

Supplementary Information

Table S1. Summary of raw reads generated for *Salix herbacea*.

Sample	before filtering			after filtering			duplication rate %	Q30 bases %	read coverage on haplotype 1
	Number of reads (x10 ⁶)	Data size (Gb)	Average length (bp)	Number of reads (x10 ⁶)	Data size (Gb)	Average length (bp)			
HiFi	NA	NA	NA	1.46	21.89	14944	NA	NA	67
HiC	308.69	46.3	150	306.76	45.82	149	6.33	96.53	140
Transcriptome	207.48	31.1	150	201.05	28.76	142	NA	NA	88
Female pool	294.42	44.46	151	292.36	43.61	149	1.68	93.05	133
Male pool	237.62	35.88	151	234.56	34.99	149	1.62	92.66	107
ind.f05	294.42	44.46	151	292.36	43.61	149	1.68	92.39	133
ind.f16	90.9	13.73	151	89.43	13.3	149	1.4	92.41	41
ind.f40	80.58	12.17	151	79.51	11.82	149	1.47	92.91	36
ind.f06	97.93	14.79	151	96.73	14.41	148	21.69	93.32	44
ind.f08	152.26	22.99	151	150.58	22.47	149	24.48	93.64	69
ind.f09	120.39	18.18	151	119.09	17.75	149	21.31	92.78	54
ind.f11	116.79	17.63	151	115.45	17.17	148	23.76	93.22	52
ind.f22	114.89	17.35	151	113.29	16.91	149	21.25	93.08	52
ind.f32	104.41	15.77	151	103.16	15.36	148	21.78	93.24	47
ind.f36	98.71	14.91	151	97.43	14.58	149	20.86	93.15	44
ind.m05	147.93	22.34	151	146.6	21.9	149	1.42	92.81	67
ind.m16	85.3	12.88	151	84.47	12.6	149	1.4	92.94	38
ind.m40	89.21	13.47	151	88.13	13.2	149	1.49	92.82	40
ind.m06	105.75	15.97	151	104.44	15.63	149	22.13	93.38	48
ind.m08	93.08	14.06	151	92.02	13.8	149	22.36	93.47	42
ind.m09	108.66	16.41	151	107.25	16.04	149	20.62	92.25	49
ind.m11	107.73	16.27	151	106.24	15.86	149	20.92	92.76	48
ind.m22	104.6	15.8	151	103.39	15.45	149	19	92.92	47
ind.m32	95.5	14.42	151	94.49	14.14	149	21.5	93.41	43
ind.m36	100.55	15.18	151	99.17	14.82	149	18.95	93.26	45

Table S2. BUSCOs results for the genome assembly of dwarf willow *Salix herbacea* based on the eudicots_odb10 database.

	Haplotype 1		Haplotype 2	
	No.	Prop.	No.	Prop.
Complete BUSCOS	2267	97.5 %	2285	98.3 %
Complete and single-copy BUSCOS	1944	83.6 %	1965	84.5 %
Complete and duplicated BUSCOS	323	13.9 %	320	13.8 %
Fragmented BUSCOS	7	0.3 %	7	0.3 %
Missing BUSCOS	52	2.2 %	34	1.4 %
Total BUSCO searched	2326		2326	

Table S3. Repeat annotation in the *Salix herbacea* genome assembly.

	Haplotype 1	Haplotype 2
Retroelements	20.88 %	20.85 %
SINEs	1.00 %	0.97 %
LINEs	0.70 %	0.73 %
LTR elements	19.18 %	19.15 %
DNA transposons	3.84 %	3.60 %
Unclassified	16.31 %	16.42 %
Small RNA	2.68 %	3.18 %
Total bases masked	49.01 %	49.33 %

Table S4. Published genomic data used.

Species	Data type	Version /Accession	Download from	Reference
<i>A. thaliana</i>	Annotation	Araport11	TAIR	Cheng, C. <i>et al.</i> Araport11: a complete reannotation of the <i>Arabidopsis thaliana</i> reference genome. <i>The Plant Journal</i> 89 , 789–804 (2017).
<i>P. deltoides</i>	Assembly and annotation	JGI WV94 v2.1	Phytozome	Xue, L. <i>et al.</i> Evidences for a role of two Y-specific genes in sex determination in <i>Populus deltoides</i> . <i>Nat. Commun.</i> 11 , 5893 (2020).
<i>P. trichocarpa</i>	Assembly and annotation	JGI v4.1, AARH04000000	Phytozome	Tuskan, G. A. <i>et al.</i> The genome of black cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> 313 , 1596–1604 (2006).
<i>P. qiongdaoensis</i>	Assembly and annotation	PRJCA007862	BIG Data Center	Li, Y. <i>et al.</i> A chromosome-level <i>Populus qiongdaoensis</i> genome assembly provides insights into tropical adaptation and a cryptic turnover of sex determination. <i>Molecular Ecology</i> 32 , 1366–1380 (2023).
<i>P. alba</i>	Assembly and annotation	PRJCA002485	BIG Data Center	Yang, W. <i>et al.</i> A general model to explain repeated turnovers of sex determination in the Salicaceae. <i>Mol. Biol. Evol.</i> 38 , 968–980 (2021).
<i>S. arbutifolia</i>	Assembly and annotation	PRJCA016000	NCBI	Wang, Y. <i>et al.</i> Gap-free X and Y chromosome assemblies of <i>Salix arbutifolia</i> reveal an evolutionary change from male to female heterogamety in willows, without a change in the position of the sex-determining locus. <i>New Phytol.</i> (2024).
<i>S. brachista</i>	Assembly and annotation	PRJNA472210	NCBI	Chen, J.-H. <i>et al.</i> Genome-wide analysis of Cushion willow provides insights into alpine plant divergence in a biodiversity hotspot. <i>Nat. Commun.</i> 10 , 5230 (2019).
<i>S. dunnii</i>	Assembly and annotation	PRJNA1136512	NCBI	He, L. <i>et al.</i> Chromosome-scale assembly of the genome of <i>Salix dunnii</i> reveals a male-heterogametic sex determination system on chromosome 7. <i>Molecular Ecology Resources</i> 21 , 1966–1982 (2021).
<i>S. exigua</i>	Assembly	SE967M, PRJNA1009227	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (<i>Salix</i>) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. koriyanagi</i>	Assembly and annotation	SH3, PRJNA892598	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (<i>Salix</i>) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. purpurea</i>	Assembly and annotation	JGI v5.1	Phytozome	Zhou, R. <i>et al.</i> A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biol.</i> 21 , 38 (2020).

<i>S.suchowensis</i>	Assembly and annotation	XY12, PRJNA668632	NCBI	Wei, S., Yang, Y. & Yin, T. The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Hortic. Res.</i> 7 , 45 (2020).
<i>S.suchowensis</i>	Assembly and annotation	P295, PRJNA892596	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S.suchowensis</i>	Assembly and annotation	P63, PRJNA892593	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. udensis</i>	Assembly	04-BN-051, PRJNA892602	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. viminalis</i>	Assembly and annotation	JORR, PRJNA892601	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. viminalis</i>	Assembly and annotation	PRJEB15049	ENA	Pucholt, P., Wright, A. E., Conze, L. L., Mank, J. E. & Berlin, S. Recent sex chromosome divergence despite ancient dioecy in the willow <i>Salix viminalis</i> . <i>Mol. Biol. Evol.</i> 34 , 1991–2001 (2017).
<i>S.suchowensis</i>	Illumina sequencing	P63, SRX14893761	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S.suchowensis</i>	Illumina sequencing	P295, SRX14893739	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S.suchowensis</i>	Illumina sequencing	P294, SRX14893691	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. purpurea</i>	Illumina sequencing	94006, SRX14893669	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. purpurea</i>	Illumina sequencing	94001, SRX14893727	NCBI	Hyden, B. <i>et al.</i> De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. <i>Int. J. Mol. Sci.</i> 24 , (2023).
<i>S. purpurea</i>	Illumina sequencing	FishCreek, SRX2139496	NCBI	Zhou, R. <i>et al.</i> A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biol.</i> 21 , 38 (2020).
<i>S. viminalis</i>	Illumina sequencing	PRJNA1199981	NCBI	

Table S5. Gene numbers and proportions of annotated sequences of the dwarf willow *Salix herbacea*, both for the entire chromosome (h1_chr15, h2_chr15), for the sex-linked region (W-SLR, Z-SLR) and for the five regions of the W-chromosome including two pseudoautosomal regions (PAR1, PAR2, two-female specific regions (FS1, FS2), and the inversion region (INV). Regions on the W-chromosome are ordered according to their position.

Chr./Regions	Length (Mb)	No. gene	Prop. gene	Prop. LTR	Prop. Pseudogene	No. Z-W homologs	No. Z/W Specific genes	Ancestral gene loss
h1_chr15	15.8	1288	0.235	0.361	0.00468	1075	192	0.16
h2_chr15	16.6	1488	0.235	0.342	0.00469	1115	263	0.08
W-SLR	8.4	426	0.146	0.516	0.00589	300	109	0.23
Z-SLR	8	477	0.153	0.487	0.00626	336	120	0.15
PAR1	3.1	319	0.292	0.218	0.00387			
FS1	2.8	171	0.188	0.419	0.0111			
INV	5	228	0.121	0.569	0.00268			
FS2	0.6	27	0.149	0.547	0.00727			
PAR2	4.3	543	0.367	0.161	0.00293			

Table S6. Summary of sex-linked genes on the W haplotype of *Salix herbacea*. Gene ID, location on the female-specific regions (FS1, FS2), sex-specific pattern of variation (hemi: W-hemizygous sites; poly: W-specific polymorphisms; disruptive mutations are indicated with an asterisk), information on homologs on chromosome 15 in other *Salix* species (ancestral: shared with other species with different sex determination systems, specific: *S. herbacea* specific, none: none of these two groups) and information on whether the sex-specific pattern are shared by other three *Salix* species (svim: only shared with *S. viminalis*, all: shared with *S. viminalis*, *S. purpurea* and *S. suchowensis*, none: not shared) are given together with gene name and description, gene model, putative function according to the TAIR gene model and a function category (female function, male function, or general flowering formation function (flower)). Further sex-linked genes and references are listed in Supplementary table S6.

Gene ID	Region	Sex-specific pattern	Homologs	Common alleles	Gene Name	Gene description	Gene model	Putative function	Category	Reference
h1_chr15-_g23451	FS1	poly	ancestral	none	VQ20	VQ motif-containing protein	AT3G18360.1	stress responses and reproductive development	stress	1
h1_chr15+_g23452	FS1	poly	ancestral	none	ATSYTF	C2 domain-containing protein	AT3G18370.1	abiotic stress response	stress	2
h1_chr15-_g23453	FS1	hemi	specific	none	NAC058	NAC domain containing protein 58	AT3G18400.1	control of flowering time and cold response	flower	3
h1_chr15-_g23454	FS1	poly	ancestral	svim	NAC058	NAC domain containing protein 58	AT3G18400.1	control of flowering time and cold response	flower	3
h1_chr15+_g23455	FS1	hemi	none	svim	SecA	translocase subunit seca	AT1G68490.1	photosynthetic development	growth	4
h1_chr15+_g23477	FS1	hemi	specific	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15-_g23478	FS1	hemi	specific	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15+_g23479	FS1	hemi	none	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15-_g23484	FS1	hemi	specific	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15-_g23515	FS1	hemi	specific	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15+_g23516	FS1	hemi	specific	none	SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	AT1G49040.1	seedling growth, root elongation and flower morphogenesis	flower	5
h1_chr15+_g23571	FS1	poly	ancestral	svim	HIK	ARABIDOPSIS NPK1-ACTIVATING KINESIN 1	AT1G18370.1	required for cytokinesis in pollen	male	6
h1_chr15-_g23580	FS1	poly	ancestral	none	GGR	geranylgeranyl reductase	AT4G38460.1	reproduction and stress response	stress	7
h1_chr15-_g23583	FS1	poly	ancestral	none	PAPS1	poly(A) polymerase 1	AT1G17980.1	mediate pollen maturation by regulating sperm cell differentiation	male	8
h1_chr15-_g23584	FS1	poly	ancestral	none	CP2	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	AT3G18210.1	epigenetic repression of flowering genes	flower	9
h1_chr15+_g23587	FS1	hemi	specific	none	ADT2	arogenate dehydratase 2	AT3G07630.1	seed development	growth	10

h1_chr15+_g23588	FS1	poly	ancestral	none	GRDP	Glycine-rich domain-containing protein-like	AT2G22660.2 stress responses	stress	11
h1_chr15-_g23589	FS1	poly	ancestral	none	CCT4	TCP-1/cpn60 chaperonin family protein	AT3G18190.1 tubulin folding, essential for growth	growth	12.
h1_chr15-_g23599	FS1	poly	none	none	FATB	fatty acyl-ACP thioesterases B	AT1G08510.1 a major determinant of saturated fatty acid synthesis	growth	13
h1_chr15-_g23600	FS1	hemi, poly	specific	none	GT61	Glycosyltransferase family 61 protein	AT3G18170.2 arabinoxylan biosynthesis	growth	14
h1_chr15-_g23601	FS1	hemi, poly	none	none	TPR	Tetratricopeptide repeat (TPR)-like superfamily protein	AT5G62370.1 hormone responses and regulation of flowering	flower	15
h1_chr15+_g23602	FS1	hemi, poly	none	none	DEAD/H	DEA(D/H)-box RNA helicase family protein	AT1G48650.2 stress responses and regulate flowering time	stress	16
h1_chr15+_g23604	FS1	hemi, poly	none	svim	Q1PEN6	Gag-Pol-related retrotransposon family protein	AT3G21000.1 LTR retrotransposition	growth	17
h1_chr15+_g23605	FS1	hemi	none	svim	CRK8	cysteine-rich RLK (RECEPTOR-like protein kinase) 8	AT4G23160.2 stress responses	stress	18
h1_chr15-_g23606	FS1	hemi, poly	none	none	GT61	Glycosyltransferase family 61 protein	AT3G18170.2 arabinoxylan biosynthesis	growth	14
h1_chr15-_g23607	FS1	poly	none	none	GT61	Glycosyltransferase family 61 protein	AT3G18180.1 arabinoxylan biosynthesis	growth	14
h1_chr15+_g23836	FS2	poly	ancestral	none	ENODL6	Early nodulin-like protein 6	AT1G48940.1 seedling growth, pollen tube elongation, embryogenesis and cell proliferation	male	19
h1_chr15+_g23838	FS2	poly	ancestral	none	ARID	AT-rich interactive domain protein	AT1G73885.1 pollen tube growth	male	20
h1_chr15-_g23839	FS2	poly	ancestral	none	LPTG10	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	AT1G73890.1 resistance against abiotic stress	stress	21
h1_chr15+_g23840	FS2	poly	ancestral	none	ALMT9	aluminum-activated malate transporter 9	AT3G18440.1 a dicarboxylic acid transporter mediate malate transportation	growth	22
h1_chr15-_g23841	FS2	poly	ancestral	none	APCB1	Eukaryotic aspartyl protease family protein	AT1G49050.1 stress responses and reproductive development	stress	23
h1_chr15-_g23842	FS2	poly	ancestral	svim	ARP4	actin-related protein 4	AT1G18450.1 male sterility due to defects in pollen and anther	male	24
h1_chr15-_g23843	FS2	poly*	specific	none	MEE29	maternal effect embryo arrest 29, DEAH RNA helicase homolog PRP2	AT2G35340.1 female gametophyte development and function	female	25.
h1_chr15-_g23844	FS2	poly*	specific	none	GSTT3	glutathione S-transferase THETA 3, No apical meristem-associated C-terminal domain	AT5G41220.1 control of flowering time and cold response	flower	3
h1_chr15-_g23846	FS2	poly	ancestral	none	-	-			
h1_chr15-_g23847	FS2	poly	none	none	CRF9	cytokinin response factor 9	AT1G49120.1 a repressor of cytokinin ARR6 during reproductive development	growth	26
h1_chr15-_g23848	FS2	poly*	ancestral	svim	CRF9	cytokinin response factor 9	AT1G49120.1 a repressor of cytokinin ARR6 during reproductive development	growth	26
h1_chr15+_g23849	FS2	hemi	specific	none	NOF1	U3 small nucleolar RNA-associated protein, DEAD-box RNA helicase-like	AT1G17690.1 female gametogenesis and embryo development	female	27

h1_chr15-_g23850	FS2	hemi	specific	none	SWEETIE HEAT repeat-containing protein		AT1G67140.2	growth and development phenotypes, such as dwarfism, lanceolate-shaped leaves, early senescence and flower sterility.	growth	28
h1_chr15-_g23851	FS2	hemi	specific	none	SWEETIE HEAT repeat-containing protein		AT1G67140.2	growth and development phenotypes, such as dwarfism, lanceolate-shaped leaves, early senescence and flower sterility.	growth	28
h1_chr15-_g23852	FS2	hemi, poly	none	svim	MiP1	Leucine-zipper of ternary complex factor MIP1	PF14389	regulate flowering time, interacting with B-box zinc finger protein	flower	29
h1_chr15-_g23853	FS2	poly	common	none	BBX15	B-box type zinc finger protein with CCT domain	AT1G25440.1	regulate flowering time and abiotic stress	flower	30
h1_chr15-_g23854	FS2	hemi, poly	none	all	ARP4	actin-related protein 4	AT1G18450.1	male sterility due to defects in pollen and anther	male	24
h1_chr15+_g23855	FS2	poly	none	none	RR5	response regulator 5	AT3G48100.1	response to cytokinin	growth	31

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Table S7. Summary of sex-linked genes on the Z haplotype of *Salix herbacea*. Gene ID) are given together with gene name and description, gene model according to the TAIR gene model.

Gene model	Description	Tair 11
ASPG1	Eukaryotic aspartyl protease family protein	AT3G18490.1
CDPK2	calcium-dependent protein kinase 2	AT1G35670.1
CYP77A5P	cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene	AT3G18270.1
CYP81D11	Cytochrome P450 superfamily protein	AT3G28740.1
ELO3	radical SAM domain-containing protein / GCN5-related N-acetyltransferase (GNAT) family protein	AT5G50320.1
ENO1	enolase 1	AT1G74030.1
LBD27	LOB domain-containing protein 27	AT3G47870.1
mTERF26	Mitochondrial transcription termination factor family protein	AT4G19650.2
MYB17	myb domain protein 17	AT3G61250.1
NEET	2 iron, 2 sulfur cluster binding protein2 iron, 2 sulfur cluster binding	AT5G51720.1
None	jagunal-like protein	AT5G51510.1
None	Pentatricopeptide repeat (PPR-like) superfamily protein	AT4G38010.1
None	Ribosomal protein L19 family protein	AT4G11630.1
None	F-box family protein	AT3G56470.1
None	alpha/beta-Hydrolases superfamily protein	AT3G49050.1
None	transferring glycosyl group transferase	AT3G23760.1
None	Glycosyltransferase family 61 protein	AT3G18180.1
None	Leucine-rich repeat (LRR) family protein	AT2G15042.1
None	zinc ion binding / nucleic acid binding protein	AT2G01050.1
None	DNase I-like superfamily protein	AT1G40390.1
None	thionin-like protein	AT1G25275.3

PCP2	hypothetical protein	AT1G18850.1
PI	a MADS domain transcription factor. Required for the specification of petal and stamen identities.	AT5G20240.1
RAE1	RNI-like superfamily protein	AT5G01720.1
SEC61	secE/sec61-gamma protein transport protein	AT5G50460.1
SMA1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	AT2G33730.1

Table S8. Copy number of intact and partial duplicates of *PI* and *ARR16/17* in 12 Salicaceae species with different sex determination systems (SD). W/Y chromosomes in female heterogamety (ZW) or male heterogamety (XY) samples are enclosed in brackets if the genome assembly is not haplotype-resolved. Assemblies without brackets indicate haplotype-resolved genomes or ZZ male samples.

Species	SD system	PI		ARR17		ARR16 complete
		complete	partial	complete	partial	
<i>S. herbacea</i>	15ZW	2 on chr02, 3 on h1chr05 and 1 on h2chr05, 1 on chr15Z	16 on chr15W	2 on chr19	no	1 on chr19, 2 on chr15W
<i>S. pupurea</i>	15ZW	1 on chr02, 1 on chr05	2 inverted on chr15W	2 on chr19, 4 on chr15W	9 on chr15Z	1 on chr19
<i>S. udensis</i> (ZZ)	15ZW	1 on chr02, 1 on chr05	not on Z	no	4 on chr15Z	1 on chr19
<i>S. suchowensis</i>	15ZW	1 on chr02, 1 on chr05	1 on chr15 (W)	1 on chr19	5 on chr15 (W)	1 on chr19
<i>S. koriyanagi</i>	15ZW	1 on chr02, 1 on chr05, 1 on chr17	1 on chr15 (W)	no	3 on chr15 (W)	1 on chr19
<i>S. brachista</i>	15ZW	2 on chr02, 1 on chr05	2 inverted on chr15 (W)	2 on chr19, 2 on chr15	4 on chr15 (W)	1 on chr19
<i>S. viminalis</i>	15ZW	1 on chr02, 1 on chr05	no	1 on chr19	1 on chr19, 3 on chr15Z	1 on chr19, 1 on chr15 (W)
<i>S. dunnii</i>	7XY	1 on chr02, 1 on chr05	no	2 on chr19	no	1 on chr19
<i>S. arbutifolia</i>	15XY	1 on chr02, 1 on chr05	no	2 on chr19	9 on chr15Y	1 on chr19
<i>S. exigua</i>	15XY	1 on chr02, 1 on chr05	no	3 on chr19	3 on chr15 (Y)	1 on chr19
<i>P. trichocarpa</i> ¹	19XY	1 on chr02, 1 on chr05	no	1 on chr19	2 on chr19 (Y)	1 on chr19
<i>P. qiongdaoensis</i> ¹	19ZW	3 on chr05	no	2 on chr19 (W)	2 on chr19	1 on chr19

¹ Li, Y. *et al.* A chromosome-level *Populus qiongdaoensis* genome assembly provides insights into tropical adaptation and a cryptic turnover of sex determination. *Molecular Ecology* **32**, 1366–1380 (2023).