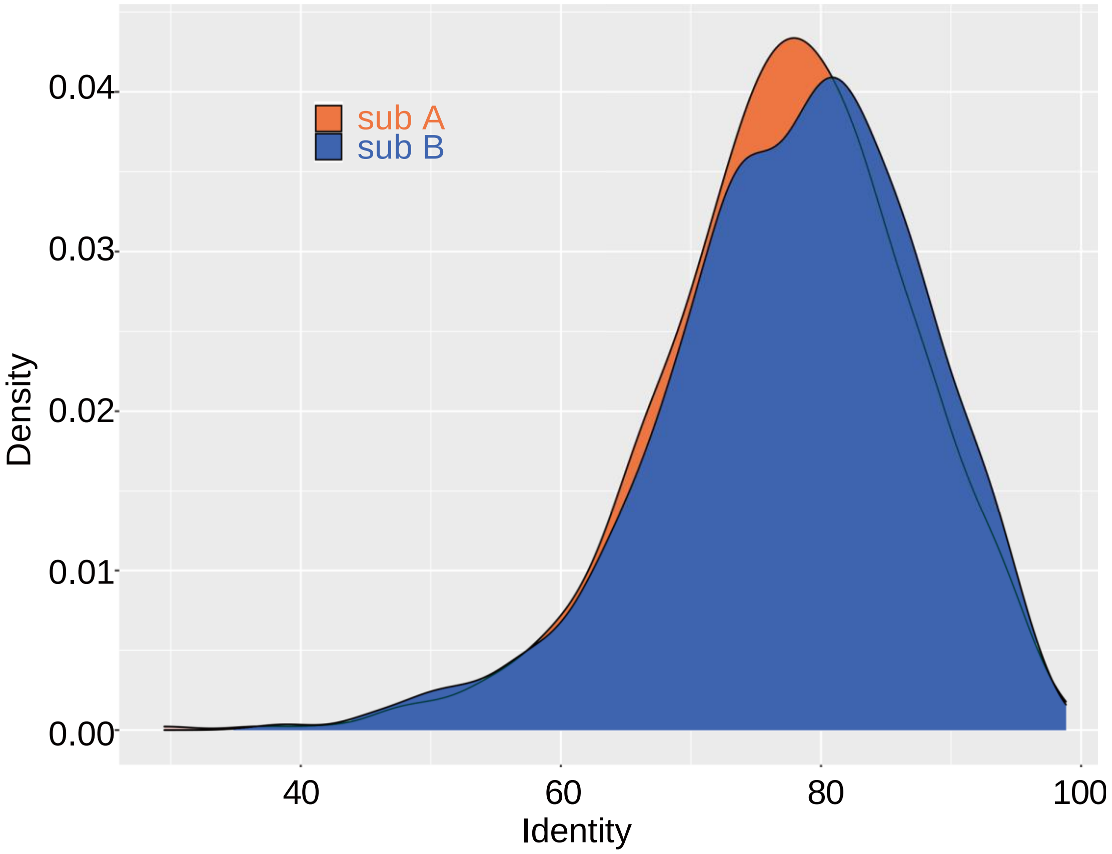


Figure S9. Identity analysis between subgenomes in pecan.



52 Figure S10. *Ka/Ks* analysis between subgenomes in pecan.

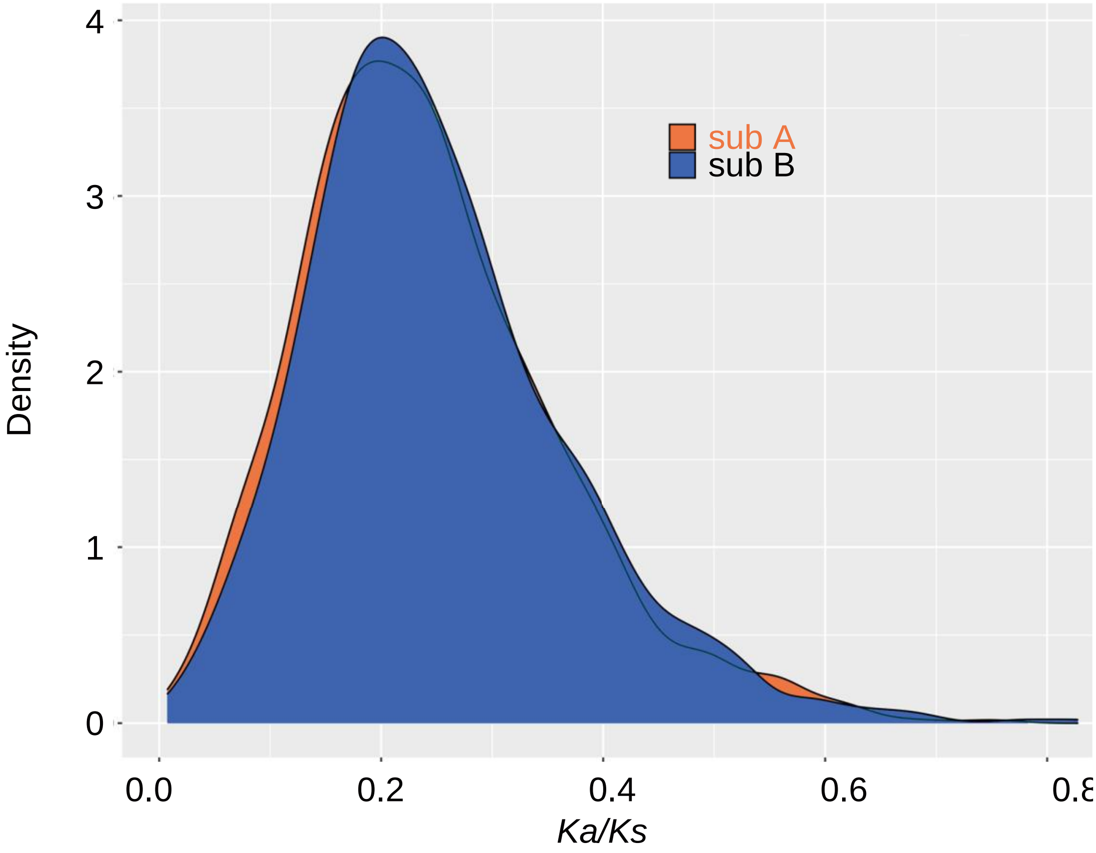


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Figure S11. The frequency distributions (upper) and correlation analyses (lower) of *Ka*, *Ks*, and *Ka/Ks*. blue line represented the fitted curve, and the shaded part represented the confidence interval.

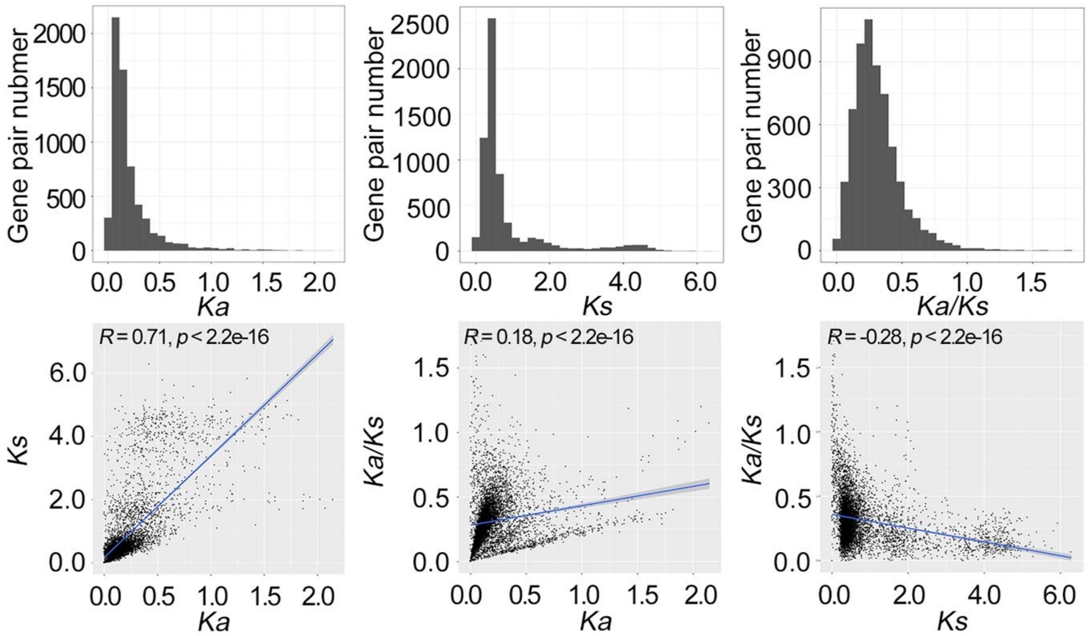
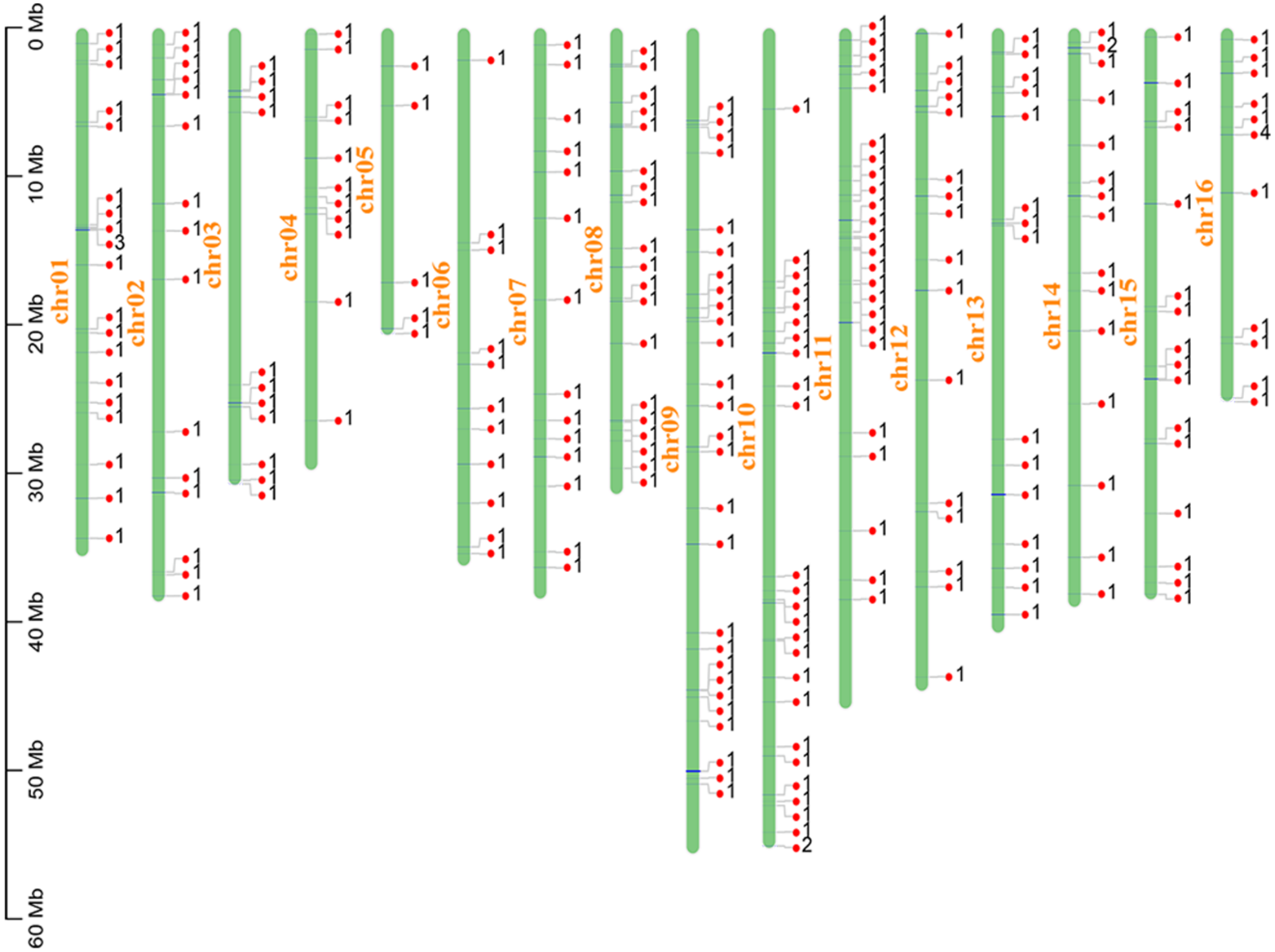


Figure S12. Distribution of *FAR1* transcription factor family members on chromosomes.



Supplemental Tables

Table S1. Data statistics for pecan genome survey and assembly.

Platform	**Data type**	**Number of Reads**	**Total length (bp)**	**N50 Length of Reads**	**N90 Length of Reads**	**Average Read Length (bp)**	**Maxmum Read Length (bp)**	**Mean Qualigy**
Nanopore	Raw Data	5,925,714	76,162,104,265	43,224	18,376	12,852	663,065	4.45
	Clean Data	2,184,040	71,697,987,348	44,087	20,238	32,828	663,065	8.84
Hiseq X-Ten (PE150)*	Raw Data	1,122,405,046	168,360,756,900	-	-	-	-	94.17% (Q20) 88.6% (Q30)
	Clean Data	1,121,333,120	168,199,968,000	-	-	-	-	-

	Number of Reads	**Total length (bp)**	**Mapped**	**Mapping Ratio**	**Valid Pairs**	**Percentage**
Hi-C (PE100)	1,518,592,046	151,859,204,600	1,139,158,524	75.01%	196,757,892	25.91%

[*] Our previously published data (Huang et al., 2019).

Table S2. Nanopore clean data length distribution.

Length	**Reads Number**	**Total Length (bp)**	**Percentage (%)**	**Average Length (bp)**
2,000~5,000	166,917	572,320,083	0.79	3,428.77
5,000~10,000	232,711	1,728,955,943	2.41	7,429.62
10,000~20,000	321,955	4,719,951,481	6.58	14,660.28
20,000~30,000	327,150	8,230,356,547	11.47	25,157.74
30,000~40,000	438,229	15,243,432,557	21.26	34,784.17
40,000~50,000	272,129	12,137,281,885	16.92	44,601.20
50,000~60,000	173,608	9,481,705,172	13.22	54,615.60
60,000~70,000	106,138	6,851,483,605	9.55	64,552.59
70,000~80,000	62,318	4,644,803,948	6.47	74,533.90
>=80,000	82,885	8,087,696,127	11.28	97,577.31

Table S3. Summary of the pecan genome assembly.

	Sequence Type	**Total Number**	**Total Length (bp)**	**N50 (bp)**	**N90 (bp)**	**Longest Read (bp)**	**Shortest Read (bp)**	**Gap Length (bp)**	**GC Content (%)**
Nanopore	contig	341	636,255,455	4,195,733	1,070,318	23,879,822	1,663	0	35.89
Hi-C	scaffold	124	636,406,555	38,784,058	25,295,717	55,745,374	1,663	263,863	35.89
	contig	564	636,142,692	2,893,887	789,098	11,551,424	112	-	35.89

Table S4. The statistics of pecan chromosome length.

Chromosome ID	**Length (bp)**	**Percentage of assembly (%)**
chr01	35,734,486	5.62
chr02	38,784,058	6.09
chr03	30,933,461	4.86
chr04	29,925,508	4.70
chr05	20,838,255	3.27
chr06	36,373,273	5.72
chr07	38,592,383	6.06
chr08	31,550,154	4.96
chr09	55,745,374	8.76
chr10	55,374,445	8.70
chr11	45,985,284	7.23
chr12	44,801,196	7.04
chr13	40,882,215	6.42
chr14	39,152,115	6.15
chr15	38,648,230	6.07
chr16	25,295,717	3.97
Total	608,616,154	95.63
un-anchored	63,793,453	4.37

Table S5. Assessment of the gene coverage rate for pecan assembly and predicted protein-coding genes by BUSCO.

	Percentage (%)	
	Assembly	**Protein-coding genes**
Complete BUSCOs	95.1 (409 genes)	93.7 (403 genes)
Complete Single-Copy BUSCOs	85.3 (367 genes)	85.6 (368 genes)
Complete Duplicated BUSCOs	9.8 (42 genes)	8.1 (35 genes)
Fragmented BUSCOs	1.2 (5genes)	4.2 (18 genes)
Missing BUSCOs	3.7 (16 genes)	2.1 (9 genes)

Table S6. Reads coverage statistics of pecan genome assembly.

Reads mapping rate (%)	95.95
Coverage of genome (%)	96.38
Coverage of genome > 4×(%)	95.25
Coverage of genome > 10× (%)	94.45
Coverage of genome > 20× (%)	93.72
Genome average sequencing depth (×)	215.49

Table S7. Repeat sequence prediction.

Type	**Repeat Size(bp)**	**% of genome**
TRF	23,381,072	3.67
RepeatMasker	87,654,647	13.77
RepeatProteinMask	76,449,465	12.01
De novo	279,886,295	43.98
Total	304,405,087	47.83

Table S8. Repeat category statistics.

	Repbase TEs		**De novo**		**TE Proteins**		**Combined TEs**	
	Length (bp)	**% in Genome**	**Length (bp)**	**% in Genome**	**Length (bp)**	**% in Genome**	**Length (bp)**	**% in Genome**
DNA	11,627,231	1.83	543,601	0.09	30,704,387	4.82	37,638,398	5.91
LINE	11,392,813	1.79	7,268,375	1.14	29,105,229	4.57	37,741,823	5.93
SINE	15,026	0	0	0	169,332	0.03	184,288	0.03
LTR	65,295,660	10.26	69,106,873	10.86	213,465,587	33.54	223,597,995	35.13
Other	1,510	0	0	0	0	0	1,510	0
Unknown	0	0	0	0	7,712,931	1.21	7,712,931	1.21
Total	87,654,647	13.77	76,449,465	12.01	272,008,903	42.74	288,757,673	45.37

Table S9. Statistics of repeat sequences and subfamilies of transposable elements (TEs).

Repeat category	subfamily	Size (bp)	% of repeat	Size in sub A (bp)	Size in sub B (bp)
TEs	DNA/Academ	5,469	0.0018	9,341	2,354
	DNA/CMC-Chapaev	62,165	0.0204	32,422	60,462
	DNA/CMC-Chapaev-3	4,573	0.0015	16,279	1,779
	DNA/CMC-EnSpm	13,705,125	4.5023	7,187,368	5,294,574
	DNA/CMC-Transib	37,776	0.0124	25,999	37,221
	DNA/Crypton	11,841	0.0039	8,124	4,542
	DNA/Crypton-H	30	0.0000	30	0
	DNA/Crypton-V	32,639	0.0107	20,358	14,472
	DNA/Dada	27,039	0.0089	16,247	11,406
	DNA/DNA	4,349,717	1.4289	1,878,329	1,913,326
	DNA/Ginger	224,921	0.0739	56,442	39,807
	DNA/Harbinger	157	0.0001	0	42,725
	DNA/hAT	257,672	0.0846	76,133	113,094
	DNA/hAT-Ac	6,752,533	2.2183	3,657,022	2,122,439
	DNA/hAT-Blackjack	5,768	0.0019	3,612	2,440
	DNA/hAT-Charlie	89,895	0.0295	31,249	34,502
	DNA/hAT-hAT5	932	0.0003	516	34
	DNA/hAT-hATm	23,540	0.0077	24,983	568
	DNA/hAT-hATw	44,907	0.0148	1,806	10,499
	DNA/hAT-hobo	1,073	0.0000	131	942
	DNA/hAT-Pegasus	6,548	0.0022	5,483	357
	DNA/hAT-Tag1	212,854	0.0699	103,730	139,728
	DNA/hAT-Tip100	890,171	0.2924	419,440	486,037
	DNA/hAT-Tol2	1,571	0.0005	581	1,268
	DNA/Helitron	3,984,983	1.3091	2,733,752	1,235,857
	DNA/IS3EU	40,653	0.0134	31,592	20,232
	DNA/Kolobok	4,864	0.0016	3,152	2,163
	DNA/Kolobok-Hydra	46,173	0.0152	30,274	18,947
	DNA/Kolobok-T2	21,446	0.0070	14,732	9,034
	DNA/Maverick	208,700	0.0686	149,653	43,345
	DNA/Merlin	24,885	0.0082	14,570	12,415
	DNA/MuLE-MuDR	2,461,172	0.8085	1,003,829	243,805
	DNA/MULE-MuDR	1,555,016	0.5108	776,984	806,123
	DNA/MULE-NOF	586	0.0002	605	180
	DNA/Novosib	406,496	0.1335	39,528	24,091
	DNA/P	60,621	0.0199	81,580	27,582
	DNA/PIF-Harbinger	1,371,592	0.4506	654,087	846,539
	DNA/PIF-HarbS	77	0.0000	77	0
	DNA/PIF-ISL2EU	75,979	0.0250	27,052	47,067
	DNA/PiggyBac	7,110	0.0023	2,477	3,840

DNA/Sola	176,894	0.0581	37,257	33,279
DNA/TcMar	25,474	0.0084	85,690	11,261
DNA/TcMar-Fot1	70,520	0.0232	33,800	54,152
DNA/TcMar-ISRm11	82,655	0.0272	4,336	2,761
DNA/TcMar-Pogo	56	0.0000	72	0
DNA/TcMar-Stowaway	11,676	0.0038	6,794	4,918
DNA/TcMar-Tc1	22,562	0.0074	2,531	25,253
DNA/TcMar-Tc4	42	0.0000	111	62
DNA/TcMar-Tigger	2,420,774	0.7953	1,099,620	442,736
DNA/Zator	42	0.0000	42	0
DNA/Zisupton	33,249	0.0109	3,637	2,548
LINE/Ambal	204	0.0001	61	131
LINE/CR1	1,591	0.0005	252,970	220
LINE/CRE	145	0.0000	10,563	924
LINE/Dong-R4	1,633	0.0005	306	521
LINE/DRE	3,854	0.0013	1,432	11,786
LINE/I	1,253	0.0004	415	784
LINE/Jockey	7,477	0.0025	4,970	3,341
LINE/L1	36,940,270	12.1354	17,420,214	13,392,696
LINE/L1-Tx1	87,445	0.0287	71,425	47,860
LINE/L2	608,135	0.1998	205,047	235,900
LINE/LINE	11,721	0.0039	5,016	5,624
LINE/Penelope	64,425	0.0212	84,909	23,469
LINE/Proto1	1,633	0.0005	726	301
LINE/R1	6,649	0.0022	50,145	1,863
LINE/R2	60,729	0.0200	31,170	27,900
LINE/Rex-Babar	1,415	0.0005	718	625
LINE/RTE-BovB	11,161	0.0037	6,676	2,657
LINE/RTE-RTE	59	0.0000		59
LINE/RTE-X	5,055	0.0017	1,824	1,598
LINE/Tad1	268	0.0001	3,059	35,899
LTR/Cassandra	24,252	0.0080	5425	704
LTR/Caulimoviru	1,189,232	0.3907	661,600	429,225
LTR/Caulimovirus	2,309,802	0.7588	1,308,128	1,095,708
LTR/Copia	**104,193,921**	**34.2293**	**51,853,612**	**35,515,454**
LTR/DIRS	78,269	0.0257	38,803	7,854
LTR/ERV	20,131	0.0066	858	281
LTR/ERV1	221,271	0.0727	89,544	59,614
LTR/ERV4	670	0.0002	381	7554
LTR/ERV-Foamy	61	0.0000	61	0
LTR/ERVK	118,769	0.0390	161,658	130,585
LTR/ERVL	3,191	0.0010	1,618	1,506
LTR/ERVL-MaLR	46	0.0000	46	0
LTR/Gypsy	**105,595,920**	**34.6899**	**46,854,456**	**44,036,255**

	LTR/LTR	23,178,086	7.6144	9,812,895	6,951,532
	LTR/Ngaro	7,059	0.0023	5,619	2,028
	LTR/Pao	166,864	0.0548	25,964	54,808
	SINE/Alu	72	0.0000	3,380	0
	SINE/B2	54	0.0000	54	0
	SINE/B4	4,668	0.0015	3,080	2,061
	SINE/ID	2,600	0.0009	1,719	1,303
	SINE/SINE	169,564	0.0557	16,485	88,089
	SINE/tRNA-7SL	577	0.0002	503	214
	SINE/tRNA-C	4,672	0.0015	2,839	2,508
	SINE/tRNA-Core	655	0.0002	450	0
	SINE/tRNA-Deu-L2	275	0.0001	263	57
	SINE/tRNA-L2	132	0.0000	132	0
	SINE/tRNA-RTE	1,135	0.0004	607	280
	SINE/U	136	0.0000	132	68
Satellite	Satellite	246,671	0.0810	287,088	139,547
Other	Composite	252	0.0001	126	126
Other	DNA_virus	1,258	0.0004	640	637
Simple	Simple_repeat	7,630,721	2.5068	4,184,870	4,107,352
Unknown	Unknown	7,712,931	2.5338	6,531,303	7,424,836

Table S10. Statistics of gene structure prediction in pecan genome assembly.

	Gene set	**Number of genes**	**CDS+intron length (bp)**	**CDS length (bp)**	**exon length (bp)**	**intron (bp)**	**Exons per gene**
Homolog	*Arabidopsis thaliana*	36,944	8,410.66	1,262.22	206.68	1,399.73	6.11
	Cucumis sativus	22,467	6,573.42	1,194.11	231.52	1,293.82	5.16
	Glycine max	21,176	7,865.64	1,300.34	226.89	1,387.66	5.73
	Prunus persica	30,693	12,085.40	1,220.08	240.04	2,661.25	5.08
	Citrullus lanatus	41,721	9,415.54	1,246.60	229.94	1,847.63	5.42
	Eucalyptus grandis	43,556	13,258.85	1,144.50	235.99	3,146.84	4.85
	Malus domestica	18,803	6,188.82	1,003.87	207.23	1,348.76	4.84
	Populus trichocarpa	32,661	10,064.20	1,313.59	237.69	1,933.22	5.53
	Vitis vinifera	24,743	13,946.90	1,328.17	236.56	2,734.52	5.61
De novo	Augustus	49,803	4333.06	1276.33	233.22	683.43	5.47
Transcript	Trinity	154,647	/				
Total		33,472	5482.63	1460.04	220.81	716.76	6.61

Table S11. Comparison of gene structure among the close relatives.

Species	**Number**	**Average transcript length (bp)**	**Average CDS length (bp)**	**Average intron length (bp)**	**Average exon length (bp)**	**Average exons per gene**
Carya illinoinensis	33,472	5,482.63	1460.04	716.76	220.81	6.61
Arabidopsis thaliana	27,465	1,890.03	1223.07	161.1	237.88	5.14
Eucalyptus grandis	36,625	2,568.35	1136.77	409.07	252.64	4.5
Glycine max	46,949	3,616.50	1289.18	537.56	241.89	5.33
Populus trichocarpa	31,612	3,314.73	1392.68	421.85	250.65	5.56
Vitis vinifera	25,726	5,619.01	1348.43	1008.82	257.66	5.23

Table S12. Statistics of function annotation of protein-coding genes in pecan genome assembly (version 2.0).

Database	**Number**	**Percentage (%)**
Swissprot	24,359	72.77
KEGG	25,885	77.33
TrEMBL	30,885	92.27
Interpro	26,047	77.82
GO	18,205	53.39
all annotated	31,247	93.35
Total	33,472	100

Table S13. Comparison on genomic features of all assemblies of pecan.

	GigaScience[a]	**Cil_V. 2.0**	**Nature Communications[b]**			
Genomic features	**Pawnee**	**Pawnee**	**Oaxaca**	**Lakota**	**Elliott**	**Pawnee**
Total length of scaffolds (Mb)	651.31	636.41	649.96	668.99	656.69	674.27
Number of scaffolds & contigs	3860/17542	125 & 433	298 & 552	261 & 499	431 & 829	16 & 34
Longest scaffold (Mb)	4.92	55.75	58.44	57	56.14	58.06
N50 of contig length	77.2Kb	3.04Mb	4.4Mb	3.7Mb	4.4Mb	26.5Mb
Number of predicted protein-coding genes	31,075	33,472	31,911	33,280	31,042	32,267
Pseudochromosomes	/	16	16	16	16	16
Anchored sequence to pseudochromosome (Mb)	/	608.6	637.0	642.9	627.1	674.3
Genome in chromosomes (%)	/	96%	98%	96.10%	95.50%	100%
Average number of exons per gene	5.0	6.6	5.4	5.5	5.5	5.5
Percentage of repeat sequences (%)	50.43	47.83	46.5	33.8	32.3	49.7

Note: a, Huang et al., 2019. b, Lovell et al, 2021.

Table S14. Statistics of key genes related to non-structural polyphenol metabolism and oil accumulation in pecan genome versions 2.0 and 1.0.

		Cil_V. 2.0				**Vertion 1.0**
		subA	**subB**	**scaffold**	**Total**	
Polyphenol metabolism	**4CL**	16	12	1	**29**	**34**
	C4H	2	1	0	**3**	**6**
	LAC15	30	11	1	**42**	**49**
	MAY123	8	7	0	**15**	**14**
	PAL	1	2	0	**3**	**8**
	WDR	0	1	0	**1**	**2**
	CHS	2	1	0	**3**	**4**
	CHI	1	1	0	2	2
	F3H	1	0	0	1	1
	F3'H	4	1	0	5	5
	DFR	3	0	0	3	3
	LDOX	1	0	0	1	1
	ANR	1	1	0	**2**	**3**
	GSTF	0	1	0	1	1
	MATE	2	0	0	2	2
	HATPase	0	1	0	**1**	**2**
	Sum	**72**	**40**	**2**	**114**	**137**
Oil accumulation	**ABCAT**	1	1	0	2	2
	ABI3	1	0	0	1	1
	ABI4	1	0	0	1	1
	ACP4	1	1	0	2	2
	alpha-CT	1	2	0	3	3
	alpha-PDH	1	1	0	**2**	**1**
	BC	1	0	0	1	1
	BCCP1	1	1	0	**2**	**4**
	beta-CT	0	0	0	**0**	**1**
	beta-PDH	1	0	0	**1**	**2**
	DHLAT/EMB3003(E2)	0	1	0	1	1
	DHLAT/LTA2(E2)	1	1	0	2	2
	ER/ENR1(MOD1)	0	1	0	**1**	**2**
	FATA	1	0	0	**1**	**2**
	FATB	1	1	0	2	2
	HACPS	1	0	0	1	1
	HAD	1	0	0	**1**	**2**

KAR	1	1	0	**2**	**3**
KASI	1	1	0	**2**	**3**
KASII	1	1	0	**2**	**3**
KASIII	1	1	0	2	2
LACS8	1	0	0	1	1
LACS9	1	0	0	**1**	**2**
LPD2(E3)	1	0	0	1	1
LS	1	1	0	2	2
LT	0	1	0	1	1
MCMT	1	1	0	2	2
PII	1	0	0	**1**	**2**
SAD/DES5	0	0	1	1	1
SAD/DES6	0	1	0	**1**	**2**
SAD/FAB2	1	0	0	**1**	**4**
TGD1	1	0	0	1	1
WRI1	3	1	0	**4**	**5**
WRI3	2	2	0	4	4
Sum	**31**	**21**	**1**	**53**	**69**

Table S15. Predicted non-coding RNAs in pecan genome assembly (version 2.0).

Type		**Copy number**	**Average length (bp)**	**Total length (bp)**	**% of genome**
miRNA		121	126.8	15,343	0.0024
tRNA		565	74.86	42,295	0.0066
rRNA	rRNA	414	180.32	74,651	0.0117
	18S	82	505.44	41,446	0.0065
	28S	69	107.87	7,443	0.0012
	5.8S	21	122.29	2,568	0.0004
	5S	242	95.84	23,194	0.0036
snRNA	snRNA	1,318	109.55	144,382	0.0227
	CD-box	1,118	105.23	117,642	0.0185
	HACA-box	52	124.08	6,452	0.001
	splicing	147	137.13	20,158	0.0032

Table S16. Statistics of synteny and genes in Cil_V. 2.0 and gap-free 'Pawnee' assembly by Lovell et al. (2021).

Chromosome Pair	Sub-genome	Chromosome[a]	Gene Number[a]	Chromosome[b]	Gene Number[b]	Genes in Block[b]	Block Number	Average gene number/Block
PAIR1	sub A	CHR09	3,011	chr1	3,080	2,001	16	125.06
	sub B	CHR01	1,984	chr2	1,995	1,422	3	474.00
PAIR2	sub A	CHR10	2,967	chr3	2,845	1,967	10	196.70
	sub B	CHR02	1,911	chr4	1,984	1,292	9	143.56
PAIR3	sub A	CHR11	2,561	chr5	2,644	1,790	7	255.71
	sub B	CHR03	1,626	chr6	1,772	1,147	10	114.70
PAIR7	sub A	CHR15	2,305	chr7	2,377	1,781	3	593.67
	sub B	CHR07	2,003	chr8	1,830	1,255	8	156.88
PARI6	sub A	CHR14	2,173	chr9	2,253	1,569	9	174.33
	sub B	CHR06	1,836	chr10	1,677	1,126	8	140.75
PAIR5	sub A	CHR13	2,106	chr11	2,110	1,353	10	135.30
	sub B	CHR05	1,385	chr12	1,430	955	7	136.43
PAIR8	sub A	CHR16	1,431	chr13	1,802	1,016	15	67.73
	sub B	CHR08	1,493	chr14	1,374	939	6	156.50
PAIR4	sub A	CHR12	1,944	chr15	1,864	1,097	9	121.89
	sub B	CHR04	1,368	chr16	1,197	794	6	132.33
Sum		16	32,104	16	32,234	21,504	136	158.12

Note: [a], Chromosome number and genes in Cil_V. 2.0 assembly; [b], Chromosome number and genes in the gap-free 'Pawnee' assembly by Lovell et al. (2021).

Table S17. Statistics of sub-genomes features.

Chromosome Pair	Sub-genome	Chromosome	Chromosome length	Gene number	TE	Identity	Ka/Ks
PAIR1	subA	CHR09	55,745,374	3,011	0.446	78.64	0.2261
	subB	CHR01	35,734,486	1,984	0.449	78.33	0.2298
PAIR2	subA	CHR10	55,374,445	2,967	0.451	77.72	0.2499
	subB	CHR02	38,784,058	1,911	0.474	75.99	0.2507
PAIR3	subA	CHR11	45,985,284	2,561	0.452	77.79	0.2419
	subB	CHR03	30,933,461	1,626	0.468	76.95	0.2524
PAIR4	subA	CHR12	44,801,196	1,944	0.511	78.73	0.2456
	subB	CHR04	29,925,508	1,368	0.502	77.17	0.2531
PAIR5	subA	CHR13	40,882,215	2,106	0.469	77.48	0.2602
	subB	CHR05	20,838,255	1,385	0.413	76.17	0.2600
PAIR6	subA	CHR14	39,152,115	2,173	0.44	79.06	0.2396
	subB	CHR06	36,373,273	1,836	0.47	77.20	0.2551
PAIR7	subA	CHR15	38,648,230	2,305	0.409	76.99	0.2475
	subB	CHR07	38,592,383	2,003	0.467	75.24	0.2769
PAIR8	subA	CHR16	25,295,717	1,431	0.436	78.84	0.2540
	subB	CHR08	31,550,154	1,493	0.489	77.40	0.2627

Table S18. Statistics of transcription factor families among pecan, walnut and bayberry.

TF_family	***Cil*_sub A**	***Cil*_sub B**	***Cil*_Scaffold**	***Cil* sum**	***Jre*_sub A**	***Jre*_sub B**	***Jre* sum**	***Mru***	***Ath***	**Included_domains**	**P-value(chi-square test)**
ABI3VP1	23	17	2	42	20	17	37	60	89	B3	0.068
AP2-EREBP	105	85	3	193	109	93	202	128	145	AP2	1
ARF	20	10	1	31	17	16	33	18	23	Auxin_resp	1
ARR-B	7	4	1	12	7	5	12	9	13	G2-like,Myb_DNA-binding,Response_reg	0.9827
Alfin-like	11	12	2	25	10	12	22	27	19	Alfin-like	0.872
BBR/BPC	5	6	0	11	6	5	11	6	8	GAGA_bind	1
BES1	5	4	1	10	4	5	9	6	8	DUF822	1
BSD	5	7	1	13	6	6	12	10	12	BSD	1
C2C2-CO-like	9	4	0	13	10	6	16	7	17	CCT,zf-B_box	0.8128
C2C2-Dof	22	19	3	44	26	22	48	27	36	zf-Dof	1
C2C2-GATA	18	13	0	31	18	15	33	30	30	GATA	0.6565
C2C2-YABBY	5	4	0	9	6	5	11	9	7	YABBY	0.8887
C2H2	39	38	4	81	46	46	92	55	65	zf-C2H2	0.8879
C3H	37	28	6	71	46	32	78	49	63	zf-CCCH	0.8617
CAMTA	3	2	0	5	5	4	9	7	5	CG-1,IQ	0.5713
CCAAT	16	19	0	35	12	14	26	22	43	CBFB_NFYA,CBFD_NFYB_HMF,CCAAT-Dr1,NF-YB,NF-YC	1
CPP	4	3	0	7	6	4	10	5	10	TCR	0.7437
CSD	2	1	0	3	3	1	4	4	3	CSD	0.815
DBP	0	0	0	0	1	0	1	1	1	DNC,PP2C	0.9268
E2F-DP	7	3	1	11	7	4	11	7	8	E2F_TDP	1
EIL	3	2	1	6	4	2	6	5	6	EIN3	0.9774

FAR1	154	107	3	264	22	18	40	26	18	FAR1	**1.39E-09**
FHA	10	8	1	19	12	9	21	14	16	FHA	0.9653
G2-like	28	23	2	53	33	26	59	36	43	G2-like	0.8481
GRAS	41	29	3	73	50	27	77	49	34	GRAS	0.8219
GRF	5	8	0	13	8	7	15	10	9	QLQ,WRC	1
GeBP	3	4	0	7	4	4	8	7	22	DUF573	0.2378
HB	9	7	0	16	9	6	15	8	8	Homeobox,KNOX1,KNOX2	0.7427
HRT	1	0	0	1	1	0	1	0	2	HRT	1
HSF	16	13	2	31	19	15	34	18	24	HSF_DNA-bind	1
LFY	0	1	0	1	0	1	1	1	1	FLO_LFY	1
LIM	12	5	0	17	9	6	15	11	12	LIM	1
LOB	26	24	2	52	29	22	51	34	43	DUF260	1
MADS	38	29	1	68	41	25	66	65	108	SRF-TF	0.2382
MYB	192	157	14	363	205	179	384	247	274	Myb_DNA-binding	1
MYB-related	159	130	12	301	167	148	315	205	227	Myb_DNA-binding	1
NAC	72	51	4	127	70	56	126	75	114	NAM	1
NOZZLE	2	2	0	4	1	1	2	2	3	NOZZLE_Angio	0.9087
OFP	15	7	3	25	17	9	26	13	19	Ovate	1
PBF-2-like	2	1	0	3	1	0	1	2	3	Whirly	1
PLATZ	12	9	1	22	7	4	11	16	12	PLATZ	0.5853
RWP-RK	7	4	1	12	6	5	11	9	15	RWP-RK	0.8289
S1Fa-like	2	0	0	2	2	1	3	2	3	S1FA	0.8413
SAP	1	0	0	1	1	0	1	2	1	STER_AP	1
SBP	13	16	2	31	16	12	28	16	17	SBP	0.6644
SRS	6	6	0	12	5	6	11	5	11	DUF702	1
Sigma70-like	1	6	0	7	1	6	7	5	6	Sigma70_r2,Sigma70_r3,Sigma70_r4	1

TAZ	3	3	0	6	3	4	7	4	5	zf-TAZ	1
TCP	12	19	2	33	18	19	37	17	24	TCP	1
TIG	4	5	0	9	4	5	9	6	4	TIG	0.9576
TUB	5	5	2	12	6	6	12	10	11	Tub	0.9827
Tify	8	8	1	17	11	12	23	13	15	tify	0.7606
Trihelix	24	20	1	45	25	23	48	33	30	trihelix	1
ULT	2	1	0	3	4	1	5	2	2	ULT	1
VARL	1	2	0	3	1	2	3	1	3	VARL	1
VOZ	5	2	1	8	3	3	6	3	5	VOZ	0.9053
WRKY	45	39	3	87	51	40	91	57	73	WRKY	0.9704
bHLH	91	74	6	171	97	85	182	111	141	HLH	0.9583
bZIP	19	17	0	36	21	19	40	24	22	bZIP_1,bZIP_2,bZIP_Maf	1
mTERF	19	27	2	48	22	30	52	33	36	mTERF	1
zf-HD	9	6	2	17	11	7	18	11	17	ZF-HD_dimer	1

Note: *Jre*, *Juglans regia* (walnut); *Mru*, *Myrica rubra* (bayberry); *Cil*, *Carya illinoisnensis* (pecan).

Table S19. Information of samples for whole genome re-sequencing.

Sample ID	Plant ID	Scab resistance*	Source**	Sampling location	Population***
Barton	ML11	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Melrose	HL35	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Osage	HL16	1	Foreign	China: Paiyashan Farm, Hunan	R
Peruque	HL38	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
PoSey	HL30	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Pvilop	HL32	1	Foreign	China: Paiyashan Farm, Hunan	R
Surprize	HL25	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Woodroof	ML38	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Owens-1	ML32	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Yalin13	YL13	1	Domestic	China: Jing'an, Jiangxi	R
Yalin30	YL30	1	Domestic	China: Jing'an, Jiangxi	R
Farley	ML20	2	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Mandan	ML25	2.3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Caddo	ML13	3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Dependable	ML1	3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Forkert	ML21	3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Kiowa	ML23	3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Oconee	HL17	3	Foreign	China: Paiyashan Farm, Hunan	S
Stuart	ML5	3	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Cheyenne	HL12	4	Foreign	China: Paiyashan Farm, Hunan	S
Hirschi/Steuck	HL29	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Mahan	ZL57	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Moore	ML29	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S

Schley	ML6	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Shawnee	ZL59	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Shoshoni	ML34	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Tejas	ZL60	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Woodard	ML37	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
VC1-68	VC1-68	4	Foreign	USA: NCGR Provenance Orchards, Somerville	S
Excell	ML3	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-2	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-3	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-4	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-5	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-6	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-7	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-8	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-9	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-11	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Excell	ML3-12	1	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-4	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-6	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-7	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-8	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-9	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Elliott	ML7-10	1.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	R
Sumner	ML8	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-2	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S

Sumner	ML8-3	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-4	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-6	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-7	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-8	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-9	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-10	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-11	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sumner	ML8-12	2.67	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Desirable	ML9	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Desirable	ML9-2	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Desirable	ML9-3	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Desirable	ML9-4	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Desirable	ML9-5	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-1	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-2	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-3	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-5	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-6	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-7	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-8	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-9	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-10	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-11	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-13	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-14	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S

Pawnee	ZL49-16	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Pawnee	ZL49-17	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sioux	HL8	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Sioux	HL42	4	Foreign	China: Paiyashan Farm, Hunan	S
Western Schley	ZL58-3	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58-4	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58-11	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58-12	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58-13	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S
Western Schley	ZL58-15	4	Foreign	China: Zhejiang A&F University campus, Hangzhou	S

Note: *, the grade of pecan scab resistance were assessed by integrating the record from XXX. **, "Foreign" indicates the original germplasms were introduced from outside China and "Domestic" means the accessions were collected from seed-germinated seedling in China. ***, the populations were defined based on the pecan scab resistance grade: R, resistance population with the grade <=2; S, susceptiable population with the grade >2.

Table S20. Statistics of the resequencing data and the SNPs for each accessions.

Sample ID	Plant ID	Raw_reads (M)	Raw_bases (Gb)	Clean_reads (M)	Clean_bases (Gb)	Clean_ratio(%)	Clean_coverage (X)	Q20(%)	Q30(%)	GC(%)
Barton	ML11	190.80	19.08	190.12	19.01	99.64	27.50	98.47	94.91	37.09
Melrose	HL35	202.54	20.25	201.85	20.19	99.66	29.21	97.09	91.73	37.49
Osage	HL16	237.93	23.79	235.60	23.56	99.02	34.08	98.80	94.91	37.66
Peruque	HL38	169.97	17.00	169.41	16.94	99.67	24.51	97.19	92.05	37.17
PoSey	HL30	185.78	18.58	185.12	18.51	99.64	26.78	97.03	91.58	37.61
Pvilop	HL32	188.53	18.85	186.61	18.66	98.98	26.99	98.56	94.99	36.83
Surprize	HL25	192.61	19.26	192.09	19.21	99.73	27.79	96.97	91.36	37.39
Woodroof	ML38	203.03	20.30	202.10	20.21	99.54	29.24	98.45	94.62	36.95
Owens-1	ML32	173.03	17.30	172.27	17.23	99.56	24.92	98.52	94.90	37.58
Yalin13	YL13	227.62	22.76	226.89	22.69	99.68	32.82	97.88	93.66	37.41
Yalin30	YL30	179.08	17.91	178.60	17.86	99.73	25.84	97.81	93.28	37.14
Farley	ML20	168.36	16.84	167.87	16.79	99.71	24.29	98.44	94.53	37.05
Mandan	ML25	172.26	17.23	171.73	17.17	99.69	24.84	98.49	94.77	37.25
Caddo	ML13	248.04	24.80	246.72	24.67	99.47	35.69	98.73	96.10	38.69
Dependable	ML1	222.27	22.23	221.56	22.16	99.68	32.06	98.70	95.70	37.03
Forkert	ML21	183.42	18.34	182.89	18.29	99.71	26.46	98.53	94.91	37.01
Kiowa	ML23	185.02	18.50	184.47	18.45	99.70	26.69	98.34	94.07	37.03
Oconee	HL17	193.78	19.38	191.95	19.19	99.05	27.76	98.51	94.74	37.01
Stuart	ML5	159.09	15.91	158.64	15.86	99.72	22.94	98.62	95.60	37.26
Cheyenne	HL12	175.20	17.52	173.82	17.38	99.21	25.14	98.42	94.61	37.15
Hirschi/Steuck	HL29	150.11	15.01	149.70	14.97	99.73	21.66	96.98	91.40	37.53
Mahan	ZL57	159.84	15.98	159.42	15.94	99.74	23.06	98.09	94.31	37.96

Moore	ML29	185.77	18.58	184.87	18.49	99.52	26.75	98.52	94.72	37.01
Schley	ML6	198.88	19.89	198.20	19.82	99.66	28.67	98.61	95.88	37.22
Shawnee	ZL59	264.27	26.43	263.20	26.32	99.60	38.07	98.37	94.44	37.64
Shoshoni	ML34	170.75	17.07	169.97	17.00	99.55	24.59	98.54	95.18	37.39
Tejas	ZL60	148.16	14.82	147.24	14.72	99.38	21.29	98.02	93.71	44.20
Woodard	ML37	169.32	16.93	168.55	16.85	99.55	24.38	98.59	95.16	37.23
VC1-68	VC1-68	226.99	22.70	225.88	22.59	99.51	32.68	98.26	94.16	40.06
Excell	ML3	199.76	19.98	199.22	19.92	99.73	28.82	98.65	95.48	36.72
Excell	ML3-2	151.03	15.10	149.99	15.00	99.32	21.70	98.53	94.95	36.02
Excell	ML3-3	179.32	17.93	178.84	17.88	99.73	25.87	98.17	94.75	37.02
Excell	ML3-4	234.32	23.43	233.75	23.37	99.75	33.81	98.62	95.49	36.61
Excell	ML3-5	190.18	19.02	189.92	18.99	99.87	27.47	98.57	94.93	37.38
Excell	ML3-6	152.70	15.27	152.56	15.26	99.90	22.07	98.56	94.72	36.94
Excell	ML3-7	166.64	16.66	166.47	16.65	99.90	24.09	98.50	94.55	37.25
Excell	ML3-8	179.47	17.95	179.29	17.93	99.90	25.94	98.59	94.97	37.21
Excell	ML3-9	192.67	19.27	192.36	19.24	99.84	27.83	98.65	95.33	37.00
Excell	ML3-11	214.80	21.48	214.52	21.45	99.87	31.03	98.60	95.05	37.03
Excell	ML3-12	195.12	19.51	194.80	19.48	99.84	28.18	98.64	95.41	36.91
Elliott	ML7	202.68	20.27	202.05	20.21	99.69	29.24	98.71	95.96	37.32
Elliott	ML7-4	190.73	19.07	190.44	19.04	99.85	27.54	98.46	94.83	37.14
Elliott	ML7-6	151.99	15.20	151.79	15.18	99.87	21.96	98.39	94.53	37.45
Elliott	ML7-7	193.29	19.33	192.97	19.30	99.83	27.92	98.41	94.53	36.95
Elliott	ML7-8	197.55	19.76	197.27	19.73	99.85	28.54	98.47	94.75	36.75
Elliott	ML7-9	211.40	21.14	211.00	21.10	99.81	30.52	98.54	95.20	36.90
Elliott	ML7-10	174.58	17.46	174.26	17.43	99.82	25.21	98.55	95.25	36.92
Sumner	ML8	200.54	20.05	200.03	20.00	99.75	28.93	98.64	95.31	37.62

Sumner	ML8-2	162.36	16.24	161.90	16.19	99.72	23.42	97.62	92.08	37.27
Sumner	ML8-3	142.77	14.28	141.83	14.18	99.34	20.51	97.59	92.69	43.50
Sumner	ML8-4	173.06	17.31	172.38	17.24	99.61	24.94	98.38	94.16	36.47
Sumner	ML8-6	249.19	24.92	247.15	24.71	99.15	35.75	97.52	92.34	37.80
Sumner	ML8-7	165.17	16.52	164.73	16.47	99.74	23.83	97.67	92.30	37.12
Sumner	ML8-8	165.01	16.50	164.56	16.46	99.73	23.81	97.73	92.75	38.47
Sumner	ML8-9	236.38	23.64	235.56	23.56	99.65	34.08	96.86	90.98	37.28
Sumner	ML8-10	234.48	23.45	233.70	23.37	99.67	33.81	96.88	91.03	37.49
Sumner	ML8-11	153.29	15.33	152.79	15.28	99.67	22.10	96.76	90.70	37.79
Sumner	ML8-12	376.17	37.62	374.53	37.45	99.56	54.17	98.50	94.89	38.88
Desirable	ML9	185.56	18.56	185.06	18.51	99.73	26.78	98.61	95.07	37.44
Desirable	ML9-2	155.46	15.55	155.05	15.51	99.74	22.44	97.65	92.21	37.79
Desirable	ML9-3	126.63	12.66	126.31	12.63	99.75	18.27	97.54	91.85	37.36
Desirable	ML9-4	127.31	12.73	127.02	12.70	99.77	18.37	97.66	92.34	38.05
Desirable	ML9-5	202.03	20.20	200.85	20.09	99.42	29.06	98.46	95.08	40.67
Pawnee	ZL49-1	194.92	19.49	193.96	19.40	99.51	28.06	98.33	94.39	37.72
Pawnee	ZL49-2	221.20	22.12	220.25	22.02	99.57	31.85	98.42	94.92	37.59
Pawnee	ZL49-3	291.60	29.16	290.82	29.08	99.73	42.07	98.19	94.59	38.83
Pawnee	ZL49-5	192.43	19.24	191.92	19.19	99.74	27.76	98.20	94.43	37.34
Pawnee	ZL49-6	152.36	15.24	151.95	15.19	99.73	21.97	98.25	94.69	37.43
Pawnee	ZL49-7	159.84	15.98	159.37	15.94	99.71	23.06	98.09	94.09	37.42
Pawnee	ZL49-8	134.35	13.43	134.01	13.40	99.75	19.38	98.15	94.38	37.80
Pawnee	ZL49-9	172.45	17.24	171.95	17.19	99.71	24.87	98.16	94.30	37.80
Pawnee	ZL49-10	191.63	19.16	190.99	19.10	99.67	27.63	98.15	94.25	37.98
Pawnee	ZL49-11	165.03	16.50	164.61	16.46	99.74	23.81	98.22	94.48	37.62
Pawnee	ZL49-13	159.89	15.99	159.49	15.95	99.75	23.07	98.09	94.21	37.75

Pawnee	ZL49-14	194.60	19.46	194.00	19.40	99.69	28.06	98.07	94.12	37.36
Pawnee	ZL49-16	188.31	18.83	187.66	18.77	99.65	27.15	98.13	94.53	37.27
Pawnee	ZL49-17	190.62	19.06	190.03	19.00	99.69	27.49	98.11	94.30	37.55
Sioux	HL8	224.19	22.42	223.53	22.35	99.70	32.33	96.88	91.08	37.39
Sioux	HL42	262.74	26.27	260.80	26.08	99.26	37.73	98.58	95.39	37.23
Western Schley	ZL58	185.75	18.58	185.17	18.52	99.69	26.79	98.34	94.75	38.12
Western Schley	ZL58-3	229.59	22.96	228.81	22.88	99.65	33.10	97.79	92.62	37.24
Western Schley	ZL58-4	177.26	17.73	176.75	17.67	99.70	25.56	97.75	92.34	36.83
Western Schley	ZL58-11	191.00	19.10	190.52	19.05	99.74	27.56	96.31	87.93	39.03
Western Schley	ZL58-12	139.21	13.92	138.60	13.86	99.55	20.05	96.16	87.50	37.10
Western Schley	ZL58-13	171.53	17.15	170.76	17.07	99.53	24.69	96.96	91.19	36.83
Western Schley	ZL58-15	146.53	14.65	146.04	14.60	99.66	21.12	96.03	88.07	36.66
Total		16303.12	1630.31	16244.28	1624.41	8569.52	-	-	-	-
Average		189.57	18.96	188.89	18.89	99.65	27.32	98.08	93.85	37.59

Table S21. Parents information and estimate ancestral sources and types in subgenomes for each cultivar.

Accession	**Subgenome A**	**Subgenome B**	**Parents (Female X Male)**
Barton	K2	K1	Moore X Success
Caddo	K1,K4,K3,K2	K3,K1	Brooks X Alley
Cheyenne	K1	K1	Clark X Odom
Dependable	K4,K2	K4,K1	Jewett X Success
Desirable	K4,K3	K3,K4	Success X Jewett
Elliott	K4,K2	K4,K1	Not known (Seedling)
Excell	K1,K2	K4,K1	Not known (Seedling)
Farley	K1,K2	K3,K4,K1	Not known (Seedling)
Forkert	K1,K3,K2	K3,K1	Success X Schley
Hirschi/Steuck	K1,K4,K3,K2	K3,K2,K4,K1	Not known (Seedling)
Kiowa	K1,K3,K2	K3,K1	Mahan X Desirable
Mahan	K3	K3	Not known (Seedling)
Mandan	K1,K3,K2	K2,K1	BW-1 X Osage
Melrose	K1,K3	K3,K2,K1	Not known (Seedling)
Moore	K1	K1	Not known (Seedling)
Oconee	K3,K2	K3,K1	Schley X Barton
Osage	K1	K3,K4,K1	Major X Evers
Owens-1	K1,K4,K3,K2	K3,K2,K4,K1	Not known (Chance seedling)
Pawnee	K3	K3	Mohawk X Starking Hardy Giant
Peruque	K2	K1	Not known (Seedling)
PoSey	K3	K3	Not known (Seedling)
Pvilop	K1,K4,K3	K3,K4,K1	No record
Schley	K4	K4	Not known (Seedling)
Shawnee	K4	K4	Schley X Barton
Shoshoni	K1	K1	Odom X Evers
Sioux	K1,K3	K3,K1	Schley X Carmichael
Stuart	K3	K3	Not known (Seedling)
Sumner	K4,K3	K3,K4	Not known (Seedling)
Surprize	K3	K2	Not known (Chance seedling)
Tejas	K4	K4	Mahan X Risien 1
VC1-68	K1,K3	K3,K1	Not known (Seedling)
Western Schley	K1,K3	K3,K2,K4,K1	Not known (Seedling)
Woodard	K1,K2	K3,K4,K1	Not known (Seedling)
Woodroof	K1,K4,K3	K3,K4,K1	Not known (Seedling)
Yalin13	K1,K4,K3,K2	K3,K2,K4,K1	Not known (Seedling)
Yalin30	K1	K3,K4,K1	Not known (Seedling)

Note: Pink=K1, Oringe=K2, lake blue=K3, sky blue=K.

Table S22. Nuecleotide diversity (π) and pairwise population differentiation level (*Fst*) between the pecan scab resistance and susceptible populations (100 Kb per window).

Table S23. Information of candidate genes in the selected regions (Top 5% of *Fst* and π ratio).

Table S24. Phenotypes of two selected regions including the protein-encoding genes of chitinases (*CHIs*) and ionotropic glutamate receptors (*GRIPs*).

(Tables S22-S24 are shown by separate files)

Table S25. Primers information for real-time qPCR.

Gene ID	**Gene name**	**Forward primer**	**Reverse primer**	**Tm**	**Product length (bp)**
Cil_09G_00199V2	*CHI-1*	CTAATAATGTCTCGGTGTCTG	CATCTATCTCCTCTATGTAGCA		243
Cil_09G_00200V2	*CHI-2*	CAACGATGTCTCAGTGTCT	CAGCAATCTCACGCATAGA		182
Cil_15G_00015V2	*GLR-1*	CCACAGTTACAGTTCCAAGA	GCCTGACTTACAACACTACT		264
Cil_15G_00016V2	*GLR-2*	TGATGCGAAGTGAATATGTG	TCAAGTGAATGAGCAAGAAG		184
Cil_15G_00017V2	*GLR-3*	TTCCAAGAGATTCGCCAAT	AAGCAGAGCAAGCAAGAA		209
Cil_15G_00018V2	*GLR-4*	GAGTTACACTGCAAGTCTGA	ATTCTTCTGCCGAGTTGAG		191
Cil_15G_00019V2	*GLR-5*	AGTCTGACCTCAATCCTTAC	CATATCCTTCTTCCGAGTTG		181
Cil_03G_00295V2	*MAPKKK3*	TCAACGAGGACACATACAAG	TCTCCGATGAAGCCGATT		208
Cil_12G_00571V2	*FAR-1*	CCTGGCGGAGATTGATAC	GTGGACACTTAGACAGAGAA		233
Cil_03G_00293V2	*FAR-2*	AGAAGAGGAGAGCATAGACT	AAGCAAGGCATACCGTAAT		249
Internal control*	*18S rRNA*	ACATCTTACCACGATACATAAC	AACTTGCGTTCAAAGACTC		134

Note: *, 18S rRNA (NCBI accession no. AF174619.1) were used as the interal control according to Mattison et al. (2017).