

Supplementary Table S1. Summary of published genome assemblies in *Populus*

Species	Assembly / Resource description	Publication year	Assembly level	Sequencing technology	Genome size (Mb)	N50 (<contig / scaffold>)	Reference
<i>Populus trichocarpa</i>	Nisqually-1 draft genome	2006	Chromosome-anchored	Sanger shotgun	485	-	Tuskan et al. 2006 Science ^[1]
<i>Populus euphratica</i>	Desert poplar draft genome	2013	Scaffold-level	Illumina	496.5	contig 40.4 kb scaffold 482 kb	Ma et al. 2013 Nature Communications ^[2]
<i>Populus tremula</i> × <i>Populus alba</i> clone	INRA 717-1B4 draft genome(highly heterozygous)	2017	Scaffold-level	Illumina	900	contig 3.85 kb	Mader et al. 2016 Silvae Genetica ^[3]
<i>Populus pruinosa</i>	Desert tree draft genome	2017	Scaffold-level	Illumina	479.3	contig 14.0 kb scaffold 698.5 kb	Yang et al. 2017 GigaScience ^[4]
<i>Populus tremula</i>	European aspen genome(map-anchored)	2018	Scaffold-level	Illumina	390.1	scaffold 42.8 kb	Lin et al. 2018 PNAS ^[5]
<i>Populus tremuloides</i>	American aspen genome(map-anchored)	2018	Scaffold-level	Illumina	377.4	scaffold 15.2 kb	Lin et al. 2018 PNAS ^[5]
<i>Populus ilicifolia</i>	Southernmost poplar genome	2020	Scaffold-level	Illumina	402	contig 57.7 kb scaffold 20.73 Mb	Chen et al. 2020 The Plant Journal ^[6]
<i>Populus alba</i> var. <i>pyramidalis</i>	Poplar draft genome (widely distributed cultivar)	2019	Scaffold-level	PacBio, Illumina	406.8	contig 9.8 kb scaffold 348.9 kb	Ma et al. 2019 Plant Biotechnology Journal ^[7]
<i>Populus alba</i> × <i>Populus tremula</i> var. <i>glandulosa</i>	De novo reference genome	2019	Chromosome-level	PacBio, Illumina, Hi-C	747.5	contig 1.99 Mb scaffold 19.6 Mb	Qiu et al. 2019 DNA Research ^[8]
<i>Populus alba</i>	White poplar genome	2019	Contig-level	PacBio, Illumina	415.99	contig 1.18 Mb	Liu et al. 2019 Science China Life Sciences ^[9]
<i>Populus euphratica</i>	Improved desert poplar genome	2020	Chromosome-level	PacBio, Hi-C	574.34	contig 900.00 kb scaffold 28.59 Mb	Zhang et al. 2020 Molecular Ecology Resources ^[10]
<i>Populus tomentosa</i>	High-quality reference genome assembly	2024	Chromosome-level Haplotype-resolved	ONT, Hi-C	714.9	contig 1.0 Mb scaffold 17.0 Mb	Li J et al.2024 Molecular Ecology Resources ^[11]
<i>Populus simonii</i>	De novo genome assembly	2020	Chromosome-level	PacBio, Illumina	441.38	contig 1.94 Mb	Wu et al. 2020 G3 ^[12]

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<i>Populus sibirica</i>	Male and female genomes	2021	Chromosome-level	ONT, Illumina	female 816 male 818	female 0.5 Mb male 1.5 Mb	Melnikova et al. 2021 <i>Frontiers in Plant Science</i> ^[13]
<i>Populus deltoides</i>	Eastern cottonwood I-69 genome	2021	Chromosome-level	ONT, Hi-C	429.3	contig 2.62 Mb	Bai et al. 2021 <i>Journal of Heredity</i> ^[14]
<i>Populus alba</i> × <i>Populus tremula</i> var. <i>glandulosa</i>	Draft improved hybrid assembly	2021	Contig-level	PacBio, Illumina	781.36	contig 3.66 Mb	Huang et al. 2021 <i>Journal of Forestry Research</i> ^[15]
<i>Populus euphratica</i>	Sex-specific reference genomes (male and female)	2022	Chromosome-level	PacBio, Illumina, Hi-C	female 564.21 male 542.59	scaffold: female 23.89 Mb male 24.55 Mb	Zhang et al. 2022 <i>Communications Biology</i> ^[16]
<i>Populus koreana</i>	Keystone forest tree genome	2022	Chromosome-level	ONT, Illumina, Hi-C	401.4	contig 6.41 Mb	Sang et al. 2022 <i>Nature Communications</i> ^[17]
<i>Populus tomentosa</i>	Haplotype-resolved genomes	2022	Chromosome-level Haplotype-resolved	PacBio, Hi-C	740.2(2n)	contig 5.47 Mb scaffold 46.68 Mb	An et al. 2022 <i>Molecular Ecology Resources</i> ^[18]
<i>Populus wilsonii</i>	Chromosome-scale genome	2022	Chromosome-level	PacBio, Illumina, Hi-C	477.35	contig 16.3 Mb scaffold 22.2 Mb	Li, C. et al. 2022 <i>Communications Biology</i> ^[19]
<i>Populus tomentosa</i>	Heterozygous alleles genome	2023	Chromosome-level	PacBio, Hi-C	395.58	contig 1.30 Mb scaffold 19.10 Mb	Li et al. 2023 <i>Plant Biotechnology Journal</i> ^[20]
<i>Populus alba</i> 'Berolinensis'	Triploid genome	2023	Chromosome-level	PacBio, Hi-C	1560(~3n)	scaffold 1.63 Mb	Chen et al. 2023 <i>Molecular Ecology Resources</i> ^[21]
<i>Populus davidiana</i>	Asian aspen genome	2023	Chromosome-level	PacBio, Illumina, Hi-C	408.1	scaffold 20.3 Mb	Bae EK et al. 2023 <i>Scientific Data</i> ^[22]
<i>Populus adenopoda</i>	Chromosomal-level genome	2023	Chromosome-level	PacBio, Illumina, Hi-C	383	contig 8.3 Mb	Liu et al. 2023 <i>bioRxiv preprint</i> ^[23]
<i>Populus qionghaoensis</i>	Tropical adaptation genome	2023	Chromosome-level	ONT, Illumina, Hi-C	391.2	contig 1.61 Mb scaffold 20.69 Mb	Li et al. 2023 <i>Molecular Ecology</i> ^[24]
<i>Populus tremula</i> × <i>Populus alba</i>	Telomere-to-telomere phased assemblies (hap1/hap2)	2023	Chromosome-level Haplotype-resolved T2T	PacBio, Hi-C	hap1:394.3 hap2:402.6	contig: hap1:12.8 Mb hap2:18.4 Mb scaffold: hap1:21.6 Mb hap2:22.2 Mb	Zhou et al. 2023 <i>The Plant Journal</i> ^[25]

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<i>Populus cathayana</i>	Genome and population resequencing	2024	Chromosome-level	PacBio, Illumina, Hi-C	406.55	scaffold 20.86 Mb	Xiang et al. 2024 Horticulture Research ^[26]
<i>Populus lasiocarpa</i>	Chromosome-level reference genome integrated with population genomics and climate-adaptation analyses	2023	Chromosome-level	ONT, Illumina, Hi-C	419.54	contig 9.19 Mb	Long et al. 2025 Molecular Biology and Evolution ^[27]
<i>Populus alba</i> × <i>Populus tremula</i> var. <i>glandulosa</i>	Phased T2T long-read assembly	2024	Chromosome-level Haplotype-resolved T2T	PacBio, ONT, Illumina, Hi-C	816.95 (combined haplotypes)	contig 22.4 Mb	Shi et al. 2024 Plant Physiology ^[28]
<i>Populus ussuriensis</i>	Doubled haploid T2T genome	2024	Chromosome-level near-T2T	PacBio, Hi-C	412.13	contig 19.50 Mb	Liu et al. 2024 Forestry Research ^[29]
<i>Populus deltoids</i> × <i>Populus euramericana</i>	NL895 haplotype-resolved genome	2024	Chromosome-level Haplotype-resolved	PacBio, Hi-C	412.6 (monoploid)	contig 14.8 Mb	Luo et al. 2024 Forestry Research ^[30]
<i>Populus tremula</i>	Updated reference genome assembly	2024	Chromosome-level	PacBio, Illumina	408.8	contig 16.9 MB	Robinson et al. 2024 Physiologia Plantarum ^[31]
<i>Populus nigra</i> subsp. <i>betulifolia</i> L.	Chromosome-scale genome	2024	Chromosome-level	PacBio, Illumina, Hi-C	413.2	contig 3.5Mb scaffold 22.5 Mb	Christenhusz M J M et al. 2024 Wellcome Open Research ^[32]
<i>Populus pruinosa</i>	v2.0 chromosome-scale genome assembly + population genomics	2024	Chromosome-level	PacBio, Illumina, Hi-C	521.09	contig 21.06 Mb	Sun et al. 2024 Horticulture Research ^[33]
<i>Populus alba</i> 'Villafranca'	Villafranca genome	2025	Chromosome-level	PacBio	498.95	contig 18.18 Mb	Sarfraz I et al. 2025 bioRxiv preprint ^[34]
<i>Populus alba</i> var. <i>pyramidalis</i>	Near-complete genome	2025	Chromosome-level Near-complete	PacBio	423.05	scaffold 22.3 Mb	Wang et al. 2025 Genome Biology ^[35]
<i>Populus euphratica</i>	Near-complete genome	2025	Chromosome-level Near-complete	PacBio	528.42	scaffold 31.9 Mb	Wang et al. 2025 Genome Biology ^[35]
<i>Populus lasiocarpa</i>	Haplotype-resolved T2T genome	2025	Chromosome-level Haplotype-resolved T2T	PacBio, Hi-C	hap1:455.72 hap2:466.29	scaffold: hap1:23.23 Mb hap2:24.46 Mb	Shen et al. 2025 The Plant Journal ^[36]

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<i>Populus deltoides</i>	Gap-free <i>P. deltoides</i> reference genome for karyotype evolution	2025	Chromosome-level T2T	PacBio, Hi-C	395.9	contig 22.73 Mb	Bi et al. 2025 BMC Biology ^[37]
<i>Populus deltoides</i>	<i>P. deltoides</i> ‘Danhong’ core parent genome + genomic selection resource	2025	Chromosome-level T2T	PacBio, Hi-C	419.4	scaffold 22 Mb	Zhou et al. 2025 Horticulture Research ^[38]
<i>Populus trichocarpa</i>	Haplotype-resolved genome	2025	Chromosome-level Haplotype-resolved near-T2T	PacBio, Hi-C	hap1:391.76 Mb hap2:397.43 Mb	scaffold: hap1: 21.8 Mb hap2: 20.9 Mb	Gao et al. 2025 Horticulture Research ^[39]
<i>Populus</i> × <i>euramericana</i> cv. ‘74/76’	Haplotype-resolved genome	2025	Chromosome-level Haplotype-resolved	PacBio, Hi-C	hap1:428.50 Mb hap2:414.20 Mb	hap1:21.30 Mb hap2:21.26 Mb	Zhang et al. 2025 Scientific Data ^[40]
<i>Populus nigra</i> ‘NL-1976’	Near telomere-to-telomere phased assemblies (hap1/hap2)	2025	Chromosome-level Haplotype-resolved near-T2T	PacBio, ONT, Hi-C	hap1:385.18 Mb hap2:390.48 Mb	contig: hap1: 22.31 Mb hap2: 22.05 Mb	Liu et al. 2026 Scientific Data ^[41]
<i>Populus</i> × <i>euramericana</i> ‘Bofeng 3’	Reference genome assembly	2025	Chromosome-level	PacBio, Illumina, Hi-C	445.53	contig 21.72 Mb	Zhong et al. 2025 Int. J. Mol. Sci ^[42]
<i>Populus</i> spp.	Genus-level pangenome	2019	Pangenome	Illumina	-	-	Zhang et al. 2019 Communications Biology ^[43]
<i>Populus</i> spp.	Super-pangenome	2024	Super-pangenome	PacBio, Illumina	-	-	Shi et al. 2024 Molecular Plant ^[44]
<i>Populus</i> spp.	3D-genome and multi-omics resource for 11 <i>Populus</i> species	2026	3D-genome	Hi-C	-	-	Shi et al. 2026 Nature Ecology & Evolution ^[45]

References

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