Table S1. Genome information of seven *Euphorbiaceae*

Subfamily	Species	Assembly Version	BioProject ID	Assembly Level	Reference
Crotonaceae	*Jatropha curcas*	GCF_014843425.1	PRJNA601606	Scaffold	Exploitation of Hi-C sequencing for improvement of genome assembly and in-vitro validation of differentially expressing genes in *Jatropha curcas* L
	Hevea brasiliensis	GCF_030052815.1	PRJNA945562	Chromosome	Chromosome-level wild *Hevea brasiliensis* genome provides new tools for genomic-assisted breeding and valuable loci to elevate rubber yield
	Manihot esculenta	Mesculenta_305_v6.1	PRJNA234389, PRJNA394209	Chromosome	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity
	Vernicia fordii	CRA001732	N\A	Scaffold	Dissection of leucine-rich repeat receptor-like protein kinases: insight into resistance to Fusarium wilt in tung tree
Acalyphoideae	*Ricinus communis*	GCF_019578655.1	PRJNA589181	Chromosome	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert
	Mercurialis annua	GCF_937616625.2	PRJEB52246	Chromosome	N\A
Euphorbioideae	*Euphorbia peplus*	GCA_028411795.1	PRJNA837952	Chromosome	Chromosome-level Genome Assembly of Euphorbia peplus, a Model System for Plant Latex, Reveals that Relative Lack of Ty3 Transposons Contributed to Its Small Genome Size

The genomes of *Manihot esculenta* and *Vernicia fordii* were downloaded from Phytozome (https://phytozome-next.jgi.doe.gov/) and GSA (https://ngdc.cncb.ac.cn/gsa/); the genomes of other species were downloaded from NCBI (https://www.ncbi.nlm.nih.gov/).