

1 Phased genome sequence of an interspecific hybrid

2 flowering cherry, Somei-Yoshino (*Cerasus* × *yedoensis*)

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13 14 **Abstract**

15 We report the phased genome sequence of an interspecific hybrid, the flowering cherry
16 Somei-Yoshino (*Cerasus* × *yedoensis*). The sequence was determined by single-molecule
17 real-time sequencing technology and assembled using a trio-binning strategy in which allelic
18 variation was resolved to obtain phased sequences. The resultant assembly consisting of two
19 haplotype genomes spanned 690.1 Mb with 4,552 contigs and an N50 length of 1.0 Mb. We
20 predicted 95,076 high-confidence genes, including 94.9% of the core eukaryotic genes. Based
21 on a high-density genetic map, we established a pair of eight pseudomolecule sequences, with
22 highly conserved structures between two genome sequences with 2.4 million sequence
23 variants. A whole genome resequencing analysis of flowering cherry varieties suggested that
24 Somei-Yoshino is derived from a cross between *C. spachiana* and either *C. speciose* or its
25 derivative. Transcriptome data for flowering date revealed comprehensive changes in gene
26 expression in floral bud development toward flowering. These genome and transcriptome
27 data are expected to provide insights into the evolution and cultivation of flowering cherry
28 and the molecular mechanism underlying flowering.

29
30 **Keywords:** floral bud, flowering cherry; interspecific hybrid; phased genome sequence;
31 transcriptome

1

2 **Introduction**

3 Flowering cherry, called sakura, is Japan's unofficial national flower and is a popular
4 ornamental tree in Japan and elsewhere. Cherry blossoms are symbols of spring, when
5 blooming typically occurs. Accordingly, flowering cherries are important resources for the
6 tourism industry in the spring season in Japan. More than 200 varieties of flowering cherry
7 are grown (Kato et al. 2012). The nomenclature and, in particular, the genus name (*Prunus*
8 or *Cerasus*) has been under discussion. We use the genus name *Cerasus* in accordance with
9 recent molecular and population genetic analyses (Katsuki and Iketani 2016). Most varieties
10 belong to a species complex with ten basic diploid founders ($2n=16$), *C. apetala*, *C. incisa*, *C.*
11 *jamasakura*, *C. kumanoensis*, *C. leveilleana*, *C. maximowiczii*, *C. nipponica*, *C. sargentii*, *C.*
12 *spachiana*, and *C. speciosa*.

13 Somei-Yoshino (*C.* × *yedoensis*), also known as Yoshino cherry, is the most popular
14 variety of flowering cherry. Somei-Yoshino is believed to have been originally bred in a nursery
15 in the Somei area of Edo (the former name of Tokyo), followed by its spread throughout Japan.
16 Somei-Yoshino is probably derived from an interspecific hybrid between two diploids ($2n=16$)
17 (Oginuma and Tanaka 1976), *C. spachiana* and *C. speciosa* (Innan et al. 1995; Nakamura et
18 al. 2015a; Takenaka 1963). An alternative hypothesis is that Somei-Yoshino arose from a cross
19 between *C. spachiana* and a hybrid of *C. jamasakura* and *C. speciosa* (Kato et al. 2014). It is
20 self-incompatible, like other members of the Rosaceae family, and accordingly no seeds are
21 produced by self-pollination. Even if self-pollinated seeds are obtained, genotypes would be
22 segregated owing to the high heterozygosity. Therefore, Somei-Yoshino is clonally propagated
23 by grafting or cutting and distributed. The clonality is supported by DNA analyses (Iketani et
24 al. 2007; Innan et al. 1995). Thus, the taxonomic classification has been well investigated.
25 However, to the best of our knowledge, there are few studies of the molecular mechanism
26 underlying flowering in flowering cherry to date, despite extensive analyses of other members
27 of the family Rosaceae.

28 Some-Yoshino trees are used as standards for forecasting the flowering date of cherry
29 blossoms in the early spring every year. Bud breaking and flowering are important and
30 scientifically intriguing growth stages. In buds, the floral primordia are generally initiated in
31 the summer (late June to August), after which the primordia start to differentiate into floral

1 organs. After differentiation is completed, the buds enter a dormancy period during the winter.
2 Recent studies have evaluated the molecular mechanisms underlying dormancy release as well
3 as flowering in fruit tree species belonging to the family Rosaceae (Lloret et al. 2018; Yamane
4 2014). Phytohormones and transcriptional regulators involved in dormancy initiation and
5 release have been characterized, including gibberellic acids (GAs) and abscisic acid (ABA).
6 *DELLA* genes, containing a conserved DELLA motif involved in GA signaling, and
7 *CBF/DREB1* (C-repeat-binding factor/dehydration responsive element-binding factor 1)
8 genes involved in cold acclimation have been analyzed in apple (Wisniewski et al. 2015;
9 Yordanov et al. 2014) and Japanese apricot (Lv et al. 2018). The involvement of ethylene
10 signaling, perhaps via crosstalk with ABA, has also been discussed based on a study of *EARLY*
11 *BUD-BREAK 1 (EBB1)*, which encodes an AP2 type/ethylene-responsive transcription
12 factor (Yordanov et al. 2014). *DORMANCY-ASSOCIATED MADS-BOX (DAM)* genes in
13 the same family as *SHORT VEGETATIVE PHASE (SVP)* genes (Leida et al. 2010; Yamane
14 et al. 2011), *FLOWERING LOCUS T (FT)*, and *CENTRORADIALIS (CEN)/ TERMINAL*
15 *FLOWER 1 (TFL1)*, encoding PEBP-like proteins involved in floral initiation and meristem
16 development, are involved in dormancy (Kurokura et al. 2013). These previous studies
17 provide insight into the genetic basis of dormancy and flowering in fruit tree species belonging
18 to the family Rosaceae.

19 Genetic and genomic analyses are straightforward approaches to gain insights into the
20 flowering mechanism in cherry blossoms. Whole genome sequences of more than 100 plant
21 species have been published (Michael and VanBuren 2015). Usually, the targets are haploids
22 or inbred lines to simplify the genomic complexity. However, advanced long-read sequencing
23 technologies and bioinformatics methods have made it possible to determine the sequences
24 of complex genomes (Belser et al. 2018; Jiao and Schneeberger 2017; Kyriakidou et al. 2018).
25 For example, an assembly strategy for single-molecule real-time sequencing data has been
26 developed to generate phased sequences in heterozygous regions of F1 hybrids (Chin et al.
27 2016). Furthermore, chromosome-scale phased genome assemblies for F1 hybrids have been
28 obtained by linked read sequencing technology, providing long-range genome information
29 (Hulse-Kemp et al. 2018), or by single-molecule real-time sequencing combined with Hi-C
30 data (Dudchenko et al. 2017; Kronenberg et al. 2018). Haplotype-resolved sequences have
31 been obtained for F1 cattle by a trio-binning strategy in which genome sequences with allelic

1 variation are resolved before assembly (Koren et al. 2018).

2 In this study, to determine the molecular mechanisms underlying cherry blossom
3 flowering, we conducted genome and transcriptome analyses of the interspecific hybrid
4 Somei-Yoshino. The genome sequence of another interspecific hybrid flowering cherry, *C.* ×
5 *nudiflora*, formerly named *P. yedoensis* (Katsuki and Iketani 2016), has been published (Baek
6 et al. 2018). However, all genomic regions derived from the two different progenitor species
7 (*C. spachiana* and *C. jamasakura*) are totally collapsed. Therefore, we established the phased
8 genome sequence of *C.* × *yedoensis*, Somei-Yoshino, representing the two genomes of the
9 probable progenitors (*C. spachiana* and *C. speciosa*). Using the genome sequences as a
10 reference, a time-course transcriptome analysis of Somei-Yoshino floral buds and flowers,
11 with a special focus on dormancy and flowering-related genes, was also conducted to
12 characterize the physiological changes during flowering.

13

14 **Materials and methods**

15 *Plant materials*

16 A Somei-Yoshino tree grown in Ueno Park (Tokyo, Japan) was used for genome assembly.
17 This tree, i.e., #136, is presumed to be the original according to a polymorphism analysis of
18 three genes and its location (Nakamura et al. 2015a; Nakamura et al. 2015b). In addition, 139
19 varieties, including a Somei-Yoshino clone maintained at Shimane University (SU), Shimane,
20 Japan, were used for a genetic diversity analysis (Supplementary Table S1). An F1 mapping
21 population, YSF1, was produced by hand pollination between Yama-Zakura and another clone
22 of Somei-Yoshino as a female and male parent, respectively, both of which are planted at the
23 Kazusa DNA Research Institute (KDRI), Chiba, Japan. The Somei-Yoshino clones at SU and
24 KDRI were used for the transcriptome analysis.

25

26 *Clustering analysis of genetically divergent varieties*

27 Genomic DNAs of the 139 varieties were extracted from young leaves using the DNeasy Plant
28 Mini Kit (Qiagen, Hilden, Germany) and double-digested with the restriction enzymes *Pst*I
29 and *Eco*RI. ddRAD-Seq libraries were constructed as described previously (Shirasawa et al.
30 2016) and sequenced using the Illumina HiSeq2000 (San Diego, CA, USA) to obtain 93 bp
31 paired-end reads. Low-quality reads were trimmed using PRINSEQ v. 0.20.4 (Schmieder and

1 Edwards 2011) and adapter sequences were removed using fastx_clipper (parameter, -a
2 AGATCGGAAGAGC) in FASTX-Toolkit v. 0.0.13 (http://hannonlab.cshl.edu/fastx_toolkit).
3 The high-quality reads were mapped onto genome sequences of either *P. avium* (Shirasawa
4 et al. 2017), *P. mume* (Zhang et al. 2012), or *P. persica* (International Peach Genome et al.
5 2013) using Bowtie2 v. 2.2.3 (Langmead and Salzberg 2012). Biallelic SNPs were called from
6 the mapping results using the mpileup command in SAMtools v. 0.1.19 (Li et al. 2009), and
7 low-quality SNPs were removed using VCFtools v. 0.1.12b (Danecek et al. 2011) with the
8 following criteria: including only sites with a minor allele frequency of ≥ 0.05 (--maf 0.05),
9 including only genotypes supported by ≥ 5 reads (--minDP 5), including only sites with a
10 quality value of ≥ 999 (--minQ 999), and excluding sites with $\geq 50\%$ missing data (--max-
11 missing 0.5). A dendrogram based on the SNPs was constructed using the neighbor-joining
12 method implemented in TASSEL 5 (Bradbury et al. 2007) and population structure was
13 investigated using ADMIXTURE v. 1.3.0 with default settings ($K = 1$ to 20) (Alexander et al.
14 2009).

15

16 *Assembly of the 'Somei-Yoshino' genome*

17 Genomic DNA was extracted from young leaves of Somei-Yoshino tree #136 using the
18 DNeasy Plant Mini Kit (Qiagen). A paired-end sequencing library (insert size of 500 bp) and
19 three mate-pair libraries (insert sizes of 2 kb, 5 kb, and 8 kb) were constructed using the
20 TruSeq PCR-free Kit (Illumina) and Mate-pair Kit (Illumina), respectively, and sequenced
21 using the MiSeq and HiSeqX platforms (Illumina). The size of the Somei-Yoshino genome
22 was estimated using Jellyfish v. 2.1.4 (Marcais and Kingsford 2011). High-quality reads after
23 removing adapter sequences and trimming low-quality reads as described above were
24 assembled using SOAPdenovo2 v. 1.10 (Luo et al. 2012) (parameter -K 121). Gaps,
25 represented by Ns in the sequence, were filled with high-quality paired-end reads using
26 GapCloser v. 1.10 (Luo et al. 2012) (parameter -p 31). The resultant sequences were
27 designated CYE_r1.0.

28 High-molecular-weight DNA was extracted from young leaves of 'Somei-Yoshino' tree
29 #136 using Genomic Tip (Qiagen) to prepare the SMRTbell library (PacBio, Menlo Park, CA,
30 USA). The sequence reads obtained from the PacBio Sequel system were assembled using
31 FALCON-Unzip (Chin et al. 2016) to obtain an assembly, CYE_r2.0. Furthermore, the

1 PacBio reads were divided into two subsets using the TrioCanu module of Canu v. 1.7 (Koren
2 et al. 2018), in which Illumina short reads of two probable ancestors of Somei-Yoshino, i.e.,
3 *C. spachiana* 'Yaebeni-shidare' and *C. speciosa* 'Ohshima-zakura,' were employed. Each
4 subset of data was assembled and polished using FALCON assembler v. 2.1.2 (Chin et al.
5 2013). The two assemblies were designated CYEspachiana_r3.0 and CYEspeciosa_r3.0, and
6 were combined to obtain CYE_r3.0, representing the Somei-Yoshino genome. Assembly
7 completeness was evaluated using BUSCO v. 3.0.2 (Simao et al. 2015), for which Plants Set
8 was employed as datasets, and a mapping rate analysis of whole genome sequence data for
9 Somei-Yoshino reads to the references was performed (see below for details).

10

11 *Genetic map construction and pseudomolecule establishment*

12 Genomic DNA was extracted from the ovules of YSF1 seeds using the Favorgen Plant Kit
13 (Ping-Tung, Taiwan) and digested with *Pst*I and *Eco*RI to construct the ddRAD-Seq library.
14 The library was sequenced on the Illumina NextSeq platform. High-quality reads were
15 mapped onto CYEspachiana_r3.0 and CYEspeciosa_r3.0 using Bowtie2 v. 2.2.3 (Langmead
16 and Salzberg 2012). Biallelic SNPs were called from the mapping results using the mpileup
17 command in SAMtools v. 0.1.19 (Li et al. 2009), and low-quality SNPs were deleted using
18 VCFtools v. 0.1.12b (Danecek et al. 2011) with the criteria used for the clustering analysis
19 described above. The SNPs from the two references were merged, grouped, and ordered using
20 Lep-Map3 v. 0.2 (Rastas 2017). Flanking sequences of the SNP sites (100 bases up- and
21 downstream of the SNPs) were compared with the genome sequence of sweet cherry,
22 PAV_r1.0 (Shirasawa et al. 2017), by BlastN with a cutoff value of 1E-40. Probable
23 misassemblies found in the mapping process were broken, and the resultant sequence set was
24 designated CYE_r3.1. According to map positions, the CYE_r3.1 sequences were oriented
25 and assigned to the genetic map of 'Somei-Yoshino' to establish pseudomolecule sequences.
26 Sequence variation between the two pseudomolecule sequences, CYEspachiana_r3.1 and
27 CYEspeciosa_r3.1, was detected using the show-snps function of MUMMER v. 3.23 (Kurtz
28 et al. 2004), for which outputs from NUCmer were employed. In parallel, the genome
29 structure of CYE_r3.1_pseudomolecule was compared with those of sweet cherry, peach,
30 Japanese apricot, and apple using D-Genies (Cabanettes and Klopp 2018).

31

1 *Gene prediction and annotation*

2 Total RNA was extracted from 12 stages of buds within 1 month in 2017 as well as from leaves,
3 stems, sepals, petals, stamens, and carpels. RNA-Seq libraries were prepared using the TruSeq
4 Stranded mRNA Sample Preparation Kit (Illumina) and sequenced by MiSeq. The obtained
5 reads were mapped to the CYE_r3.1 sequences to determine gene positions using TopHat2 v.
6 2.0.14 (Kim et al. 2013). The positional information was used in BREAKER2 v. 2.1.0 (Hoff
7 et al. 2016) to gain training data sets for AUGUSTUS v. 3.3 (Stanke et al. 2006) and
8 GeneMark v. 4.33 (Lomsadze et al. 2005). The two training sets and a preset of SNAP v.
9 2006-07-28 for *Arabidopsis* as well as peptide sequences of *P. avium* (v1.0.a1), *P. persica*
10 (v2.0.a1), and *Malus × domestica* (GDDH13 v1.1) registered in the Genome Database for
11 Rosaceae (Jung et al. 2019) and those of *P. mume* (Zhang et al. 2012) were analyzed using
12 MAKER pipeline v. 2.31.10 (Cantarel et al. 2008) to predict putative protein-coding genes in
13 the CYE_r3.1 sequences. Genes annotated using Hayai-Annotation Plants v. 1.0 (Ghelfi et al.
14 2019) (with a sequence identity threshold of 80% and query coverage of 80%) were selected
15 as a high-confidence gene set.

16

17 *Gene clustering, multiple sequence alignment, and divergence time estimation*

18 Potential orthologues were identified from genes predicted in seven genomes (two genomes
19 of Somei-Yoshino and one each of *P. avium*, *P. mume*, *P. persica*, and *M. × domestica*, as well
20 as *Arabidopsis thaliana* as an outgroup) using OrthoMCL v. 2.0.9 (Li et al. 2003). The single
21 copy orthologues in the seven genomes were used to generate a multiple sequence alignment
22 using MUSCLE v. 3.8.31 (Edgar 2004), in which indels were eliminated by Gblocks v. 0.91b
23 (Castresana 2000). A phylogenetic tree based on the maximum-likelihood algorithm was
24 constructed from the alignments with the Jones-Taylor-Thornton model in MEGA X v. 10.0.5
25 (Kumar et al. 2018). The divergence time was calculated using MEGA X v. 10.0.5 (Kumar et
26 al. 2018) assuming that the divergence time between *M. × domestica* and *P. persica* was
27 approximately 34 to 67 MYA in TIMETREE (Kumar et al. 2017).

28

29 *Repetitive sequence analysis*

30 A database of repeat sequences of the Somei-Yoshino genome was established using
31 RepeatModeler v. 1.0.11 (Smit et al. 2008-2015). The repeat database as well as that

1 registered in Repbase (Bao et al. 2015) were used to predict repetitive sequences in CYE_r3.1
2 using RepeatMasker v. 4.0.7 (Smit et al. 2013-2015).

3

4 *Whole genome resequencing analysis*

5 Genomic DNA of eight representative lines of the SU collection and one of the parental lines
6 of the mapping population, Yama-Zakura, were digested with NEBNext dsDNA Fragmentase
7 (New England BioLabs, Ipswich, MA, USA) for whole genome shotgun library preparation
8 using the Illumina TruSeq PCR-free Kit. The sequences were determined on the Illumina
9 NextSeq platform. Read trimming, read mapping to the CYE_r3.1 sequence, and SNP
10 identification were performed as described above. Effects of SNPs on gene functions were
11 evaluated using SnpEff v. 4.2 (Cingolani et al. 2012).

12

13 *Transcriptome analysis*

14 Additional RNA-Seq libraries were prepared from buds at 24 stages collected in 2017 at KDRI
15 and in 2014 and 2015 at SU using the TruSeq Stranded mRNA Library Prep Kit (Illumina)
16 and sequenced on the NextSeq500 (Illumina). High-quality reads after removing adapter
17 sequences and trimming low-quality reads as mentioned above were mapped to the
18 pseudomolecule sequences of CYE_r3.1 using HISAT2 v. 2.1.0 (Kim et al. 2015), and reads
19 on each gene model were quantified and normalized to determine FPKM values using
20 StringTie v. 1.3.5 (Pertea et al. 2015) and Ballgown v.2.14.1 (Frazee et al. 2015) in accordance
21 with the protocol paper (Pertea et al. 2016). The R package WGCNA v.1.66 (Langfelder and
22 Horvath 2008) was used for network construction and module detection.

23

24 **Results**

25 *Clustering analysis of cherry varieties*

26 We obtained approximately 1.9 million (M) high-quality reads per line after trimming
27 adapters and low-quality sequences from the ddRAD-Seq library. The reads were mapped
28 onto the genome sequences of *P. avium* (PAV_r1.0), *P. mume*, and *P. persica* (v1.0) with
29 mapping alignment rates of 70.8%, 77.8%, and 68.7%, respectively (Supplementary Table
30 S2). We detected 46,278 (*P. avium*), 31,973 (*P. mume*), and 33,199 (*P. persica*) high-
31 confidence SNPs. A clustering tree based on the 46,278 SNPs and a population structure

1 analysis indicated that the cherry collection was derived from at least eight founders ($K = 8$)
2 (Supplementary Figure S1). The Somei-Yoshino genome consisted of *C. spachiana* and *C.*
3 *speciosa* genomic features.

4

5 *Assembly of the Somei-Yoshino genome*

6 The 'Somei-Yoshino' genome size was estimated by a k-mer analysis with 14.3 Gb of paired-
7 end reads ($20.7\times$) obtained by MiSeq (Supplementary Table S3). The distribution of distinct
8 k-mers ($k = 17$) showed two peaks at multiplicities of 18 and 37, indicating heterozygous and
9 homozygous regions, respectively (Supplementary Figure S2). This result suggested that the
10 heterozygosity of the Somei-Yoshino genome was high. In other words, Somei-Yoshino is likely
11 an interspecific hybrid harboring components of two different genomes. The total size of the
12 two genomes was approximately 690 Mb.

13 Totals of 132.5 Gb of paired-end reads ($192\times$ genome coverage) and 69.1 Gb of mate-
14 pair data ($100\times$) (Supplementary Table S3) were assembled into 1.2 million scaffold
15 sequences. The total length of the resultant scaffolds, i.e., CYE_r1.0, was 686.9 Mb, including
16 63.6 Mb of Ns with an N50 length of 142.5 kb (Supplementary Table S4). Only 62.3% of
17 complete single copy orthologs in plant genomes were identified in a BUSCO analysis
18 (Supplementary Table S4). Paired-end reads of Somei-Yoshino ($20.7\times$) were mapped onto
19 CYE_r1.0 with a mapping rate of 76.6%. We found that 82.4% of SNPs were homozygous for
20 the reference type. Ideally, both rates should be close to 100% if the assembly was fully
21 extended and the two genomes were separated, or phased. Distributions of the sequence
22 depth of coverage showed a single peak at the expected value of $21\times$ (Supplementary Figure
23 S3). When we mapped the reads to the sequence of *C. \times nudiflora* (Pyn.v1) (Baek et al.
24 2018), two peaks at $22\times$ (expected) and $44\times$ (double the expected value) were observed
25 (Supplementary Figure S3), indicating a mixture of phased and unphased sequences.

26 To extend the sequence contiguity and to improve the genome coverage, PacBio long-
27 read technology was employed to obtain 37.3 Gb of reads ($54\times$) with an N50 read length of
28 17 kb (Supplementary Table S3). The long reads were assembled using FALCON-Unzip into
29 3,226 contigs [470 primary contigs (488 Mb) and 2,756 haplotigs (116 Mb)] spanning a total
30 length of 605.4 Mb with an N50 length of 2.3 Mb, i.e., CYE_r2.0 (Supplementary Table S4).
31 A BUSCO analysis indicated that 97.0% of complete BUSCOs (9.1% single copy and 87.9%

1 duplicated, as expected) were represented in the assembly (Supplementary Table S4). The
2 mapping rate of the Somei-Yoshino reads was 95.3%, and 97.1% of SNPs were homozygous
3 for the reference type. Most of the sequences were phased, with one major peak of genome
4 coverage at $21\times$ (Supplementary Figure S3); however, the total length was 13% shorter than
5 the estimated size and no haplotype information was available.

6 We used a trio-binning approach to obtain the entire sequences of the two haplotype
7 sequences. The long reads (37.3 Gb, $54\times$) were divided into two subsets based on whole
8 genome resequencing of the two lines, i.e., *C. spachiana* (Yaebini-shidare) and *C. speciosa*
9 (Ohshima-zakura). The resultant subsets included 18.9 Gb and 18.2 Gb for *C. spachiana* and
10 *C. speciosa*, respectively, and 0.3 Mb of unassigned reads. The subsets were separately
11 assembled to obtain 2,281 contigs (717 primary contigs and 1,564 associated contigs
12 including duplicated repetitive sequences) covering 350.1 Mb, i.e., CYEspachiana_r3.0, and
13 2,271 contigs (800 primary contigs and 1,471 associated contigs) covering 340.0 Mb, i.e.,
14 CYEspachiana_r3.0 (Supplementary Table S4). The total sequence (i.e., CYE_r3.0) spanned
15 690.1 Mb and consisted of 4,552 contigs with an N50 length of 1.0 Mb (Supplementary Table
16 S4). The complete BUSCO score for CYE_r3.0 was 96.8% (10.6% single copy and 86.2%
17 duplicated, as expected), while those for CYEspachiana_r3.0 and CYEspeciosa_r3.0 were
18 90.9% (69.3% single copy and 21.6% duplicated) and 88.9% (72.1% single copy and 16.8%
19 duplicated), respectively (Supplementary Table S4). The mapping rate of the Somei-Yoshino
20 reads was as high as 96.3%, and 96.2% of SNPs were homozygous for the reference type. The
21 sequence depth of coverage was distributed as expected, with a single peak at $20\times$
22 (Supplementary Figure S3). Therefore, CYE_r3.0 was used for further analyses because it
23 satisfied all of the established criteria.

24

25 *Genetic map for Somei-Yoshino*

26 Approximately 2.0 million high-quality ddRAD-Seq reads per sample were obtained from
27 YSF1 and mapped to either CYEspachiana_r3.0 or CYEspeciosa_r3.0 with alignment rates of
28 79.3% and 80.3%, respectively (Supplementary Table S5). We detected 16,145 and 17,462
29 SNPs from the alignments with the references of CYEspachiana_r3.0 and CYEspeciosa_r3.0,
30 respectively. Of these, 23,532 heterozygous SNPs in 'Somei-Yoshino' were used for a linkage
31 analysis. The SNPs were assigned to eight groups and ordered, covering 458.8 cM with 16,933

1 SNPs in 694 genetic bins (Supplementary Tables S6 and S7). The map was split into two for
2 *C. spachiana* and *C. speciosa*, covering 448.9 cM with 8,280 SNPs (628 genetic bins) and
3 446.3 cM with 8,653 SNPs (645 genetic bins), respectively. The genetic bins were common
4 for 579 loci on the two maps, suggesting that the sequences in the common bins were the
5 same loci. A comparison of the genetic maps with the genome sequence of sweet cherry,
6 PAV_r1.0 (Supplementary Figure S4), indicated a high similarity of the genome structures in
7 the two species.

8

9 *Genetic anchoring of the assemblies to the chromosomes*

10 In the genetic mapping process, we found 19 potential misassemblies in 18 contig sequences
11 of CYE_r3.0. The contigs were broken between SNPs mapped to different linkage groups.
12 Finally, we obtained 4,571 contigs with an N50 length of 918.2 kb and the same total length
13 (690.1 Mb). This final version of contigs was named CYE_r3.1, consisting of
14 CYEspachiana_r3.1 (2,292 contigs, N50 length of 1.2 Mb) and CYEspeciosa_r3.1 (2,279
15 contigs, N50 length of 800.6 kb) (Table 1). Of these, 184 CYEspachiana_r3.1 contigs (221.8
16 Mb) and 262 CYEspeciosa_r3.1 contigs (199.2 Mb) were assigned to the genetic maps
17 (Supplementary Tables S8). The contigs were connected with 10,000 Ns to establish the
18 Somei-Yoshino pseudomolecule sequences consisting of 4,571 contigs covering 418 Mb. The
19 structures of the two pseudomolecule sequences were well conserved (Fig. 1). We observed
20 2,371,773 and 2,392,937 sequence variants, including SNPs and indels, in
21 CYEspachiana_r3.1 (one variant every 93 bp) and CYEspeciosa_r3.1 (one variant every 83
22 bp), respectively, of which 0.4% were deleterious mutations (Supplementary Tables S9). The
23 structure of the Somei-Yoshino genome showed high synteny with the genomes of other
24 members of Rosaceae (Supplementary Figure S5).

25

26 *Gene prediction and annotation*

27 We initially predicted 222,168 putative genes using the MAKER pipeline. All genes were
28 annotated by a similarity search against the UniProtKB database using the Hayai-Annotation
29 Plants pipeline to select 94,776 non-redundant high-confidence genes. Then, 300 genes
30 showing sequence similarity to genes involved in flowering and dormancy in the family
31 Rosaceae (Supplementary Table S10) were manually added. A total of 95,076 genes (48,280

1 and 46,796 from CYEspachiana_r3.1 and CYEspeciosa_r3.1, respectively) were selected as a
2 high-confidence gene set for CYE_r3.1 (Table 1). The total length of the coding sequences
3 was 91.9 Mb (13.3% of the CYE_r3.1) with an N50 length of 1,512 bases and a GC content
4 of 44.8%. This gene set included 94.9% complete BUSCOs (12.8% single copy and 82.1%
5 duplicated). Out of the 95,076 genes, 26,463 (27.8%), 34,996 (36.8%), and 46,502 (48.9%)
6 were assigned to Gene Ontology slim terms in the biological process, cellular component, and
7 molecular function categories, respectively (Supplementary Table S11). Furthermore, 3,972
8 genes had enzyme commission numbers.

9 We found two pairs of self-incompatible genes, *S* determinants for pollen (S-RNase) and
10 pistils (SFB: *S* haplotype-specific F-box); CYE_r3.1SPE0_g058440.1 (S-RNase) and
11 CYE_r3.1SPE0_g058430.1 (SFB) were *S* genes of the *PyS1* haplotype, and
12 CYE_r3.1SPE0_g046700.1 (S-RNase) and CYE_r3.1SPE0_g046660.1 (SFB) were *S* genes of
13 *PyS2*. For dormancy, we detected a cluster of six *DAM*-like genes, as reported in the Japanese
14 apricot genome (Zhang et al. 2012), in the pseudomolecule sequence of SPA1
15 (CYE_r3.1SPA1_g039840.1 to CYE_r3.1SPA1_g039890.1). In addition, *CBF* gene clusters
16 were also found in SPA5 (CYE_r3.1SPA5_g014520.1 to CYE_r3.1SPA5_g014610.1) and
17 SPE5 (CYE_r3.1SPE5_g016380.1 to CYE_r3.1SPE5_g016430.1).

18

19 *Divergence time of Somei-Yoshino ancestors*

20 The predicted genes were clustered with those of apple, sweet cherry, Japanese apricot, peach,
21 and *Arabidopsis* to obtain 29,091 clusters, involving 36,396 and 35,559 genes from
22 CYEspachiana_r3.1 and CYEspeciosa_r3.1, respectively (Supplementary Table S12). Among
23 these, 8,125 clusters were common across the tested species, and 1,254 consisting of one gene
24 from each genome were selected for divergence time estimation. When the divergence time
25 between apple and peach was set to 34 to 67 MYA, the divergence time between the two
26 haplotype sequences of Somei-Yoshino was set to 5.52 MYA (Figure 2).

27

28 *Repetitive sequence analysis*

29 A total of 293.3 Mb (42.5%) of CYE_r3.1 (690.1 Mb) was identified as repetitive sequences,
30 including transposable elements (Supplementary Table S13), which occupied 142.9 Mb
31 (40.8%) and 150.4 Mb (44.2%) of CYEspachiana_r3.1 and CYEspeciosa_r3.1, respectively.

1 The most prominent repeat types were long-terminal repeat retrotransposons (104.0 Mb;
2 14.1%), e.g., *Gypsy*- and *Copia*-types, followed by DNA transposons (65.1 Mb; 8.8%).

3 *Whole genome resequencing analysis*

4 Approximately 136 million high-quality whole genome sequence reads was obtained from
5 eight representatives in a population structure analysis (Supplementary Table S14) and the
6 parents of the mapping population, Yama-Zakura and 'Somei-Yoshino.' In addition, 250
7 million sequence reads of *C. × nudiflora* (Baek et al. 2018) (SRA accession number
8 SRX3900230) was also employed. The reads were aligned to CYE_r3.1 as a reference with a
9 mapping rate of 88.0%, on average. From the alignment data, we detected 2,307,670 SNPs
10 and 169,664 indels, including 658,873 SNPs and 42,286 indels (28.3%) in
11 CYEspachiana_r3.1 and 1,648,797 SNPs and 127,378 indels (71.7%) in CYEspeciosa_r3.1.
12 Of these, 8,872 SNPs (0.4%) were deleterious mutations (Supplementary Tables S15).

13
14 In Somei-Yoshino, the reads were evenly mapped to the references of CYEspachiana_r3.1
15 (48.7%) and CYEspeciosa_r3.1 (47.6%) (Supplementary Figure S6). Most of the loci (94.5%
16 of SNPs in CYEspachiana_r3.1 and 96.9% in CYEspeciosa_r3.1) were homozygous for the
17 reference type, as expected (Supplementary Figure S7). Only 61.7% and 52.9% of SNPs in *C.*
18 *× nudiflora* were reference-type homozygotes on CYEspachiana_r3.1 and CYEspeciosa_r3.1,
19 respectively (Supplementary Figure S6), and read mapping rates were 52.2%
20 (CYEspachiana_r3.1) and 39.8% (CYEspeciosa_r3.1) (Supplementary Figure S7).

21 In *C. spachiana* (Yaebeni-shidare), 69.8% of the reads were preferentially mapped to
22 CYEspachiana_r3.1 (Supplementary Figure S6), and 80.1% of SNPs detected in
23 CYEspachiana_r3.1 were homozygous for the reference type (Supplementary Figure S7). In
24 *C. speciose* (Ohshima-zakura), 61.1% of reads were mapped to CYEspeciosa_r3.1
25 (Supplementary Figure S6) and 73.5% of SNPs in CYEspeciosa_r3.1 were homozygous for
26 the reference type (Supplementary Figure S7). In the remaining seven lines, mapping rates
27 on CYEspeciosa_r3.1 were higher than those on CYEspachiana_r3.1, as in *C. speciose*
28 (Ohshima-zakura) (Supplementary Figure S6).

29 *Transcriptome analysis of flowering dates*

30 RNA-Seq reads were obtained from 12 stages of buds collected every month from May 2014
31

1 to April 2015 (Supplementary Table S16) as well as from the 12 stages from 2 to 34 days
2 before anthesis in 2017 used for gene prediction. After trimming, the reads as well as those
3 for the six organs used in the gene prediction analyses were mapped to CYE_r3.1 with a
4 mapping rate of 67.6%, on average. Among the 95,076 predicted genes, 72,248 (76.0%) with
5 a variance across samples of ≥ 1 were selected. A WGCNA analysis was performed with the
6 expression data for the 24 buds to generate 31 highly co-expressed gene clusters, referred to
7 as modules (Supplementary Figure S8). The modules were roughly grouped into three main
8 classes expressed in the previous year of flowering, within 1 month, and within 1 week
9 (Supplementary Figure S9).

10 Based on the literature and databases for Rosaceae, we identified dormancy- and
11 flowering-associated genes (i.e., *DELLA*, *CBF/DREB1*, *EBB1*, *DAM (SVP)*, *FT*, and
12 *CEN/TFL1* genes). We detected 35 predicted genes in the Somei-Yoshino genome, 16 of
13 which were expressed in ≥ 1 sample. The expression patterns basically agreed with those of
14 the modules and could be roughly classified into five groups (Figure 3). The first group (blue
15 and magenta gene modules in Supplementary Figure S8) consisted of four genes homologous
16 to *DELLA* genes. Their expression levels were elevated in the floral buds about 1 month
17 before anthesis; expression was also observed in young vegetative buds. The second group
18 (turquoise, brown, and salmon gene modules) were highly expressed in the summer and
19 autumn (from July to November) in the floral buds. Six genes homologous to *CBF/DREB1*
20 belonged to this group; however, these were classified into three different clusters on the
21 dendrogram. The third group (turquoise gene module) consisted of two *EBB1* homologs and
22 one *DAM(SVP)* homolog; these genes were highly expressed in the autumn and winter (from
23 October to December). In the fourth group (turquoise gene module), genes were highly
24 expressed in the winter 2–3 months before anthesis and were homologous to *FT* genes. The
25 fifth group (red gene module) solely included *CEN/TFL1*-like genes specifically expressed in
26 vegetative state buds before flower differentiation.

27

28 Discussion

29 We obtained the genome sequence of the flowering cherry Somei-Yoshino. To the best of our
30 knowledge, this is the first report of a phased genome sequence of an interspecific hybrid in
31 the family Rosaceae or in the kingdom of Plantae, broadly, although genome sequences have

1 been reported for several species belonging to Rosaceae (Jung et al. 2019). Although the
2 genome of another interspecific hybrid cherry flower, *C. × nudiflora*, has been reported (Baek
3 et al. 2018), the two homoeologous ancestral genomes (*C. spachiana* and *C. jamasakura*) are
4 totally collapsed, as indicted by the double peaks of sequence depth (Supplementary Figure
5 S3), resulting in a short assembly size (323.8 Mb). The genome complexity of interspecific
6 hybrids could be compared to those of polyploids and highly heterozygous species. Genome
7 sequences of polyploids and F1 hybrids have been obtained (Chin et al. 2016; Hulse-Kemp et
8 al. 2018) by single-molecule real-time sequencing technology, linked read sequencing, optical
9 maps, and Hi-C (Belser et al. 2018; Jiao and Schneeberger 2017; Kyriakidou et al. 2018).
10 These technologies to obtain phased genome assemblies are limited by haplotype switching
11 (Kronenberg et al. 2018), where two haplotypes are patched to make mosaic genome
12 sequences.

13 We employed the trio-binning technique (Koren et al. 2018) to determine haplotype
14 phases before assembly. This technique was initially developed to construct phased genome
15 sequences of an F1 hybrid between cattle subspecies. Since sequence reads of two sub-
16 genomes were divided into two subsets according to the sequences of the parents, haplotype
17 switching is avoidable. We applied the trio-binning technique to the interspecific hybrid
18 cherry tree. We verified the quality and accuracy of the resultant assembly, CYE_r3.0, by a
19 BUSCO analysis (Supplementary Table S4), the mapping rate of Somei-Yoshino reads to the
20 assemblies (Supplementary Figure S6), and SNP genotypes detected in the mapping results.
21 In addition, the genetic map (Supplementary Table S6 and S7) and a comparative analysis of
22 the pseudomolecule sequences (Figure 1 and Supplementary Figure S4 and S5) also
23 supported the quality and accuracy of the assembly. The results of this study suggested that
24 the trio-binning strategy is useful for determining phased genome sequences for highly
25 heterozygous genomes of interspecific hybrids.

26 Our genome data provided insight into the progenitors of Somei-Yoshino. Our results
27 were consistent with the conclusions of Baek et al. (2018), who found that Somei-Yoshino, *C.*
28 *× yedoensis*, is distinct from a variety in Jeju Island, Korea, *C. × nudiflora*. In the present
29 study, a population structure analysis indicated that Somei-Yoshino was established by two
30 founders, *C. spachiana* and *C. speciosa* (Figure 2, Supplementary Figure S1), as suggested in
31 previous studies (Innan et al. 1995; Takenaka 1963). In a whole genome resequencing analysis,

1 sequence reads of *C. spachiana* ‘Yaebeni-shidare’ were preferentially mapped to SPA
2 sequences (Supplementary Figure S6), and genotypes of most SNPs were homozygous for the
3 reference type (Supplementary Figure S7). This indicated that the sequence similarity of *C.*
4 *spachiana* ‘Yaebeni-shidare’ and CYEspachiana_r3.1 was high and therefore that *C. spachiana*
5 is a candidate parent. While reads of *C. speciosa* ‘Ohshima-zakura’ were mapped to
6 CYEspeciosa_r3.1 sequences (Supplementary Figure S6), the frequency of SNP genotypes
7 homozygous for the reference type was not as high as that for *C. spachiana* (Supplementary
8 Figure S7). This observation suggests that *C. speciosa* is not an actual parent of Somei-
9 Yoshino (Kato et al. 2014). Somei-Yoshino genome data can be used in future studies of the
10 origin to determine the most likely parents.

11 We obtained a number of predicted genes. Transcriptome data for the developing bud
12 provided a comprehensive overview of genes expressed during dormancy and flowering
13 processes (Figure 3). Our analysis was based on previous studies of key genes and
14 fundamental molecular mechanisms underlying dormancy (Lloret et al. 2018; Yamane 2014).
15 Despite some discrepancies, the gene expression patterns observed in our study were
16 generally consistent with previously observed patterns in deciduous fruit tree species in
17 Rosaceae. The relatively high expression levels of *DELLA* genes observed at 1 month before
18 anthesis corresponded to the time at which the bud typically transitions from endodormancy
19 to ecodormancy (Lv et al. 2018). GA signaling may reactivate bud development internally at
20 the ecodormancy stage (Wen et al. 2016). The relatively high expression levels of
21 *CBF/DREB1* in the summer and decreased expression levels toward the winter is consistent
22 with a role in cold acclimation, as previously reported in almond (Saibo et al. 2012). We
23 detected one *DAM* gene that was highly expressed in dormant buds in the winter, in
24 agreement with previous reports (Yamane et al. 2006); however, two *EBB1* genes, assigned
25 to the same module as *DAM* genes, showed different expression patterns from those in apple
26 and poplar, in which the genes exhibit sharp increases in expression before bud breaking
27 (Wisniewski et al. 2015; Yordanov et al. 2014). This inconsistency may be explained by
28 differences in regulatory mechanisms underlying bud breaking. *FT* genes showed elevated
29 expression levels in buds in February, when endodormancy is almost completed. In addition
30 to the function of floral induction, unknown functions of *FT* genes during dormancy are
31 possible. Interestingly, transgenic plum (*Prunus domestica*) with overexpressed poplar *FT*

1 (*PtFTI*) does not enter a state of endodormancy upon cold treatment or, alternatively, has no
2 chilling requirement after dormancy is established (Srinivasan et al. 2012). Further studies of
3 the role of *FT* genes in dormancy are needed. *CEN/TFL1* was highly expressed only in
4 vegetative buds before floral initiation. This observation was consistent with other previous
5 results for species in the family Rosaceae (Esumi et al. 2010; Mimida et al. 2009). Our
6 transcriptome data for flowering cherry successfully revealed the comprehensive changes in
7 gene expression during floral bud development toward flowering. The expression patterns of
8 above genes in this study and supposed regulation network for dormancy release of woody
9 plants (Falavigna et al. 2019; Lloret et al. 2018; Singh et al. 2018) are jointly summarized in
10 Figure 4. The transcriptome data set provides a basis for further research aimed at identifying
11 additional genes involved in floral bud development and flowering. Especially, identifying
12 genes involved in the regulation of flowering under *FT* gene (protein) signaling and GA
13 signaling processes is intriguing, and those may be able to utilize for accurate forecasting the
14 flowering date of cherry blossoms.

15 The genome and transcriptome data obtained in this study are expected to accelerate
16 genomic and genetic analyses of flowering cherry. Owing to the complicated genomes, it is
17 necessary to build additional *de novo* assemblies for divergent flowering cherries, which is a
18 challenging task. Genome-graph-based pan-genome analyses could be used to characterize
19 the complex genomes (Rakocevic et al. 2019). The Somei-Yoshino genome sequence would
20 be a resource for the flowering cherry pan-genome analyses. It may provide insights into the
21 evolution and cultivation of flowering cherry as well as the molecular mechanism underlying
22 flowering traits in the species and in the family Rosaceae, and it may guide the future
23 cultivation and breeding of flowering cherry.

24

25 **Data availability**

26 The sequence reads are available from the DDBJ Sequence Read Archive (DRA) under the
27 accession numbers DRA008094, DRA008096, DRA008097, DRA008099, and DRA008100.
28 The WGS accession numbers of assembled scaffold sequences are BJCG01000001-
29 BJCG01004571 (4,571 entries). The genome assembly data, annotations, gene models,
30 genetic maps, and DNA polymorphism information are available at DBcherry
31 (<http://cherry.kazusa.or.jp>).

1

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11

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29
30 **Figure legends**

31 **Figure 1** Synteny of the two haplotype pseudomolecule sequences of the Somei-Yoshino
32 genome

33 *X*- and *Y*-axis are sequences of CYE_r3.1spachiana (SPA1 to 8) and CYE_r3.1speciosa (SPE1
34 to 8), respectively.

35 **Figure 2** Phylogenetic tree indicating the divergence time of Somei-Yoshino

1 The two genomes of Somei-Yoshino are indicated by SPA and SPE, representing *C. spachiana*
2 and *C. speciosa*, respectively. Divergence times (MYA; million years ago) between branches
3 are shown.

4 **Figure 3** Heat map representing expression patterns of dormancy and flowering genes in
5 Somei-Yoshino buds

6 Colors in each block represent a continuum of gene expression levels with Z-score-
7 transformed FPKM (low-to-high gene expression levels are represented by blue to red). May
8 to Apr are the months and 34DBA to 2DBA are days before anthesis when bud samples were
9 collected. Gene modules based on WGCNA (see also Supplementary Figure S8) are shown as
10 colored bars between the dendrogram and heatmap.

11 **Figure 4** A putative regulation model for dormancy release and flowering with expression
12 patterns of related genes in Somei-Yoshino buds

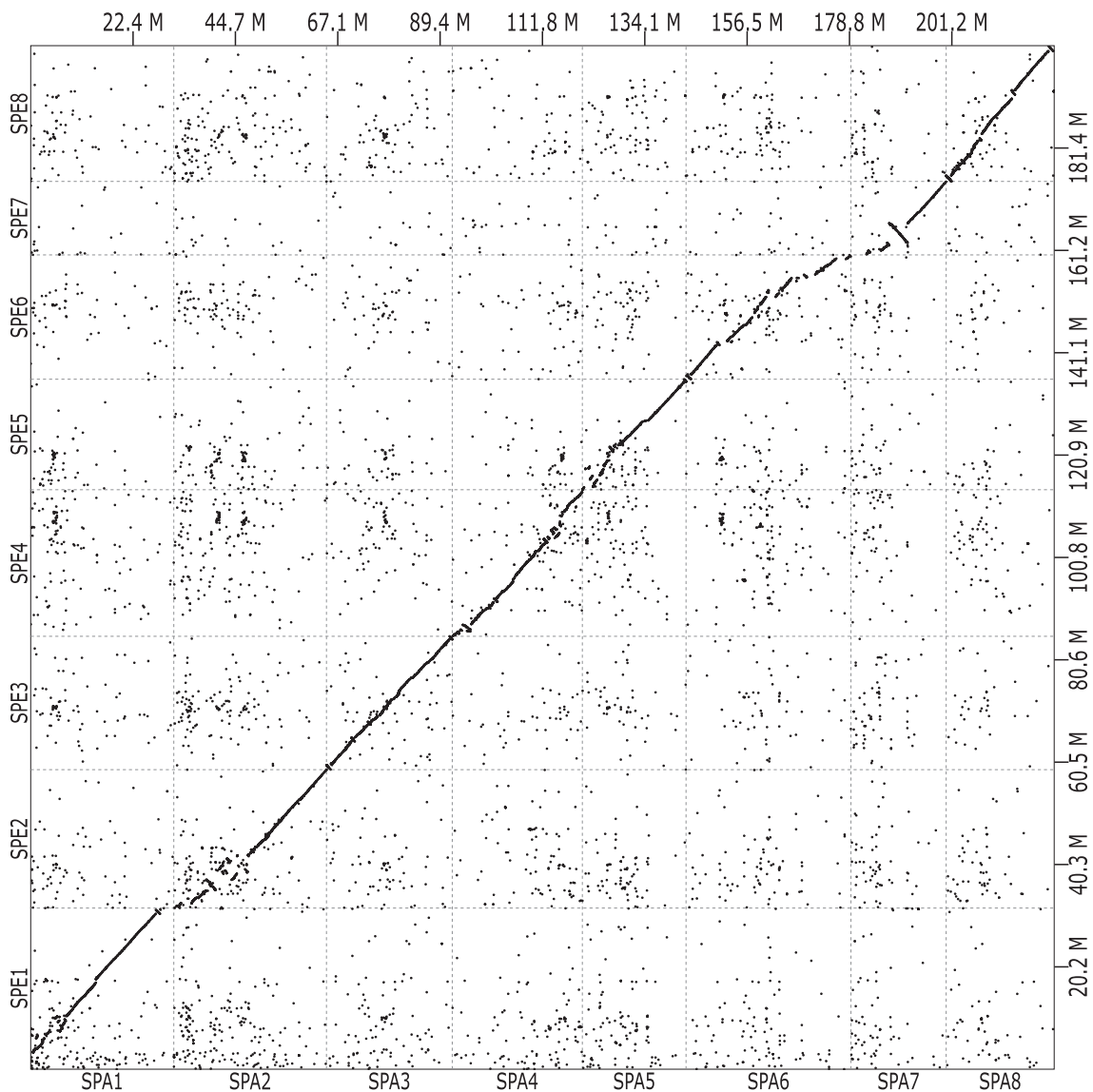
13 The supposed regulation mechanism for dormancy and flowering is based on recent studies
14 and reviews in woody plants (Falavigna et al. 2019; Lloret et al. 2018; Singh et al. 2018). The
15 gene expression patterns represented as black arrows are based on Figure 3.

16

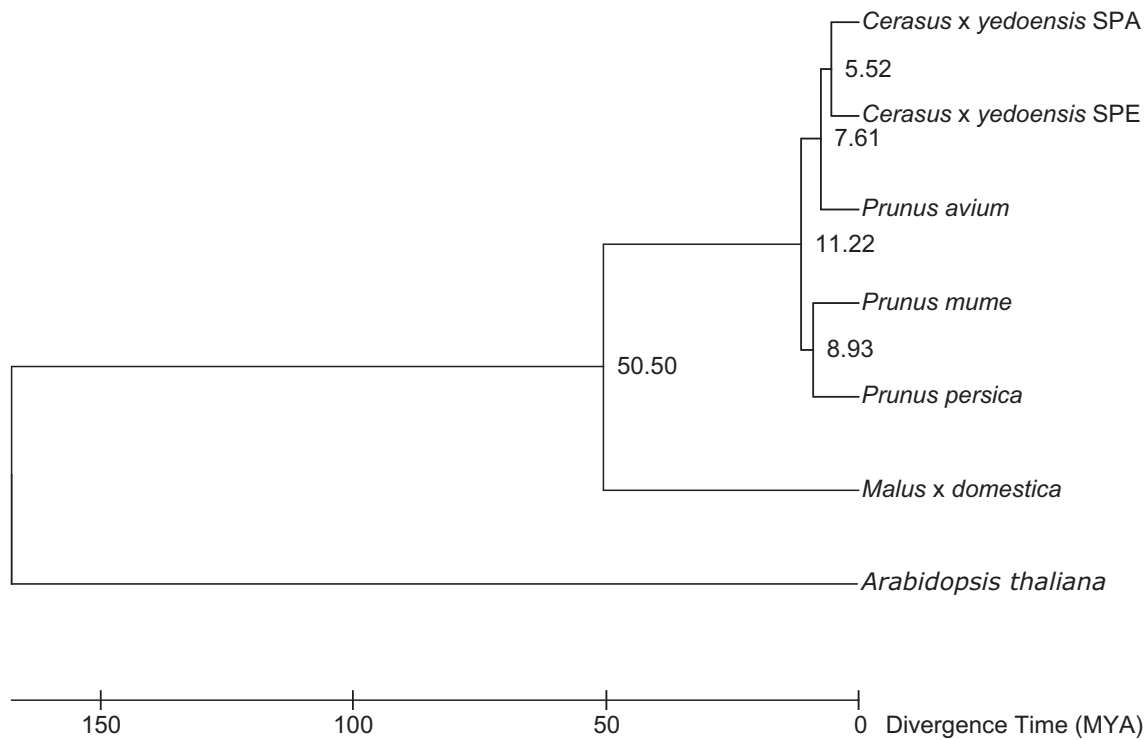
1 **Table 1** Assembly statistics of the final version of the Somei-Yoshino genome sequence

	CYE_r3.1 (Total)	CYEspachiana_r3.1	CYEspectiosa_r3.1
Number of contigs	4,571	2,292	2,279
Total length (bases)	690,105,700	350,135,227	339,970,473
Contig N50 (bases)	918,183	1,151,237	800,562
Longest contig (bases)	11,102,098	11,102,098	6,718,036
Gap length (bases)	0	0	0
GC (%)	37.9	37.8	38.1
Number of predicted genes	95,076	48,280	46,796
Mean size of genes (bases)	966	975	951

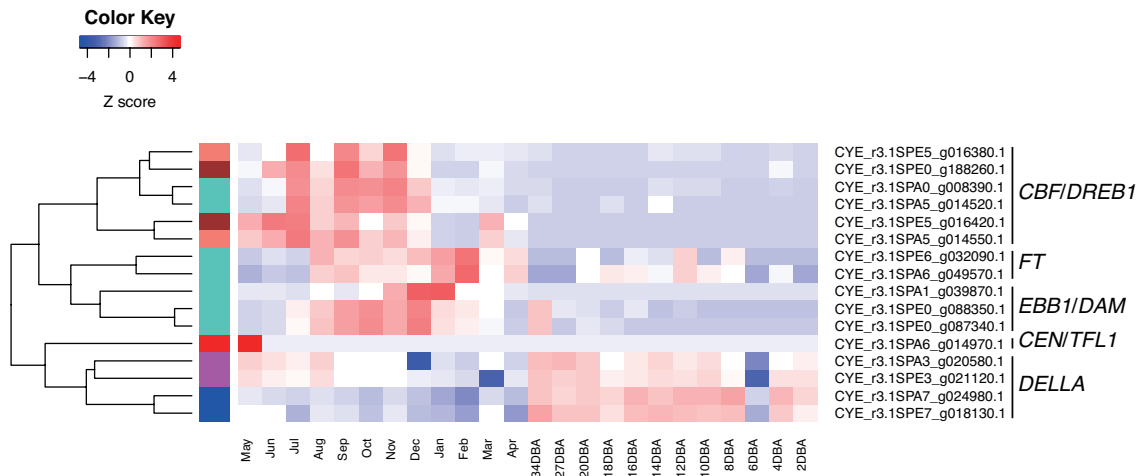
2



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4 X- and Y-axis are sequences of CYE_r3.1spachiana (SPA1 to 8) and CYE_r3.1speciosa
5 (SPE1 to 8), respectively.
6



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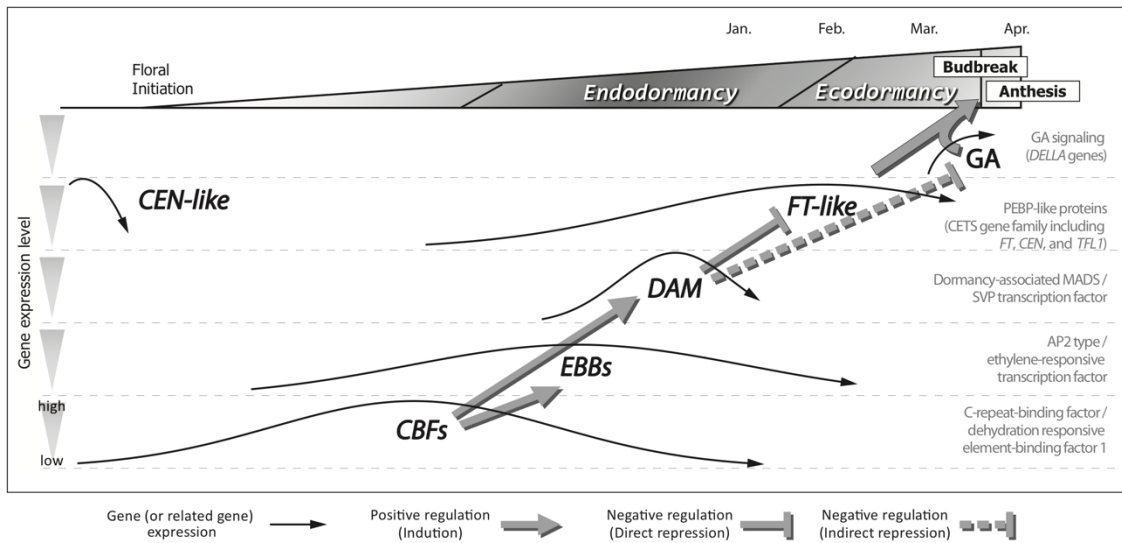
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8 colored bars between the dendrogram and heatmap.

9



1

2 **Figure 4** A putative regulation model for dormancy release and flowering with expression
3 patterns of related genes in Somei-Yoshino buds

4 The supposed regulation mechanism for dormancy and flowering is based on recent studies
5 and reviews in woody plants (Falavigna et al. 2019; Lloret et al. 2018; Singh et al. 2018). The
6 gene expression patterns represented as black arrows are based on Figure 3.

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