

Supplementary Table 1. Summary of ornamental plant genome assemblies.

NO.	Species	genome size	Number of predicted genes	Sequencing platform	Assembly level (Draft/Chromosome/T2T)	Objects/goals	Publication year	Pulication
1	<i>Acer pseudosieboldianum</i>	690.24 Mb	29,679	PacBio Sequel II, Illumina (PE)	Chromosome	Chromosome-scale genome assembly, leaf color and shape change mechanisms, anthocyanin biosynthesis pathways, gene-to-metabolite correlation network, TCP transcription factors, evolutionary history, molecular breeding foundation.	2022	Frontiers in Plant Science
2	<i>Amaranthus hypochondriacus</i>	465.2 Mb	24,829	Illumina HiSeq 2000	Draft	Lysine biosynthetic pathway	2014	DNA Research
3	<i>Amaranthus hypochondriacus</i>	377 Mb	23,059	Illumina HiSeq 2500	Draft	Systematic evolution	2016	The Plant Genome
4	<i>Antirrhinum majus</i>	510 Mb	37,714	Illumina HiSeq 2000, PacBio RS II	Chromosome	Flower asymmetry, self-incompatibility	2019	Nature Plants
5	<i>Apostasia shenzhenica</i>	349 Mb	21,841	Illumina HiSeq 2000, PacBio	Draft	Flower development, seeds without endosperm, evolution of epiphytism	2017	Nature
6	<i>Asparagus setaceus</i>	710.15 Mb	28,410	HiSeq X ten, Hi-C	Chromosome	Resistance R genes	2020	Horticulture Research
7	<i>Begonia darthvaderiana</i>	797 Mb	23444	PacBio, Hi-C	Chromosome	Evolution and shade adaptation	2022	New Phytologist
8	<i>Begonia fuchsioides</i>	374 Mb	51,638	Illumina HiSeq 2000/4000	Draft	Nitrogen-fixing root nodule symbiosis	2018	Science
9	<i>Begonia loranthoides</i>	724 Mb	22059	10x Genomics, Hi-C	Chromosome	Evolution and shade adaptation	2022	New Phytologist
10	<i>Begonia masoniana</i>	806 Mb	22861	PacBio, Hi-C	Chromosome	Evolution and shade adaptation	2022	New Phytologist
11	<i>Begonia peltatifolia</i>	349 Mb	23010	10x Genomics, Hi-C	Chromosome	Evolution and shade adaptation	2022	New Phytologist
12	<i>Boea hygrometrica</i>	1.55 Gb	49,374	Illumina HiSeq 2000, Roche 454	Draft	Desiccation tolerance	2015	Proceedings of the National Academy of Sciences
13	<i>Bombax ceiba</i>	895 Mb	52,705	Illumina HiSeq 2000, PacBio RS II	Draft	Evolutionary history	2018	GigaScience
14	<i>Camptotheca acuminata</i>	403.2 Mb	31,825	Illumina HiSeq 2000	Chromosome	Camptothecin biosynthesis	2017	GigaScience
15	<i>Carnegiea gigantea</i>	980.3 Mb	28,292	Illumina HiSeq 2000, MiSeq	Draft	Cactus phylogeny	2017	Proceedings of the National Academy of Sciences of the United States of America
16	<i>Casuarina equisetifolia</i>	301 Mb	29,827	Illumina HiSeq 2000, PacBio RS II	Draft	Secondary growth and DNA modification	2018	The Plant Journal
17	<i>Casuarina glauca</i>	283 MB	26,282	Illumina HiSeq 2000/4000	Draft	Nitrogen-fixing root nodule symbiosis	2018	Science
18	<i>Catharanthus roseus</i>	523 Mb	33,829	Illumina HiSeq 2000	Draft	Monoterpene indole alkaloid pathway	2015	The Plant Journal
19	<i>Catharanthus roseus</i> cv. 'Pacifica XP Burgundy'	561.7 Mb	30,085	Illumina, PacBio, BioNano, Hi-C	T2T(One chromosome was assembled completely from telomere to telomere, and four were assembled with a single end telomere)	Genome assembly, vinblastine biosynthesis, susceptibility to Huanglongbing pathogen.	2023	Plant Communications
20	<i>Cerasus serrulata</i>	265.40 Mb	29,094	Illumina X-ten, Nanopore, Hi-C	Chromosome	MADS-box, MYB, WRKY, and plant disease-resistance genes	2020	Horticulture Research
21	<i>Cerasus yedoensis</i>	350.1 Mb	48,280	Illumina HiSeq 2000, MiSeq, HiSeq X	Chromosome	Dormancy- and flowering-associated genes	2019	DNA Research
22	<i>Cerasus yedoensis</i>	339.97 Mb	46,796	Illumina HiSeq 2000, MiSeq, HiSeq X	Chromosome	Dormancy- and flowering-associated genes	2019	DNA Research
23	<i>Cercis canadensis</i>	330 Mb	34,023	Illumina HiSeq 2000/4000	Draft	Nitrogen-fixing root nodule symbiosis	2018	Science
24	<i>Chaenomeles speciosa</i>	632.3 Mb	45,515	PacBio HiFi, Hi-C	(T2T) 7 gaps	Telomere-to-telomere genome assembly, medicinal compound biosynthesis, genetic insight into pentacyclic triterpenoid biosynthesis, Rosaceae evolution, comparison with other species like Malus domestica, identification of expanded/contracted gene families associated with plant metabolism.	2023	Horticulture Research
25	<i>Chimonanthus praecox</i>	695.36 Mb	23,591	Illumina HiSeq 2000, PacBio RS II, HiSeq X, Hi-	Chromosome	Floral transition, floral organ specification, early blooming, strong cold resistance, terpene/benzenoid/phenylpropanoid biosynthesis	2020	Genome Biology
26	<i>Chimonanthus salicifolius</i>	820.1 Mb	36,651	Illumina HiSeq 2000, PacBio RS II, Hi-C	Chromosome	Flower development, flavonoid biosynthesis	2020	The Plant Journal

27	<i>Chrysanthemum lavandulifolium</i>	2.60 Gb	64,257	PacBio RS II, Oxford Nanopore, Hi-C	Chromosome	Understanding the molecular mechanism underlying diverse capitulum types, capitulum development in <i>Chrysanthemum</i> .	2022	Horticulture Research
28	<i>Chrysanthemum makinoi</i>	3.1 Gb	95,074	Oxford Nanopore, Pacific Biosciences, Illumina	Chromosome	Complete and contiguous genome assembly, annotation, understanding of <i>chrysanthemum</i> genome, evolution, and history.	2022	G3-Genes Genomes Genetics
29	<i>Chrysanthemum morifolium</i>	8.15 Gb	138,749	PacBio CLR, 10X Genomics, Hi-C	Chromosome	Origin and evolution of cultivated <i>chrysanthemum</i> , whole-genome triplication event, segmental allopolyploidy, genes underlying ornamental traits, flower colour breeding history, genomic resources for genetic improvement of <i>chrysanthemum</i> .	2023	Nature Communications
30	<i>Chrysanthemum nankingense</i>	2.53 Gb	56,870	HiSeq2000, PacBio RS II	Chromosome	Flower trait, flavonoid biosynthesis	2018	Molecular Plant
31	<i>Chrysanthemum seticuspe</i>	2.72 Gb	71,057	Illumina HiSeq 2000, MiSeq	Draft	Flowering time	2019	DNA Research
32	<i>Dendrobium catenatum</i>	1.01 Gb	28,910	Illumina HiSeq 2000	Draft	Polysaccharide synthase, MADS-box genes	2016	Scientific Reports
33	<i>Dendrobium officinale</i>	1.35 Gb	35,567	Illumina HiSeq 2000, PacBio RS II	Chromosome	MADS-box genes, morphology of the flower, polysaccharides, alkaloids	2014	Molecular Plant
34	<i>Dianthus caryophyllus</i>	622 Mb	43,266	Illumina HiSeq 1000, GS FLXp	Draft(emphasizing the assembly's intermediate quality between a basic draft and a more complete chromosome-level assembly.)	Phenylpropanoid biosynthetic, betalain/chlorophyll and carotenoid synthesis, disease resistance, ethylene/carbohydrate metabolism, and cell wall modification during flower opening, floral scent	2013	DNA Research
35	<i>Dionaea muscipula</i>	1.5 Gb	21,135	PacBio RS II	Draft	Carnivory genes	2020	Current Biology
36	<i>Drosera capensis</i>	264 Mb	–	Illumina HiSeq 2500	Draft	3D structures of cysteine protease	2016	Proteins: Structure, Function, and Bioinformatics
37	<i>Eschscholzia californica</i>	489 Mb	41,612	Illumina HiSeq 2500	Draft	Benzylisoquinoline alkaloid biosynthesis	2017	Plant Cell Physiology
38	<i>Forsythia suspensa</i>	737.47 Mb	33,062	Illumina HiSeq 2500, Oxford Nanopore	Chromosome	Candidate genes associated with solar radiation, temperature, and water variables	2020	Horticulture Research
39	<i>Fraxinus excelsior</i>	867 Mb	38,852	Illumina HiSeq 2000, MiSeq, Roche 454		Disease resistance	2016	Nature
40	<i>Gardenia jasminoides</i>	535 Mb	35,967	Illumina HiSeq 2000, Oxford Nanopore, Hi-C	Chromosome	Crocin and caffeine biosynthesis genes	2020	BMC Biology
41	<i>Ginkgo biloba</i>	10.61 Gb	41,840	Illumina HiSeq 2000/4000	Draft	Multiple defense mechanisms, resistant genes	2016	GigaScience
42	<i>Ginkgo biloba</i>	9.87 Gb	27,832	PacBio RSII and Illumina HiSeq 2500	Chromosome	Gymnosperm evolution, genome expansion, spermatophore flagellum formation in ginkgo, long terminal repeats, candidate genes identification, insights into gymnosperm genome evolution.	2021	Nature Plants
43	<i>Handroanthus impetiginosus</i>	503.7 Mb	31,688	Illumina HiSeq 2000	Draft	Biosynthetic pathway of specialized quinoids	2017	GigaScience
44	<i>Helianthus annuus</i>	2.94 Gb	52,232	PacBio RS II	Chromosome	Flowering time, oil production	2017	Nature
45	<i>Hibiscus syriacus</i>	1.75 Gb	87,603	Illumina HiSeq 2000	Draft	Flowering time, disease resistance	2016	DNA Research
46	<i>Ipomoea cairica</i>	733.0 Mb	38,115	PacBio Sequel II and Illumina NovaSeq 6000	Chromosome	Invasive species study, chromosome-level reference genome construction, transposable element content analysis, phylogenetic analysis, genome triplication in Convolvulaceae, molecular mechanisms of rapid growth and invasiveness.	2022	G3-Genes Genomes Genetics
47	<i>Ipomoea nil</i>	734.8 Mb	42,783	Illumina HiSeq2500, PacBio RS II	Draft	Dwarf trait	2016	Nature Communications
48	<i>Jasminum sambac</i>	537.99 Mb	39,381 (HA); 39,201 (HB); 39,843 (consensus)	Illumina; Pacific Biosciences HiFi; Hi-C data	T2T(9 chromosomes gap-free)	Molecular mechanism of jasmonate synthesis and accumulation, aromatic volatile gene expression, comparative genomic, transcriptomic, and metabolomic analysis, key genes in JA biosynthesis, insights into fragrance production, high JA synthesis and low degradation under typical conditions.	2023	Journal of Experimental Botany
49	<i>Kalanchoe fedtschenkoi</i>	256 Mb	30,964	MiSeq	Draft	Crassulacean acid metabolism	2017	Nature Communications
50	<i>Loganstroemia indica</i>	329.14 Mb	33,608	PacBio, Hi-C	Chromosome (Gap number of scaffolds=554,000)	Investigating the evolution, population structure, and differentiation of Myrtaceae species and accelerating the molecular breeding of <i>L. indica</i>	2023	Horticulture Research

51	<i>Lavandula angustifolia</i>	688 Mb	62,141	Illumina HiSeq 2000	Draft	Pathways of isoprenoid metabolism	2018	Planta
52	<i>Lavandula angustifolia</i> 'Munstead'	795 Mb	58,702	Oxford Nanopore Technologies, Hi-C	Chromosome	Genomic basis of chemical diversity in lavender, high-quality genome assembly, comparative analyses within lavender and Lamiaceae, annotation of protein-coding sequences.	2023	BMC Genomic Data
53	<i>Liriodendron chinense</i>	1.74 Gb	35,269	Illumina HiSeq 2000, PacBio RS II, Bionano	Draft	Systematic evolution of angiosperms	2018	Nature Plants
54	<i>Lolium perenne</i>	1.13 Gb	28,455	Illumina HiSeq 2000	Draft	Pollen allergens, self-incompatibility mechanism	2015	The Plant Journal
55	<i>Magnolia biondii</i>	2.23 Gb	47,547	PacBio, 10X Genomics, Hi-C	Chromosome	Evolution of Magnoliales, biosynthesis of terpenoids, phylogenetic resolution within Magnoliaceae, genome-wide duplication (WGD) event, gene family expansion in biosynthesis of secondary metabolites, phylogenomic analysis revealing relationship with Chloranthaceae, monocots, and eudicots.	2021	Horticulture Research
56	<i>Mimosa pudica</i>	557 Mb	33,108	Illumina HiSeq 2000/4000	Draft	Nitrogen-fixing root nodule symbiosis	2018	Science
57	<i>Mimulus guttatus</i>	321.7 Mb	26,718	Illumina HiSeq 2000	Draft	Recombination activity	2013	Proceedings of the National Academy of Sciences
58	<i>Nelumbo nucifera</i>	804 Mb	26,685	Illumina HiSeq 2000, Roche 454	Chromosome	Aquatic lifestyle	2013	Genome Biology
59	<i>Nelumbo nucifera</i>	792 Mb	36,385	Illumina HiSeq 2000	Draft	Seed formation, embryonic development, seed dormancy, starch synthesis	2013	The Plant Journal
60	<i>Nelumbo nucifera</i>	847.16 Mb	30,378	BioNano	Chromosome	Chromosome fusions	2018	The Plant Journal
61	<i>Nicotiana glauca</i>	2.22 Gb	38,940	Illumina HiSeq 2000	Draft	Terpenoid metabolism, alkaloid metabolism, and heavy metal transport	2013	Genome Biology
62	<i>Nymphaea colorata</i>	409 Mb	31,580	PacBio RS II, Hi-C	Chromosome	Flowering transition, flower development, floral scents, flower colors	2019	Nature
63	<i>Nymphaea thermarum</i>	–	25,760	Illumina HiSeq	Draft	Revealing variable genomic signatures of ancient vascular cambium losses through lineage-specific patterns of gene loss and divergence associated with cambium loss.	2020	Proceedings of the National Academy of Sciences
64	<i>Osmanthus fragrans</i>	740.6 Mb	45,542	HiSeq X ten, Hi-C	Chromosome	Flower scent	2018	Horticulture Research
65	<i>Paeonia suffruticosa</i>	13.79 Gb	35,687	BGISEQ-500, PacBio RS II	Draft	MADS-box genes	2019	Scientific Reports
66	<i>Papilionanthe Miss Joaquim</i> 'Agnes'	2.5 Gb	31,529	Oxford Nanopore Technology (ONT); Illumina PacBio, Hi-C	Chromosome	Genome assembly and secondary metabolite analysis. Anthocyanin and vandateroside biosynthesis study. Genetic exploration of subtle floral scent	2022	Communications biology
67	<i>Penstemon davidsonii</i>	438 Mb	18199	Illumina PacBio, Hi-C	Chromosome	Studying evolutionary history and genetic diversity	2023	G3 Genes
68	<i>Petunia axillaris</i>	1.26 Gb	32,928	Illumina HiSeq 2000, PacBio RS II	Chromosome	Floral color, pollination	2016	Nature Plants
69	<i>Petunia inflata</i>	1.29 Gb	36,697		Chromosome	Floral color, pollination	2016	Nature Plants
70	<i>Phalaenopsis aphrodite</i>	1.03 Gb	28,902	Illumina HiSeq 2000/2500	Chromosome	Flower development	2018	Plant Biotechnology Journal
71	<i>Phalaenopsis equestris</i>	1.09 Gb	29,431	Illumina HiSeq 2000	Chromosome	Crassulacean acid metabolism, MADS-box genes	2014	Nature Genetics
72	<i>Phalaenopsis orchid</i>	3.1 Gb	41,153	Illumina HiSeq 2000	Draft	Labellum organ development, flowering-time genes	2016	PeerJ
73	<i>Primula veris</i>	301.8 Mb	19,507	Illumina HiSeq 2000, PacBio RS II	Draft	Floral morphs	2015	Genome Biology
74	<i>Primula vulgaris</i>	411.1 Mb	24,599	Illumina HiSeq 2500	Draft	Flower development	2018	Scientific Reports
75	<i>Prunus mume</i>	237 Mb	31,390	Illumina GA II	Chromosome	Early blooming, endodormancy, bacterial infection, biosynthesis of flower scent.	2012	Nature Communications
76	<i>Prunus mume</i> var. <i>tortuosa</i>	237.8 Mb	29,706	Oxford Nanopore, Hi-C	Chromosome	A putative regulatory pathway for the tortuous branch trait was constructed based on genome assembly and gene expression levels.	2022	New Phytologist
77	<i>Prunus yedoensis</i>	323.8 Mb	41,294	HiSeq X Ten, PacBio RS II	Draft	S-locus genes	2018	Genome Biology
78	<i>Rhodiola crenulata</i>	344.5 Mb	31,517	Illumina HiSeq 2000/4000	Draft	Stress resistance, biosynthesis pathways of medicinal ingredients	2017	GigaScience

79	<i>Rhododendron delavayi</i>	695.09 Mb	32,938	Illumina HiSeq 2000	Draft	Biosynthesis pathways of medicinal ingredients	2017	GigaScience
80	<i>Rhododendron molle</i>	653.46 Mb	41,600	Illumina HiSeq X Ten, PromethION ONT	T2T	Divergence in flower color, LTR-RT proliferation, carotenoids/flavonols biosynthesis, chlorophyll degradation, gene regulatory networks for pigmentation.	2022	Horticulture Research
81	<i>Rhododendron molle</i>	744.36 Mb	39,288	Illumina, PacBio SMRT, Hi-C	Chromosome	Traditional medicine, grayanoid biosynthesis, non-addictive analgesic activity, terpene synthase and CYP450 gene expansion, phylogenetic analysis of CYP71AU subfamily.	2022	BMC Plant Biology
82	<i>Rhododendron ovatum</i>	549 Mb	41,264	PacBio, Hi-C	Chromosome	Exploring <i>Rhododendron ovatum</i> 's genome for low-altitude adaptability and scent evolution. Found defense response gene expansion and tandem duplications enhancing scent-related genes.	2021	Plant Biotechnology Journal
83	<i>Rhododendron simsii</i>	528.6 Mb	34,170	PacBio RS II, Hi-C	Chromosome	Metabolic pathways for anthocyanins and carotenoids	2020	Nature Communications
84	<i>Rhododendron williamsianum</i>	532 Mb	23,559	Illumina HiSeq 2000, Hi-C	Chromosome	Evolutionary history	2019	Genome Biology and Evolution
85	<i>Rhodomyrtus tomentosa</i>	470.35 Mb	33,382	PacBio Sequel II, Oxford Nanopore Technology (ONT)	T2T	Evolution, anthocyanin accumulation mechanism	2023	Horticulture Research
86	<i>Rosa chinensis</i>	515 Mb	36,377	PacBio RS II, Hi-C	Chromosome	Recurrent blooming, flower scent, and flower color	2018	Nature Genetics
87	<i>Rosa chinensis</i>	512 Mb	39,669	Illumina HiSeq 2500, PacBio RS-II	Chromosome	Rickle density, flower petals	2018	Nature Plants
88	<i>Rosa multiflora</i>	740 Mb	67,380	Illumina HiSeq 2000, MiSeq	Draft	Flower color, flower scent, floral development	2017	DNA Research
89	<i>Rosa roxburghii</i>	409.36 Mb	22,721	Illumina HiSeq 2500	Draft	Ascorbate metabolism	2016	PLOS ONE
90	<i>Rosa rugosa</i>	382.6 Mb	39,704	PacBio HiFi, Hi-C	Chromosome	<i>Rosa rugosa</i> genome study: adaptation, floral development, stress response.	2021	Horticulture Research
91	<i>Salvia splendens</i>	808 Mb	54,008	PacBio RS II	Chromosome	Flower color, bioactive secondary metabolites	2018	GigaScience
92	<i>Sedum album</i>	302 Mb	44,487	PacBio RS II	Draft	Crassulacean acid metabolism	2019	PLOS Genetics
93	<i>Sequoia sempervirens</i>	26.45 Gb	118,906	Illumina HiSeq 4000, Oxford Nanopore Technologies	Not specified	Climate adaptation genes discovery, hexaploid genome origin investigation, repetitive content characterization, species-specific gene expansions for stress responses, comparison with other conifers, autopolyploidy hypothesis support for hexaploidy.	2022	G3-Genes Genomes Genetics
94	<i>Syringa oblata</i>	1.12 Gb	35,313	-	Chromosome	Chromosome formation in Oleaceae, evolutionary history of lilacs, synteny analysis, duplication events, aromatic scent formation, phylogenetic relationship with <i>Osmanthus fragrans</i> and <i>Olea europaea</i> , biogeographic reconstruction, gene introgression, species diversity in <i>Syringa</i> .	2022	Plant Journal
95	<i>Tagetes erecta</i>	707.21 Mb	35,834	Illumina, PacBio, Hi-C	Chromosome	Genetic mechanism of lutein in marigold, chromosome-scale genome assembly, phylogenetic relationship with Asteraceae species, whole-genome duplication events, candidate genes in lutein biosynthesis, genomic resource for Asteraceae evolution and marigold breeding.	2023	Horticultural Plant Journal
96	<i>Tanacetum cinerariifolium</i>	7.08 Gb	60,080	HiSeq X, HiSeq 4000	Draft	Pyrethrin	2019	Scientific Reports
97	<i>Tarenaya hassleriana</i>	290 Mb	28,917	Illumina HiSeq 2000	Chromosome	Floral developmental, self-incompatibility	2013	The Plant Cell
98	<i>Taxus wallichiana</i>	10.9 Gb	44,008	Illumina HiSeq 2500, Nanopore, Hi-C	Chromosome	Origin and evolution of paclitaxel biosynthetic pathway, gene family evolution, tandem duplication, taxadiene synthase, P450s, transferases, neofunctionalization, chemodiversity of taxoids, medicinal value, gymnosperm genome analysis.	2021	Molecular Plant
99	<i>Thalia dealbata</i>	255.05 Mb	24,780	Pacific Biosciences, Hi-C	T2T (gaps=4)	Wetland plant adaptation, emergent wetland plant genome assembly, phylogenetic analysis, gene family expansion and contraction, genomic resource for comparative genomics of Zingiberales and flowering plants.	2023	Frontiers in Plant Science

100	<i>Trifolium pratense</i>	309 Mb	40,868	Illumina HiSeq 2000	Draft	Forage nutrition traits	2015	Scientific Reports	
101	<i>Trifolium subterraneum</i>	471.8 Mb	42,706	Illumina HiSeq 2000	Draft	Evolutionary divergence	2016	Scientific Reports	
102	<i>Zantedeschia elliottiana</i>	1,154 Mb	36,165	PacBio (120.70×)	Chromosome	(Total gap size (bp)= 6,700)	Understanding genome size differences within the Araceae family, advancing genomic research on colored calla lily	2023	Scientific Data
103	<i>Zoysia japonica</i>	334.38 Mb	59,271	Illumina HiSeq 2000, MiSeq	Draft	Comparative genome	2016	DNA Research	
104	<i>Zoysia matrella</i>	563.44 Mb	95,079	Illumina HiSeq 2000, MiSeq	Draft	Comparative genome	2016	DNA Research	
105	<i>Zoysia pacifica</i>	397.01 Mb	65,252	Illumina HiSeq 2000, MiSeq	Draft	Comparative genome	2016	DNA Research	
Polyploid species									
106	<i>Acorus calamus</i>	700.94 Mb	24,322	PacBio Sequel	Chromosome	Acorus gramineus and Ac. calamus genomes mapped to study monocot evolution, showing Ac. gramineus isn't Ac. calamus's ancestor and highlighting Ac. calamus's allotetraploid and asymmetric evolution.	2023	Nature Communications	
107	<i>Acorus gramineus</i>	391.63 Mb	25,090, 21,743	PacBio Sequel	Chromosome	Acorus gramineus and Ac. calamus genomes mapped to study monocot evolution, showing Ac. gramineus isn't Ac. calamus's ancestor and highlighting Ac. calamus's allotetraploid and asymmetric evolution.	2023	Nature Communications	
108	<i>Barringtonia asiatica</i>	0.79Gb	28 625	Illumina X-TEN platform, PacBio Sequel II, MGI-seq platform	Chromosome	Barringtonia genome analysis reveals allopolyploidy's evolutionary role; Allo5D tool for subgenome insights. Highlights speciation, coastal adaptation, and glucosinolate pathway expansion.	2023	Plant Biotechnology Journal	
109	<i>Barringtonia racemosa</i>	1.26Gb	58 875	Illumina X-TEN platform, PacBio Sequel II, MGI-seq platform	Chromosome	Barringtonia genome analysis reveals allopolyploidy's evolutionary role; Allo4D tool for subgenome insights. Highlights speciation, coastal adaptation, and glucosinolate pathway expansion.	2023	Plant Biotechnology Journal	
110	<i>Chrysanthemum morifolium</i>	-	138,749	Illumina, PacBio	Chromosome	Reveal the origin and evolution of cultivated chrysanthemum, gene identification for key ornamental traits, flower colour breeding history	2023	Nature Communications	
111	<i>Dendrocalamus brandisii</i>	2,756 Mb	-	Long-read HiFi sequencing, Oxford Nanopore Technologies	Chromosomal	D. brandisii genome mapping reveals structure and function, with transcriptome and metabolome analysis linking shoot quality to specific compounds, aiding in food/wood optimization and genetic research.	2023	Journal of Integrative Plant Biology	
112	<i>Eustoma grandiflorum</i>	1.71 Gb	54305	PacBio HiFi, Hi-C	Chromosome	Studying polyploidy and ornamental traits	2022	Plant Biotechnology Journal	
113	<i>Jerusalem Artichoke (Helianthus tuberosus)</i>	21 Gb	388,053	Illumina NovaSeq 6000 platform, PacBio Sequel II platform	Chromosome	Jerusalem artichoke genome assembly: 21 Gb, hexaploid, indicating hybrid origin and chromosome rearrangements with sunflower. Identified genes in inulin metabolism for diverse applications.	2023	Plant Communications	
114	<i>Lantana camara</i>	2.95 Gb	83775	PacBio HiFi, Hi-C, Illumina NovaSeq	Chromosome	Ornamental breeding, invasive species management	2024	Research Article	
115	<i>Nepenthes gracilis</i>	746.7 Mb	34,010	Oxford Nanopore Technology (ONT), Illumina	Chromosome	Nepenthes gracilis genome: decaploid, subgenome dominance, sex-linked flower development genes. Highlights carnivory gene origins, evolutionary innovation via gene diversification.	2023	Nature Plants	
116	<i>Papaver spp.</i>	-	-	Not stated	Chromosome	Study the early evolutionary history of eudicots, evolution of morphinan biosynthesis, propose an alternative model for the evolution and the genomic diversity of Papaver species	2021	Nature Communications	
117	<i>Rosa hybrida</i>	2,698 Mb	2,023	PacBio HiFi, Illumina, Hi-C	Chromosome	Insights into the origin and domestication of modern rose, rose improvement	2023	bioRxiv	