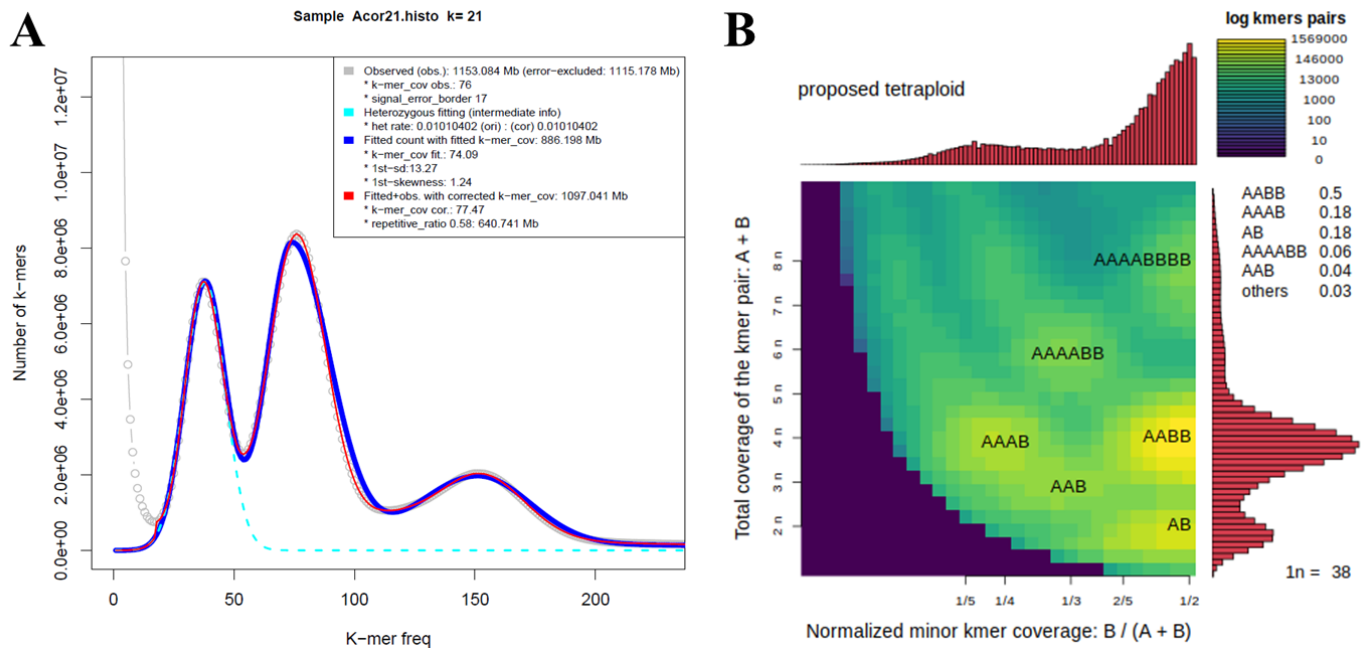
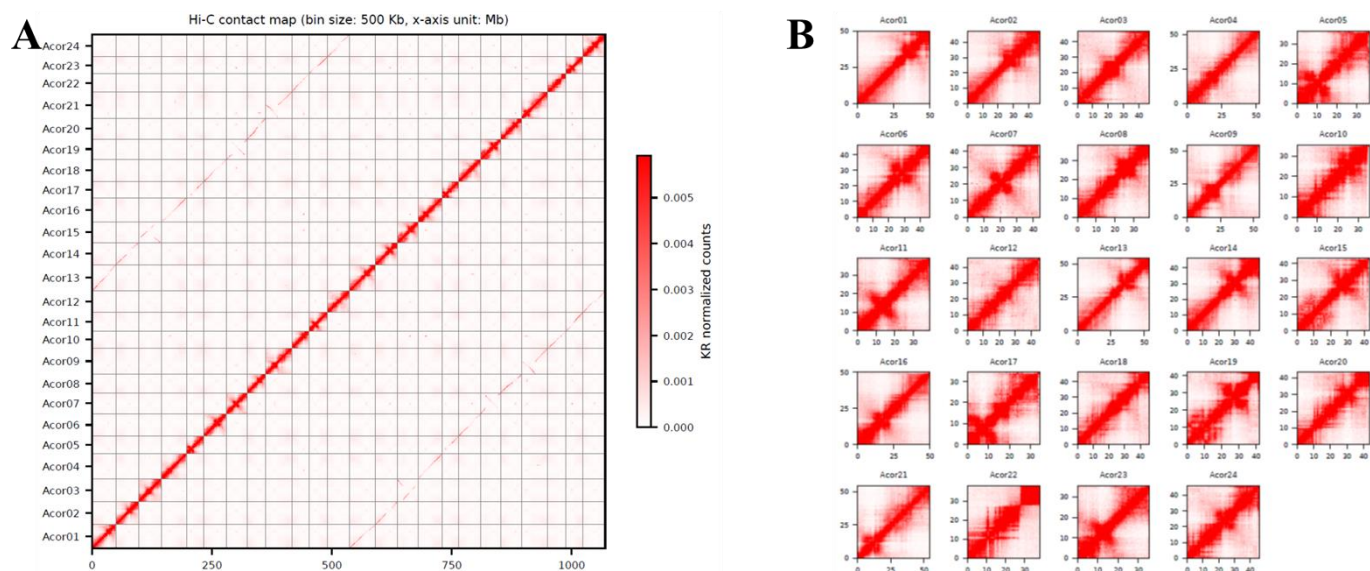
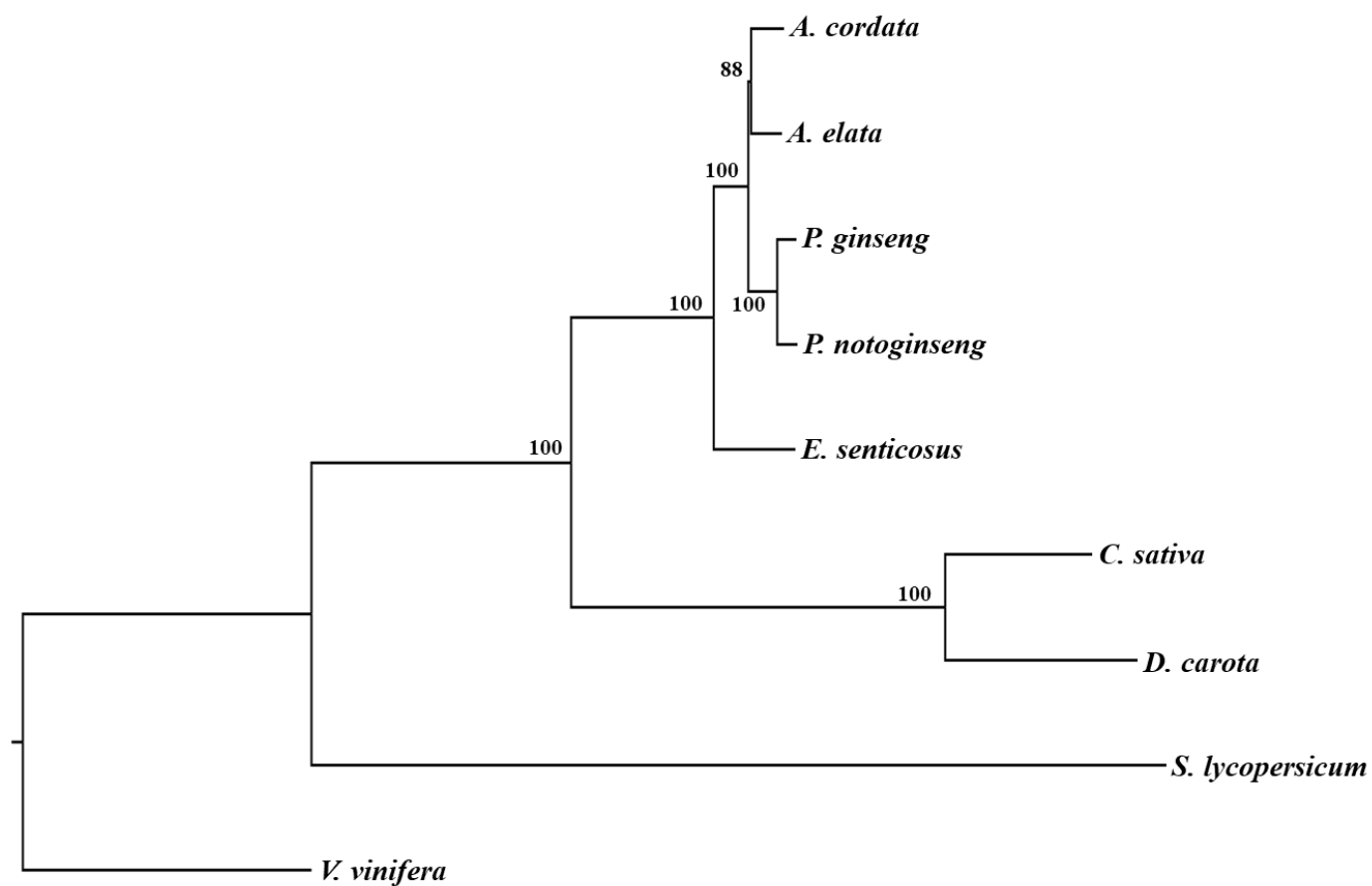




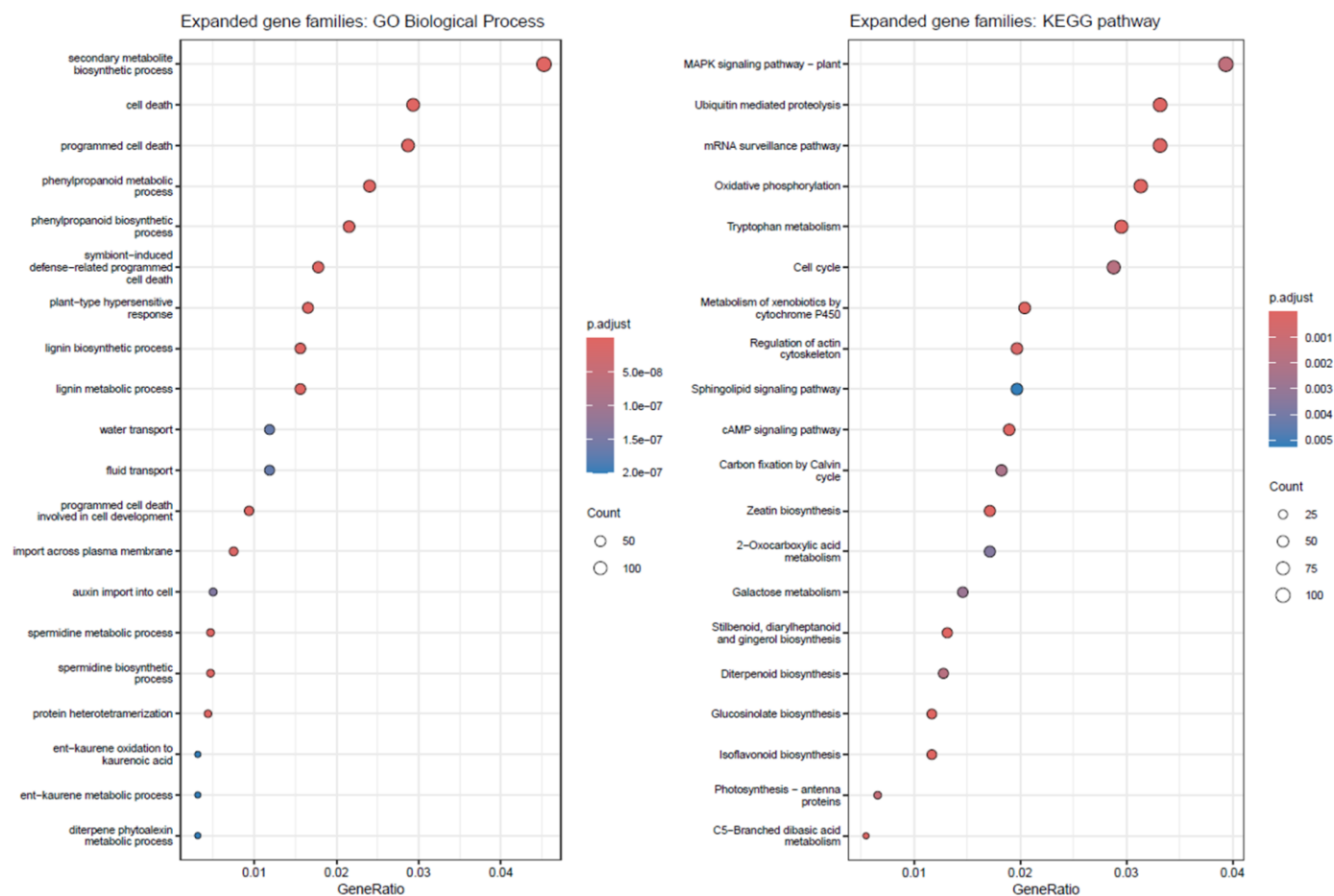
Supplementary Figure 1. Genomic characteristics of the *Aralia cordata* genome. A) Genome size estimation. B) Ploidy level estimation.



Supplementary Figure 2. Hi-C contact map of the *Aralia cordata* genome. A) Hi-C contact matrix of twenty-four chromosome-level scaffolds. B) Separate Hi-C contact matrix of twenty-four chromosome-level scaffolds.



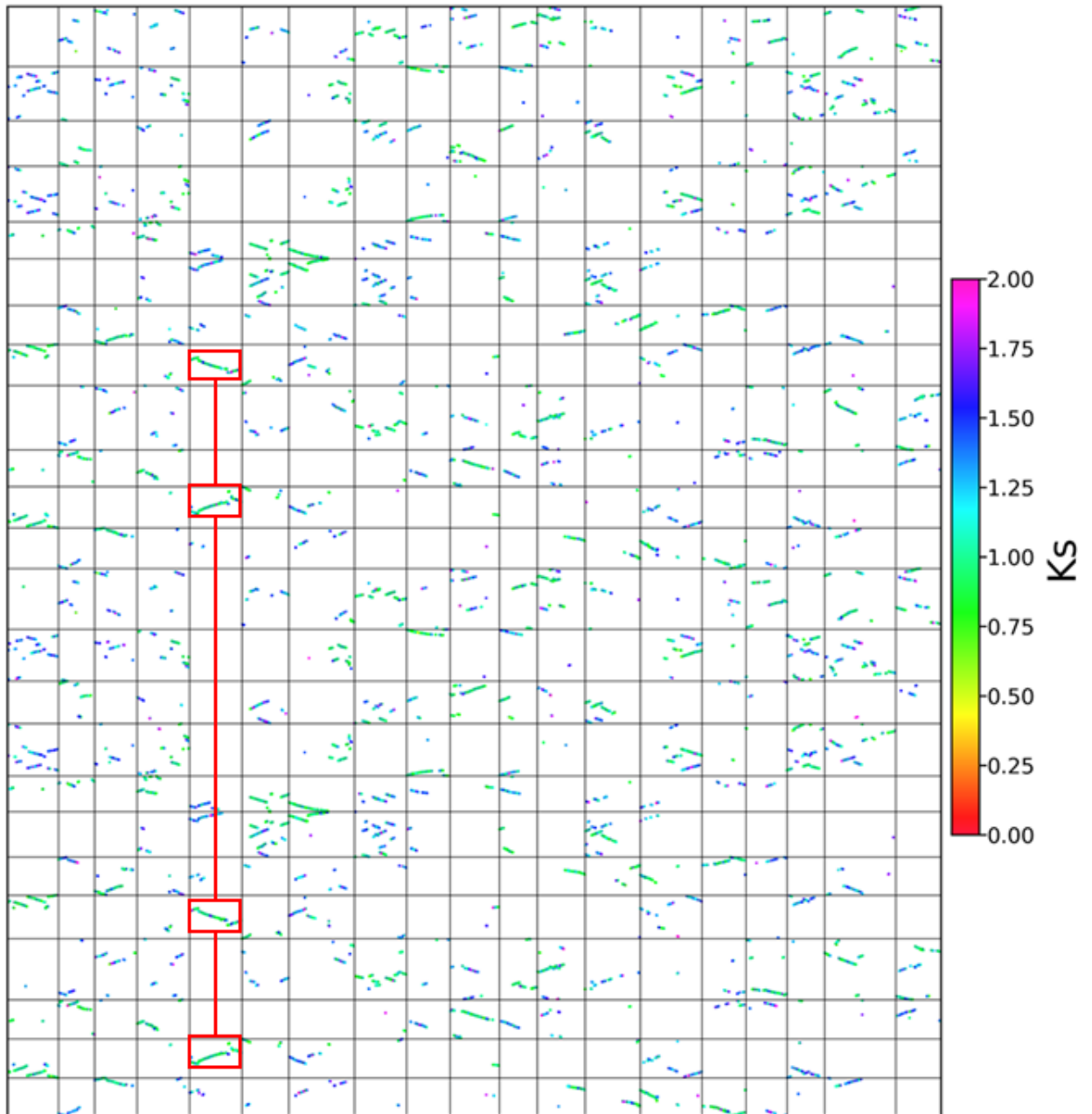
Supplementary Figure 3. Phylogenetic relationships of *A. cordata* and its related.



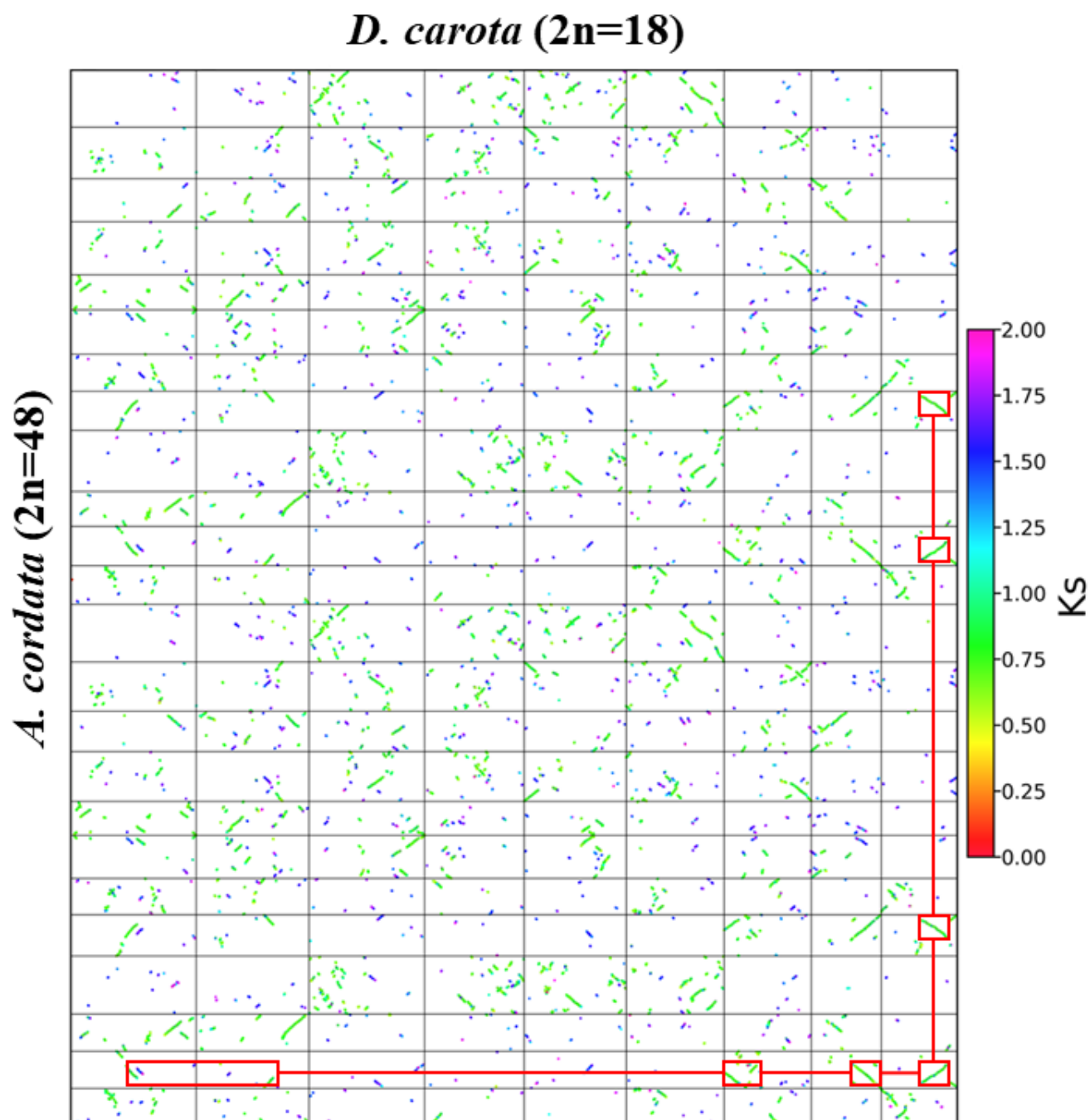
Supplementary Figure 4. Gene family expansion of *A. cordata*. Color bar indicated adjusted p-value and the circles indicated gene numbers.

V. vinifera (2n=38)

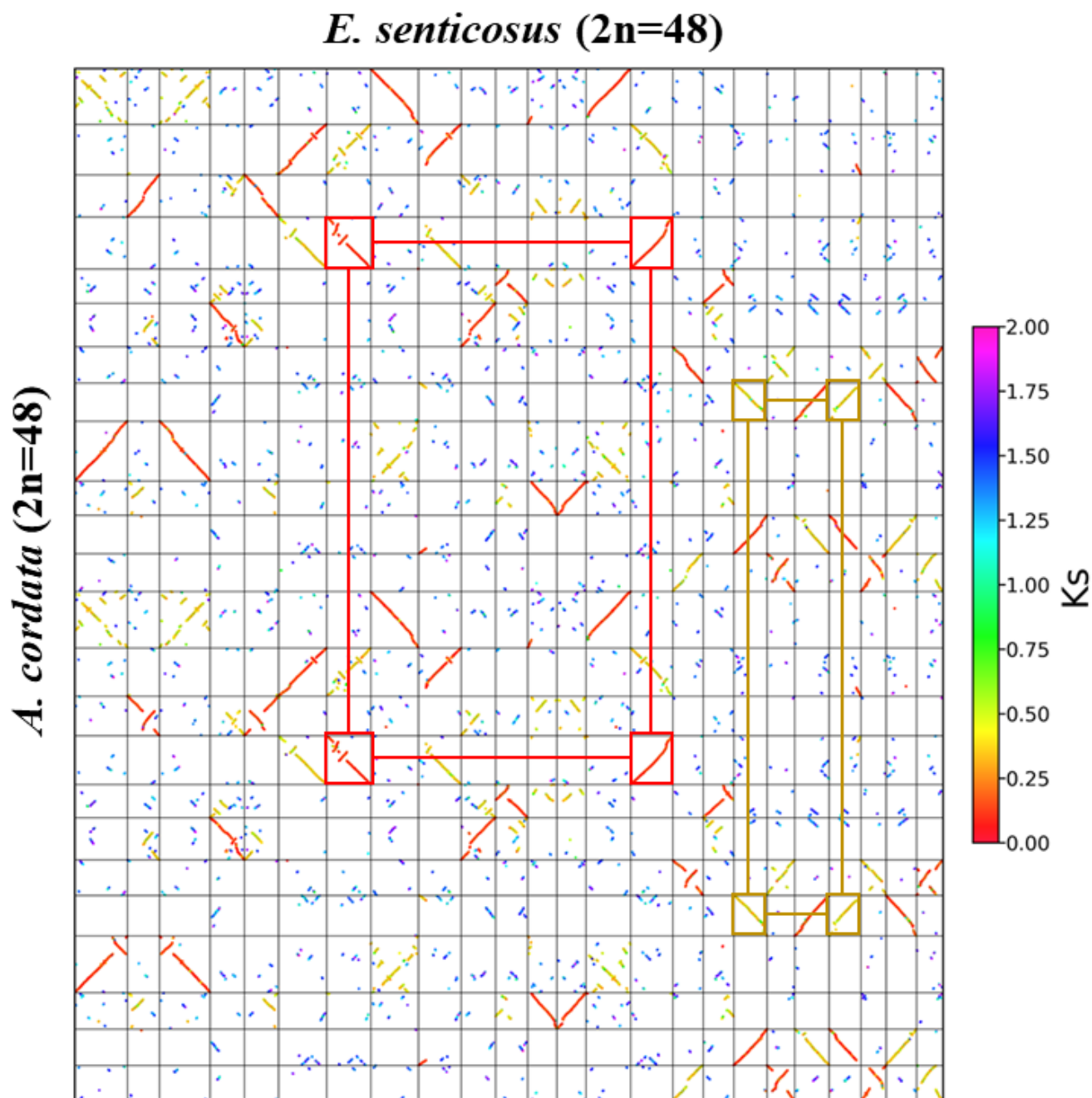
A. cordata (2n=48)



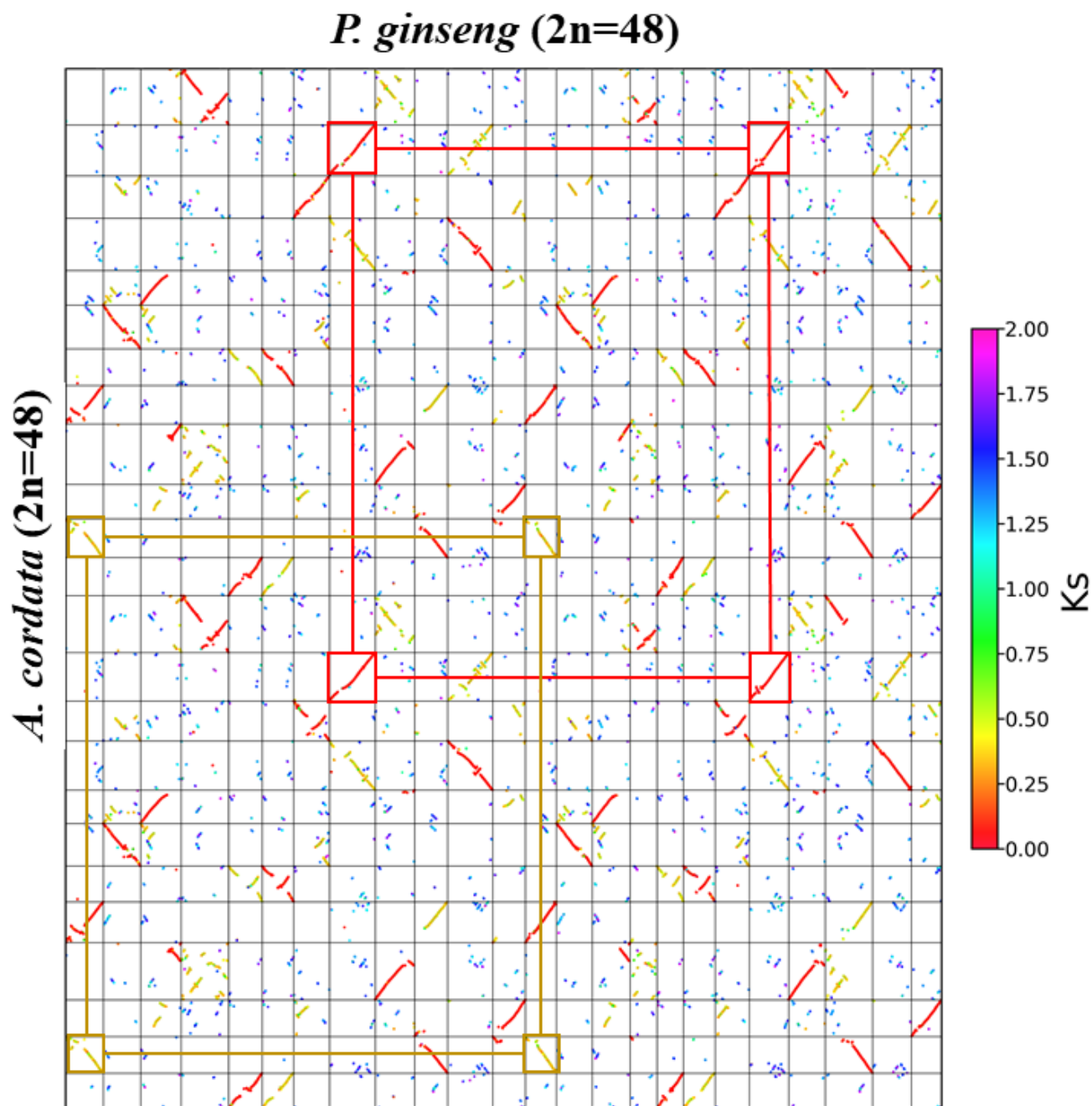
Supplementary Figure 5. Block *Ks* relationships of *A. cordata*. The colors of the dots were based on the *Ks* values of each block. A comparison between *A. cordata* and *V. vinifera*.



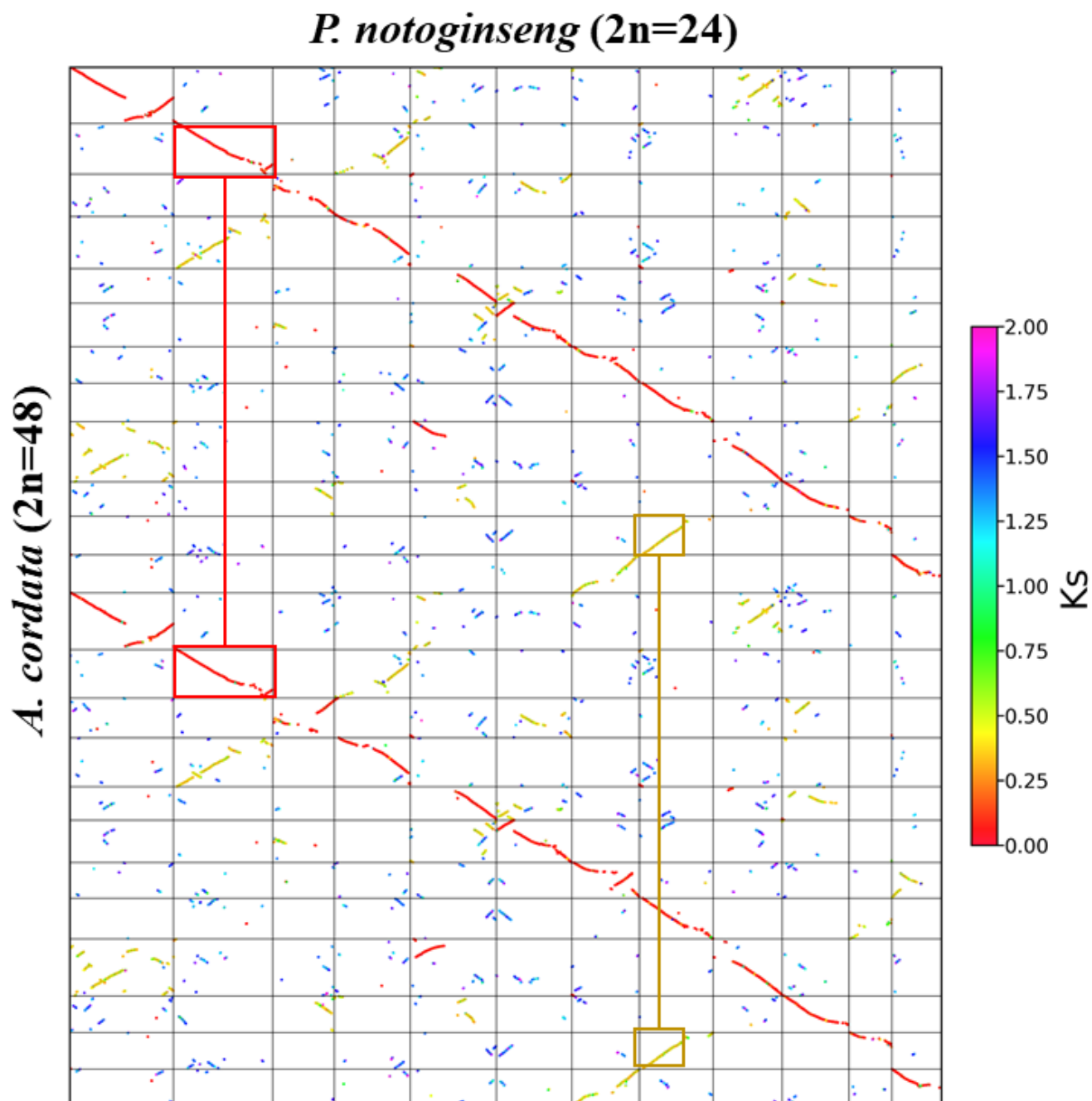
Supplementary Figure 6. Block *Ks* relationships of *A. cordata*. A comparison between *A. cordata* and *D. carota*.



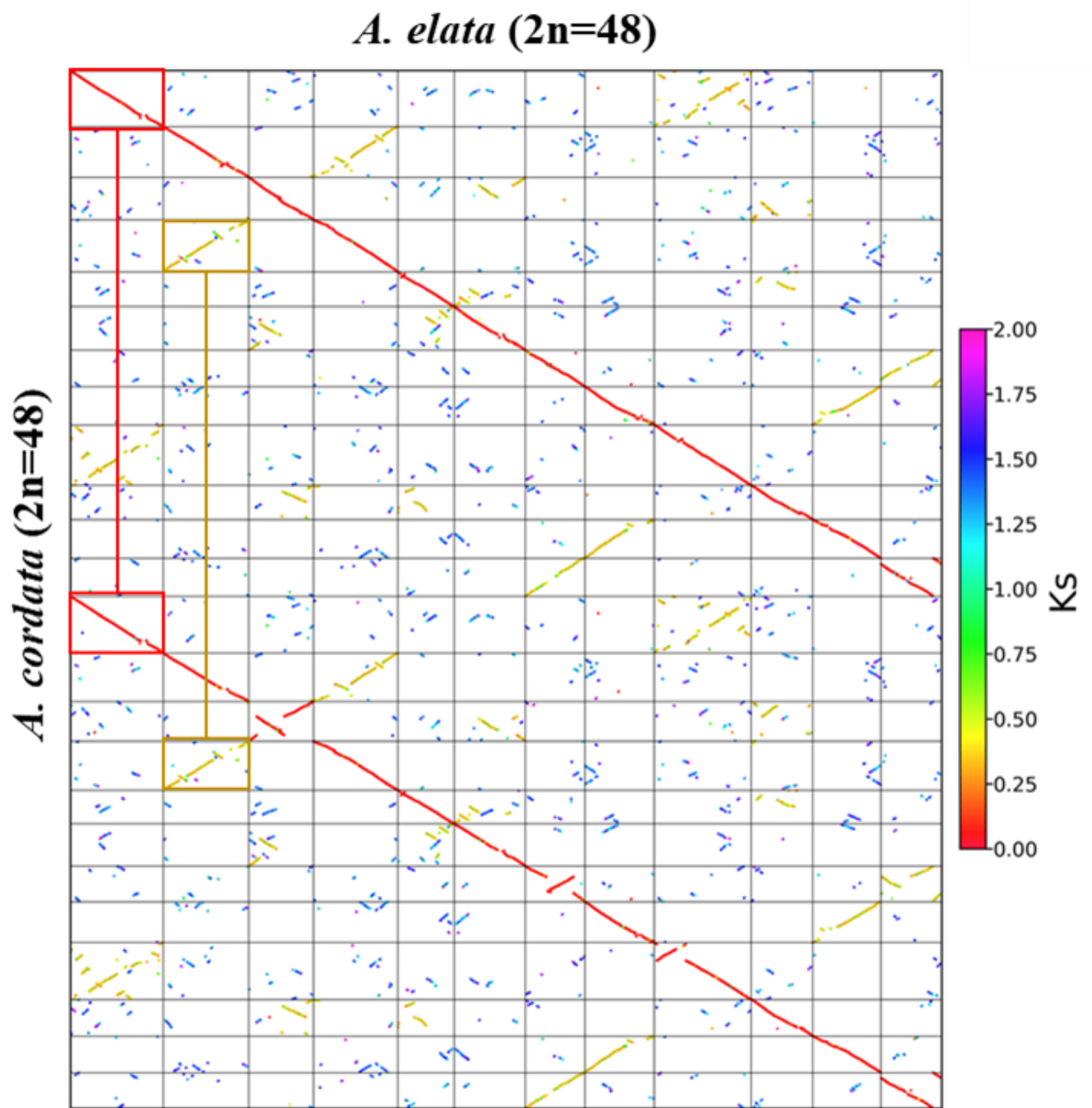
Supplementary Figure 7. Block Ks relationships of *A. cordata*. The red boxes indicated results of the WGD. The yellow boxes indicated the Araliaceae- β . A comparison between *A. cordata* and *E. senticosus*.



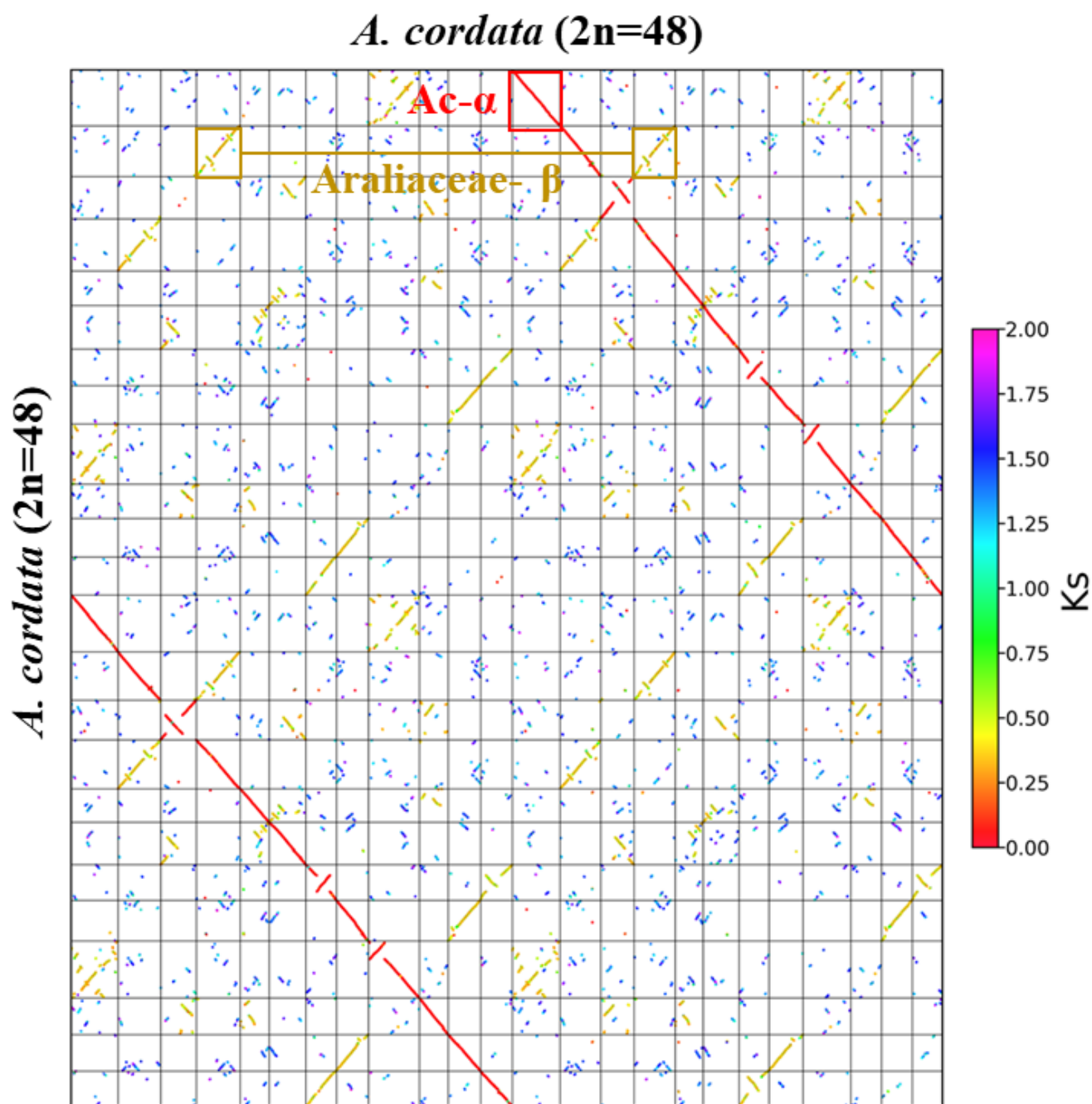
Supplementary Figure 8. Block *Ks* relationships of *A. cordata*. A comparison between *A. cordata* and *P. ginseng*.



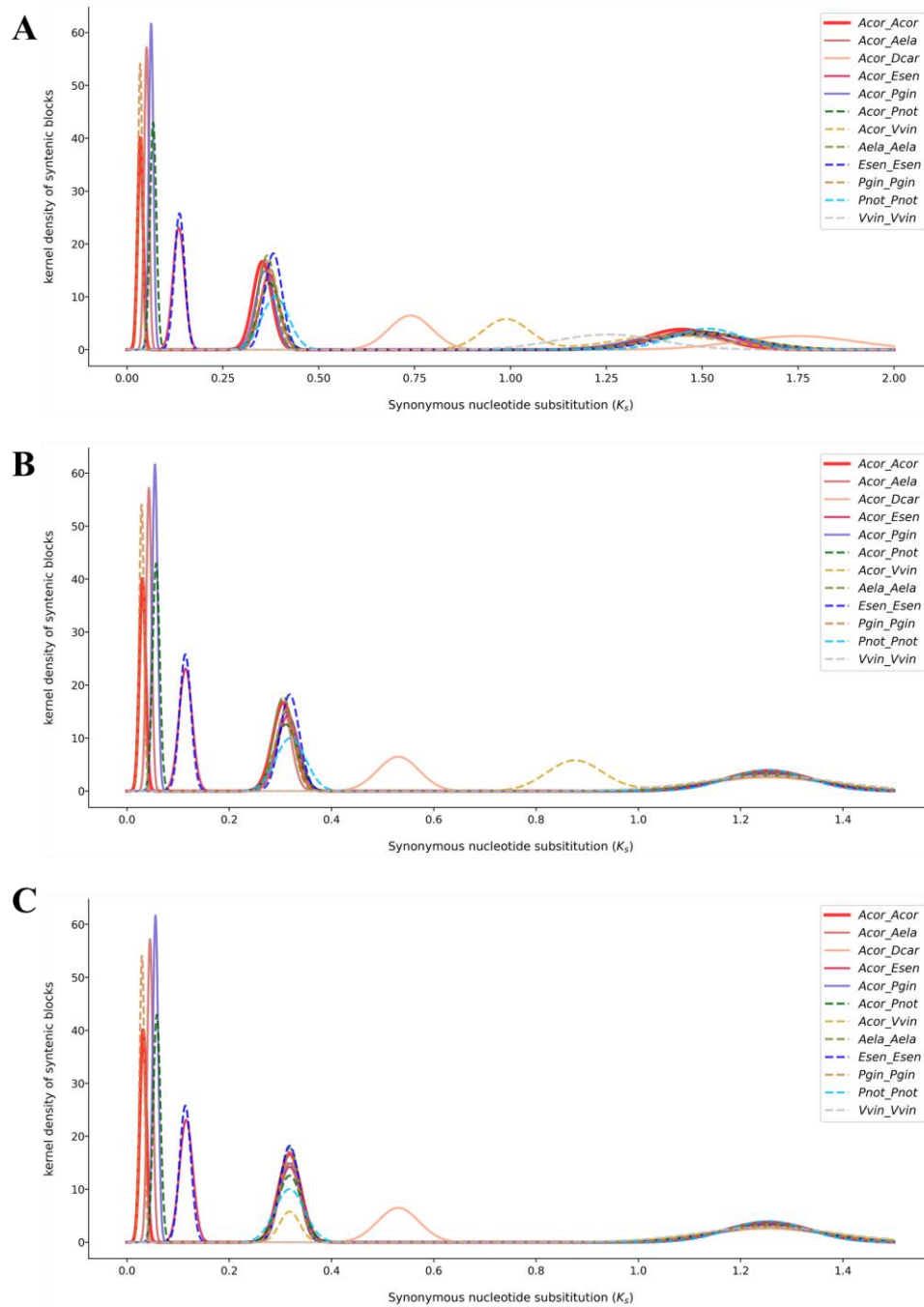
Supplementary Figure 9. Block Ks relationships of *A. cordata*. A comparison between *A. cordata* and *P. notoginseng*.



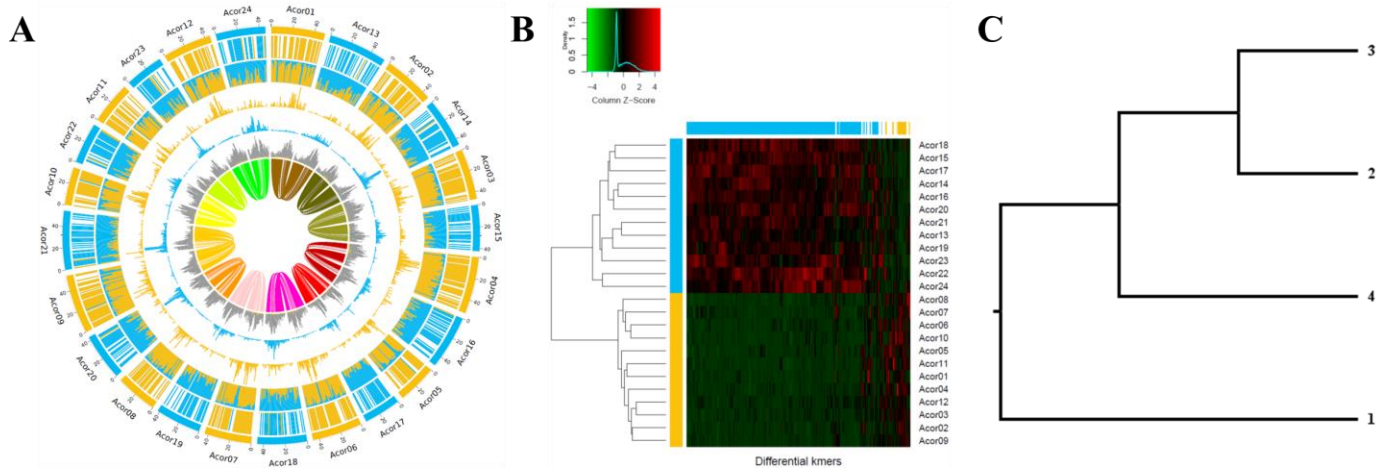
Supplementary Figure 10. Block Ks relationships of *A. cordata*. A comparison between *A. cordata* and *A. elata*.



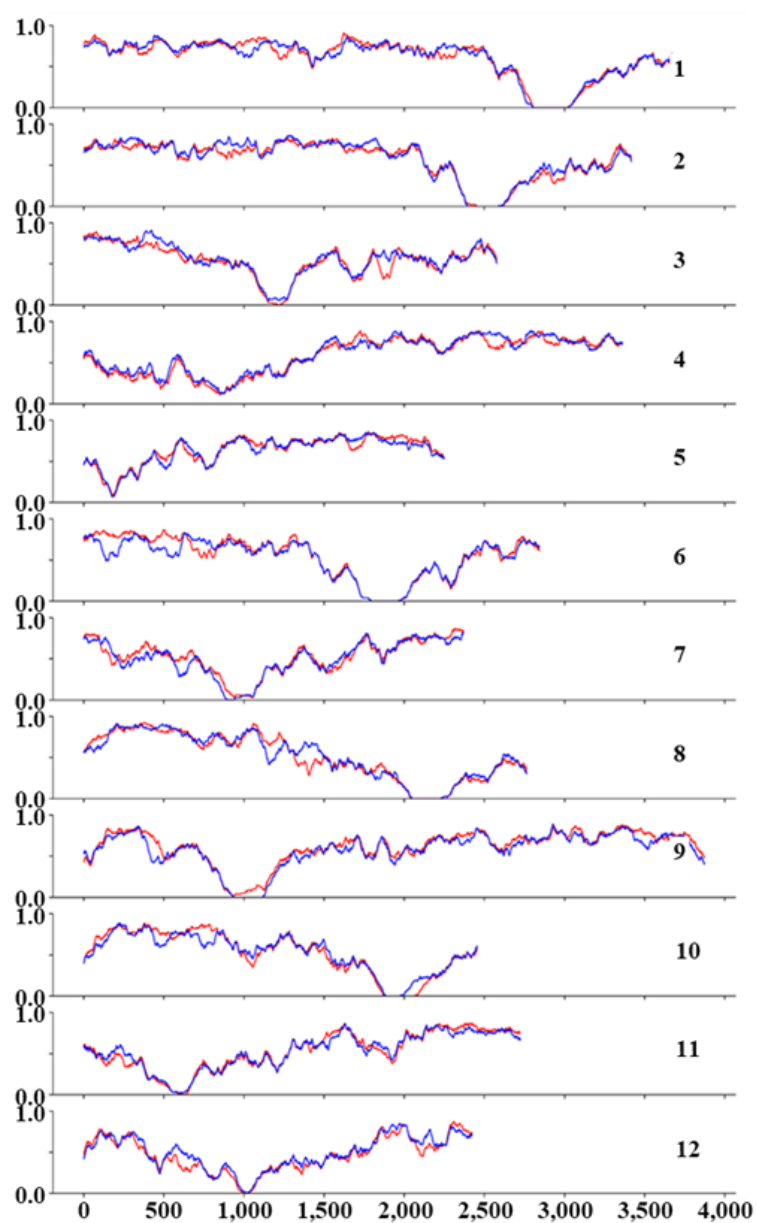
Supplementary Figure 11. Block Ks relationships of *A. cordata*. Self-comparison of *A. cordata*.



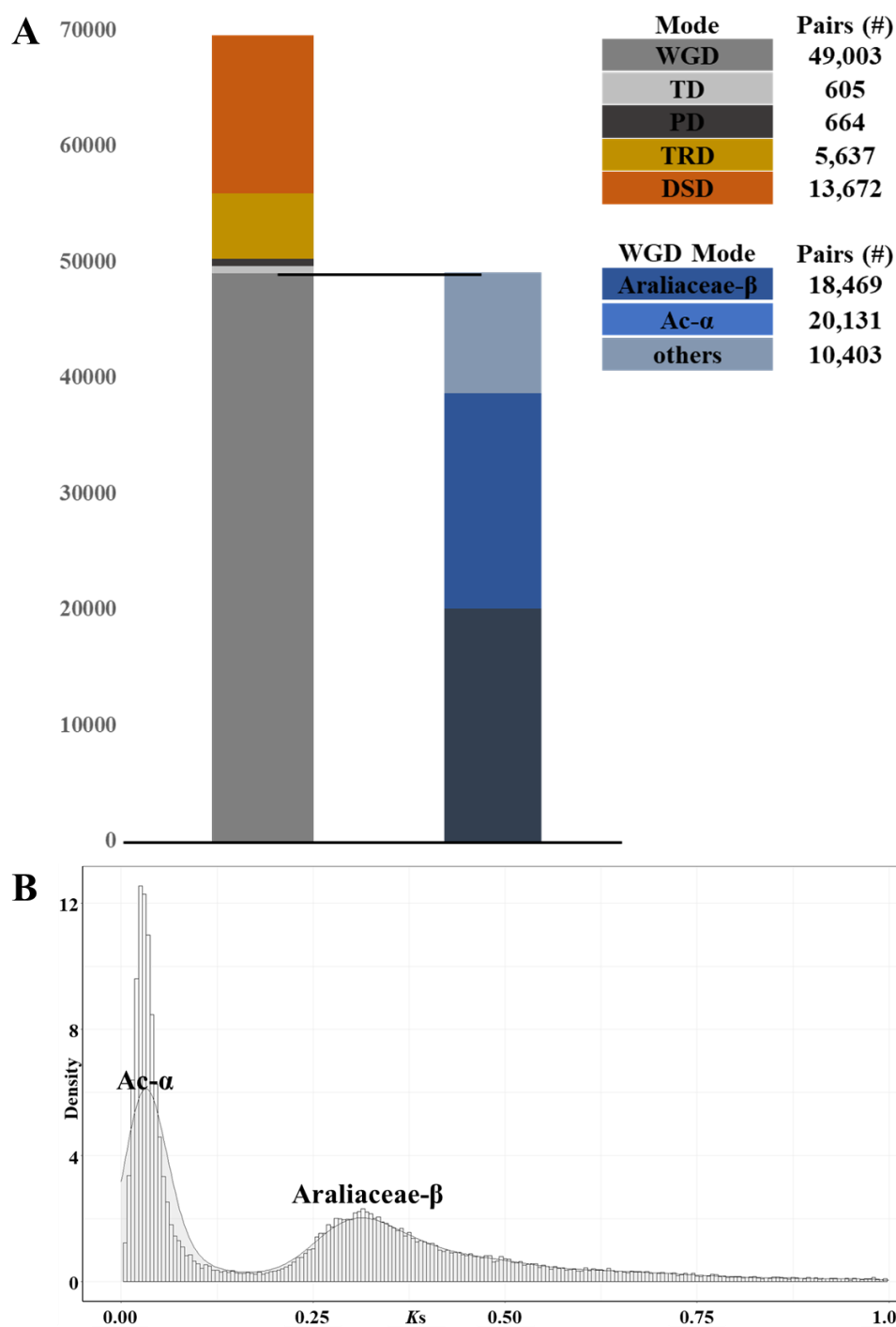
Supplementary Figure 12. Distribution of synonymous nucleotide substitution rates (K_s) of syntenic blocks. The X axis is synonymous nucleotide substitution rates, and the Y axis is kernel density of syntenic blocks. A) Raw distribution, B) K_s distribution after the first curation using *V. vinifera*, C) K_s distribution after the second curation using *E. senticosus*.



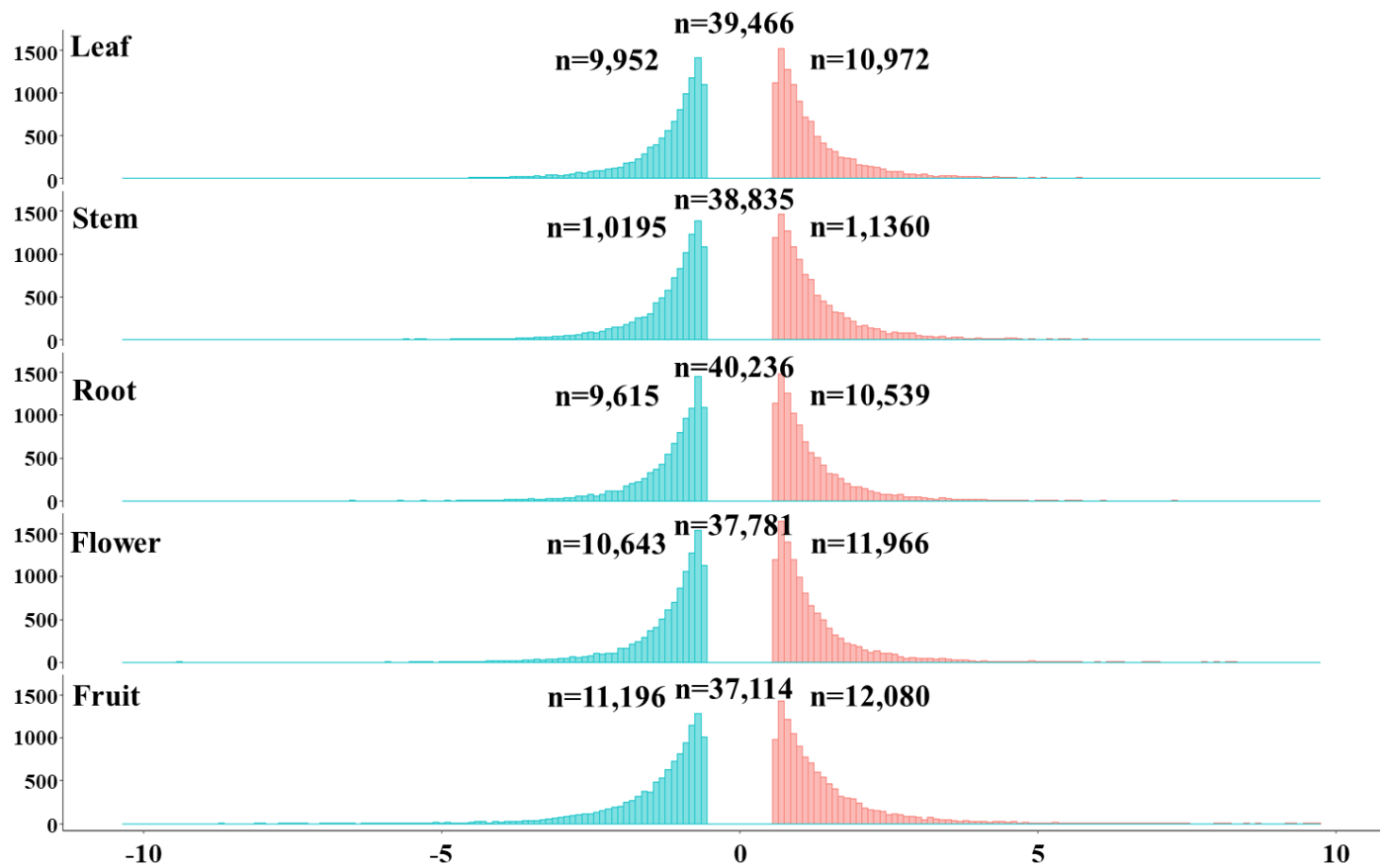
Supplementary Figure 13. Subgenome classification in *A. cordata*. A) and B) Subgenome division based on SubPhaser. A) Subgenome circos map, B) Subgenome k-mer matrix. C) Subgenome division based on phylogenetic tree. 1: One of the subgenomes of *E. senticosus*; 2, 3: each subgenome of *A. cordata*; 4: *A. elata*. Each subgenome of *A. cordata* was followed by a SubPhaser classification.



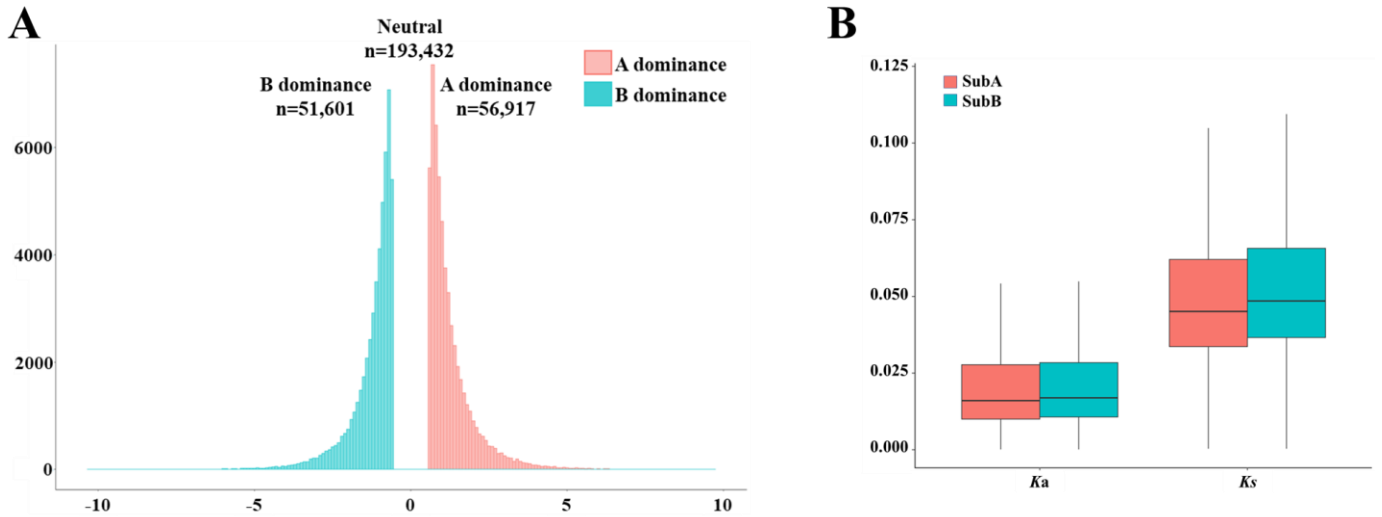
Supplementary Figure 14. Gene retention of each subgenome of *A. cordata*. *A. elata* was used as a reference genome. Red and blue lines indicated subA and subB, respectively.



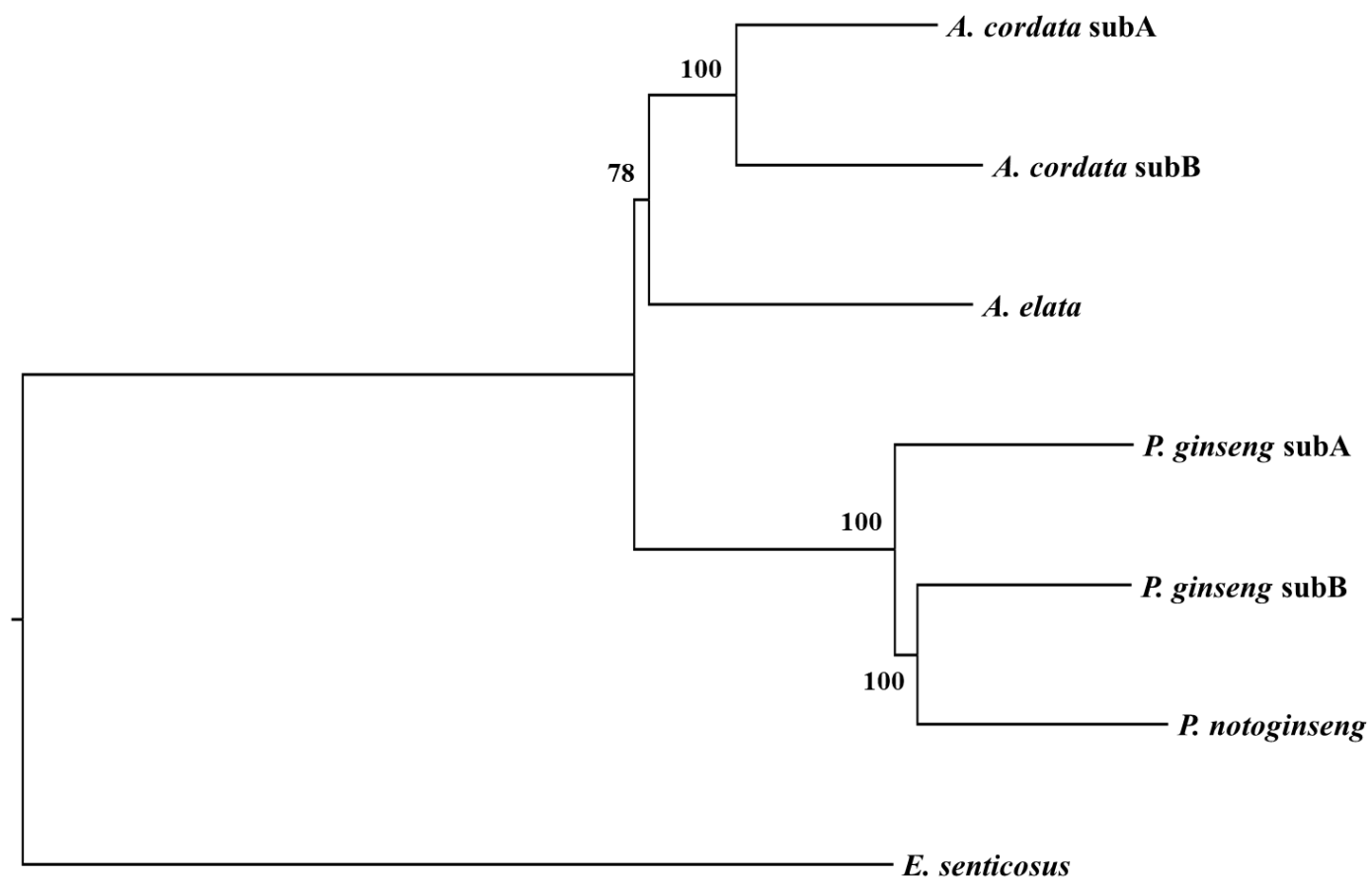
Supplementary Figure 15. Classification of duplicated gene pairs. A) Classification of duplicated gene pairs based on their duplicated mode. WGD: Whole genome duplication, TD: Tandem duplication, PD: Proximal duplication, TRD: Transposed duplication, DSD: Dispersed duplication. B) The K_s distributions of WGD gene pairs. The K_s value of 0.2 was used as a threshold to divide the Ac- α and Araliaceae- β .



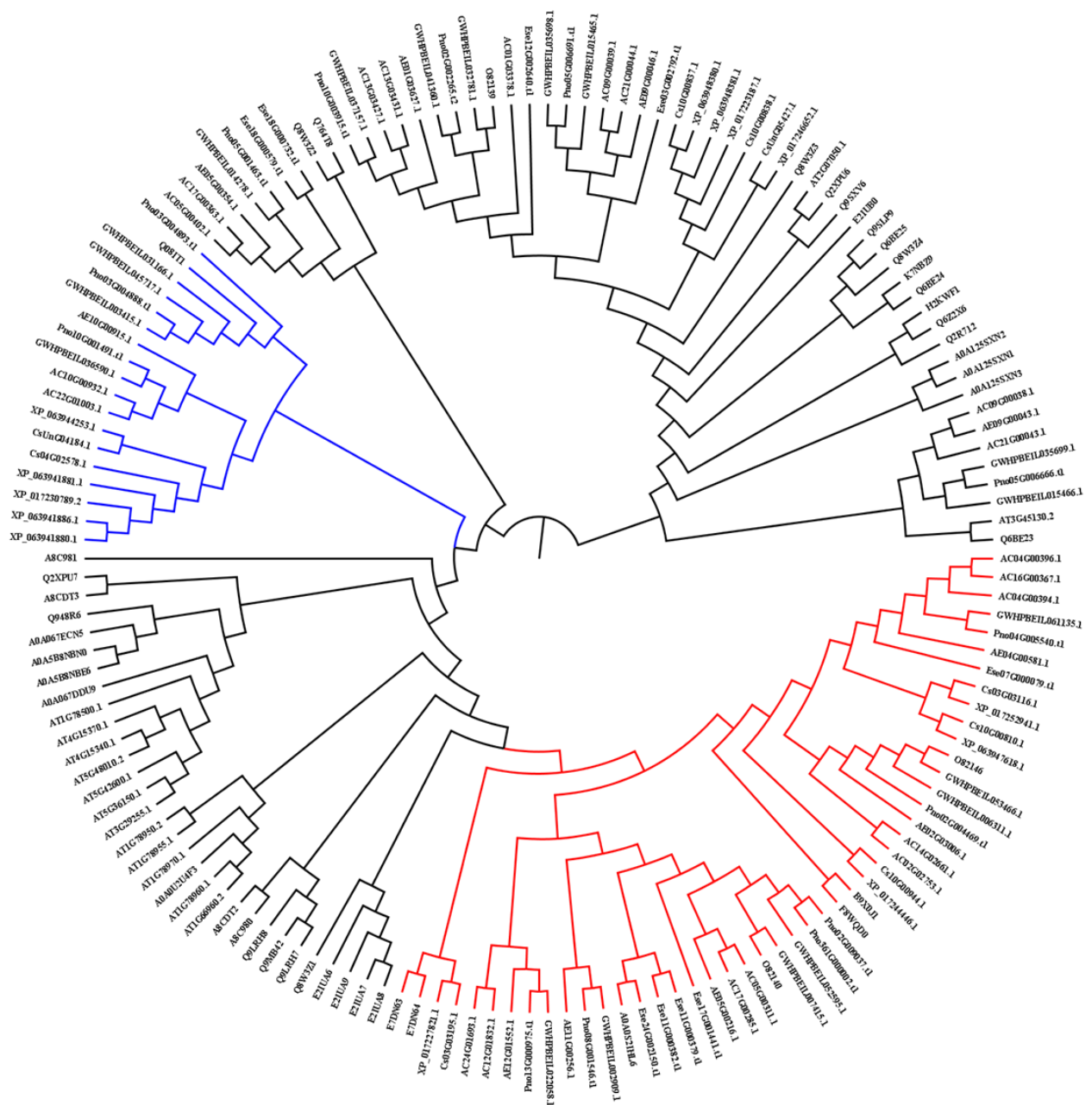
Supplementary Figure 16. Comparisons of expression bias in each organ between subgenome A and B. Five organs were compared to confirm the expression bias in the subgenomes. The red and blue bars indicated subA dominance and subB dominance, respectively.



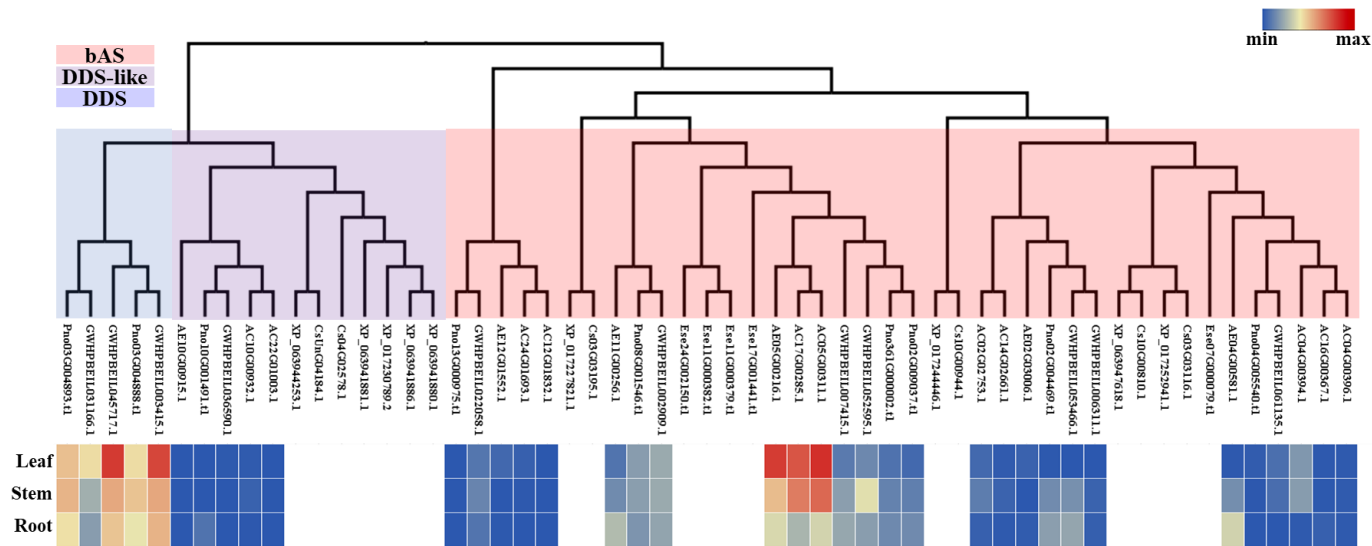
Supplementary Figure 17. Expression and substitution rate differences in the subgeomes of *A. cordata*. The red and blue bars indicated subA and subB, respectively. A) Comparison of gene expression between subgenomes A and B. Paralogous genes showing over 1.5 times the expression levels were counted as dominant expression genes for each subgenome. B) Comparison of non-synonymous mutation (Ka) and synonymous mutation (Ks) rates between subgenomes A and B.



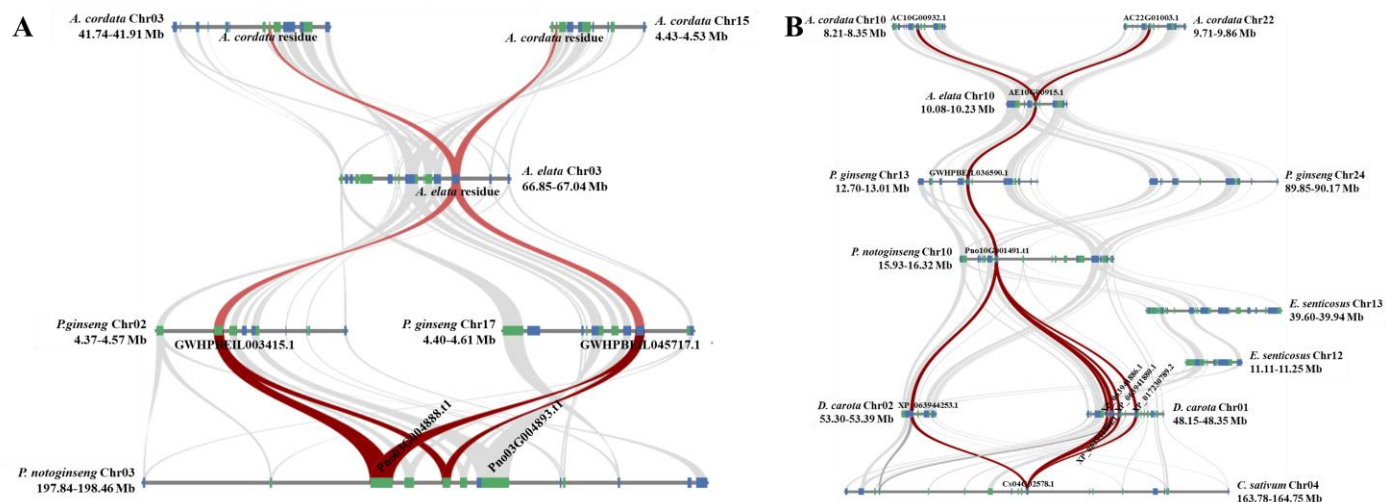
Supplementary Figure 18. Phylogenetic relationships of subgenomes of Araliaceae. A total of 3,049 single-copy orthologue genes were utilized to construct the phylogenetic tree.



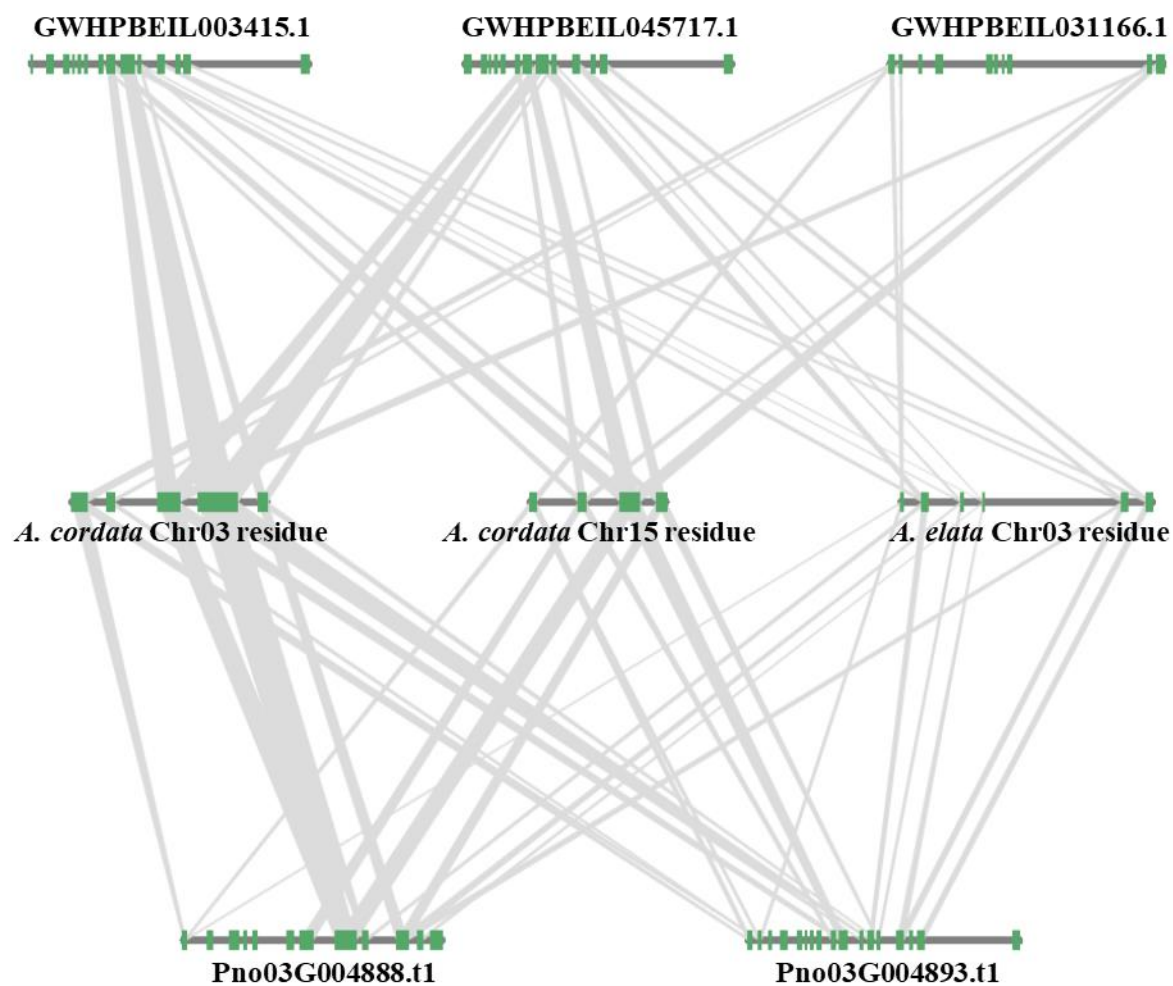
Supplementary Figure 19. Phylogenetic tree of OSC genes. The red line indicated beta-amyrin synthase-like genes, and the blue line indicated dammarenediol II synthase-like genes.



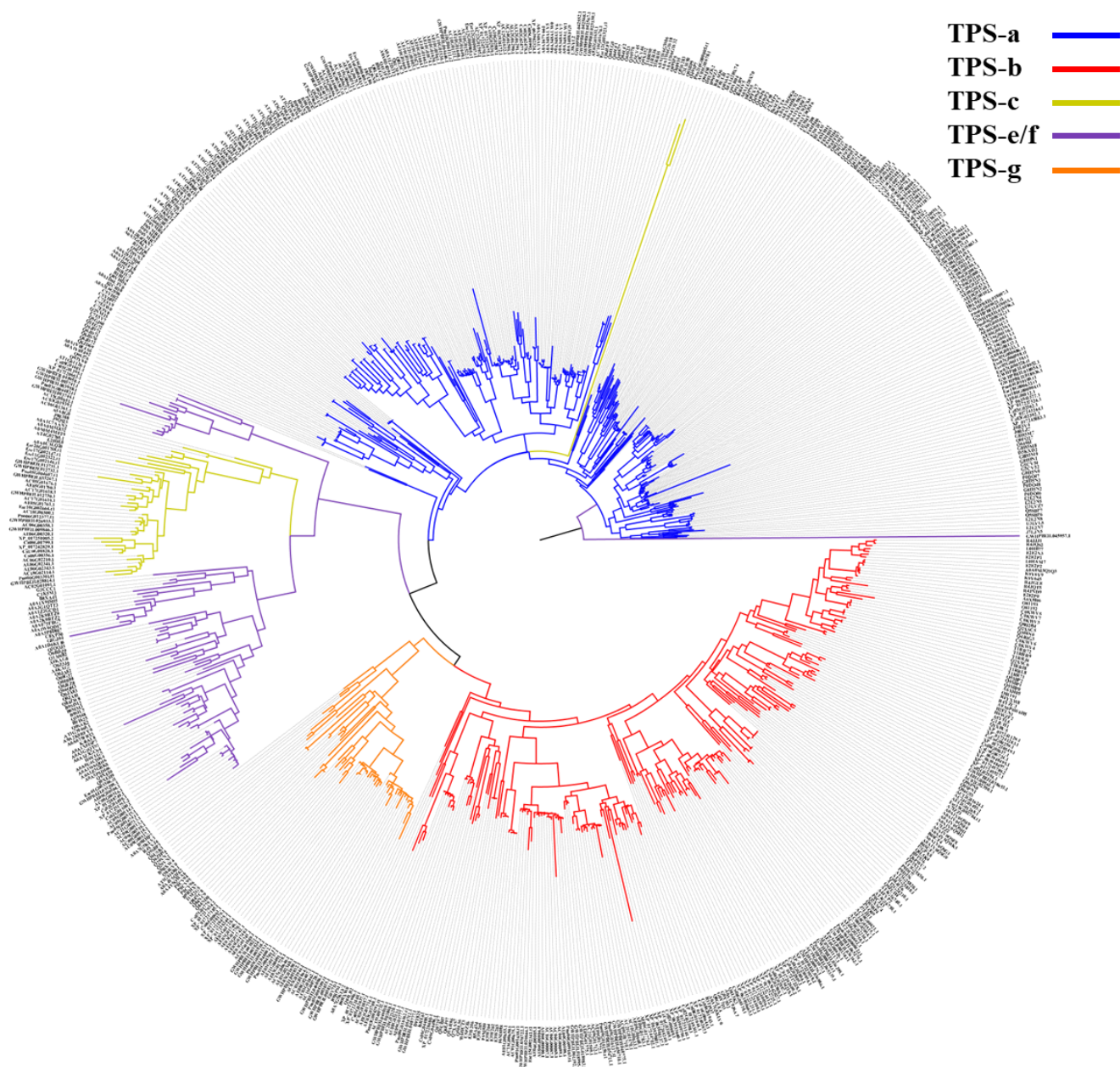
Supplementary Figure 20. Phylogenetic tree of DDS, DDS-like, and bAS genes with their expression levels. The red shadow indicated bAS, the purple shadow indicated DDS-like, and the blue shadow indicated DDS.



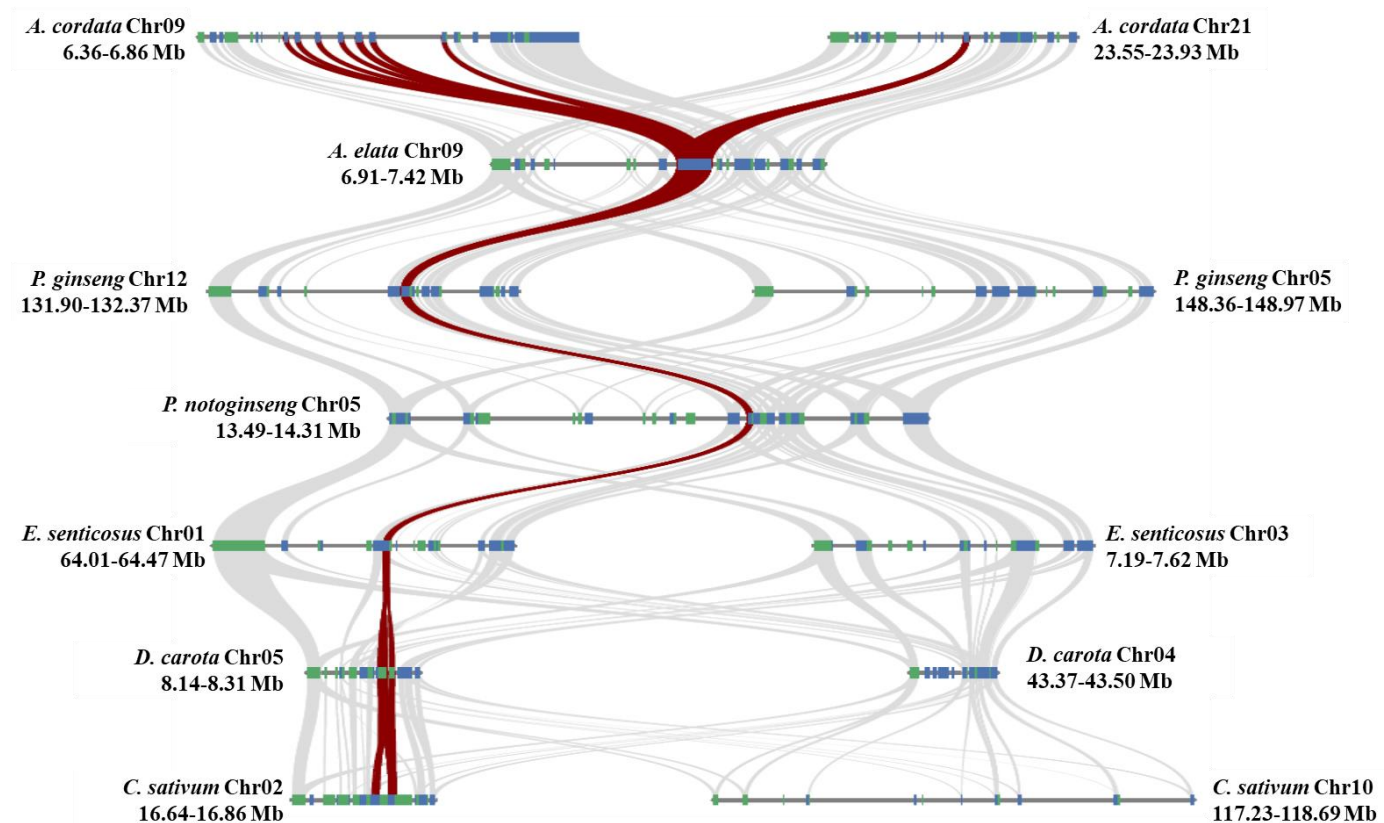
Supplementary Figure 21. Syntenic blocks of DDS and DDS-like genes. A) Micro-synteny blocks of DDS-like. B) Micro-synteny blocks of DDS and DDS residues in *Aralia* and *Panax*.



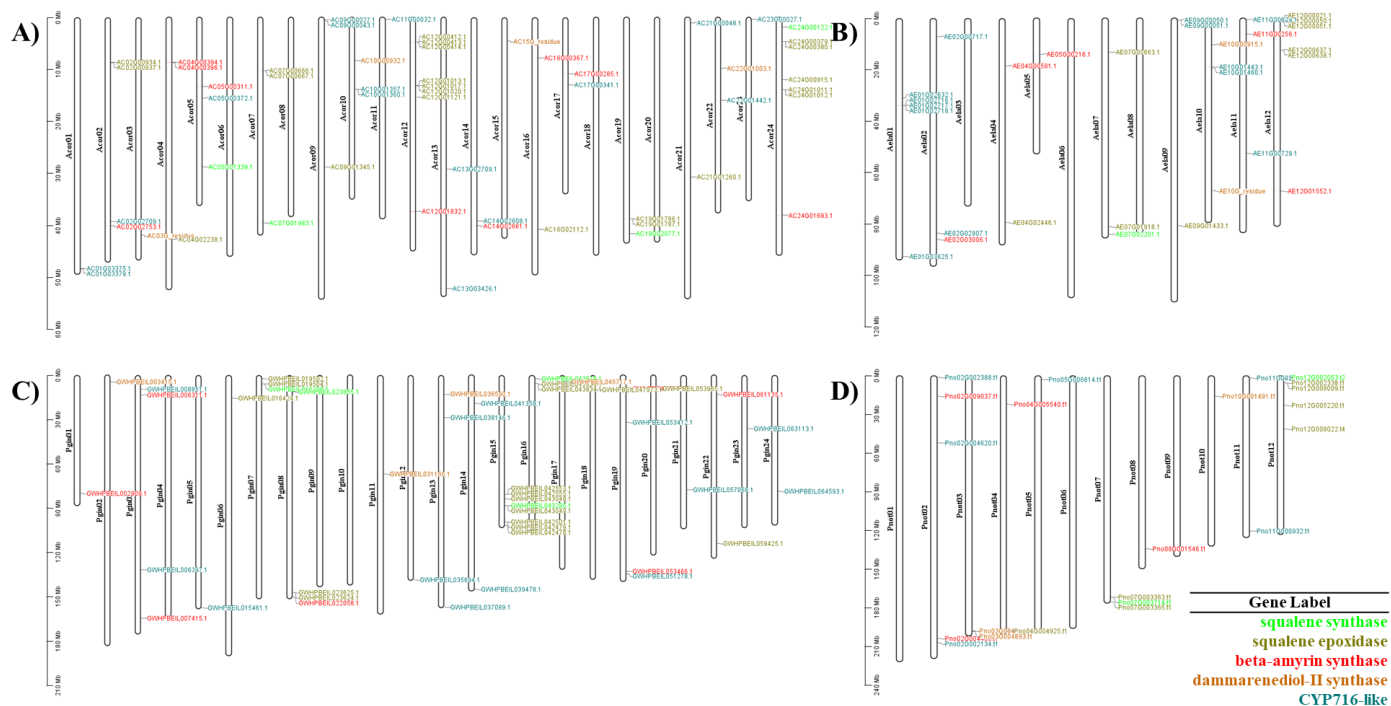
Supplementary Figure 22. Homology relationships between DDS residues in *Aralia* and DDD exons in *Panax*.



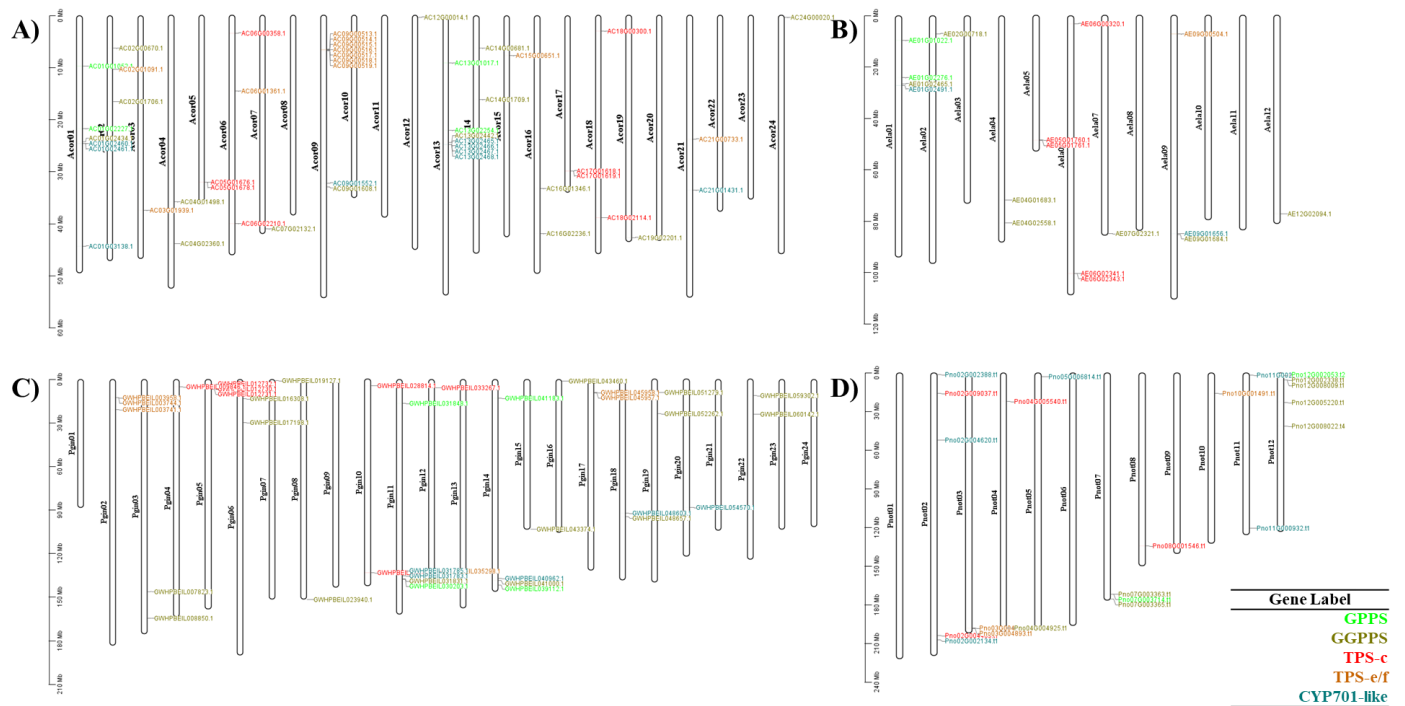
Supplementary Figure 23. Phylogenetic tree and classification of TPS genes. The yellow and purple lines indicated TPS-c and TPS-e/f, respectively.



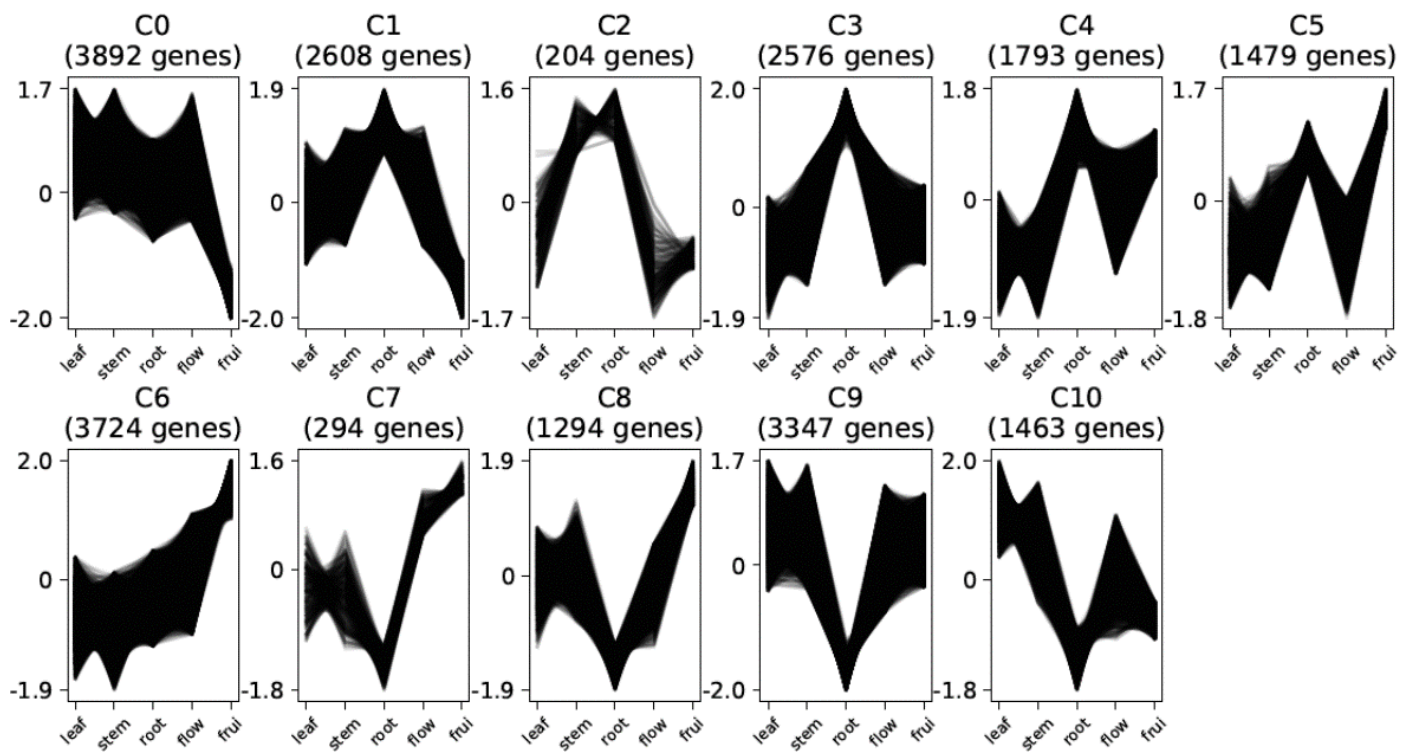
Supplementary Figure 25. Micro-synteny blocks of tandemly duplicated TPS-e/f genes in *A. cordata*.



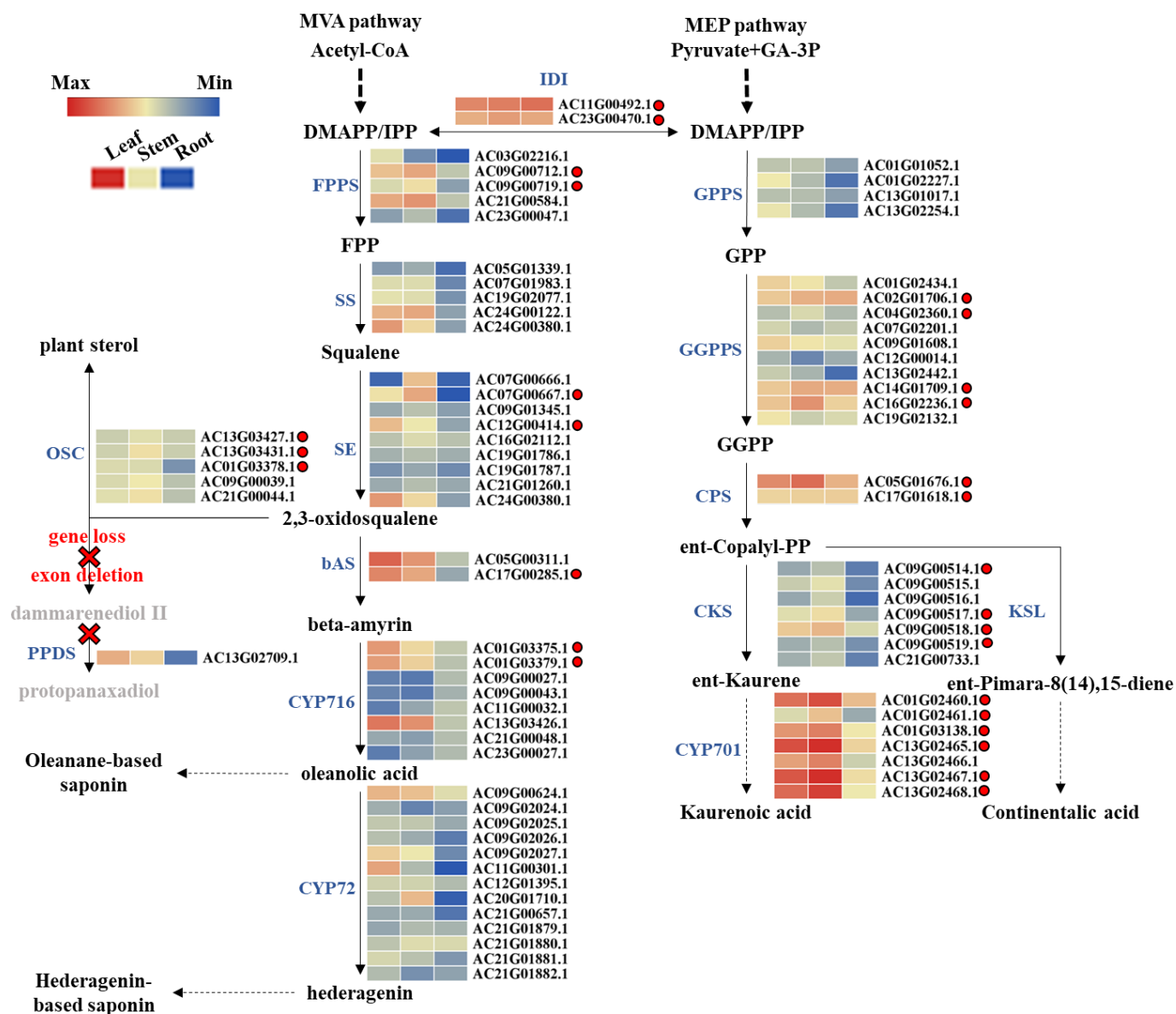
Supplementary Figure 26. Chromosomal location of genes related to synthesizing dammarene and olenane-type triterpenoids in *Aralia-Panax*. A) *A. cordata*, B) *A. elata*, C) *P. ginseng*, D) *P. notoginseng*.



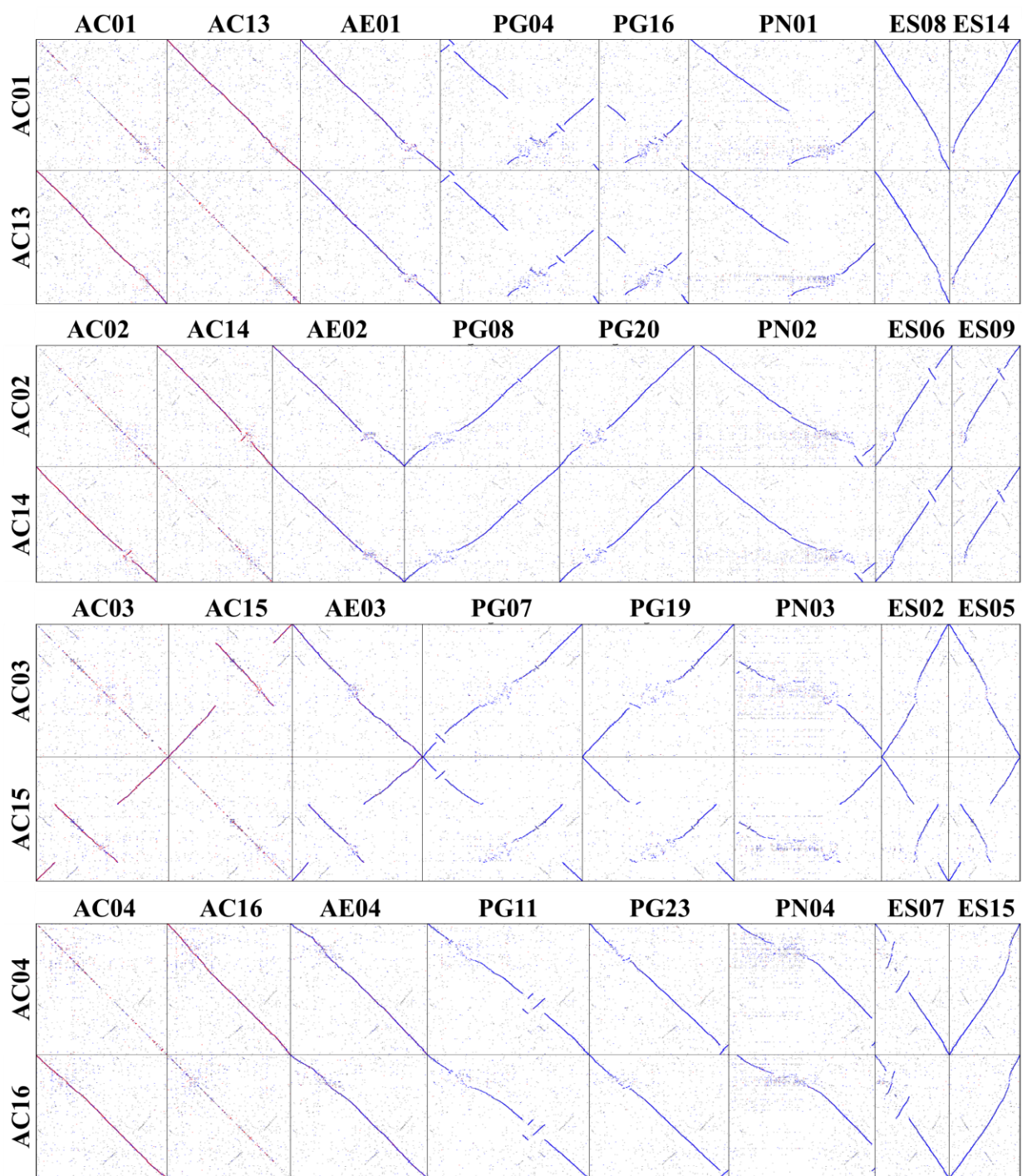
Supplementary Figure 27. Chromosomal location of genes related to synthesizing diterpenoids in *Aralia-Panax*. A) *A. cordata*, B) *A. elata*, C) *P. ginseng*, D) *P. notoginseng*.



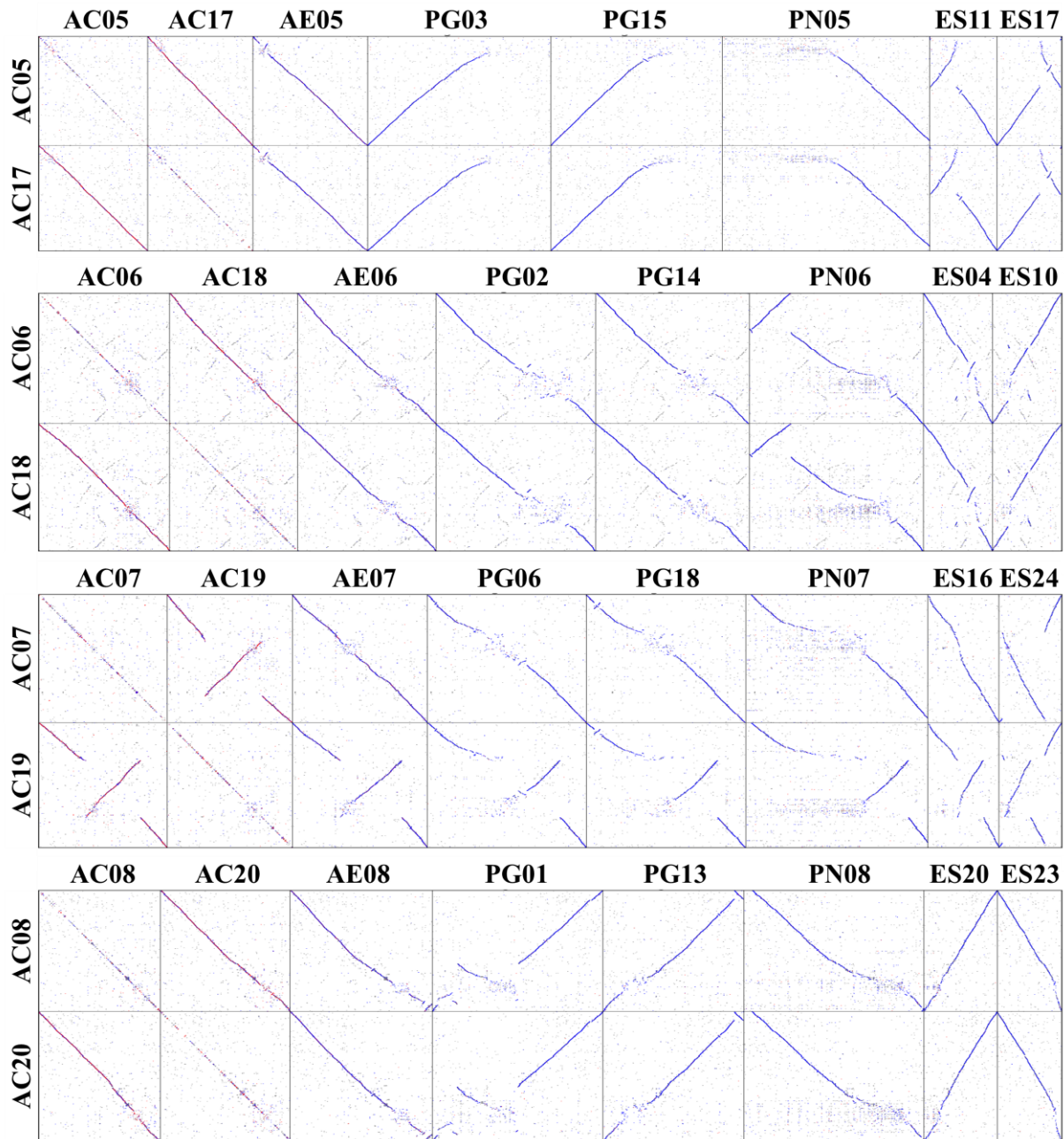
Supplementary Figure 28. Coexpressed gene clusters analysis divided into 11 clusters.
Most of the genes related to the heatmap below were included in the C0 cluster.



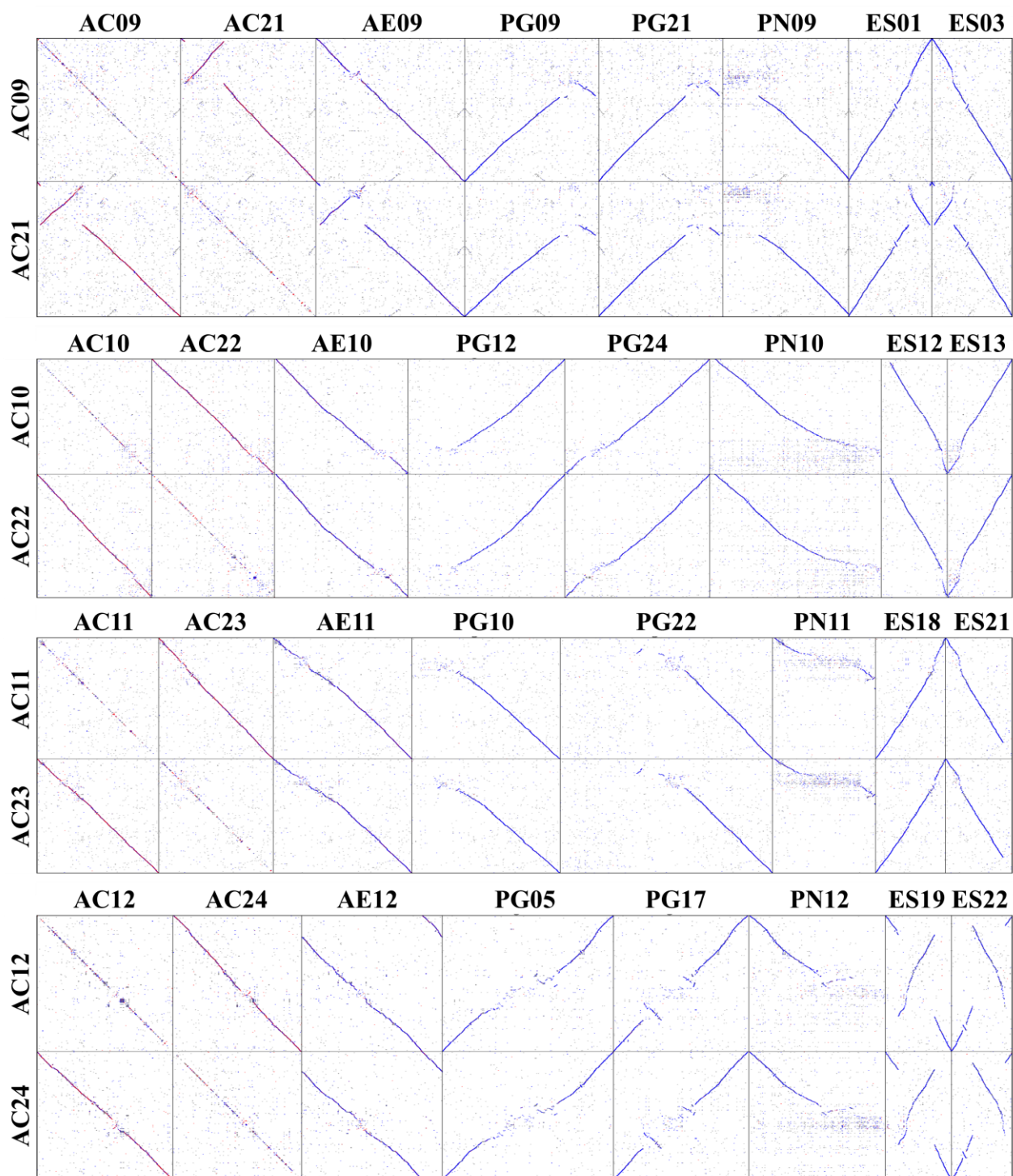
Supplementary Figure 29. Global expression heatmap of triterpenoids (left) and diterpenoids (right) in *A. cordata*. Red dots are the clustered genes in the C0 cluster.



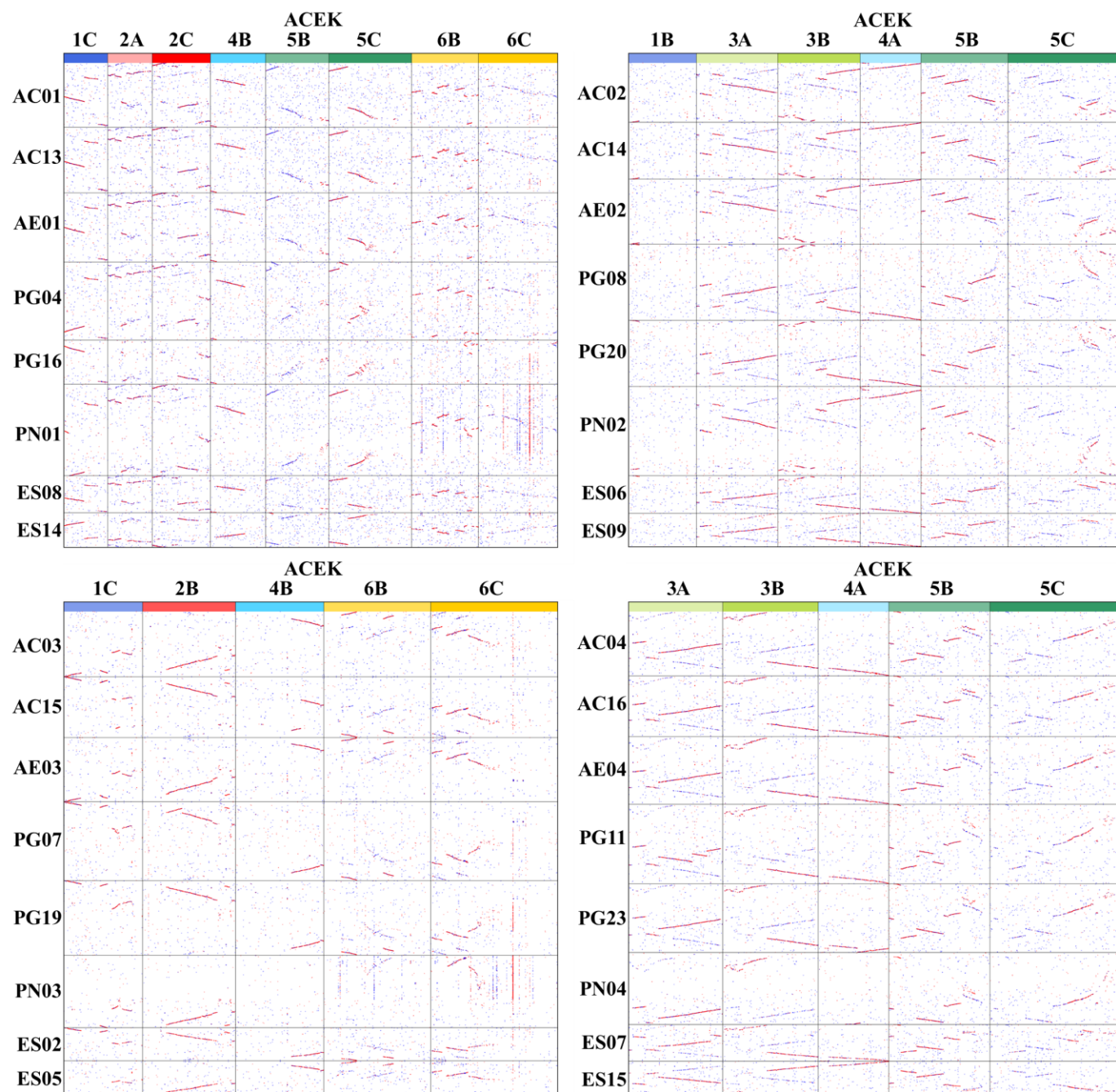
Supplementary Figure 30. Dotplots of chromosome structure comparisons. *A. cordata* Chr01-04 and Chr13-16 were used as a reference for structure comparisons. Ac: *A. cordata*, Ae: *A. elata*, Pg: *P. ginseng*, Pn: *P. notoginseng*, Es: *E. senticosus*.



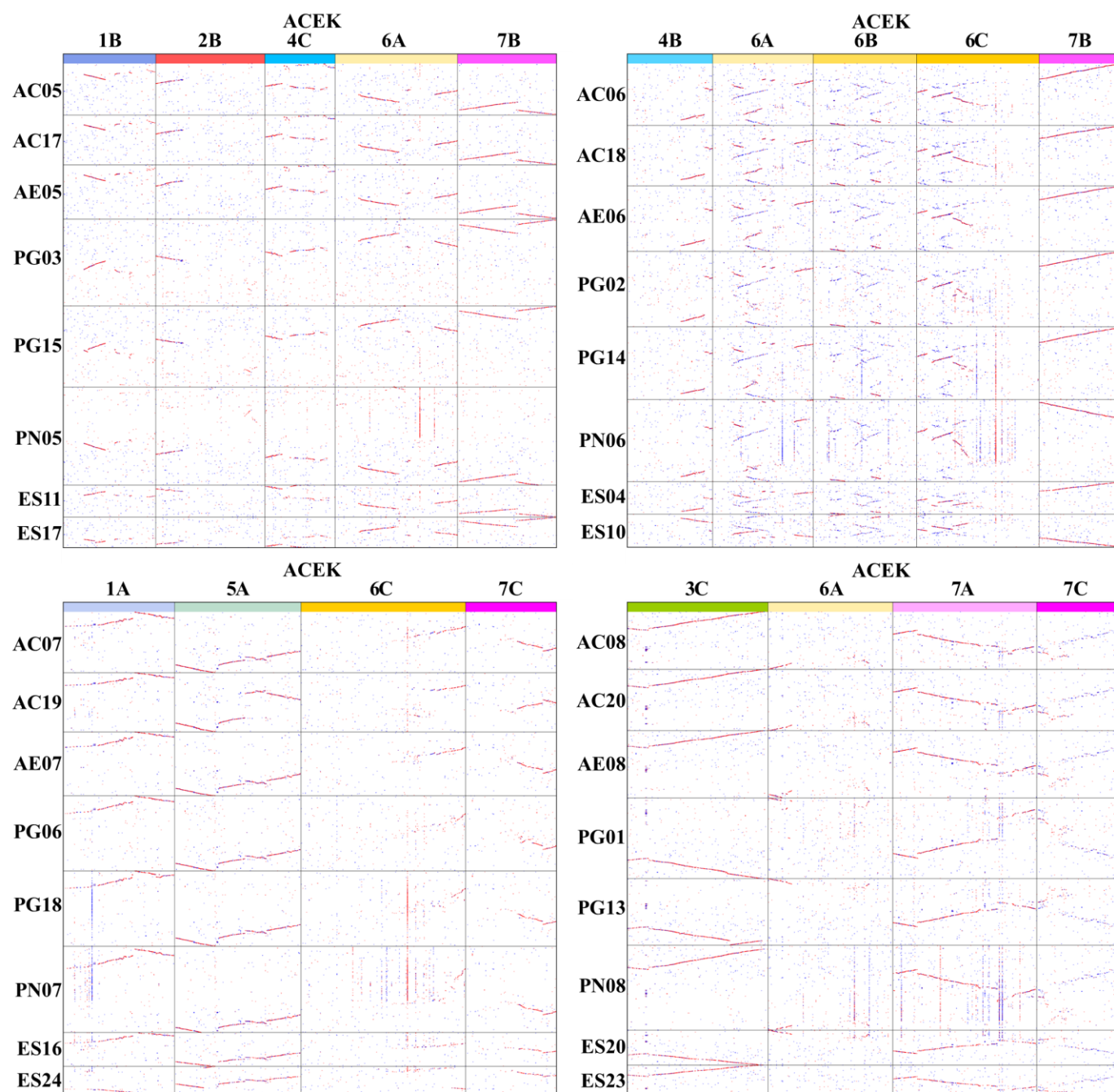
Supplementary Figure 31. Dotplots of chromosome structure comparisons. *A. cordata* Chr05-08 and Chr17-20 were used as a reference for structure comparisons. Ac: *A. cordata*, Ae: *A. elata*, Pg: *P. ginseng*, Pn: *P. notoginseng*, Es: *E. senticosus*.



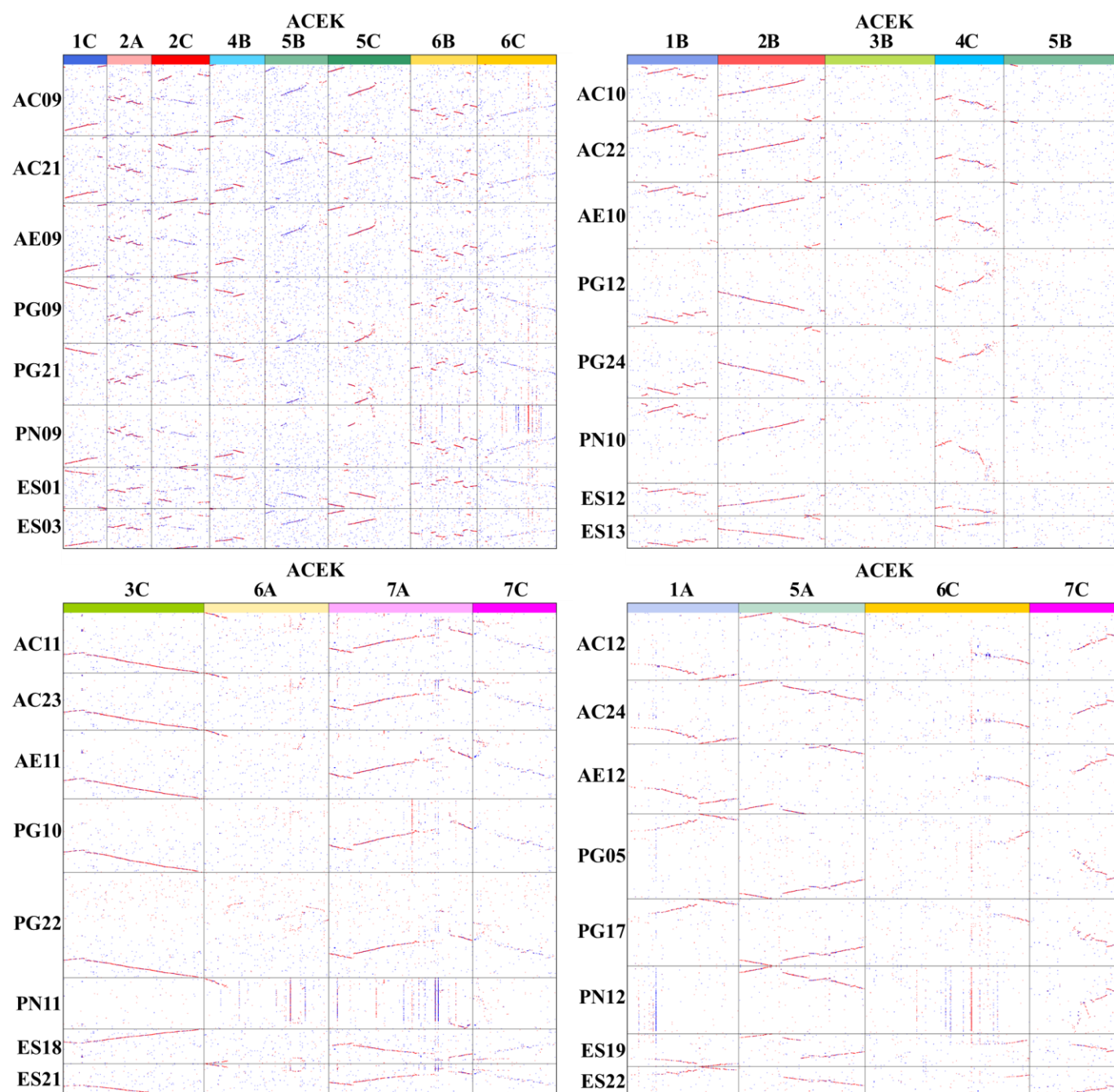
Supplementary Figure 32. Dotplots of chromosome structure comparisons. *A. cordata* Chr09-12 and Chr21-24 were used as a reference for structure comparisons. Ac: *A. cordata*, Ae: *A. elata*, Pg: *P. ginseng*, Pn: *P. notoginseng*, Es: *E. senticosus*.



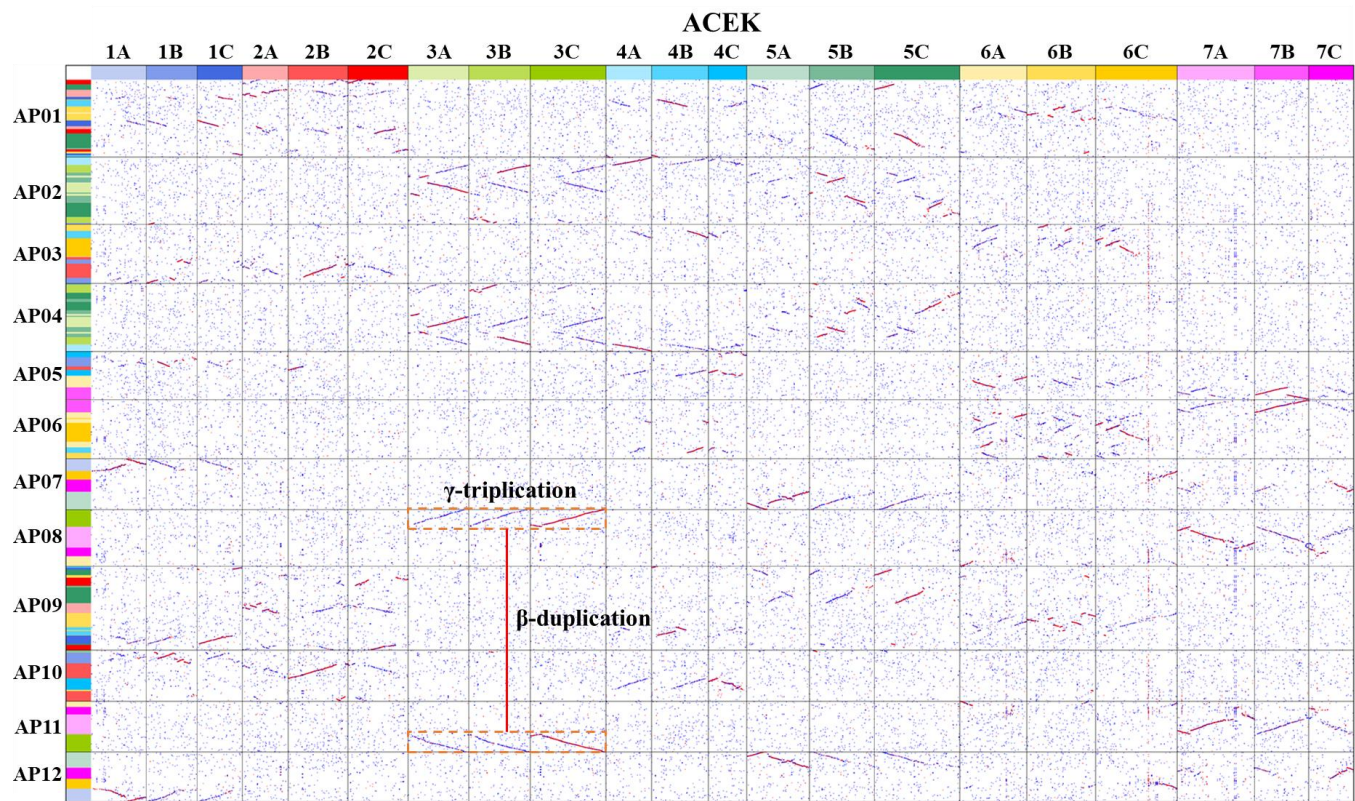
Supplementary Figure 33. Dotplot relationships between Araliaceae and ACEK. Chromosomes related to *A. cordata* Chr01-04 in Araliaceae and ACEK were compared by dotplots. Ancestral karyotypes were inferred by the structure comparisons by each species and ACEK. Red dots were the strong signal relationships between each species and ACEK. AC: *A. cordata*, AE: *A. elata*, PG: *P. ginseng*, PN: *P. notoginseng*, ES: *E. senticosus*.



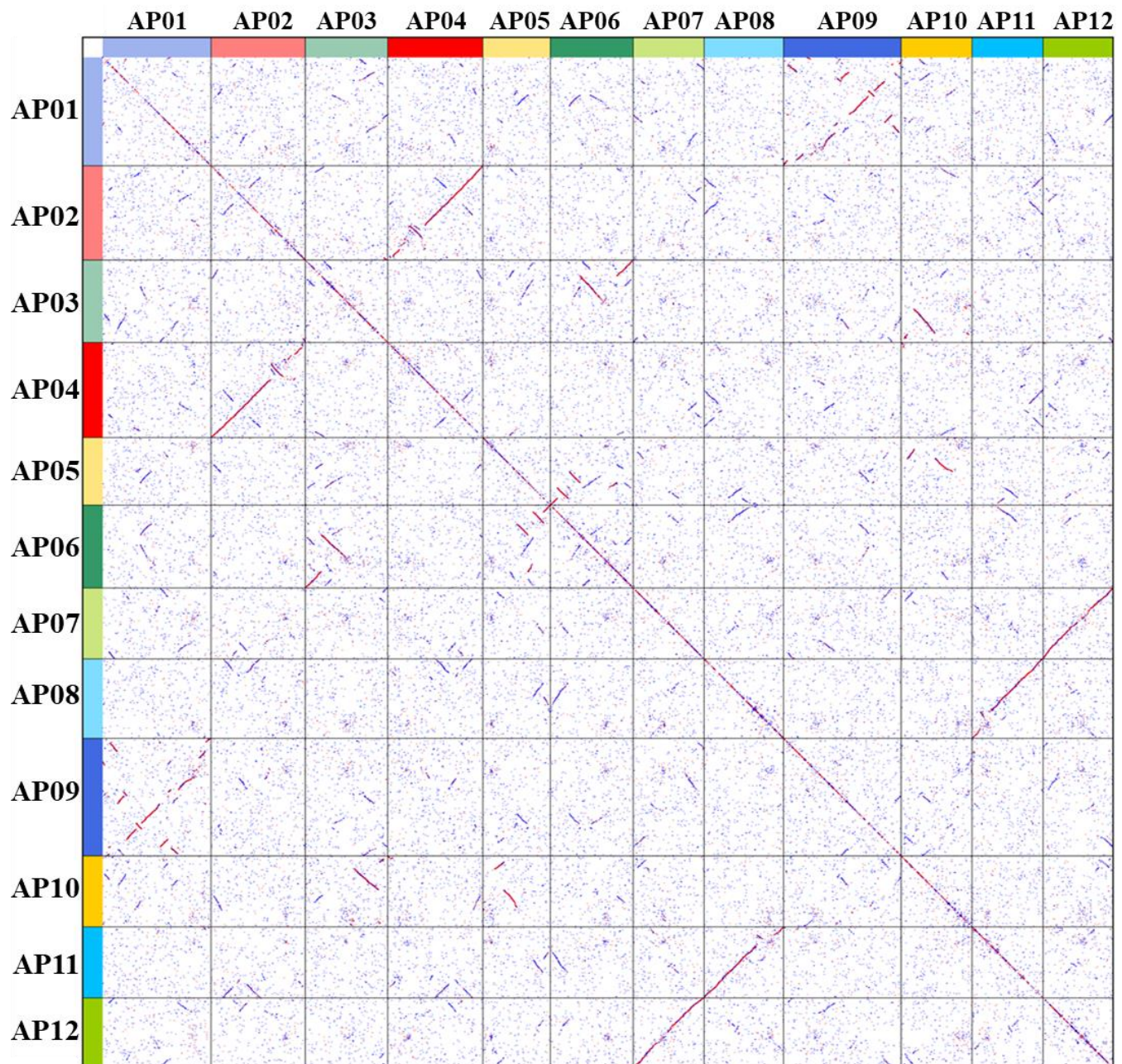
Supplementary Figure 34. Dotplot relationships between Araliaceae and ACEK. Chromosomes related to *A. cordata* Chr05-08 in Araliaceae and ACEK were compared by dotplots. The description is same with Supplementary Figure 33.



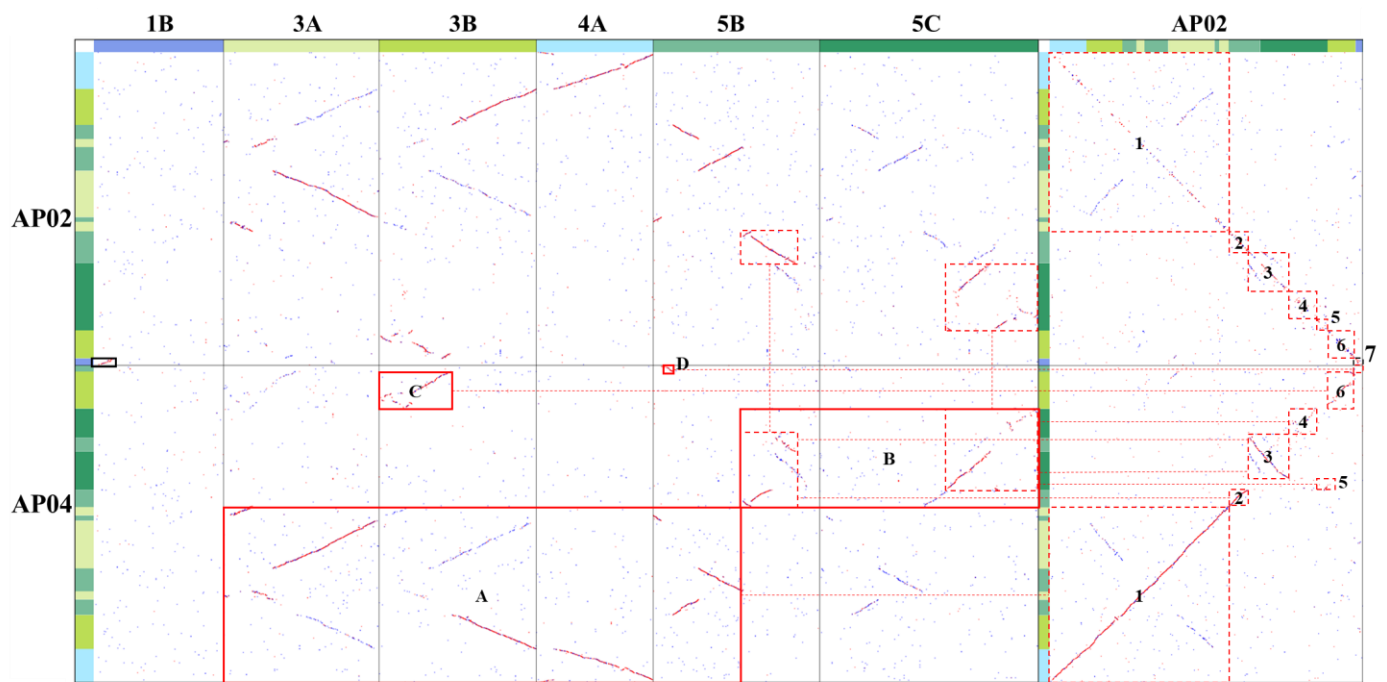
Supplementary Figure 35. Dotplot relationships between Araliaceae and ACEK. Chromosomes related to *A. cordata* Chr09-12 in Araliaceae and ACEK were compared by dotplots. The description is same with Supplementary Figure 33.



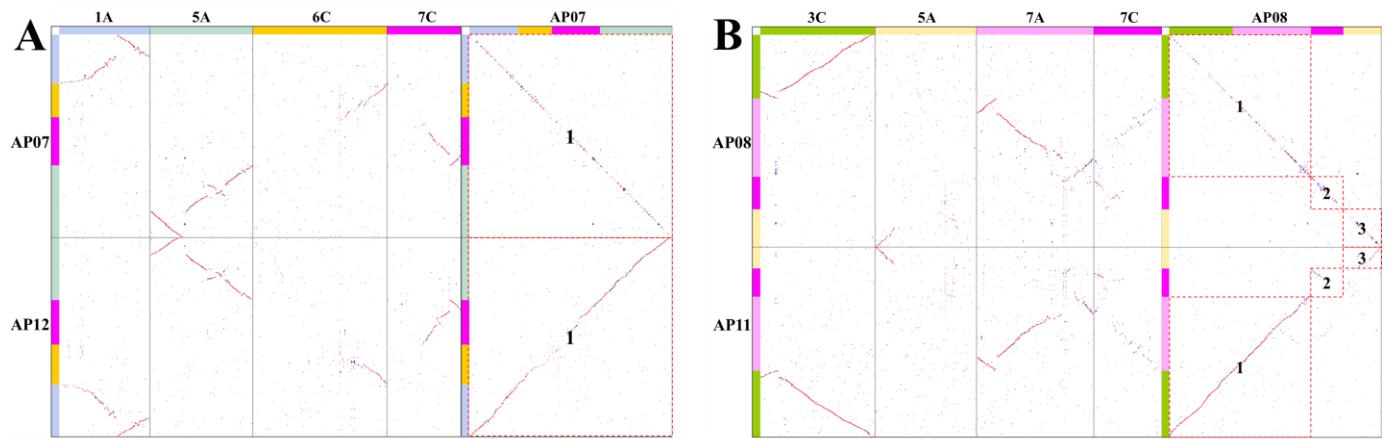
Supplementary Figure 36. Dotplot relationships between ancestral chromosomes of post- β duplication and ACEK. The orange box indicated the result of WGT, while the red line indicated the result of WGD. The color box on the top indicated the colors representing each ACEK chromosome. The color box on the left indicated the ACEK compositions of ancestral chromosomes of post- β duplication.



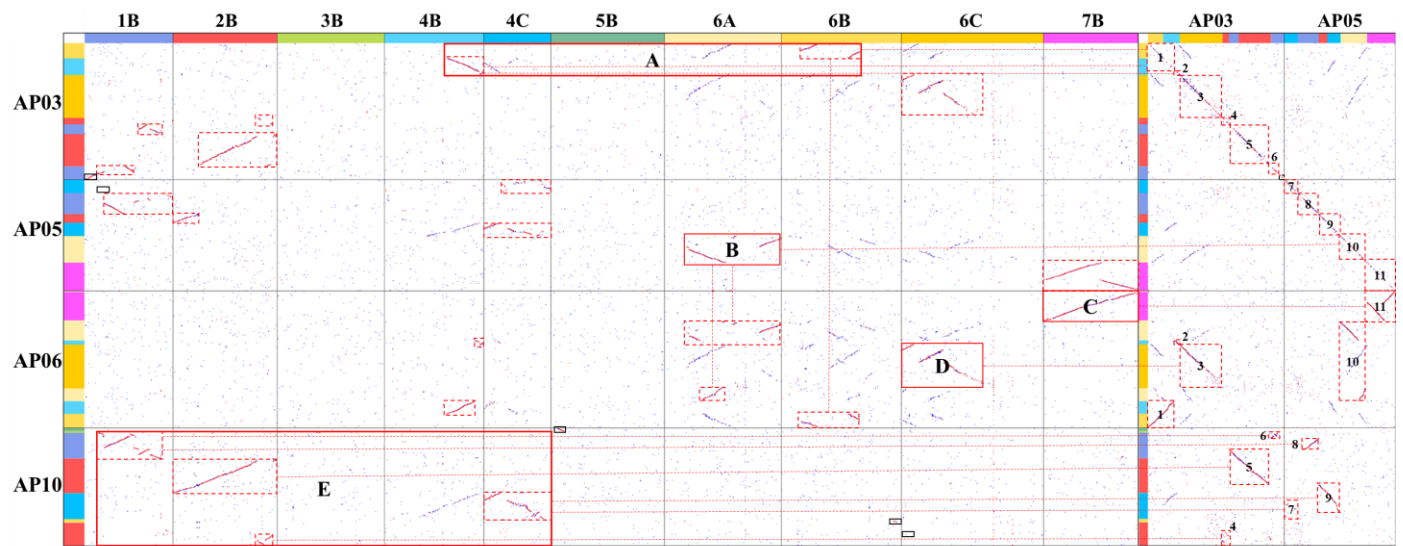
Supplementary Figure 37. Self-comparison dotplot of ancestral chromosomes of Araliaceae post- β duplication. The color box on the top and left indicated the colors representing each ancestral chromosome.



Supplementary Figure 39. Dotplot relationships of AP02:AP04 and ACEK. Red dotted boxes indicated the fragmented syntenic blocks. Red-lined boxes indicated the pre-β duplication forms inferred by the syntenic relationships.

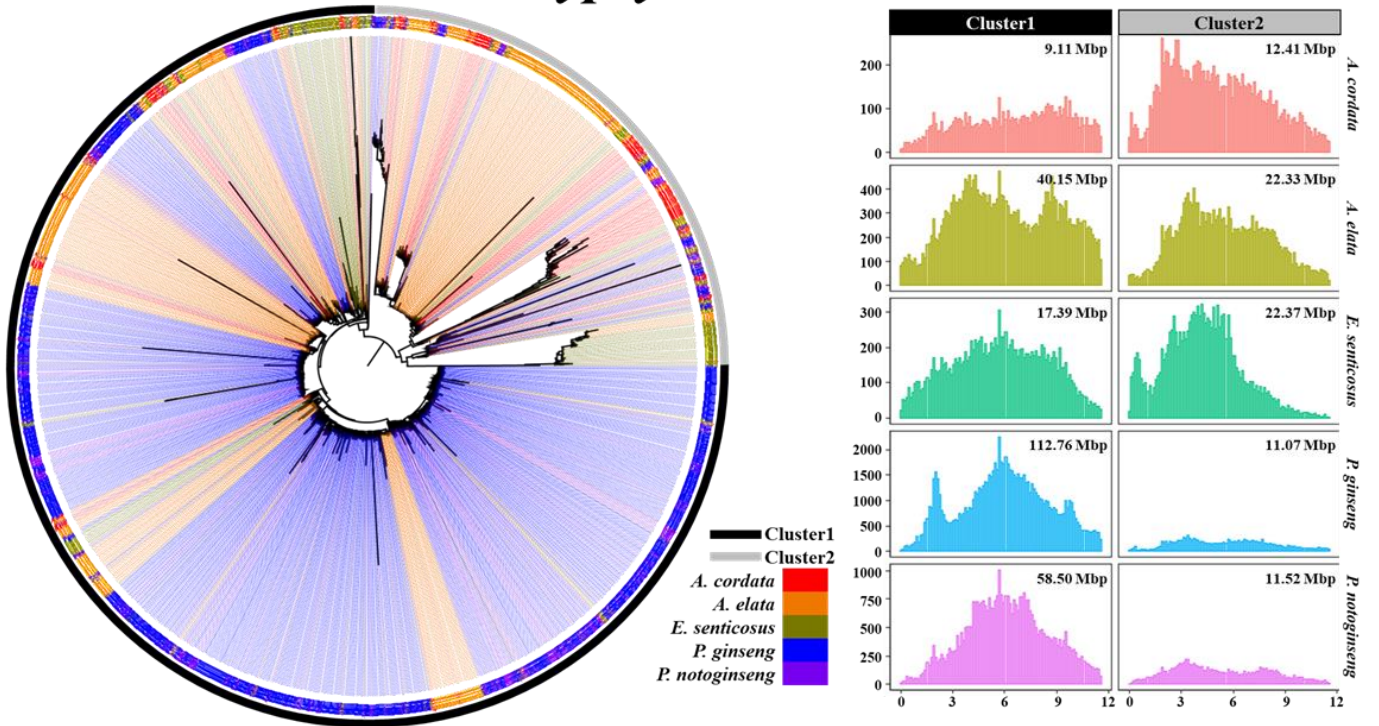


Supplementary Figure 40. Dotplot relationships with ACEK. A) Block relationships of AP07:AP12 and ACEK, B) Block relationships of AP08:AP11 and ACEK. Red dotted boxes indicated the fragmented syntenic blocks. Red-lined boxes indicated the pre- β duplication forms inferred by the syntenic relationships.

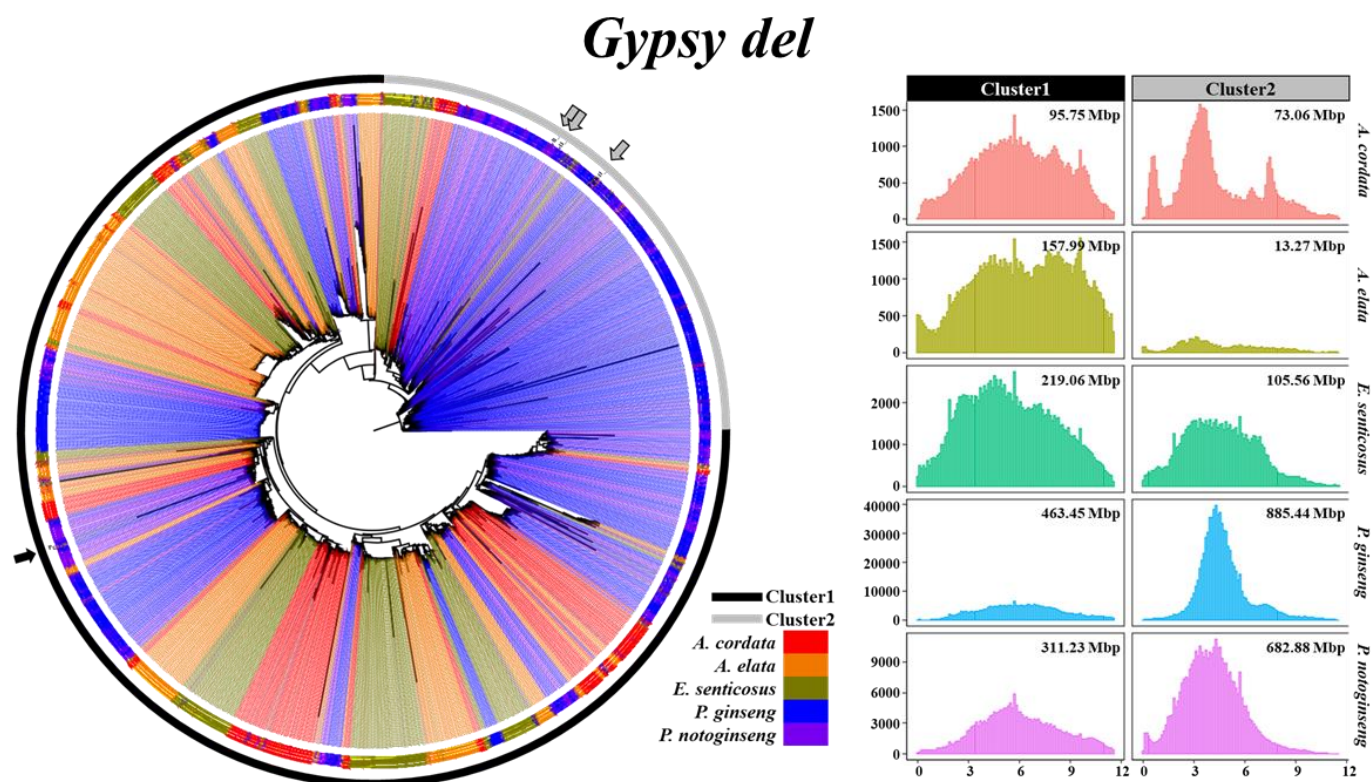


Supplementary Figure 41. Dotplot relationships of AP03:AP05:AP06:AP10 and ACEK. Red dotted boxes indicated the fragmented syntenic blocks. Red-lined boxes indicated the pre- β duplication forms inferred by the syntenic relationships.

Gypsy athila

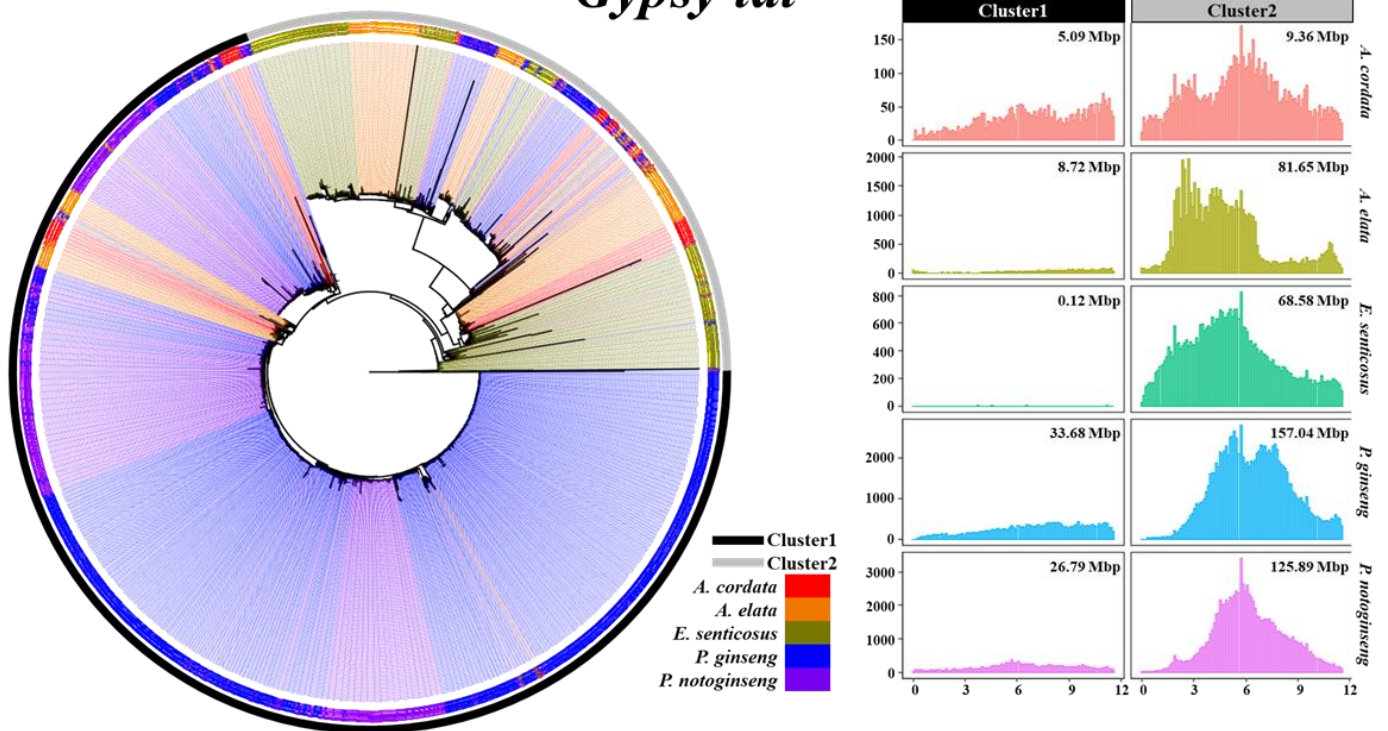


Supplementary Figure 42. Cluster-level *Gypsy athila* classification and its insertion time of five species in Araliaceae. In the phylogenetic tree, each species was indicated by different colors on the tip label. Red: *A. cordata*, Orange: *A. elata*, Dark green: *E. senticosus*, Blue: *P. ginseng*, Purple: *P. notoginseng*. Each group in the LTR element was classified based on the color arc on the tree. Black: Cluster1, Dark gray: Cluster2. In the histogram, the color bar on the top was the same as the cluster classification in the phylogenetic tree. The marked number on the top right was the composition in the genome. The X-axis indicated the insertion time of the LTR element with the unit Mya. The Y-axis indicated the count of the LTR element. As specific elements were inserted densely compared to other species. The Y-axis was not fixed.

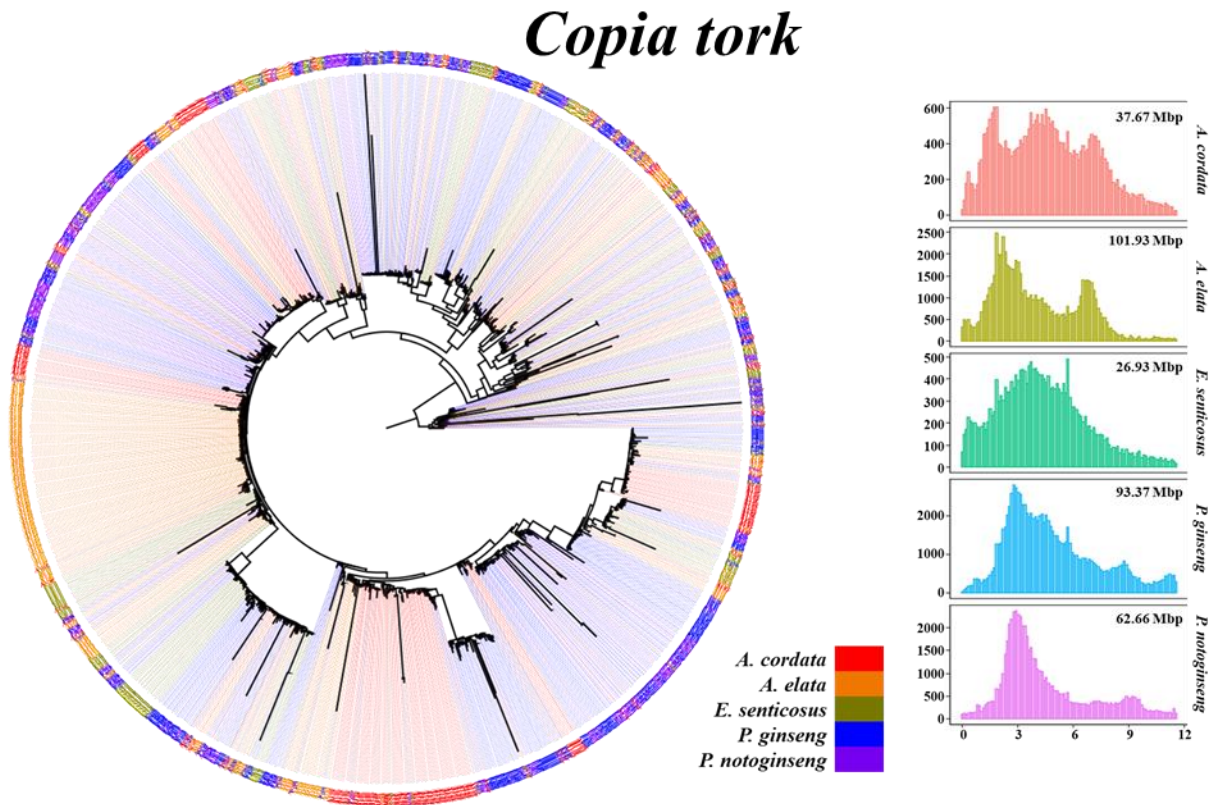


Supplementary Figure 43. Cluster-level *Gypsy del* classification and its insertion time of five species in Araliaceae. The marked gray and black arrow on the tree indicated the PgDel1 and PgDel2, respectively, which were identified in previous studies. The description is same with Supplementary Figure 42.

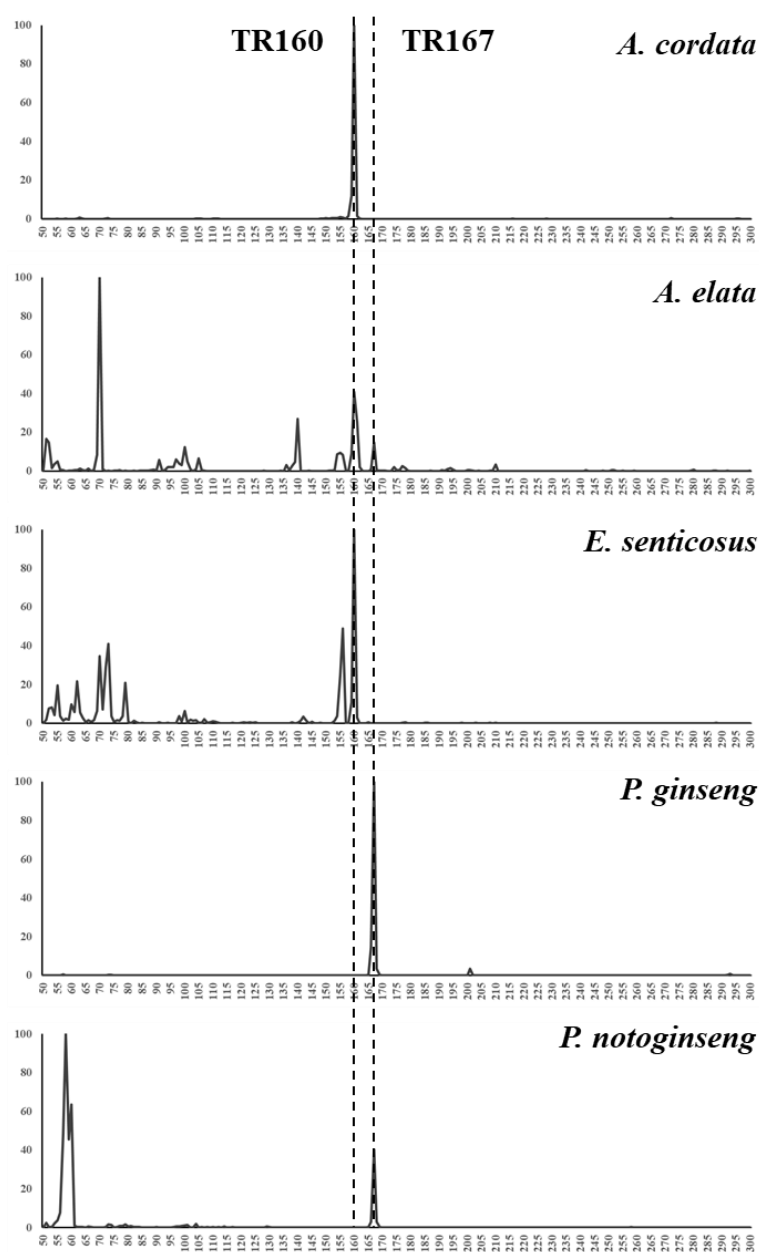
Gypsy tat



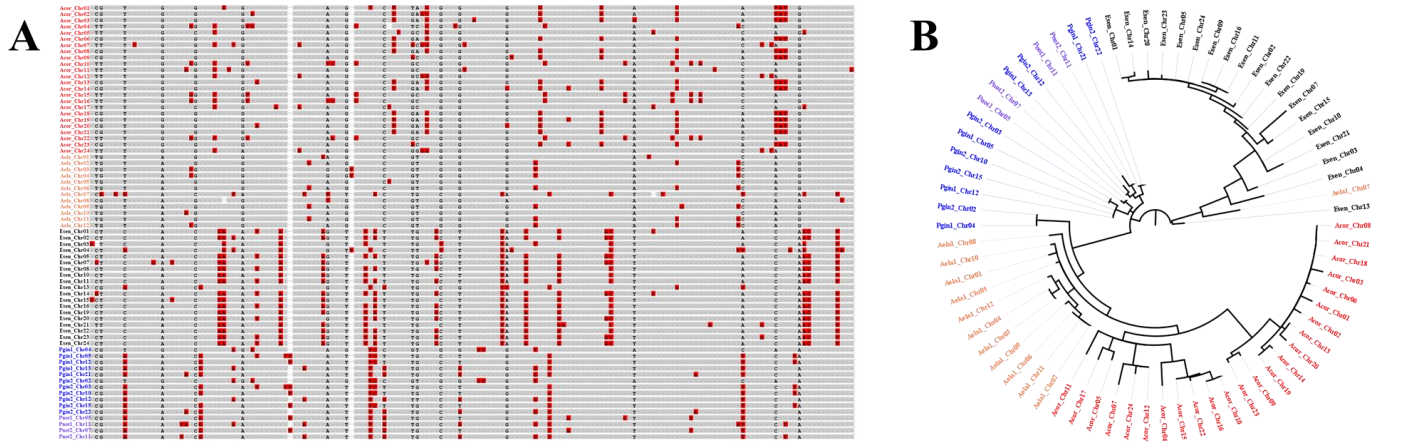
Supplementary Figure 44. Cluster-level *Gypsy tat* classification and its insertion time of five species in Araliaceae. The description is same with Supplementary Figure 42.



Supplementary Figure 45. Classification of *Copia tork* and its insertion time of five species in Araliaceae. In the phylogenetic tree, each species was indicated by different colors on the tip label. Red: *A. cordata*, Orange: *A. elata*, Dark green: *E. senticosus*, Blue: *P. ginseng*, Purple: *P. notoginseng*. *Copia tork* was not divided.



Supplementary Figure 46. Tandem repeat monomer peaks in *Aralia-Panax* and *E. senticosus*. Tandem repeats were searched for in the low k-mer diversity regions.



Supplementary Figure 47. Relationships of TR160 of five species in Araliaceae. A) Alignment of TR160 in the five species. Consensus for each chromosome in five species was collected and analyzed. B) Phylogenetic relationships of TR160. In the alignment and phylogenetic tree, each species was marked with different colors. *A. cordata*: red. *A. elata*: orange. *E. senticosus*: black. *P. ginseng*: blue. *P. notoginseng*: purple.

Supplementary Table 1. Produced raw read data for genome assembly.

	Total bases (bp)	Number of reads (#)	Mean read length (bp)	Mean read quality	Depth (X)
ONT	52,742,076,824	2,450,931	21,519.20	10.2	48.08
Illumina	112,822,327,230	747,167,730			102.85
Omni-C	35,277,221,433	233,623,983			

Supplementary Table 2. Genome assembly result.

	1: Draft	2: Polishing	3: Scaffolding	4: Final
Contigs (#)	8,520	8,520	8,662	5,625
Total length (bp)	1,330,862,824	1,331,470,231	1,331,470,231	1,088,871,566
avg length (bp)	156,205	156,276	153,714	193,577
max length (bp)	9,850,897	9,861,197	9,861,197	9,861,197
N50 (bp)	421,218	421,333	413,539	479,201
N50_num	683	681	705	489
GC content	34.24%	34.18%	34.18%	34.09%
1MB >= (#)	-	-	-	166
Scaffolds (#)	-	-	3,355	318
Total length (bp)	-	-	1,332,000,931	1,089,402,266
avg length (bp)	-	-	397,020	3,425,793
max length (bp)	-	-	54,253,215	54,253,215
N50	-	-	43,531,952	45,787,721
N50_num	-	-	14	11
GC content	-	-	34.17%	34.07%
Chromosomes (#)	-	-	-	24
Total length (bp)	-	-	-	1,062,891,754
min length (bp)	-	-	-	34,010,475
avg length (bp)	-	-	-	44,287,156
max length (bp)	-	-	-	54,253,215
GC content	-	-	-	34.04%
Gap	-	-	-	5,309
Anchored	-	-	-	97.57%
BUSCO (eudicots_odb10)	-	-	-	99.5%
LAI (LTR Assembly Index)	-	-	-	10.06

Supplementary Table 3. Information of twenty-four representative scaffolds.

ID	Length (bp)	ID	Length (bp)
Acor01	49,529,386	Acor13	53,801,769
Acor02	47,122,381	Acor14	45,749,321
Acor03	46,762,039	Acor15	42,522,970
Acor04	52,469,688	Acor16	49,544,842
Acor05	36,283,572	Acor17	34,010,475
Acor06	46,035,039	Acor18	45,787,721
Acor07	43,531,952	Acor19	41,938,036
Acor08	38,369,058	Acor20	43,266,040
Acor09	54,253,215	Acor21	54,182,953
Acor10	35,006,295	Acor22	37,668,494
Acor11	38,812,598	Acor23	35,344,174
Acor12	45,030,142	Acor24	45,869,596

Supplementary Table 4. Mapping rates of long reads and short reads.

Chr	Length (bp)	Depth (x)	Mapped	Depth ≥5X	Depth ≥10X	Depth (x)	Mapped	Depth ≥5X	Depth ≥10X
Acor01	49,529,386	43.99	99.87%	98.86%	97.62%	91.17	95.34%	94.07%	93.46%
Acor02	47,122,381	43.20	99.88%	99.01%	97.85%	88.44	95.29%	94.07%	93.51%
Acor03	46,762,039	38.44	99.85%	98.79%	97.27%	83.03	93.55%	91.66%	90.77%
Acor04	52,469,688	42.27	99.85%	98.89%	97.68%	81.97	93.70%	91.94%	91.08%
Acor05	36,283,572	48.67	99.96%	99.52%	99.20%	102.723	96.65%	95.67%	95.24%
Acor06	46,035,039	46.45	99.80%	99.02%	98.25%	96.12	95.86%	94.65%	94.13%
Acor07	43,531,952	38.50	99.89%	98.37%	96.35%	79.82	92.74%	90.73%	89.75%
Acor08	38,369,058	39.89	99.89%	99.10%	97.96%	80.75	94.49%	92.82%	91.98%
Acor09	54,253,215	42.55	99.90%	98.70%	97.22%	84.94	94.52%	93.14%	92.47%
Acor10	35,006,295	41.72	99.93%	99.35%	98.08%	80.57	94.69%	93.00%	92.13%
Acor11	38,812,598	42.14	99.93%	99.31%	98.08%	87.48	95.25%	94.01%	93.41%
Acor12	45,030,142	42.83	99.87%	98.17%	96.32%	82.77	92.82%	90.95%	89.98%
Acor13	53,801,767	39.37	99.90%	98.46%	96.63%	76.96	93.19%	91.47%	90.63%
Acor14	45,749,321	45.41	99.90%	99.20%	98.14%	91.13	96.17%	95.09%	94.59%
Acor15	42,522,970	40.48	99.85%	98.28%	96.22%	83.49	93.29%	91.59%	90.76%
Acor16	49,544,842	48.08	99.93%	99.23%	98.60%	100.40	96.49%	95.38%	94.91%
Acor17	34,010,475	44.01	99.89%	98.86%	97.87%	92.69	96.32%	95.26%	94.75%
Acor18	45,787,721	39.08	99.84%	98.91%	97.19%	78.15	93.70%	91.87%	90.97%
Acor19	41,938,036	41.72	99.90%	99.11%	97.82%	88.714	94.86%	93.44%	92.78%
Acor20	43,266,040	38.80	99.87%	98.80%	96.79%	79.99	93.83%	92.05%	91.12%
Acor21	54,182,953	40.73	99.89%	99.06%	97.66%	79.84	94.28%	92.65%	91.86%
Acor22	37,668,494	54.32	99.93%	99.54%	98.82%	112.46	96.07%	94.80%	94.24%
Acor23	35,344,174	41.73	99.81%	98.37%	96.81%	83.52	94.33%	92.82%	92.03%
Acor24	45,869,596	46.94	99.93%	99.38%	98.51%	103.51	95.53%	94.20%	93.58%
Total	1,062,891,754	42.87	99.88%	98.92%	97.60%	87.64	94.66%	93.17%	92.45%

Supplementary Table 5. Repeat annotation of *A. cordata*.

Class	Length (bp)	Proportion (%)
LTR/Gypsy	225,161,021	21.18
LTR/Copia	75,214,863	7.08
LTR/unknown	125,752,449	11.83
TIR	141,625,998	13.32
nonTIR	36,058,086	3.39
repeat_region	25,177,801	2.37
LINE	465,485	0.04
Total	629,455,703	59.22

Supplementary Table 6. Gene annotation stats of *A. cordata*.

Annotation Stats	
Gene (#)	64,215
Exon per mRNA (#)	5.4
Total Gene length (bp)	320,491,606
Total CDS length (bp)	79,772,841
Mean intron length in exon (bp)	788
Mean Gene length (bp)	4,990
Mean CDS length (bp)	1,242
BUSCO (eudicots odb10, proteins)	99.0%

Supplementary Table 7. Functional annotation stats of *A. cordata*.

Annotation Stats (#, %) 64,215	
InterPro	60,899 (94.84)
GO	44,516 (69.32)
Swissprot	50,290 (78.32)
eggNOG	59,412 (92.52)
TrEMBL (plants)	60,277 (93.87)
nr (viridiplantae)	60,311 (93.92)
Total	62,416 (97.20)

Supplementary Table 8. BUSCO assessment on the genome and gene-model (protein) of *A. cordata*.

	Genome		Gene-model (protein)	
	Count	Percentage	Count	Percentage
Complete BUSCOs (C)	2,310	99.5	2,301	99.0
Complete and single-copy BUSCOs (S)	215	9.2	334	14.4
Complete and duplicated BUSCOs (D)	2,100	90.3	1,968	84.6
Fragmented BUSCOs (F)	3	0.1	6	0.3
Missing BUSCOs (M)	8	0.4	18	0.7
Total BUSCO groups searched	2,326	100.0	2,326	100.0

Supplementary Table 9. Gene numbers related to saponin biosynthesis.

	SS	SE	bAS	DDS-like	CYP716
<i>A. cordata</i>	4	22	9	2	16
<i>A. elata</i>	1	9	5	1	13
<i>P. ginseng</i>	4	20	7	4	13
<i>P. notoginseng</i>	2	8	6	3	7
<i>E. senticosus</i>	4	9	5	0	8
<i>D. carota</i>	2	5	5	4	9
<i>C. sativum</i>	3	6	2	2	15

Supplementary Table 10. Blast hit of five species with DDS and DDS-like genes.

Species	Chr	Start	End	DDS-like		DDS		Classificaton
				Align (bp)	Identity (%)	Align (bp)	Identity (%)	
<i>A. cordata</i>	Acor03	41,844,444	41,844,575	0	0	132	96.97	DDS
<i>A. cordata</i>	Acor03	41,844,749	41,844,810	60	95	62	98.387	DDS
<i>A. cordata</i>	Acor03	41,845,183	41,845,368	0	0	174	90.86	DDS
<i>A. cordata</i>	Acor03	41,845,531	41,845,870	0	0	344	79.404	DDS
<i>A. cordata</i>	Acor03	41,846,044	41,846,128	0	0	86	91.954	DDS
<i>A. cordata</i>	Acor15	4,523,316	4,523,403	0	0	86	92.045	DDS
<i>A. cordata</i>	Acor15	4,523,544	4,523,712	0	0	179	89.385	DDS
<i>A. cordata</i>	Acor15	4,524,005	4,524,074	0	0	70	98.571	DDS
<i>A. cordata</i>	Acor15	4,524,437	4,524,491	0	0	53	94.545	DDS
<i>A. elata</i>	Chr02	16,587,843	16,587,912	0	0	67	87.143	DDS
<i>A. elata</i>	Chr03	66,907,103	66,907,185	80	90	83	98.795	DDS
<i>A. elata</i>	Chr03	66,907,714	66,907,897	181	83.978	183	97.814	DDS
<i>A. elata</i>	Chr03	66,908,807	66,908,891	0	0	86	91.86	DDS
<i>A. elata</i>	Chr03	66,909,463	66,909,501	0	0	39	97.436	DDS
<i>A. elata</i>	Chr03	66,913,430	66,913,597	0	0	166	92.857	DDS
<i>A. elata</i>	Chr03	66,914,114	66,914,308	0	0	189	96.296	DDS
<i>A. elata</i>	Chr03	71,308,632	71,308,670	0	0	36	92.308	DDS
<i>A. elata</i>	Chr04	62,786,908	62,786,949	0	0	39	92.857	DDS
<i>A. elata</i>	Chr08	4,200,930	4,200,999	0	0	67	90	DDS
<i>E. senticosus</i>	11	30,308,615	30,308,806	189	96.296	192	83.854	DDS-like
<i>E. senticosus</i>	11	30,314,889	30,315,245	355	93.521	344	82.267	DDS-like
<i>E. senticosus</i>	11	30,316,271	30,316,504	234	95.726	222	85.586	DDS-like
<i>E. senticosus</i>	11	30,320,523	30,320,601	79	94.937	63	93.651	DDS-like
<i>E. senticosus</i>	11	30,360,751	30,361,105	352	92.898	344	82.849	DDS-like
<i>C. sativum</i>	ctg3345	96,093	96,176	84	88.095	84	84.524	DDS-like
<i>C. sativum</i>	ctg9740	8,091	8,174	84	88.095	84	84.524	DDS-like
<i>D. carota</i>	NC_030382.2	53,357,351	53,357,706	356	96.067	327	79.817	DDS-like

Supplementary Table 11. Substitution rates between DDS residues and DDS-like genes.

Sequence1	Sequence2	Classification	Ka	Ks	Ka/Ks
Acor03_residue	GWHPBEIL031166.1	DDS	0.0471668	0.0783455	0.602035
Acor03_residue	Pno03G004893.t1	DDS	0.194152	0.370137	0.52454
Acor03_residue	GWHPBEIL045717.1	DDS	0.345594	0.579316	0.596556
Acor03_residue	GWHPBEIL003415.1	DDS	0.355964	0.643595	0.553087
Acor03_residue	Pno03G004888.t1	DDS	0.44818	0.843552	0.531301
Acor03_residue	Pno10G001491.t1	DDS-like	0.305956	1.26398	0.242057
Acor03_residue	GWHPBEIL036590.1	DDS-like	0.314374	1.27097	0.24735
Acor03_residue	AC10G00932.1	DDS-like	0.302924	1.32882	0.227965
Acor03_residue	AE10G00915.1	DDS-like	0.304473	1.35155	0.225277
Acor03_residue	AC22G01003.1	DDS-like	0.310818	1.43535	0.216546
Acor03_residue	XP_017230789.2	DDS-like	0.295468	1.47691	0.200058
Acor03_residue	Cs04G02578.1	DDS-like	0.498767	1.58241	0.315195
Acor03_residue	XP_063941886.1	DDS-like	0.303314	1.60778	0.188654
Acor03_residue	XP_063941880.1	DDS-like	0.302244	1.67953	0.179957
Acor03_residue	XP_063941881.1	DDS-like	0.299168	1.86201	0.160669
Acor03_residue	XP_063944253.1	DDS-like	0.328323	1.91736	0.171237
Acor03_residue	CsUnG04184.1	DDS-like	0.311835	2.10445	0.148179
Acor15_residue	GWHPBEIL031166.1	DDS	0.315501	0.333616	0.945698
Acor15_residue	Pno03G004893.t1	DDS	0.319222	0.350695	0.910256
Acor15_residue	GWHPBEIL045717.1	DDS	0.33529	0.499274	0.671555
Acor15_residue	GWHPBEIL003415.1	DDS	0.338839	0.55091	0.615053
Acor15_residue	Pno03G004888.t1	DDS	0.395443	0.677602	0.583592
Acor15_residue	XP_063944253.1	DDS-like	0.435594	1.82721	0.238392
Acor15_residue	Pno10G001491.t1	DDS-like	0.355689	2.11785	0.167948
Acor15_residue	Cs04G02578.1	DDS-like	0.522923	2.25789	0.231598
Acor15_residue	GWHPBEIL036590.1	DDS-like	0.354762	2.27841	0.155706
Acor15_residue	XP_063941880.1	DDS-like	0.387867	2.29797	0.168787
Acor15_residue	CsUnG04184.1	DDS-like	0.392267	2.33963	0.167662
Acor15_residue	AC10G00932.1	DDS-like	0.349084	2.39809	0.145568
Acor15_residue	AE10G00915.1	DDS-like	0.356559	2.44668	0.145732
Acor15_residue	XP_017230789.2	DDS-like	0.349678	2.45176	0.142623
Acor15_residue	XP_063941886.1	DDS-like	0.361671	2.46282	0.146853
Acor15_residue	XP_063941881.1	DDS-like	0.365396	2.82798	0.129207
Acor15_residue	AC22G01003.1	DDS-like	0.398724	2.93974	0.135633
Aela03_residue	GWHPBEIL045717.1	DDS	0.100731	0.135518	0.743304
Aela03_residue	GWHPBEIL003415.1	DDS	0.106612	0.165602	0.643784
Aela03_residue	Pno03G004888.t1	DDS	0.110957	0.179467	0.618259
Aela03_residue	Pno03G004893.t1	DDS	0.202395	0.267559	0.756451
Aela03_residue	GWHPBEIL031166.1	DDS	0.0464939	0.463033	0.100412
Aela03_residue	GWHPBEIL036590.1	DDS-like	0.138887	0.794243	0.174867
Aela03_residue	Pno10G001491.t1	DDS-like	0.135388	0.819679	0.165172
Aela03_residue	AC22G01003.1	DDS-like	0.148059	0.834518	0.177419
Aela03_residue	AC10G00932.1	DDS-like	0.138089	0.837808	0.164822
Aela03_residue	AE10G00915.1	DDS-like	0.135044	0.88834	0.152019
Aela03_residue	Cs04G02578.1	DDS-like	0.206787	1.06886	0.193466
Aela03_residue	XP_017230789.2	DDS-like	0.16146	1.10865	0.145637
Aela03_residue	XP_063941881.1	DDS-like	0.166576	1.20739	0.137964
Aela03_residue	XP_063941880.1	DDS-like	0.173776	1.27493	0.136302
Aela03_residue	CsUnG04184.1	DDS-like	0.157205	1.34592	0.116801
Aela03_residue	XP_063941886.1	DDS-like	0.168713	1.55053	0.10881
Aela03_residue	XP_063944253.1	DDS-like	0.157832	1.56856	0.100623

Supplementary Table 12. TPS family gene numbers in seven species.

Species	Gene-model ^a	Full-length ^b	TPS-a	TPS-b	TPS-c	TPS-e/f	TPS-g
<i>A. cordata</i>	71	58	16	19	7	10	6
<i>A. elata</i>	63	53	22	16	5	1	9
<i>P. ginseng</i>	57	42	13	13	6	5	5
<i>P. notoginseng</i>	23	18	4	7	3	2	2
<i>E. senticosus</i>	20	17	9	2	5	1	0
<i>D. carota</i>	61	56	17	30	2	3	4
<i>C. sativum</i>	43	28	9	12	2	4	1

a: Total number of TPS genes identified in this study.

b: Putative full length TPS genes which longer than 500 aa.

Supplementary Table 13. Subgenome relationships among Araliaceae.

<i>A. cordata</i> (This study)		<i>A. elata</i> (Wang <i>et al.</i> , 2022) ^a	<i>P. ginseng</i> (Song <i>et al.</i> , 2024) ^b		<i>P. notoginseng</i> (Yang <i>et al.</i> , 2021) ^c	<i>E. senticosus</i> (Yang <i>et al.</i> , 2021) ^d
subA	subB		subA	subB		
1	13	1	4	16	1	8, 14
2	14	2	8	20	2	6, 9
3	15	3	7	19	3	2, 5
4	16	4	11	23	4	7, 15
5	17	5	3	15	5	11, 17
6	18	6	2	14	6	4, 10
7	19	7	6	18	7	16, 24
8	20	8	1	13	8	20, 23
9	21	9	9	21	9	1, 3
10	22	10	12	24	10	12, 13
11	23	11	10	22	11	18, 21
12	24	12	5	17	12	19, 22

a: <https://doi.org/10.1038/s41467-022-29908-y>

b: <https://doi.org/10.1093/hr/uhae107>

c: <https://doi.org/10.1111/pbi.13558>

d: <https://doi.org/10.1111/1755-0998.13403>

Supplementary Table 14. Ancestral chromosome assignment using *A. cordata*.

Ancestor	<i>A. cordata</i>
AP01	Acor01
AP02	Acor14
AP03	Acor03
AP04	Acor16
AP05	Acor05
AP06	Acor18
AP07	Acor07
AP08	Acor20
AP09	Acor09
AP10	Acor22
AP11	Acor23
AP12	Acor24

Supplementary Table 15. Repeat compositions of five species in Araliaceae family.

Unit (Mbp)	<i>A. cordata</i>	<i>A. elata</i>	<i>P. ginseng</i>	<i>P. notoginseng</i>	<i>E. senticosus</i>
Genome size	1,062.89	1,038.02	3,455.43	2,089.72	1,201.30
Total TE	629.46	756.74	3,007.60	1,850.96	849.59
Total LTR	426.13	638.69	2,679.58	1,718.82	698.01
LTR/Gypsy	225.16	369.19	1,680.42	1,098.72	456.09
LTR/Copia	75.21	142.53	202.46	88.81	70.54
LTR/unknown	125.75	126.97	796.70	531.29	171.37
TIR	141.63	77.07	238.50	88.32	102.60
nonTIR	36.06	15.47	30.75	8.43	18.62
LINE	0.47	0.19	0.98	0.71	1.23
repeat_region	25.18	25.23	57.78	34.66	29.12

Supplementary Table 16. Representative LTR compositions of five species in Araliaceae family.

Unit (Mbp)	<i>A. cordata</i>	<i>A. elata</i>	<i>P. ginseng</i>	<i>P. notoginseng</i>	<i>E. senticosus</i>
Genome size	1,062.89	1,038.02	3,455.43	2,089.72	1,201.3
Total LTR	426.13	638.69	2,679.58	1,718.82	698.01
Classified LTR	315.87	524.87	2,248.51	1,474.71	569.99
<i>Copia 1731</i>	0.02	1.98	13.75	0.47	0.23
<i>Copia codi</i>	2.81	0.97	54.96	9.47	3.71
<i>Copia copia</i>	5.93	2.30	7.28	4.15	20.2
<i>Copia hydra</i>	1.58	0.02	7.38	6.29	2.33
<i>Copia oryco</i>	1.76	4.88	5.65	3.28	2.35
<i>Copia pCretro</i>	1.35	0.06	29.95	10.56	0.65
<i>Copia pseudovirus</i>	1.21	0.15	17.04	26.48	1.98
<i>Copia retrofit</i>	7.19	6.83	24.21	8.07	9.51
<i>Copia sire</i>	11.41	18.07	70.20	27.82	18.31
<i>Copia tork</i>	37.67	103.63	94.32	62.66	26.93
<i>Copia tyl/copia</i>	0.27	0.01	1.02	0.83	1.62
<i>Gypsy 17</i>	0.93	5.04	36.62	10.92	0.32
<i>Gypsy 412</i>	0.84	1.19	2.34	14.93	2.26
<i>Gypsy a</i>	0.29	0.38	2.61	0.04	2.93
<i>Gypsy athila</i>	21.6	67.35	132.22	71.00	39.86
<i>Gypsy b</i>	0.52	0.28	4.95	5.24	2.72
<i>Gypsy cer2</i>	0.06	0.66	4.29	0.09	0.02
<i>Gypsy crm</i>	16.00	26.53	15.46	11.18	16.65
<i>Gypsy csrn1</i>	1.99	0.48	15.56	5.29	0.20
<i>Gypsy del</i>	168.81	180.26	1,366.57	994.11	324.62
<i>Gypsy galadriel</i>	0.28	1.73	15.22	0.92	0.40
<i>Gypsy gmr1</i>	0.48	1.10	0.65	0.58	0.01
<i>Gypsy gypsy</i>	0.89	2.46	28.35	7.55	0.06
<i>Gypsy maggy</i>	0.86	2.17	12.05	5.71	0.85
<i>Gypsy micropia</i>	5.85	0.45	41.37	21.66	2.35
<i>Gypsy osvaldo</i>	1.39	0.41	15.52	5.20	0.11
<i>Gypsy pyret</i>	0.63	0.39	4.08	1.37	0.95
<i>Gypsy reina</i>	6.65	2.37	7.72	2.11	16.9
<i>Gypsy tat</i>	14.46	92.65	202.56	152.67	68.7
<i>Gypsy TF</i>	2.17	0.07	14.6	4.09	2.25

Supplementary Table 17. Ten most frequent tandem repeat unit in whole genome.

TRunit	Acor	TRunit	Aela	TRunit	Pgin	TRunit	Pnot	TRunit	Esen
160	200876	70	52507.6	167	231374	58	35463.9	70	15374.1
320	56701	140	15972.7	334	40952.3	60	24702.6	73	15337.8
480	38269	51	9455	166	31489.2	57	19430.9	55	11886.8
159	23616.7	52	6453.8	57	18318.2	59	15847.6	72	11452
73	10783	100	5937.8	168	11348.8	167	5842.5	60	5538
479	5959	69	4576.3	73	8975	56	3114	62	5437.5
63	4942.5	160	4224.5	201	7538.2	55	1974.1	79	5388.8
72	4823.9	54	3547.9	74	7188.7	51	1501.2	61	5106
319	3987.1	139	3357.5	58	5852.4	73	1380.1	53	4033.4
158	3026.7	55	3170.8	333	4900.1	54	1336.2	69	3946.1

Acor: *A. cordata*Pgin: *P. ginseng*Esen: *E. senticosus*Aela: *A. elata*Pnot: *P. notoginseng***Supplementary Table 18. Ten most frequent tandem repeat unit in low k-mer diversity regions.**

TRunit	Acor	TRunit	Aela1	TRunit	Pgin	TRunit	Pnot	TRunit	Esen
160	198724	70	7692.5	167	219084	58	6206.9	160	2497.6
320	56433.2	160	3156.5	334	37163.6	60	3948.3	156	1220.1
480	38323.8	140	2063.9	166	32064.7	57	3013.6	73	1027
159	23307.8	161	1957.1	168	7672.3	59	2834.7	70	868.8
479	5888.1	51	1277.9	201	7538.2	167	2506.4	72	727.6
319	3847	52	1146.8	436	3981.2	334	507.1	155	613.6
161	2879.4	167	1130.3	333	3903.5	56	480.7	62	542.3
158	2844.3	100	956.3	402	3776.1	333	285.6	79	520.5
321	2592.7	155	721.9	336	3306.7	55	234	55	492
478	2557.2	159	686.6	293	2112	166	188.1	159	268.6

Acor: *A. cordata*Pgin: *P. ginseng*Esen: *E. senticosus*Aela: *A. elata*Pnot: *P. notoginseng***Supplementary Table 19. Primer information for PLOP-FISH analysis.**

Oligo name	PLOP sequences	Length (bp)	Modification
AraTR4_160_OP1	GGTGATTTCGAGTCCTACTACTTCGTTCTA	30	5'-Cy3
AraTR4_160_OP2	GTTTGTTTAGCATCGAAAGGAGCAATCCTA	30	
AraTR4_160_OP3	CGTTATTTCTTTGAAATTCGCAAACAAAGA	30	