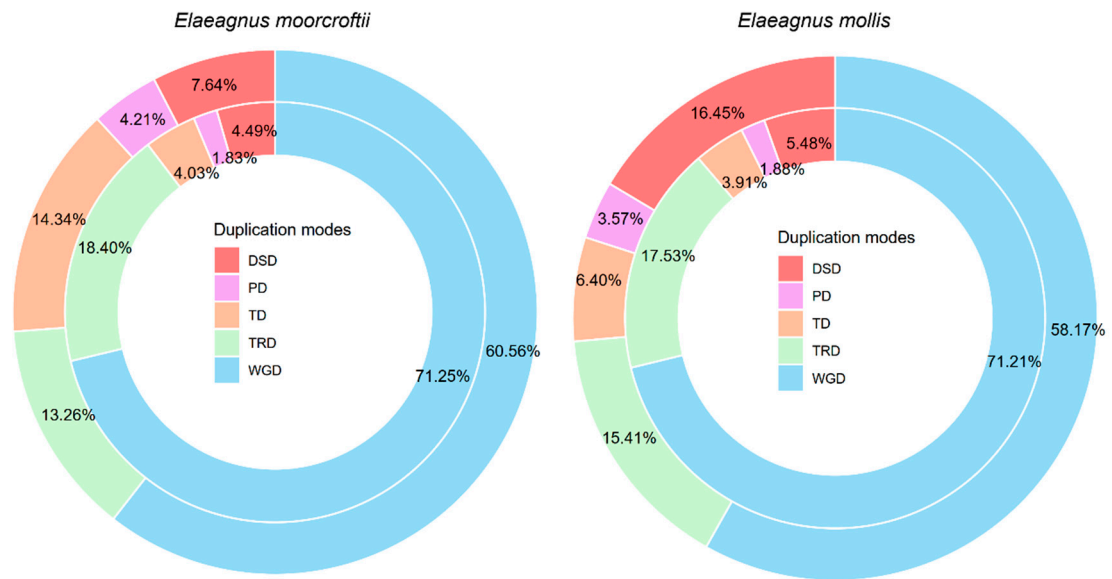
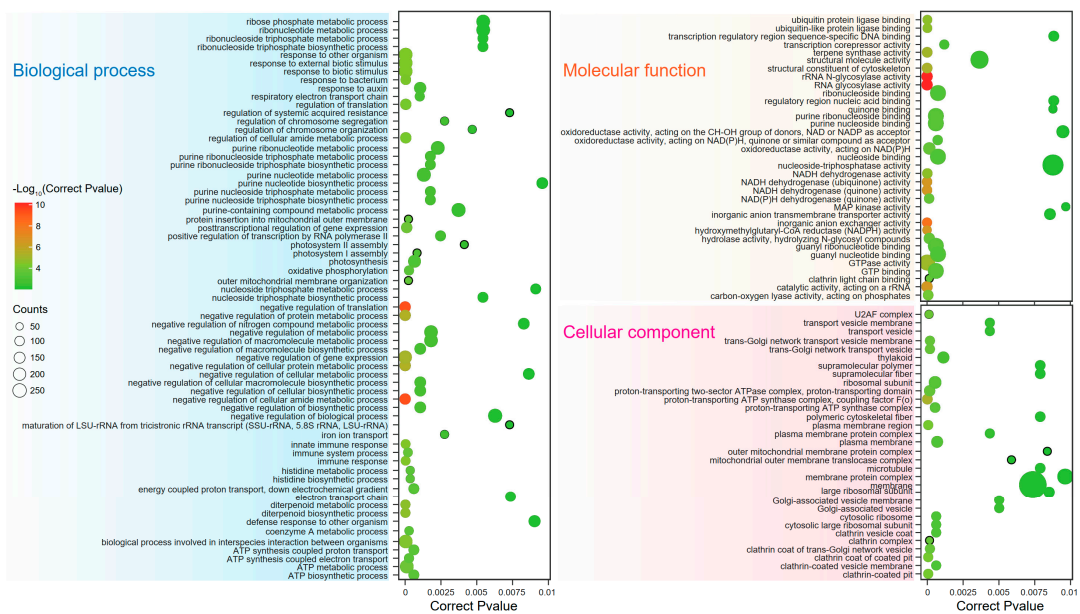


**Figure S1. The distribution frequency of PacBio's HiFi sequencing data.** Abscissa axis represents the length of reads (bp), and vertical axis shows the number of reads.



**Figure S2. The different modes of gene duplications related to expanded and contracted gene families in *E. moorcroftii* and *E. mollis*.** DSD: dispersed duplications; PD: proximal duplications; TD: tandem duplications; TRD: transposed duplications; WGD: whole genome duplications. The outer and inner circles indicate the expanded and contracted gene families in each species, respectively.



**Figure S3. The enriched GO terms for the expanded gene families of *E. moorcroftii*.**

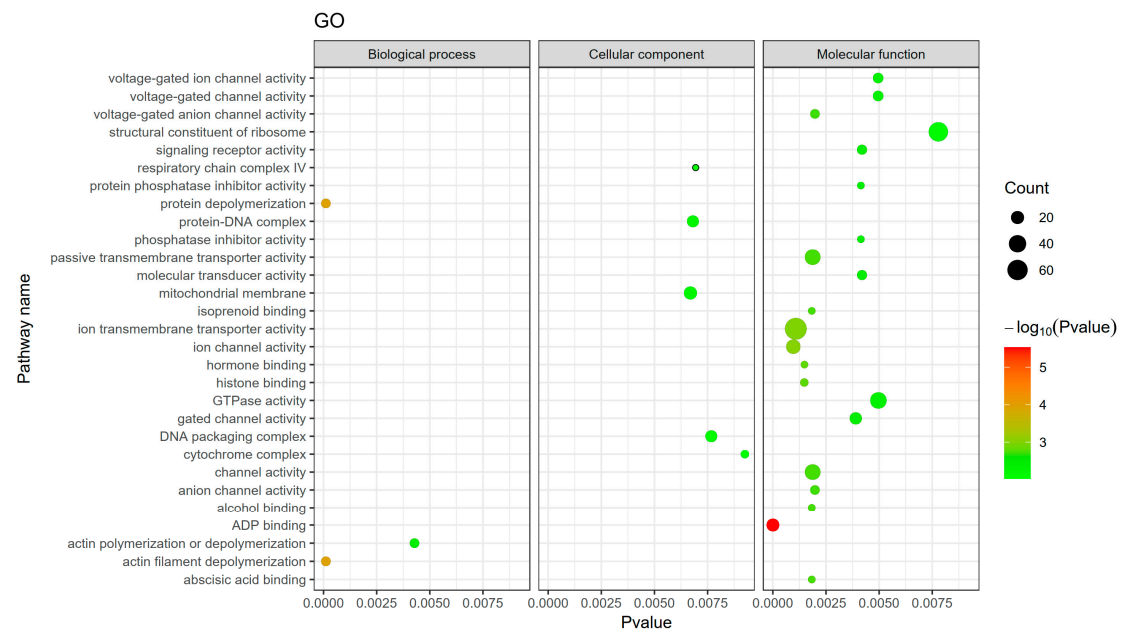


Figure S4. The enriched GO terms for the contracted gene families of *E. moorcroftii*.

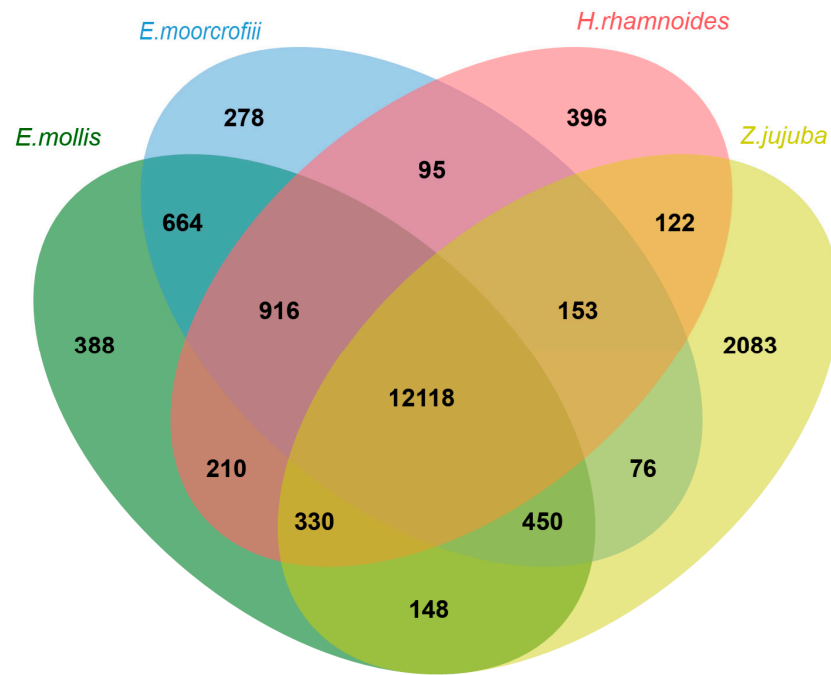


Figure S5. Venn diagram showing the shared and specific gene families among *E. moorcroftii*, *E. mollis*, *H. rhamnoides*, and *Z. jujuba*.

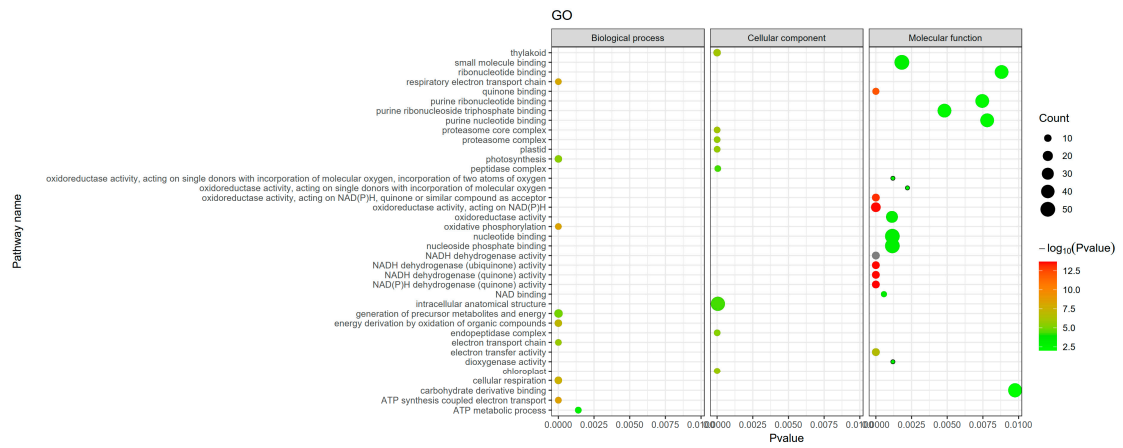
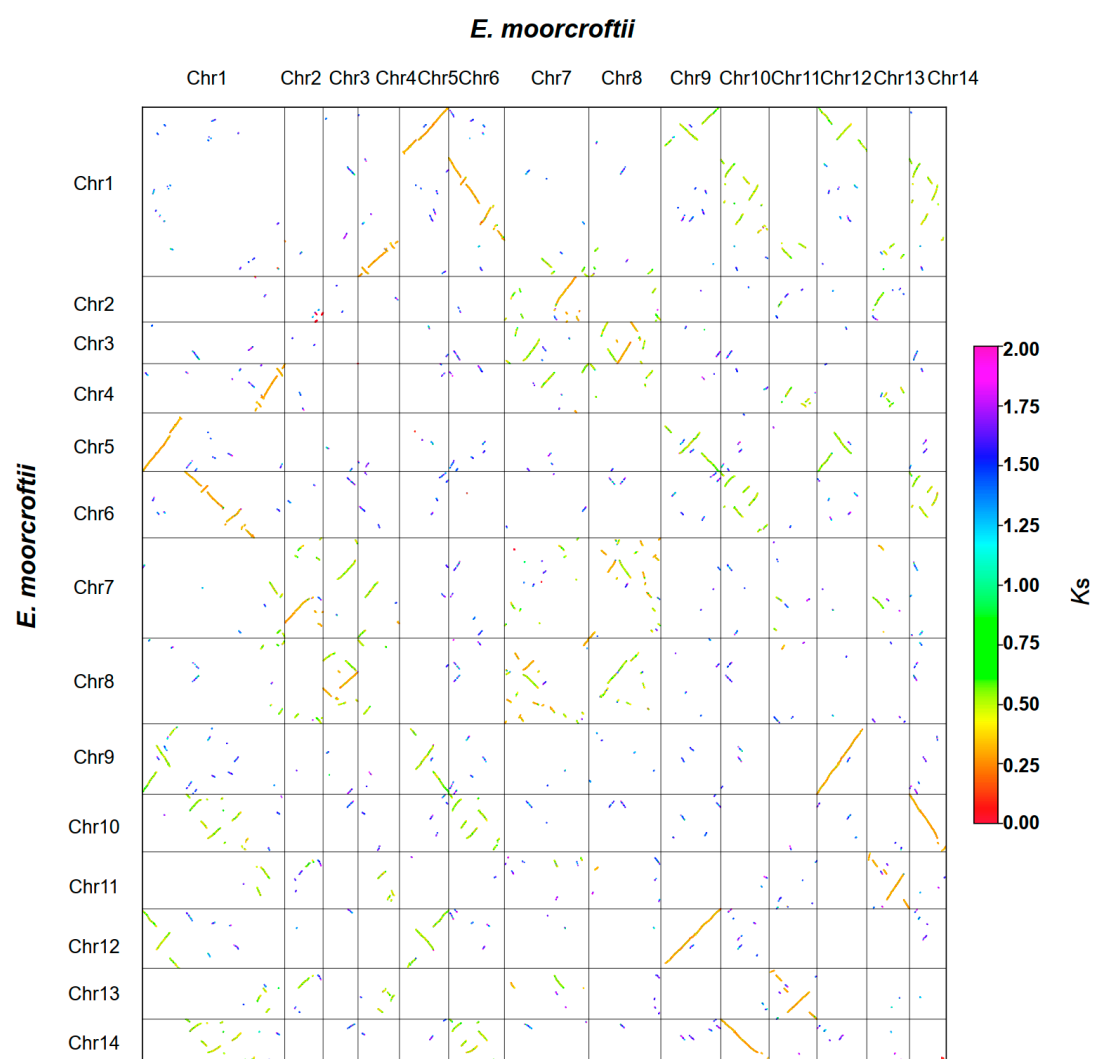


Figure S6. The enriched GO terms for the unique gene families of *E. moorcroftii*.



**Figure S7. Syntenic dot plot of the self-comparison of *E. moorcroftii*.**

**Table S1. Information of plant genomes used in this study.**

Family	Species name	Version	Gene number	Data source
Brassicaceae	<i>Arabidopsis thaliana</i>	TAIR v10	27,380	Phytozome v9
Salicaceae	<i>Populus trichocarpa</i>	Version 4.1	34,699	Phytozome v13
Vitaceae	<i>Vitis vinifera</i>	Version 2.1	31,730	Phytozome v13
Cannabaceae	<i>Cannabis sativa</i>	Version 1.21	33,556	NCBI
Rosaceae	<i>Malus domestica</i>	Version 1.1	45,105	Phytozome v12
	<i>Prunus persica</i>	Version 2.1	26,873	Phytozome v10
Elaeagnaceae	<i>Elaeagnus mollis</i>	Version 1.0	33,446	Ren et al., 2021
	<i>Elaeagnus moorcroftii</i>	Version 1.0	29,243	This study
	<i>Hippophae rhamnoides</i>	Version 1.0	30,812	Wu et al., 2022
Moraceae	<i>Morus notabilis</i>	Version 1.21	27,100	NCBI
Rhamnaceae	<i>Ziziphus jujuba</i>	Version 1.21	43,012	NCBI

**Table S2. Basic statistics of PacBio's HiFi sequencing data.**

Read number	Max read length (bp)	Mean read length (bp)	N50 of read(bp)
1,630,175	64,203	14,783	15,012

**Table S3. Mapping rates of RNA-seq reads onto the assembly genome.**

Accession number	Mapping rate (%)
SRR12569922	93.14
SRR12569923	94.12
SRR12569923	94.27

**Table S4. Genome assembly completeness evaluated based on BUSCO.**

Type (gene)	Number	Percent (%)
Complete BUSCOs (C)	1,546	95.80
Complete and single-copy BUSCOs (S)	1,365	84.60
Complete and duplicated BUSCOs (D)	181	11.20
Fragmented BUSCOs (F)	15	0.90
Missing BUSCOs (M)	53	3.3
Total BUSCO groups searched	1,614	100

**Table S5. Information of different classes of repetitive sequences in *E. moorcroftii* genome.**

Order	Super family	Length of sequence (bp)	Percent of sequence (%)
DNA		18,960,827	95.80
	DNA_CMC-EnSpm	3,115,353	0.588
	DNA_MuDR	6,932,482	1.309
	DNA_PIF-		
	Harbinger	1,158,088	0.219
	DNA_hAT-Ac	5,112,542	0.965
	DNA_hAT-Tip100	901,009	0.17
	DNA_other	1,933,355	0.365
LINE		8,004,781	1.512
	LINE_L1	7,588,087	1.433
	LINE_L2	243	0
	LINE_other	419,200	0.079
LTR		169,178,687	31.947
	LTR_Copia	84,853,051	16.023
	LTR_Gypsy	70,425,005	13.299
	LTR_other	14,562,811	2.75
Low_complexity		1,583,252	0.299
SINE		43,867	0.008
Satellite		3,123,906	0.59

Simple_repeat	38,925,148	7.35
Small_RNA	5,324,239	1.005
Unclassified_ARTEFACT	203	0
Unclassified_RC	6,076	0.001
Unclassified_RC/Helitron	1,799,103	0.34
Unclassified_Retroposon	148,909	0.028
Unclassified_Retroposon/ L1-dep	44	0
Unclassified_Unknown	115,622,651	21.834
Total Repeats	322,779,888	60.95

**Table S6. Functional annotation of the predicted genes in *E. moorcroftii*.**

	Database	Gene number	Percent (%)
Total		29,243	100
	InterProScan	25,178	86.10
	GO	18,982	64.91
	KEGG	1,131	3.87
	NR	27,709	94.75
	SwissProt	23,799	81.38
	KOG	26,682	91.24
Annotated		27,810	95.10
Unannotated		1,433	4.90

**Table S7. *E. moorcroftii* genome annotation completeness evaluated based on BUSCO.**

Type (gene)	Number	Percent (%)
Complete BUSCOs (C)	1,572	97.40
Complete and single-copy BUSCOs (S)	1,366	84.6
Complete and duplicated BUSCOs (D)	206	12.8
Fragmented BUSCOs (F)	18	1.1
Missing BUSCOs (M)	24	1.5
Total BUSCO groups searched	1,614	100

**Table S8. List of non-coding RNA genes in *E. moorcroftii* genome.**

Type	Number	Average length (bp)
miRNA	183	124.86
snRNA	2,461	107.52
tRNA	1,636	75.21
rRNA	20,568	238.47