Genome-wide Identification and Expression Analysis of NAC Transcription Factor Family Genes during Fruit and Kernel Development in Siberian Apricot

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ABSTRACT. The NAC (NAM, ATAF1/2, and CUC2) family is a group of plant-specific transcription factors that have vital roles in the growth and development of plants, and especially in fruit and kernel development. This study aimed to identify members of the NAC gene (*PsNACs*) family and investigate their functions in siberian apricot (*Prunus sibirica*). A total of 102 predicted *PsNAC* proteins (*PsNACs*) were divided into 14 clades and the genes were mapped to the eight chromosomes in siberian apricot. The *PsNACs* of the same clade had similar structures. A synteny analysis showed that the *PsNACs* had close relationships with the NAC genes of japanese apricot (*Prunus mume*). An expression pattern analysis of the *PsNACs* revealed many differences in various tissues and at different stages of fruit and kernel development. All eight *PsNACs* in clade XI have crucial roles in fruit and kernel development. Seven *PsNACs* (*PsNACs* 18, 64, 23, 33, 9, 4, and 50) in clades I, III, VI, VII, and XIII are related to fruit development. Eight *PsNACs* (*PsNACs* 6, 13, 46, 51, 41, 67, 37, and 59) in clades I, II, V, VIII, and XIII are involved in fruit ripening. Five *PsNACs* (*PsNACs* 6, 94, 41, 32, and 17) in clades I, IV, V, VII, and XI regulated the rapid growth of the kernel. Four *PsNACs* (*PsNACs* 50, 4, 67, and 84) in clades I, III, V, and XIII affected the hardening of the kernel. Four *PsNACs* (*PsNACs* 17, 82, 13, and 51) in clades II, XI, and IX acted on kernel maturation. We have characterized the NAC genes in siberian apricot during this study. Our results will provide resources for future research of the biological roles of *PsNACs* in fruit and kernel development in siberian apricot.

Siberian apricot (*Prunus sibirica*) belongs to the family Rosaceae and is widely distributed in northern and northeastern China, eastern and southeastern Mongolia, eastern Siberia, and the Maritime Territory of Russia (Wang and Yu, 2012). Siberian apricot can grow in harsh environmental conditions and has been used for afforestation in northern China because of its strong environmental adaptability (Wang et al., 2017; Zhang et al., 2006). The kernels of siberian apricot have commercial value; for example, they can be processed into protein drinks

(Sharma et al., 2010) and biodiesel fuel (Wang et al., 2017). They are also used in traditional Chinese medicine.

NAC proteins are plant-specific transcription factors that contain an N-terminal DNA-binding domain [no apical meristem (*NAM*)], a nuclear localization signal sequence [*Arabidopsis* transcription activation factor (*ATAF1/2*)], and a C-terminal transcriptional activation domain [cup-shaped cotyledon (*CUC2*)] (Hu et al., 2015b; Ooka et al., 2003; Shen et al., 2020). The N-terminal DNA-binding domain usually contains ≈150 amino acid residues and is further divided into five subdomains (A to E) (Apweiler et al., 2001; Duval et al., 2002; Kikuchi et al., 2000). The diverse C-terminal domain contains a transcriptional regulatory region (TRR) that activates or represses transcriptional activity (Delessert et al., 2005; Fang et al., 2008; Kim et al., 2007; Yamaguchi et al., 2010).

The NAC gene family has been intensively studied in various plant species since its discovery. In monocotyledons, 138 and 115 NAC genes have been identified in rice [*Oryza sativa* (Fang et al., 2008)] and maize [*Zea mays* (Zhu et al., 2012)], respectively. In dicotyledons, there are 105 NAC genes in *Arabidopsis*

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Fig. 1. Phylogenetic tree of the NAC genes in siberian apricot. Phylogenetic analysis of NAC genes from siberian apricot and arabidopsis using the complete protein sequences. Each of the 14 clades is indicated by a specific color.

[*Arabidopsis thaliana* (Ooka et al., 2003)], 74 in grape [*Vitis vinifera* (Wang et al., 2013)], 96 in cassava [*Manihot esculenta* (Hu et al., 2015b)], 93 in tomato [*Solanum lycopersicum* (Jin et al., 2020)], and 88 in pigeonpea [*Cajanus cajan* (Satheesh et al., 2014)]. In the Rosaceae, there are 180 NAC genes in apple [*Malus domestica* (Su et al., 2013)], 183 in white pear [*Pyrus bretschneideri* (Gong et al., 2019)], 114 in peach [*Prunus persica* (Gong et al., 2019)], and 113 in japanese apricot [*Prunus mume* (Zhuo et al., 2018)]. However, studies of the NAC gene

family in siberian apricot are still limited (García-Gómez et al., 2019; Niu et al., 2016).

Previous reports have described the multiple functions of NAC transcription factors in plants, for example, controlling leaf senescence in arabidopsis (Guo and Gan, 2006), responding to ABA hormone signaling in arabidopsis (Jensen et al., 2008), forming secondary walls in woody plants (Mitsuda et al., 2007), controlling the growth transition between stamens and petals in arabidopsis (Sablowski and Meyerowitz, 1998), and regulating

Fig. 2. The conserved motifs and gene structures of *PsNACs*. (A) The motif composition of 102 *PsNACs*. (B) Exon/intron structures of *PsNACs*. The motifs, numbered 1 to 20, are displayed in boxes with different colors. The sequence information for each motif is provided in Supplemental Fig. 1. The length of the protein could be estimated using the scale at the bottom. Green boxes indicate untranslated 5' and 3' regions; yellow boxes indicate exons; black lines indicate introns.

shoot branching in rice (Mao et al., 2007). Additionally, the NAC gene family has crucial roles in fruit and seed development. For example, 13 NAC genes in cucumber (*Cucumis sativus*) impact fruit spine development (Liu et al., 2018). *Solanum lycopersicum* NAC gene 4 (SINAC4), a tomato NAC domain protein, accumulates to high levels at the onset of fruit ripening (Zhu et al., 2014). No-ripening-like 1 (NOR-like1), a NAC transcription factor, is a positive regulator of tomato fruit ripening (Gao et al., 2018). Six strawberry (*Fragaria × ananassa*) NAC proteins have been identified that have important regulatory roles in fruit development and ripening (Moyano et al., 2018). *AtNAM* is specifically expressed in developing arabidopsis seeds (Duval et al., 2002).

The availability of the siberian apricot genome is a valuable resource for the identification of gene families that allows us to gain further insight into their functions. Here, we report that the siberian apricot NAC gene (*PsNAC*) family may impact plant development, especially during fruit and kernel development. This study provides information regarding the functional characteristics and role of *PsNACs* in the development of siberian apricot.

Materials and Methods

IDENTIFICATION OF NAC FAMILY GENES.

The hidden Markov model (HMM) file of the NAC domain (PF 02365) was downloaded from the Pfam protein family database (El-Gebali et al., 2019) to identify NAC family genes in siberian apricot genome (Genome Sequence Archive PRJCA001987) using HMMER 3.3 software (default parameters) (Finn et al., 2011) with a cutoff of 0.01. All candidate proteins were submitted to the National Center for Biotechnology Information Conserved Domain Database (Marchler-Bauer et al., 2017) and Simple Modular Architecture Research Tool (Letunic and Bork, 2018) to confirm the presence and completeness of the NAM domain. The molecular weights, isoelectric point, and subcellular localization tools were predicted on the ExPasy website (Gasteiger et al., 2003). The positions of all NAC family gene from the siberian apricot genome general feature format file were detected using TBtools program (Chen et al., 2018).

PHYLOGENETIC TREE ANALYSIS. NAC protein sequences from siberian apricot (102) and arabidopsis (105) were used to construct the phylogenetic tree. We performed multiple sequence alignment

Fig. 3. Distribution and segmental duplication of *PsNACs*. Orange lines represent the chromosomes of siberian apricot. The scale on the chromosomes represents the chromosome length. The *PsNACs* in red are involved in duplication events. The brown lines indicate duplicated NAC gene pairs.

using MUSCLE (Edgar, 2004) set at the default parameters and constructed phylogenetic trees by using a maximum likelihood approach with 1000 bootstrap replicates using MEGA X (Kumar et al., 2018). The classification of *PsNACs* was performed according to their phylogenetic relationship with corresponding NAC genes of arabidopsis. The phylogenetic tree was displayed using the online tool iTOL (version 4) (Letunic and Bork, 2016).

GENE STRUCTURES AND CONSERVED MOTIFS OF *PsNACs*. The gene structures of each *PsNAC* was drawn using the Gene Structure Display Server online software package (Hu et al., 2015a). The MEME tool (Bailey et al., 2009) was used to identify conserved motifs shared among siberian apricot NAC proteins (*PsNACs*) (Bailey and Gribskov, 1998; Bailey et al., 2009). The analysis parameters were set as follows: maximum number of different motifs, 20; minimum motif width, 6; and maximum motif width, 50.

GENE DUPLICATION AND EVOLUTIONARY ANALYSIS OF *PsNACs*. We used the Multiple Collinearity Scan Toolkit (MCScanX, default parameters) (Wang et al., 2012) to examine whole-genome duplication (WGD) or segmental, tandem, and dispersed duplicates in the *PsNACs*. We analyzed the collinear relationship of the NAC genes of siberian apricot and peach, japanese apricot, and apple (Gong et al., 2019) using a dual synteny plotter (Chen et al.,

2018). Synonymous substitution (K_s) values were used to calculate the dates of duplication events (T) according to the following equation: $T = K_s/2\lambda$, where $\lambda = 1.5 \times 10^{-8}$ for dicots (Blanc and Wolfe, 2004; Koch et al., 2000). The mode of selection was identified according to the standard protocol described by Kayum using the nonsynonymous to synonymous substitutions (K_a/K_s) value, where $K_a/K_s < 1$ indicates a negative selection, $K_a/K_s = 1$ indicates a neutral selection, and $K_a/K_s > 1$ indicates a positive selection (Gong et al., 2019).

EXPRESSION ANALYSIS USING RNA-SEQUENCING DATA. RNA-sequencing (RNA-seq) data were used to gain insight into the temporal and spatial transcription patterns and were obtained from the Genome Sequence Archive (PRJCA001987). Leaf, flower bud, and flower of the siberian apricot were collected on 15 Mar., 20 Mar., and 5 Apr. 2016, respectively. The fruit and kernel were collected on 16 May, 26 May, 5 June, 15 June, 25 June, and 5 July 2017, representing 25 d (S1), 35 d (S2), 45 d (S3), 55 d (S4), 65 d (S5), and 75 d (S6) after full bloom, respectively. Two biological replicates for each sample were used. The expression levels of genes were measured as fragments per kilobase million (FPKM). The heat maps were created by Heatmap (Chen

et al., 2018) based on the transformed data of $\log_2$ (FPKM+1) values.

QUANTITATIVE REAL-TIME POLYMERASE CHAIN REACTION. For quantitative real-time polymerase chain reaction (qRT-PCR) analysis, 1 μ g of DNA-free RNA was transcribed into first-strand complementary DNA (cDNA) using All-in-One First-Strand Synthesis MasterMix with dsDNase (CodonX Biotechnology Co., Beijing, China). The qRT-PCR was performed with a fluorescent quantitative PCR instrument (LightCycler 480; Roche Diagnostics, Mannheim, Germany) using $2 \times$ SYBR Green qPCR Premix Universal (CodonX Biotechnology Co.). The reaction conditions were 45 cycles at 95 °C for 15 s, 60 °C for 15 s, and 60 °C for 35 s. The primer sequences of target genes were designed with Primer 3 software (Untergasser et al., 2012) and listed in Supplemental Table 1. The housekeeping siberian apricot Ubiquitin-conjugating enzyme (*UBC*) gene (Niu et al., 2014) was used as an internal control (Supplemental Table 1). Each reaction was performed with three repeats from different biological samples. The data from real-time PCR amplification were analyzed using the $2^{-\Delta\Delta C_t}$ method. Statistical analysis using Student's *t* test was performed with Microsoft Excel (version 2010 for Windows; Microsoft Corp., Redmond, WA). Data are provided as means $\pm$ SD of three

Fig. 4. Synteny analysis of NAC genes between siberian apricot and three Rosaceae species: (A) apple, (B) peach, and (C) japanese apricot. Orange, purple, blue, and green blocks present chromosomes of siberian apricot (Ps1–8), apple (Md1–18), japanese apricot (Pm1–8), and peach (Pp1–8), respectively. Red lines denote syntenic NAC gene pairs.

independent biological replicates. The Pearson correlation value, linear fitting equation, and R^2 values of the RNA-seq data and qRT-PCR were assumed using IBM SPSS Statistics (version 23; IBM Corp., Armonk, NY).

Results

IDENTIFICATION OF *PsNACs* IN SIBERIAN APRICOT GENOME. A total of 102 putative NAC protein genes were identified in siberian apricot genome and named after their locations on the chromosomes (*PsNAC1–PsNAC102*) (Supplemental Table 2). The lengths of the predicted proteins ranged from 64 to 860 amino acids (aa), with isoelectric point values between 4.38 and 9.80 and molecular weights between 7.52 and 95.98 kDa. Subcellular localization prediction indicated that most of the *PsNACs* (90) are located in the nucleus, whereas only single *PsNACs* were predicted to be localized in the plasma membrane (*PsNAC28*),

vacuole (*PsNAC17*), and chloroplast (*PsNAC67*). Two *PsNACs* were predicted to localize in the mitochondrion (*PsNACs* 35 and 44), three were predicted to localize in the extracellular space (*PsNACs* 11, 19, and 43), and four were predicted to localize in the cytoplasm (*PsNACs* 34, 87, 93, and 99) (Supplemental Table 2).

PHYLOGENETIC ANALYSIS AND CLASSIFICATION OF *PsNACs*. Based on the homology of the *PsNACs* with those from arabidopsis, 105 *AtNACs* and 102 *PsNACs* were grouped into 14 phylogenetic clades: I (NAP); II (*AtNAC3/ATAF*); III (SENU5); IV (ONAC22/TERN); V (*NAC1/NAM*); VI (*OsNAC7*); VII (ANAC001); VIII (TIP); IX (*OsNAC8*); X (ANAC011); XI (*NAC2*); XII and XIII (ONAC003); and XIV (ANAC063) (Fig. 1). Clade XII contained the largest number of *PsNACs* (21), followed by clades VII (18) and VI (11). Clade IX had the fewest members, with only one *PsNAC*. Additionally, the proteins in clade XII were found to be specific to siberian apricot (Supplemental Table 3).

Fig. 5. Gene expressions of *PsNACs* in leaf, flower bud, flower, fruit, and kernel. RNA-sequencing (RNA-seq) expressions of fruit and kernel are from 75 d after full bloom (S6). Color scale of the upper right represents the value in fragments per kilobase million (FPKM).

PREDICTED PROTEIN MOTIFS AND STRUCTURES OF *PsNACs*. To understand the structural diversity of the *PsNACs*, we determined the conserved protein motifs in the predicted *PsNACs* and the exon/intron composition of the genes (Fig. 2). A total of 20 conserved motifs were identified (Fig. 2A, Supplemental Fig. 1), and all of the *PsNACs* contained at least one conserved motif (motifs 1–7). Specifically, motifs 1 to 7 occurred in a specific order (motifs 1, 5, 4, 3, 6, 2, and 7) in the proteins because they represent the conserved subdomains A, B, C1, C2, D1, D2, and E, respectively, of the N-terminal NAC domains. Except for clade XII, most of the conserved motifs were found in the N-terminal regions of the *PsNACs*, indicating their importance to the function of the NAC proteins. In addition, the motifs present in clade VII and clade XII proteins (13) were the most diverse. We found that all of the members of clade XI contained motifs 4, 5, and 10, except for *PsNAC10*. Motifs 8 and 15 were only absent from proteins in clades XII and VII, respectively. Motifs 4 and 5 were absent from all of the proteins in clade XIII. To further study the gene structures, we predicted the exon/intron composition in the 102 *PsNACs*. We found that the numbers of introns ranged from 0 to 11 (Fig. 2B, Supplemental Table 2). The majority (40; 39.22%) of the genes contained 2 introns, followed by 3 introns (20; 19.61%), 0 introns (11; 10.78%), 1 intron (10; 9.80%), 4 introns (7; 6.86%), 5 introns (6; 5.88%), 6 introns (4; 3.92%), 7 introns (2; 1.96%), 8 introns (1; 0.98%), and 11 introns (1; 0.98%). There were no *PsNACs* with 9 or 10 introns. Most of the *PsNACs* within a clade had similar exon/intron compositions; for example, all members of

clades I, II, III, IV, and V had two introns except for *PsNAC1*, *PsNAC11*, *PsNAC58*, and *PsNAC83*. In contrast, members of clade VII had highly variable intron numbers, ranging from 0 to 11. The conserved motifs and gene structures analyses suggested that *PsNACs* in the same clades may have similar biological functions.

CHROMOSOMAL LOCATION AND SYNTENY ANALYSIS OF *PsNACs* The 102 *PsNACs* were unevenly distributed on the eight siberian apricot chromosomes (Fig. 3). Chromosome 2 had the most *PsNACs* (22; 21.57%), followed by chromosome 4 (16; 15.69%) and chromosome 1 (15; 14.71%), whereas, only eight *PsNACs* were predicted to be located on chromosome 3 (7.84%) (Fig. 3, Supplemental Table 2).

To identify any potential duplication events in *PsNACs*, we performed a collinearity analysis. Nine pairs of segmentally duplicated genes were found in the 102 *PsNACs*. Segmentally duplicated genes were located on chromosomes 1 to 7. Seven duplicated gene pairs were from the same clade, except *PsNAC4* (clade XI) and *PsNAC38* (clade II) and *PsNAC66* (clade XI) (Fig. 3). The nonsynonymous substitution (K_a) and K_s ratios were calculated

to estimate the selection pressure and divergence times of the gene duplication events. All K_a/K_s ratios were <1 (Supplemental Table 4), which indicated that purifying selection was the main force behind the evolution of *PsNACs*. The divergence times of *PsNACs* in siberian apricot ranged from 104.77 to 3.49 million years ago, and most of the duplication events traced back to 40 to 80 million years ago (Supplemental Table 4).

We further performed synteny analyses to compare the siberian apricot genome with apple, peach, and japanese apricot. The results identified 129 pairs of homologous genes between 69 *PsNACs* from siberian apricot and 109 NAC genes in apple (Fig. 4A), followed by 101 pairs between siberian apricot (79) and peach (80) (Fig. 4B) and 86 pairs between siberian apricot (70) and japanese apricot (70) (Fig. 4C) (Supplemental Tables 5–7).

The divergence times of NAC genes in apple ranged from 86.59 to 7.42 million years ago, and most of them occurred 10 to 30 million years ago based on duplication events; for peach, the divergence times ranged from 110.81 to 0.76 million years ago, and most of them occurred between 1 and 10 million years ago. For japanese apricot, the divergence times ranged from 108.65 to 0.13 million years ago, with most of them occurring from 0.3 to 6 million years ago (Supplemental Tables 5–7). Comparisons of the divergence times among the four species showed the shortest time of speciation occurred in japanese apricot and siberian apricot, thereby providing further evidence of the close evolutionary relationship between these two species.

EXPRESSION PATTERNS OF *PsNACs* IN FIVE PLANT TISSUES. The expression patterns of *PsNACs* were investigated in leaves,

Fig. 6. Gene expression of *PsNACs* during (A) fruit and (B) kernel development. Color scale of the upper right represents the scale value in fragments per kilobase million (FPKM).

flower buds, flowers, fruit, and kernels. Most *PsNACs* showed diverse expression patterns within each clade, indicating that these genes may have different functions in all tested tissues (Fig. 5). The expressions of clade VIII and clade XI genes were higher than those of genes from the other clades, indicating that genes in these clades may be involved in growth, development, and morphogenesis in the five tissues; each gene acquired a different function during evolution. *PsNAC93* in clade V showed the highest expression level in the flower, whereas *PsNAC41* and *PsNAC67* were highly expressed in fruit. Additionally, the functions of the different clade proteins could be distinguished because most *PsNACs* had higher expression levels than others in the specific tissues: *PsNAC6* (clade I), *PsNAC33* (clade VII), and *PsNAC9* (clade XIII) in the leaf; *PsNAC33* (clade VII) and *PsNAC68* (clade XII) in the flower bud; and *PsNAC93* (clade V) and *PsNAC37* (clade VIII) in the flower. Eleven *PsNACs* were found to be highly expressed in the fruit, including *PsNAC6*, *PsNAC50*, and *PsNAC92* (clade I), *PsNAC13* (clade II), *PsNAC4* and *PsNAC38* (clade III), *PsNAC41* and *PsNAC67* (clade V), *PsNAC37* (clade VIII), *PsNAC17* (clade XI), and *PsNAC59* (clade XIII). Four genes were highly expressed in the kernel, including *PsNAC13* (clade II), *PsNAC51* (clade II), *PsNAC82* (clade IX), and *PsNAC17* (clade XI). The expression patterns of all the aforementioned *PsNACs*, which were from clades I to III, V, VII, IX, and XI to XIII, showed overlap in the various tissues, indicating that *PsNACs* from these clades may have diverse functions.

EXPRESSION OF *PsNACs* DURING FRUIT AND KERNEL DEVELOPMENT. The expression levels of *PsNACs* during fruit development were evaluated (Fig. 6A). Twenty-six *PsNACs* showed constitutive expression (FPKM>1 in all tested samples). Eight of the 26 genes from clade XI showed a general trend in which gene expression continued to increase during fruit development, indicating that these eight genes could have similar functions. Some *PsNACs* showed diverse expression patterns based on the different expression patterns from the same clade. For example, the expression of *PsNAC9* from clade XIII peaked at S1 during all stages of fruit

development, whereas *PsNAC59*, also from clade XIII, showed the opposite expression pattern.

Eight *PsNACs* were highly expressed in S6, including *PsNAC6* (clade I), *PsNAC13*, *PsNAC46*, and *PsNAC51* (clade II), *PsNAC41* and *PsNAC67* (clade V), *PsNAC37* (clade VIII), and *PsNAC59* (clade XIII), suggesting these *PsNACs* are associated with fruit maturation. Five *PsNACs*, including *PsNAC18* and *PsNAC64* (clade VI), *PsNAC23* and *PsNAC33* (clade VII), and *PsNAC9* (clade XIII), are highly expressed in S1; therefore, they may have important roles in fruit growth. The expression levels of *PsNAC4* (clade III) peaked in S4 and *PsNAC50* (clade I) in S5, respectively, suggesting that they may be involved in fruit development.

The expression levels of the *PsNACs* during kernel development were evaluated (Fig. 6B). The expression patterns in the kernel of *PsNACs* from most clades showed similar trends in the fruit; for example, genes from clade XI were the only group that showed constitutive expression, which suggests that clade XI genes have crucial roles in fruit and kernel development. Four *PsNACs* were found to be highly expressed in S1, including *PsNAC6* (clade I), *PsNAC94* (clade IV), *PsNAC41* (clade V), and *PsNAC32* (clade VII), and these genes may regulate the rapid growth of the kernel. Three *PsNACs* expressed in S6, *PsNAC82* (clade IX), and *PsNAC13* and *PsNAC51* (clade II) may impact dry matter accumulation and maturation of the kernel. *PsNAC17* (clade XI) is highly expressed in both S1 and S6. Four *PsNACs* are highly expressed in S2, including *PsNAC50* (clade I), *PsNAC4* (clade III), *PsNAC67* (clade V), and *PsNAC84* (clade XIII), which indicated that these genes may affect the hardening of the kernel.

To further evaluate the validity of the RNA-seq data, 15 *PsNACs* were selected and their expressions were analyzed by qRT-PCR (Supplemental Fig. 2). The results showed that 14 of the 15 selected *PsNACs* had expression patterns that were consistent with those determined by RNA-seq (Supplemental Table 8). Therefore, the qRT-PCR results validated the reliability of the RNA-seq data.

Discussion

Characterization of the NAC gene family has been reported for many species in the Rosaceae, including strawberry (Moyano et al., 2018), apple (Su et al., 2013), white pear (Gong et al., 2019), peach (Gong et al., 2019), and japanese apricot (Zhuo et al., 2018), whereas studies of the NAC gene family in siberian apricot have provided unclear results (García-Gómez et al., 2019; Niu et al., 2016). In the present study, we systematically analyzed the NAC gene family in the siberian apricot genome. A total of 102 *PsNACs* were identified and divided into 14 clades based on the phylogenetic analysis; these results were similar to those of japanese apricot (Zhuo et al., 2018). This may be a result of the close evolutionary relationship between siberian apricot and japanese apricot. Interestingly, among the 14 *PsNAC* clades, the 21 members of clade XII had no corresponding *AtNAC* proteins, suggesting that the diversification and expansion of the *PsNACs* in clade XII occurred after the divergence of siberian apricot and arabidopsis.

Many of the *PsNACs* (40/102; 39.22%) had 2 introns. These results are similar to those for japanese apricot (48/113; 42.48%) (Zhuo et al., 2018), apple (79/180; 43.89%) (Su et al., 2013), and white pear (86/183; 46.99%) (Gong et al., 2019). Most of

the *PsNACs* that encode proteins in the same clade showed similar exon/intron compositions, suggesting that the structures of *PsNACs* are relatively conserved.

Each *PsNAC* was predicted to contain at least one conserved motif (motifs 1–7). Motifs 1 to 7 correspond to subdomains A, D2, C2, C1, B, D1, and E, respectively, which is consistent with previous findings for japanese apricot (Zhuo et al., 2018). Additionally, most of the conserved motifs were found in the N-terminal regions of the predicted *PsNACs*, indicating that the N-terminus is an important part of the NAC proteins, as has been shown previously for potato (*Solanum tuberosum*) (Koch et al., 2000) and cassava (Hu et al., 2015b). Therefore, our results provide evidence that the conserved motifs are significant to the functions of the NAC proteins.

Gene duplication events are an important way of generating new genes that encode proteins with improved or novel functions, and they are vital to the evolution of genomes and genetic systems (Moore and Purugganan, 2003). The recent occurrence of a WGD was found in apple and white pear (Su et al., 2013); in contrast, siberian apricot, peach, and japanese apricot showed evidence of an ancient WGD, but no recent WGD (Gong et al., 2019). Considering that most gene duplication events between japanese apricot and peach occurred ≈ 1 to 5 million years ago (Zhuo et al., 2018), we inferred that siberian apricot has the closest evolutionary relationships with japanese apricot, followed by peach, and is evolutionarily most distant from apple.

We performed RNA-seq transcriptome analyses of five tissues to understand the expression patterns of the *PsNACs* and their physiological or reproductive functions. Three *PsNACs* had relatively higher expression levels in leaves, two in flower buds, two in flowers, four in kernels, and 11 (the highest number) during fruit development. These results suggest that the *PsNACs* may have acquired different functions during evolution. Similar tissue-specific expression profiles were found for other species, including tomato (Jin et al., 2020), cassava (Hu et al., 2015b), and soybean (Le et al., 2011).

According to the RNA-seq analysis of the *PsNACs* involved in fruit and kernel development, we found that *PsNAC4* (clade III) in S4, *PsNAC50* (clade I) in S5, and *PsNAC41* (clade V) and *PsNAC59* (clade XIII) in S6 were homologous with *FvNAC042*, *FvNAC035*, *FvNAC092*, and *FvNAC006* in strawberry, respectively; of these, *FvNAC035* impacts fruit ripening, *FvNAC042* is involved in fruit growth and development, and *FvNAC006* and *FvNAC092* may be related to fruit senescence (Moyano et al., 2018). These results imply that the functions of *PsNACs* may be related to the characteristics of the NAC gene family. *PsNAC50* (clade I) and *PsNAC67* (clade V) in S2 of kernel development are homologous with arabidopsis *AtNAM* (Duval et al., 2002) and maize *APN-1* (*NAM*-related protein 1-like) (Verza et al., 2011); *AtNAM* is associated with developing seeds and *APN-1* (*NAM*-related protein 1-like) in maize has a role in regulating the late phases of endosperm development.

In summary, we identified and characterized the *PsNAC* gene/protein family in siberian apricot genome. We also performed systematic investigations of the gene structures and evolutionary relationships among the *PsNACs* and the proteins they are predicted to encode. Our results create a foundation for

future research of the biological functions of *PsNACs* involved in fruit and kernel development in siberian apricot.

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Supplemental Table 1. Primer sequences used for quantitative real-time polymerase chain reaction (qRT-PCR).

Gene name	Sense primer	Anti-sense primer
<i>UBC^z</i>	GAGACCAGCAATAACCGTGAA	TCTTGTAATCCGTGGCATCCT
<i>PsNAC9</i>	GATGTTCGCTGGCACAAGACT	CCTTCTCATCCTCCTCAGTTCC
<i>PsNAC59</i>	TGGCACAAGACAGGGAAGACAA	ACTTTTGAGACCACCAGCTCCC
<i>PsNAC6</i>	TTCTTTACCCCAAGGGACAGGA	GCTTTCTTCACCCCCACATACT
<i>PsNAC33</i>	CTTGGGATTACCTGGGATGTT	CTCGCTTAGTGACCCTGTTGG
<i>PsNAC51</i>	CTCTGGTTTTCTATGTCGGCAA	ACGACACAAAACCCATTTCATCC
<i>PsNAC67</i>	GTCTGAGGACAAACAGGGCAAC	GCTCTGCCTCTGTAGAAAACCAAG
<i>PsNAC4</i>	GGCAACTGGGTAGACAAGCAA	GCCAAAACAAGGCGATATTTCAT
<i>PsNAC37</i>	GGTCTTCCATACTGGTCGTGCT	CAGACGACAAAGAACAAGGGAT
<i>PsNAC13</i>	ACAAATACAAACCCCTGGGACCT	CCAAAGCCTTCTTAATCCCGACT
<i>PsNAC50</i>	CAGGGACTGATAAGCCCGTGT	TGGTCTTGTTATCAGCCAGCCTA
<i>PsNAC64</i>	AGAATCGGGTTGAGAAAGACGC	ATACTCGGCATACCACCCACC
<i>PsNAC94</i>	CGTTTGCTGATAACTGCCACT	GTTGGCTGCAAAATGAGATGGT
<i>PsNAC32</i>	TTTAGGGATACTTCCGCTGACG	CGGCAGTTTGAGGATATGGAGG

^zUBC = Ubiquitin-conjugating enzyme gene.

Supplemental Table 2. Information for NAC genes in siberian apricot genome.

Gene name	Gene	Chromosome	Start	End	Strand	aa ^z	CDS ^z	Exon no.	pI ^z	MW ^z	Cell location
<i>PsNAC1</i>	PaF106G0100001051.01.T02	Chr1	6804341	6805605	-	304	911	4	5.94	34608.19	Nucleus
<i>PsNAC2</i>	PaF106G0100001251.01.T01	Chr1	8404432	8405592	-	386	1160	1	4.76	44225.08	Nucleus
<i>PsNAC3</i>	PaF106G0100001279.01.T01	Chr1	8567150	8568717	+	363	1091	1	5.01	41486.18	Nucleus
<i>PsNAC4</i>	PaF106G0100002691.01.T01	Chr1	20140448	20141909	-	258	774	3	9.16	29439.4	Nucleus
<i>PsNAC5</i>	PaF106G0100003290.01.T01	Chr1	23997571	23999385	+	484	1452	3	7.26	53697.01	Nucleus
<i>PsNAC6</i>	PaF106G0100003324.01.T01	Chr1	24162587	24163966	-	288	864	3	7.01	33193.55	Nucleus
<i>PsNAC7</i>	PaF106G0100003398.01.T02	Chr1	24487653	24489336	-	162	485	5	5.04	18457.53	Nucleus
<i>PsNAC8</i>	PaF106G0100003399.01.T02	Chr1	24494068	24495808	-	204	612	4	5.17	23330.42	Nucleus
<i>PsNAC9</i>	PaF106G0100003636.01.T01	Chr1	25687665	25691020	+	454	1359	6	4.84	51532.22	Nucleus
<i>PsNAC10</i>	PaF106G0100004524.01.T01	Chr1	30089751	30092820	+	382	1144	6	7.91	42409.48	Nucleus
<i>PsNAC11</i>	PaF106G0100005052.01.T03	Chr1	32558219	32560259	+	287	860	4	9.36	33034.65	Extracellular
<i>PsNAC12</i>	PaF106G0100005288.01.T01	Chr1	33802255	33804582	+	342	1026	3	8.95	38086.85	Nucleus
<i>PsNAC13</i>	PaF106G0100005713.01.T02	Chr1	36334023	36335570	+	297	891	3	8.09	34149.33	Nucleus
<i>PsNAC14</i>	PaF106G0100006471.01.T01	Chr1	41134752	41136214	+	209	627	3	5.15	23852.47	Nucleus
<i>PsNAC15</i>	PaF106G0100006718.01.T01	Chr1	42716774	42718051	+	367	1102	2	4.85	40933.42	Nucleus
<i>PsNAC16</i>	PaF106G0200008014.01.T01	Chr2	11802179	11808156	+	641	1922	4	5.79	69822.65	Nucleus
<i>PsNAC17</i>	PaF106G0200008016.01.T04	Chr2	11821460	11825086	+	591	1770	6	4.51	66277.37	Vacuole
<i>PsNAC18</i>	PaF106G0200009314.01.T01	Chr2	20032319	20034084	-	400	1200	4	5.92	45208.13	Nucleus
<i>PsNAC19</i>	PaF106G0200009318.01.T01	Chr2	20062396	20063511	-	290	871	2	4.8	33108.47	Extracellular
<i>PsNAC20</i>	PaF106G0200009362.01.T03	Chr2	20317704	20323951	-	788	2360	7	5.05	84824.2	Nucleus
<i>PsNAC21</i>	PaF106G0200009364.01.T02	Chr2	20326120	20329544	-	598	1791	8	5.06	64473.71	Nucleus
<i>PsNAC22</i>	PaF106G0200009366.01.T01	Chr2	20332537	20334505	-	313	939	3	5.37	34380.65	Nucleus
<i>PsNAC23</i>	PaF106G0200009367.01.T01	Chr2	20335987	20338951	-	324	972	4	5.51	35736.17	Nucleus
<i>PsNAC24</i>	PaF106G0200009369.01.T01	Chr2	20342925	20345373	-	460	1378	5	4.69	51859.21	Nucleus
<i>PsNAC25</i>	PaF106G0200009371.01.T01	Chr2	20348339	20350573	-	248	744	5	8.32	28128.51	Nucleus
<i>PsNAC26</i>	PaF106G0200009372.01.T01	Chr2	20355733	20358036	-	457	1369	5	4.51	51503.89	Nucleus
<i>PsNAC27</i>	PaF106G0200009374.01.T02	Chr2	20362068	20363313	-	329	987	3	8.68	38064.08	Nucleus
<i>PsNAC28</i>	PaF106G0200009376.01.T01	Chr2	20401724	20402105	-	100	302	1	5.21	11283.31	Plasma membrane
<i>PsNAC29</i>	PaF106G0200009380.01.T01	Chr2	20437996	20443271	-	494	1477	12	5.04	57082.2	Nucleus
<i>PsNAC30</i>	PaF106G0200009381.01.T02	Chr2	20445394	20447732	-	446	1332	9	4.62	51962.39	Nucleus
<i>PsNAC31</i>	PaF106G0200009383.01.T01	Chr2	20449886	20452725	-	494	1479	6	6.79	57559.45	Nucleus
<i>PsNAC32</i>	PaF106G0200009384.01.T06	Chr2	20459703	20462470	-	475	1421	7	7.21	55305.04	Nucleus
<i>PsNAC33</i>	PaF106G0200009404.01.T01	Chr2	20567897	20569176	+	152	456	4	9.76	17941.81	Nucleus
<i>PsNAC34</i>	PaF106G0200009406.01.T01	Chr2	20571304	20572535	+	186	557	4	5.22	21887.67	Cytoplasm
<i>PsNAC35</i>	PaF106G0200009409.01.T01	Chr2	20589188	20590871	+	113	340	4	9.8	13442.35	Mitochondrion
<i>PsNAC36</i>	PaF106G0200010296.01.T01	Chr2	24966612	24969376	-	221	663	4	8.56	26134.61	Nucleus
<i>PsNAC37</i>	PaF106G0200010786.01.T02	Chr2	27262191	27265562	-	385	1153	6	5.17	43566.53	Nucleus
<i>PsNAC38</i>	PaF106G0300010962.01.T01	Chr3	430522	431723	-	237	711	3	9.38	27123.66	Nucleus
<i>PsNAC39</i>	PaF106G0300011153.01.T01	Chr3	1275832	1279258	-	389	1164	6	5.18	42813.48	Nucleus
<i>PsNAC40</i>	PaF106G0300011420.01.T01	Chr3	2467978	2469483	-	395	1185	3	6.02	44068.17	Nucleus
<i>PsNAC41</i>	PaF106G0300011468.01.T01	Chr3	2652398	2653995	+	352	1056	3	6.56	40144.96	Nucleus
<i>PsNAC42</i>	PaF106G0300012473.01.T01	Chr3	8261982	8264494	+	305	915	3	8.35	35325.99	Nucleus
<i>PsNAC43</i>	PaF106G0300013351.01.T01	Chr3	15562474	15562668	+	64	194	1	4.44	7517.43	Extracellular
<i>PsNAC44</i>	PaF106G0300013354.01.T01	Chr3	15588895	15589284	+	103	311	1	6.57	11759.22	Mitochondrion
<i>PsNAC45</i>	PaF106G0300013852.01.T01	Chr3	19401906	19402978	-	321	965	1	4.92	35761.65	Nucleus
<i>PsNAC46</i>	PaF106G0400014754.01.T01	Chr4	1314360	1315884	-	292	876	3	6.19	33694.09	Nucleus
<i>PsNAC47</i>	PaF106G0400015194.01.T01	Chr4	6757960	6759582	+	383	1149	3	8.28	44502.24	Nucleus
<i>PsNAC48</i>	PaF106G0400015523.01.T01	Chr4	9268251	9269240	-	329	989	1	4.88	36895.89	Nucleus
<i>PsNAC49</i>	PaF106G0400015525.01.T01	Chr4	9280734	9281824	-	362	1087	2	5.02	41186.2	Nucleus
<i>PsNAC50</i>	PaF106G0400015969.01.T01	Chr4	12618287	12620308	-	371	1113	3	7.18	41158.12	Nucleus

(Continued on next page)

Supplemental Table 2. (Continued)

Gene name	Gene	Chromosome	Start	End	Strand	aa ^z	CDS ^z	Exon no.	pI ^z	MW ^z	Cell location
<i>PsNAC51</i>	PaF106G0400015972.01.T01	Chr4	12640569	12642193	-	350	1050	3	8.14	39213.97	Nucleus
<i>PsNAC52</i>	PaF106G0400016087.01.T01	Chr4	13324581	13326270	-	290	871	3	8.8	31870.59	Nucleus
<i>PsNAC53</i>	PaF106G0400016422.01.T01	Chr4	15293662	15295771	+	385	1155	3	8.41	43665.14	Nucleus
<i>PsNAC54</i>	PaF106G0400016439.01.T01	Chr4	15405087	15405854	-	255	767	1	5.47	29722.26	Nucleus
<i>PsNAC55</i>	PaF106G0400016619.01.T01	Chr4	16375152	16377035	-	322	966	3	6.67	37184.41	Nucleus
<i>PsNAC56</i>	PaF106G0400016793.01.T01	Chr4	17500303	17503440	-	354	1061	4	4.77	40320.58	Nucleus
<i>PsNAC57</i>	PaF106G0400016834.01.T02	Chr4	17751495	17752879	-	293	879	3	7.04	33458.48	Nucleus
<i>PsNAC58</i>	PaF106G0400017046.01.T01	Chr4	19111398	19113864	+	328	983	4	8.97	37526.37	Nucleus
<i>PsNAC59</i>	PaF106G0400017722.01.T01	Chr4	22771175	22773638	-	317	951	3	8.47	35771.22	Nucleus
<i>PsNAC60</i>	PaF106G0400017892.01.T01	Chr4	23532747	23534514	+	365	1095	3	8.76	40148.64	Nucleus
<i>PsNAC61</i>	PaF106G0400018075.01.T01	Chr4	24441507	24444272	+	213	640	4	5.7	24282.87	Nucleus
<i>PsNAC62</i>	PaF106G0500018516.01.T01	Chr5	631098	633597	+	437	1311	3	6.33	49275.31	Nucleus
<i>PsNAC63</i>	PaF106G0500019383.01.T01	Chr5	7301548	7305242	-	362	1086	4	6.4	42228.94	Nucleus
<i>PsNAC64</i>	PaF106G0500020061.01.T01	Chr5	11974628	11976100	-	394	1182	3	5.94	45450.45	Nucleus
<i>PsNAC65</i>	PaF106G0500020096.01.T01	Chr5	12160028	12164081	-	860	2575	8	5.04	95982.39	Nucleus
<i>PsNAC66</i>	PaF106G0500020210.01.T01	Chr5	12737137	12738204	-	262	786	3	8.21	29696.28	Nucleus
<i>PsNAC67</i>	PaF106G0500020796.01.T01	Chr5	15443847	15445816	+	360	1080	3	7.64	40281.49	Chloroplast
<i>PsNAC68</i>	PaF106G0500020907.01.T02	Chr5	16125215	16126014	+	189	568	2	7.79	21790.59	Nucleus
<i>PsNAC69</i>	PaF106G0500021114.01.T01	Chr5	17089806	17091486	+	353	1059	3	6.61	39611.23	Nucleus
<i>PsNAC70</i>	PaF106G0500021325.01.T01	Chr5	18137845	18140144	-	261	783	3	5.07	29853.16	Nucleus
<i>PsNAC71</i>	PaF106G0600022049.01.T02	Chr6	3943738	3945341	+	350	1051	2	5.15	39864.78	Nucleus
<i>PsNAC72</i>	PaF106G0600022464.01.T01	Chr6	6149190	6150307	+	366	1099	2	4.71	42209.09	Nucleus
<i>PsNAC73</i>	PaF106G0600022544.01.T01	Chr6	6675482	6676147	-	221	665	1	8.54	26077.31	Nucleus
<i>PsNAC74</i>	PaF106G0600022545.01.T01	Chr6	6680851	6682501	-	163	489	3	8.79	19337.88	Nucleus
<i>PsNAC75</i>	PaF106G0600022547.01.T01	Chr6	6688780	6690470	-	344	1032	3	8.81	39185.23	Nucleus
<i>PsNAC76</i>	PaF106G0600022604.01.T01	Chr6	7085247	7086174	+	261	784	2	8.32	30169.42	Nucleus
<i>PsNAC77</i>	PaF106G0600022607.01.T01	Chr6	7094122	7095475	+	410	1231	2	4.38	46410.02	Nucleus
<i>PsNAC78</i>	PaF106G0600022711.01.T01	Chr6	7930679	7932577	-	304	913	2	5.68	34799.28	Nucleus
<i>PsNAC79</i>	PaF106G0600022722.01.T01	Chr6	7973329	7974426	+	365	1097	1	4.77	42331.88	Nucleus
<i>PsNAC80</i>	PaF106G0600022733.01.T01	Chr6	8064375	8065537	-	356	1070	2	4.69	41315.79	Nucleus
<i>PsNAC81</i>	PaF106G0600023030.01.T01	Chr6	10543449	10545038	+	198	595	3	6.19	21988.6	Nucleus
<i>PsNAC82</i>	PaF106G0600023066.01.T01	Chr6	10951041	10955242	+	389	1166	4	5.84	43480.38	Nucleus
<i>PsNAC83</i>	PaF106G0600024369.01.T01	Chr6	22291525	22293375	+	356	1068	4	7.55	40413.21	Nucleus
<i>PsNAC84</i>	PaF106G0700026542.01.T01	Chr7	3116989	3121707	-	485	1452	7	6.63	54591.53	Nucleus
<i>PsNAC85</i>	PaF106G0700027143.01.T01	Chr7	6153741	6157924	-	335	1005	4	5	38649.15	Nucleus
<i>PsNAC86</i>	PaF106G0700027914.01.T01	Chr7	10349543	10351137	+	257	771	3	9.64	29567.39	Nucleus
<i>PsNAC87</i>	PaF106G0700028020.01.T02	Chr7	10981600	10985010	-	372	1113	7	4.94	41460.6	Cytoplasm
<i>PsNAC88</i>	PaF106G0700028379.01.T01	Chr7	13627838	13629260	+	401	1203	3	6.32	46086.95	Nucleus
<i>PsNAC89</i>	PaF106G0700028380.01.T01	Chr7	13631687	13634769	+	290	870	3	5.9	33560.09	Nucleus
<i>PsNAC90</i>	PaF106G0700028413.01.T01	Chr7	13869695	13871283	-	400	1200	3	4.86	45270.23	Nucleus
<i>PsNAC91</i>	PaF106G0700029093.01.T03	Chr7	20891518	20893369	-	479	1436	4	5.09	53507.76	Nucleus
<i>PsNAC92</i>	PaF106G0700029265.01.T01	Chr7	22450132	22451918	-	384	1152	3	7.76	42977.5	Nucleus
<i>PsNAC93</i>	PaF106G0800029902.01.T01	Chr8	2990380	2994055	-	239	717	3	8.6	27565.43	Cytoplasm
<i>PsNAC94</i>	PaF106G0800030484.01.T01	Chr8	5916364	5917998	-	291	873	3	7.03	33868.74	Nucleus
<i>PsNAC95</i>	PaF106G0800031447.01.T01	Chr8	11262037	11262976	+	286	860	1	5.59	33051.85	Nucleus
<i>PsNAC96</i>	PaF106G0800031681.01.T01	Chr8	12998406	13000349	+	299	896	4	8.77	34038.83	Nucleus
<i>PsNAC97</i>	PaF106G0800032053.01.T01	Chr8	16472387	16474230	-	306	918	3	6.21	35519.6	Nucleus
<i>PsNAC98</i>	PaF106G0800032290.01.T01	Chr8	18879434	18883273	+	577	1729	5	5.1	65381.9	Nucleus
<i>PsNAC99</i>	PaF106G0800032439.01.T01	Chr8	20206705	20209321	-	432	1295	4	4.55	48114.89	Cytoplasm
<i>PsNAC100</i>	PaF106G0800032441.01.T02	Chr8	20212858	20214900	-	372	1114	5	5.01	41963.01	Nucleus
<i>PsNAC101</i>	PaF106G0800032442.01.T01	Chr8	20223298	20226512	-	351	1052	5	5.32	39292.02	Nucleus
<i>PsNAC102</i>	PaF106G0800032900.01.T01	Chr8	23458676	23460601	-	378	1134	3	7.29	42968.71	Nucleus

^zaa = amino acids, CDS = coding sequence, pI = isoelectric point, MW = molecular weight.

Supplemental Table 3. Grouping of NAC proteins in siberian apricot and arabidopsis.

Clade	PsNAC	AtNAC
I (NAP)	PsNAC1, PsNAC6, PsNAC11, PsNAC47, PsNAC50, PsNAC60, PsNAC75, PsNAC83, PsNAC92	AT1G52880.1, AT3G15510.1, AT1G61110.1, AT1G69490.1, AT3G04070.1
II (AtNAC3/ATAF)	PsNAC51, PsNAC13, PsNAC46, PsNAC14	AT1G52890.1, AT3G15500.1, AT4G27410.2, AT1G01720.1, AT1G77450.1, AT5G08790.1, AT5G63790.1, AT5G50820.1, AT5G64530.1
III (SENU5)	PsNAC66, PsNAC88, PsNAC89, PsNAC4, PsNAC38	AT5G13180.1, AT2G33480.1, AT5G14000.1, AT5G41090.1
IV (ONAC22/TERN)	PsNAC5, PsNAC40, PsNAC42, PsNAC55, PsNAC58, PsNAC94, PsNAC81, PsNAC86	AT5G39820.1, AT1G26870.1, AT2G43000.1, AT2G17040.1, AT2G02450.1, AT2G02450.2, AT3G44350.1, AT5G22380.1
V (NAC1/NAM)	PsNAC12, PsNAC41, PsNAC52, PsNAC62, PsNAC67, PsNAC69, PsNAC93	AT5G07680.1, AT5G07680.2, AT5G61430.1, AT3G29035.1, AT5G39610.1, AT3G04060.1, AT5G18270.1, AT1G76420.1, AT5G53950.1, AT3G15170.1, AT3G18400.1, AT2G24430.1, AT2G24430.2, AT1G56010.1, AT1G56010.2, AT4G28530.1
VI (OsNAC7)	PsNAC18, PsNAC36, PsNAC57, PsNAC61, PsNAC63, PsNAC64, PsNAC85, PsNAC96, PsNAC97, PsNAC102	AT1G12260.1, AT1G62700.1, AT5G62380.1, AT1G71930.1, AT5G66300.1, AT2G18060.1, AT4G36160.1, AT1G33280.1, AT4G10350.1, AT1G79580.1, AT1G32770.1, AT2G46770.1, AT3G61910.1
VII (ANAC001)	PsNAC20, PsNAC21, PsNAC22, PsNAC23, PsNAC24, PsNAC25, PsNAC26, PsNAC27, PsNAC28, PsNAC29, PsNAC30, PsNAC31, PsNAC32, PsNAC33, PsNAC34, PsNAC35, PsNAC91, PsNAC8	AT1G01010.1, AT1G02220.1, AT3G04420.1, AT1G02230.1, AT1G02250.1, AT4G01550.1, AT4G01520.1, AT4G01540.1, AT1G64105.1, AT5G18300.1, AT3G04430.1, AT1G03490.1
VIII (TIP)	PsNAC37, PsNAC65	AT1G33060.1, AT3G49530.1, AT5G24590.2
IX (OsNAC8)	PsNAC82	AT3G44290.1, AT5G22290.1, AT2G27300.1
X (ANAC011)	PsNAC56, PsNAC70	AT1G54330.1, AT3G17730.1, AT1G65910.1, AT3G03200.1, AT5G17260.1, AT1G32510.1, AT4G17980.1, AT5G46590.1
XI (NAC2)	PsNAC10, PsNAC16, PsNAC17, PsNAC87, PsNAC98, PsNAC99, PsNAC100, PsNAC101	AT5G09330.1, AT5G64060.1, AT3G10500.1, AT5G04410.1, AT5G04400.1, AT3G10480.1, AT3G10490.1, AT3G10490.2, AT1G34180.1, AT1G34190.1, AT1G32870.1
XII	PsNAC2, PsNAC3, PsNAC15, PsNAC43, PsNAC44, PsNAC45, PsNAC48, PsNAC49, PsNAC53, PsNAC54, PsNAC68, PsNAC71, PsNAC72, PsNAC73, PsNAC74, PsNAC76, PsNAC77, PsNAC78, PsNAC79, PsNAC80, PsNAC95	

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Supplemental Table 3. (Continued)

Clade	PsNAC	AtNAC
X III (ONAC003)	PsNAC9, PsNAC39, PsNAC59, PsNAC84	AT1G28470.1, AT4G28500.1, AT5G56620.1, AT4G29230.1, AT1G25580.1, AT3G01600.1, AT5G14490.1
X IV (ANAC063)	PsNAC19, PsNAC7, PsNAC90	AT3G56560.1, AT3G56530.1, AT3G55210.1, AT5G39690.1, AT1G60280.1, AT1G60350.1

Supplemental Table 4. Estimated non-synonymous (Ka) to synonymous (Ks) substitution ratios and divergence times of the duplicated PsNACs.

Duplication gene pairs	Ka	Ks	Ka/Ks	Selection type	Divergence time (Mya) ^z
<i>PsNAC4</i> vs. <i>PsNAC38</i>	0.460	1.874	0.245	Purifying	62.48
<i>PsNAC4</i> vs. <i>PsNAC66</i>	0.271	1.159	0.234	Purifying	38.63
<i>PsNAC5</i> vs. <i>PsNAC40</i>	0.307	1.223	0.251	Purifying	40.77
<i>PsNAC18</i> vs. <i>PsNAC64</i>	0.323	2.041	0.158	Purifying	68.02
<i>PsNAC36</i> vs. <i>PsNAC61</i>	0.079	0.105	0.756	Purifying	3.49
<i>PsNAC37</i> vs. <i>PsNAC65</i>	0.424	3.143	0.135	Purifying	104.77
<i>PsNAC38</i> vs. <i>PsNAC66</i>	0.635	2.539	0.250	Purifying	84.65
<i>PsNAC75</i> vs. <i>PsNAC83</i>	0.442	1.750	0.253	Purifying	58.34
<i>PsNAC81</i> vs. <i>PsNAC86</i>	0.624	2.303	0.271	Purifying	76.78

^zMillion years ago.

Supplemental Table 5. Estimated non-synonymous (Ka) to synonymous (Ks) substitution ratios and divergence times of the systemic gene pairs of NAC between siberian apricot and apple.

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC4</i> vs. <i>MD06G1135700</i>	0.277	1.371	0.202	45.69
<i>PsNAC4</i> vs. <i>MD13G1125000</i>	0.117	0.667	0.175	22.23
<i>PsNAC4</i> vs. <i>MD14G1150900</i>	0.301	1.660	0.181	55.34
<i>PsNAC4</i> vs. <i>MD16G1125800</i>	0.073	0.542	0.134	18.07
<i>PsNAC5</i> vs. <i>MD09G1050400</i>	0.319	1.426	0.224	47.53
<i>PsNAC5</i> vs. <i>MD13G1072500</i>	0.076	0.386	0.197	12.87
<i>PsNAC5</i> vs. <i>MD16G1073300</i>	0.066	0.401	0.165	13.38
<i>PsNAC6</i> vs. <i>MD13G1069200</i>	0.107	0.780	0.138	26.02
<i>PsNAC6</i> vs. <i>MD16G1069500</i>	0.109	0.777	0.140	25.89
<i>PsNAC7</i> vs. <i>MD13G1063900</i>	0.395	0.868	0.454	28.94
<i>PsNAC7</i> vs. <i>MD16G1062600</i>	0.393	0.821	0.479	27.35
<i>PsNAC9</i> vs. <i>MD13G1046600</i>	0.088	0.242	0.365	8.06
<i>PsNAC9</i> vs. <i>MD16G1048300</i>	0.088	0.223	0.395	7.42
<i>PsNAC11</i> vs. <i>MD08G1096700</i>	0.207	0.507	0.408	16.89
<i>PsNAC11</i> vs. <i>MD15G1079400</i>	0.191	0.450	0.425	15.01
<i>PsNAC12</i> vs. <i>MD08G1121300</i>	0.075	0.350	0.215	11.66
<i>PsNAC12</i> vs. <i>MD15G1100100</i>	0.057	0.407	0.139	13.58
<i>PsNAC13</i> vs. <i>MD15G1344900</i>	0.078	0.605	0.130	20.16
<i>PsNAC14</i> vs. <i>MD08G1222300</i>	0.085	0.400	0.211	13.33
<i>PsNAC14</i> vs. <i>MD15G1415700</i>	0.091	0.398	0.228	13.26
<i>PsNAC16</i> vs. <i>MD02G1243800</i>	0.417	1.551	0.269	51.70
<i>PsNAC17</i> vs. <i>MD02G1243200</i>	0.135	0.424	0.318	14.15
<i>PsNAC17</i> vs. <i>MD07G1073100</i>	0.688	1.907	0.361	63.58
<i>PsNAC18</i> vs. <i>MD01G1088100</i>	0.107	0.556	0.193	18.54
<i>PsNAC18</i> vs. <i>MD07G1158300</i>	0.073	0.469	0.155	15.64
<i>PsNAC18</i> vs. <i>MD14G1137900</i>	0.308	1.432	0.215	47.73
<i>PsNAC20</i> vs. <i>MD01G1092200</i>	0.363	1.075	0.338	35.82
<i>PsNAC21</i> vs. <i>MD01G1092200</i>	0.296	0.715	0.414	23.82
<i>PsNAC21</i> vs. <i>MD07G1162700</i>	0.461	0.807	0.571	26.89
<i>PsNAC22</i> vs. <i>MD01G1092900</i>	0.424	0.888	0.478	29.58
<i>PsNAC23</i> vs. <i>MD01G1093000</i>	0.538	0.753	0.714	25.11
<i>PsNAC25</i> vs. <i>MD07G1162800</i>	0.363	0.407	0.893	13.56
<i>PsNAC27</i> vs. <i>MD01G1092600</i>	0.410	0.816	0.503	27.19
<i>PsNAC28</i> vs. <i>MD01G1093500</i>	0.391	0.670	0.584	22.34
<i>PsNAC29</i> vs. <i>MD01G1093900</i>	0.219	0.337	0.651	11.23
<i>PsNAC30</i> vs. <i>MD01G1093800</i>	0.249	0.590	0.422	19.66
<i>PsNAC31</i> vs. <i>MD01G1094700</i>	0.319	0.490	0.650	16.33
<i>PsNAC31</i> vs. <i>MD07G1163400</i>	0.389	0.514	0.757	17.14
<i>PsNAC32</i> vs. <i>MD01G1094700</i>	0.373	0.546	0.683	18.20
<i>PsNAC36</i> vs. <i>MD07G1254800</i>	0.018	0.345	0.051	11.50
<i>PsNAC37</i> vs. <i>MD01G1229900</i>	0.141	0.485	0.290	16.18
<i>PsNAC37</i> vs. <i>MD06G1124800</i>	0.422	2.557	0.165	85.24
<i>PsNAC37</i> vs. <i>MD07G1301800</i>	0.134	0.481	0.278	16.02
<i>PsNAC38</i> vs. <i>MD06G1135700</i>	0.560	1.824	0.307	60.78
<i>PsNAC38</i> vs. <i>MD09G1006400</i>	0.200	0.478	0.419	15.94
<i>PsNAC38</i> vs. <i>MD14G1150900</i>	0.525	1.759	0.299	58.63
<i>PsNAC38</i> vs. <i>MD16G1125800</i>	0.491	2.598	0.189	86.59
<i>PsNAC38</i> vs. <i>MD17G1010300</i>	0.208	0.485	0.429	16.16
<i>PsNAC39</i> vs. <i>MD09G1023600</i>	0.096	0.235	0.408	7.83
<i>PsNAC39</i> vs. <i>MD17G1023100</i>	0.128	0.319	0.400	10.62
<i>PsNAC40</i> vs. <i>MD09G1050400</i>	0.069	0.495	0.140	16.49
<i>PsNAC40</i> vs. <i>MD13G1072500</i>	0.341	1.769	0.193	58.96
<i>PsNAC40</i> vs. <i>MD16G1073300</i>	0.348	1.450	0.240	48.34
<i>PsNAC40</i> vs. <i>MD17G1050600</i>	0.084	0.469	0.178	15.63
<i>PsNAC41</i> vs. <i>MD09G1053700</i>	0.082	0.562	0.145	18.74

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Supplemental Table 5. (Continued)

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC41</i> vs. <i>MD17G1051600</i>	0.082	0.591	0.140	19.70
<i>PsNAC42</i> vs. <i>MD09G1147500</i>	0.117	0.311	0.376	10.35
<i>PsNAC42</i> vs. <i>MD17G1134400</i>	0.100	0.282	0.356	9.39
<i>PsNAC46</i> vs. <i>MD15G1136600</i>	0.083	0.593	0.140	19.76
<i>PsNAC47</i> vs. <i>MD03G1172900</i>	0.257	0.680	0.378	22.67
<i>PsNAC47</i> vs. <i>MD11G1190900</i>	0.279	0.704	0.396	23.46
<i>PsNAC50</i> vs. <i>MD03G1222600</i>	0.076	0.581	0.131	19.37
<i>PsNAC50</i> vs. <i>MD05G1321800</i>	0.147	1.474	0.100	49.13
<i>PsNAC50</i> vs. <i>MD10G1299900</i>	0.292	2.215	0.132	73.84
<i>PsNAC50</i> vs. <i>MD11G1239900</i>	0.065	0.641	0.102	21.36
<i>PsNAC51</i> vs. <i>MD03G1222700</i>	0.106	0.627	0.169	20.90
<i>PsNAC52</i> vs. <i>MD11G1253500</i>	0.069	0.624	0.110	20.79
<i>PsNAC54</i> vs. <i>MD03G1255100</i>	0.255	0.488	0.523	16.25
<i>PsNAC55</i> vs. <i>MD05G1221100</i>	0.087	0.489	0.178	16.29
<i>PsNAC56</i> vs. <i>MD05G1239300</i>	0.045	0.341	0.133	11.38
<i>PsNAC56</i> vs. <i>MD10G1217500</i>	0.043	0.325	0.132	10.85
<i>PsNAC57</i> vs. <i>MD10G1220600</i>	0.047	0.479	0.098	15.95
<i>PsNAC58</i> vs. <i>MD05G1258300</i>	0.112	0.428	0.262	14.27
<i>PsNAC58</i> vs. <i>MD10G1238200</i>	0.102	0.494	0.207	16.46
<i>PsNAC59</i> vs. <i>MD05G1309700</i>	0.033	0.503	0.065	16.76
<i>PsNAC59</i> vs. <i>MD10G1288300</i>	0.036	0.525	0.068	17.50
<i>PsNAC60</i> vs. <i>MD05G1321800</i>	0.081	0.605	0.133	20.16
<i>PsNAC60</i> vs. <i>MD10G1299900</i>	0.123	0.561	0.220	18.70
<i>PsNAC61</i> vs. <i>MD07G1254700</i>	0.054	0.411	0.132	13.69
<i>PsNAC61</i> vs. <i>MD11G1195600</i>	0.038	0.536	0.072	17.85
<i>PsNAC62</i> vs. <i>MD06G1004900</i>	0.161	0.644	0.250	21.46
<i>PsNAC64</i> vs. <i>MD06G1121400</i>	0.042	0.481	0.087	16.02
<i>PsNAC64</i> vs. <i>MD07G1158300</i>	0.314	NaN	NaN	NaN
<i>PsNAC64</i> vs. <i>MD14G1137900</i>	0.051	0.440	0.115	14.67
<i>PsNAC65</i> vs. <i>MD06G1124800</i>	0.128	0.393	0.327	13.09
<i>PsNAC66</i> vs. <i>MD06G1135700</i>	0.087	0.613	0.142	20.43
<i>PsNAC66</i> vs. <i>MD14G1150900</i>	0.117	0.513	0.228	17.09
<i>PsNAC66</i> vs. <i>MD16G1125800</i>	0.299	2.267	0.132	75.58
<i>PsNAC67</i> vs. <i>MD06G1196100</i>	0.079	0.522	0.151	17.42
<i>PsNAC67</i> vs. <i>MD09G1053700</i>	0.269	1.400	0.192	46.67
<i>PsNAC67</i> vs. <i>MD14G1203000</i>	0.085	0.447	0.191	14.91
<i>PsNAC68</i> vs. <i>MD14G1210000</i>	0.219	0.539	0.406	17.96
<i>PsNAC69</i> vs. <i>MD06G1216500</i>	0.124	0.531	0.233	17.71
<i>PsNAC69</i> vs. <i>MD14G1226900</i>	0.133	0.510	0.261	17.02
<i>PsNAC70</i> vs. <i>MD06G1236800</i>	0.185	0.764	0.241	25.48
<i>PsNAC70</i> vs. <i>MD14G1243700</i>	0.107	0.494	0.216	16.48
<i>PsNAC71</i> vs. <i>MD11G1074200</i>	0.412	1.076	0.383	35.88
<i>PsNAC75</i> vs. <i>MD03G1115100</i>	0.134	0.428	0.314	14.26
<i>PsNAC75</i> vs. <i>MD11G1133000</i>	0.132	0.369	0.357	12.28
<i>PsNAC76</i> vs. <i>MD11G1138500</i>	0.451	0.981	0.460	32.69
<i>PsNAC79</i> vs. <i>MD03G1130400</i>	0.554	1.604	0.345	53.45
<i>PsNAC81</i> vs. <i>MD03G1148500</i>	0.284	0.682	0.417	22.73
<i>PsNAC81</i> vs. <i>MD11G1167900</i>	0.219	0.588	0.372	19.60
<i>PsNAC81</i> vs. <i>MD12G1030200</i>	0.627	1.525	0.411	50.84
<i>PsNAC81</i> vs. <i>MD14G1031000</i>	0.695	2.054	0.339	68.47
<i>PsNAC82</i> vs. <i>MD03G1150800</i>	0.140	0.396	0.354	13.21
<i>PsNAC82</i> vs. <i>MD11G1170300</i>	0.113	0.299	0.379	9.95
<i>PsNAC83</i> vs. <i>MD03G1115100</i>	0.479	1.810	0.265	60.34
<i>PsNAC83</i> vs. <i>MD04G1100400</i>	0.082	0.479	0.172	15.97
<i>PsNAC83</i> vs. <i>MD11G1133000</i>	0.464	1.500	0.309	49.99
<i>PsNAC84</i> vs. <i>MD02G1068700</i>	0.041	0.279	0.148	9.29

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Supplemental Table 5. (Continued)

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC84</i> vs. <i>MD15G1200200</i>	0.045	0.315	0.143	10.49
<i>PsNAC85</i> vs. <i>MD02G1134500</i>	0.044	0.359	0.123	11.95
<i>PsNAC85</i> vs. <i>MD15G1247800</i>	0.038	0.421	0.091	14.04
<i>PsNAC86</i> vs. <i>MD12G1030200</i>	0.200	0.544	0.368	18.15
<i>PsNAC86</i> vs. <i>MD14G1030700</i>	0.237	0.535	0.444	17.82
<i>PsNAC88</i> vs. <i>MD14G1069400</i>	0.364	0.608	0.598	20.28
<i>PsNAC90</i> vs. <i>MD14G1071200</i>	0.421	0.646	0.653	21.52
<i>PsNAC92</i> vs. <i>MD12G1000800</i>	0.102	0.385	0.264	12.85
<i>PsNAC92</i> vs. <i>MD14G1001000</i>	0.100	0.417	0.240	13.89
<i>PsNAC93</i> vs. <i>MD05G1195300</i>	0.064	0.339	0.188	11.29
<i>PsNAC94</i> vs. <i>MD05G1130500</i>	0.074	0.370	0.201	12.34
<i>PsNAC94</i> vs. <i>MD10G1133400</i>	0.072	0.335	0.215	11.16
<i>PsNAC97</i> vs. <i>MD05G1042100</i>	0.100	0.385	0.260	12.83
<i>PsNAC97</i> vs. <i>MD10G1048600</i>	0.075	0.346	0.218	11.55
<i>PsNAC98</i> vs. <i>MD05G1037700</i>	0.109	0.289	0.376	9.64
<i>PsNAC98</i> vs. <i>MD10G1041500</i>	0.108	0.272	0.397	9.08
<i>PsNAC99</i> vs. <i>MD05G1029800</i>	0.378	0.762	0.496	25.41
<i>PsNAC99</i> vs. <i>MD10G1030400</i>	0.250	0.460	0.544	15.33

^zMillion years ago.

Supplemental Table 6. Estimated non-synonymous (Ka) to synonymous (Ks) substitution ratios and divergence times of the syntenic gene pairs of NAC between siberian apricot and peach.

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC2</i> vs. <i>Prupe.1G106100.1</i>	0.020	0.054	0.371	1.80
<i>PsNAC4</i> vs. <i>Prupe.1G220400.1</i>	0.012	0.023	0.500	0.78
<i>PsNAC4</i> vs. <i>Prupe.3G310600.1</i>	0.465	1.891	0.246	63.03
<i>PsNAC4</i> vs. <i>Prupe.5G146100.1</i>	0.271	1.222	0.222	40.75
<i>PsNAC5</i> vs. <i>Prupe.1G274300.1</i>	0.018	0.055	0.324	1.85
<i>PsNAC5</i> vs. <i>Prupe.3G268400.1</i>	0.320	1.499	0.213	49.96
<i>PsNAC6</i> vs. <i>Prupe.1G277500.1</i>	0.007	0.087	0.085	2.89
<i>PsNAC7</i> vs. <i>Prupe.1G284800.1</i>	0.162	0.208	0.777	6.94
<i>PsNAC9</i> vs. <i>Prupe.1G305300.1</i>	0.014	0.025	0.573	0.83
<i>PsNAC10</i> vs. <i>Prupe.1G383200.1</i>	0.017	0.045	0.382	1.48
<i>PsNAC11</i> vs. <i>Prupe.1G432600.2</i>	0.108	0.138	0.784	4.60
<i>PsNAC12</i> vs. <i>Prupe.1G454900.2</i>	0.004	0.026	0.145	0.87
<i>PsNAC13</i> vs. <i>Prupe.1G493100.1</i>	0.016	0.074	0.218	2.48
<i>PsNAC14</i> vs. <i>Prupe.1G560100.1</i>	0.019	0.086	0.220	2.88
<i>PsNAC16</i> vs. <i>Prupe.2G091300.1</i>	0.012	0.023	0.532	0.78
<i>PsNAC18</i> vs. <i>Prupe.2G196600.1</i>	0.009	0.036	0.241	1.19
<i>PsNAC18</i> vs. <i>Prupe.5G131900.1</i>	0.321	1.976	0.162	65.87
<i>PsNAC20</i> vs. <i>Prupe.2G201200.1</i>	0.105	0.116	0.905	3.88
<i>PsNAC21</i> vs. <i>Prupe.2G201200.1</i>	0.175	0.223	0.786	7.43
<i>PsNAC25</i> vs. <i>Prupe.2G202200.1</i>	0.276	0.277	0.999	9.22
<i>PsNAC26</i> vs. <i>Prupe.2G201300.1</i>	0.266	0.316	0.842	10.55
<i>PsNAC28</i> vs. <i>Prupe.2G201800.1</i>	0.241	0.378	0.638	12.59
<i>PsNAC28</i> vs. <i>Prupe.2G202600.1</i>	0.477	0.789	0.604	26.30
<i>PsNAC29</i> vs. <i>Prupe.2G202500.1</i>	0.021	0.025	0.860	0.83
<i>PsNAC31</i> vs. <i>Prupe.2G202500.5</i>	0.531	1.214	0.437	40.48
<i>PsNAC31</i> vs. <i>Prupe.2G202800.1</i>	0.079	0.130	0.612	4.32
<i>PsNAC32</i> vs. <i>Prupe.2G202800.1</i>	0.193	0.212	0.912	7.05
<i>PsNAC33</i> vs. <i>Prupe.2G204700.1</i>	0.157	0.256	0.613	8.53
<i>PsNAC36</i> vs. <i>Prupe.2G278100.1</i>	0.040	0.089	0.449	2.96
<i>PsNAC37</i> vs. <i>Prupe.2G320600.1</i>	0.026	0.068	0.378	2.27
<i>PsNAC37</i> vs. <i>Prupe.5G135400.1</i>	0.437	3.324	0.131	110.81

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Supplemental Table 6. (Continued)

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC38</i> vs. <i>Prupe.1G220400.1</i>	0.484	1.449	0.334	48.32
<i>PsNAC38</i> vs. <i>Prupe.3G310600.1</i>	0.020	0.026	0.791	0.85
<i>PsNAC38</i> vs. <i>Prupe.5G146100.1</i>	0.635	3.093	0.205	103.09
<i>PsNAC39</i> vs. <i>Prupe.3G293200.2</i>	0.009	0.036	0.247	1.19
<i>PsNAC40</i> vs. <i>Prupe.1G274300.1</i>	0.312	1.226	0.254	40.88
<i>PsNAC40</i> vs. <i>Prupe.3G268400.1</i>	0.010	0.028	0.348	0.93
<i>PsNAC41</i> vs. <i>Prupe.3G264600.1</i>	0.012	0.050	0.243	1.67
<i>PsNAC42</i> vs. <i>Prupe.3G178000.1</i>	0.014	0.064	0.220	2.13
<i>PsNAC43</i> vs. <i>Prupe.3G111400.1</i>	0.036	0.027	1.320	0.91
<i>PsNAC45</i> vs. <i>Prupe.3G065000.1</i>	0.035	0.055	0.641	1.83
<i>PsNAC46</i> vs. <i>Prupe.4G279600.1</i>	0.009	0.044	0.198	1.47
<i>PsNAC47</i> vs. <i>Prupe.4G253600.1</i>	0.048	0.071	0.679	2.36
<i>PsNAC48</i> vs. <i>Prupe.4G230600.1</i>	0.505	1.215	0.415	40.50
<i>PsNAC50</i> vs. <i>Prupe.4G187100.1</i>	0.011	0.059	0.183	1.96
<i>PsNAC51</i> vs. <i>Prupe.4G186800.1</i>	0.015	0.065	0.233	2.15
<i>PsNAC52</i> vs. <i>Prupe.4G175800.1</i>	0.005	0.050	0.091	1.66
<i>PsNAC54</i> vs. <i>Prupe.4G151900.1</i>	0.017	0.074	0.232	2.46
<i>PsNAC55</i> vs. <i>Prupe.4G138500.1</i>	0.009	0.056	0.165	1.87
<i>PsNAC56</i> vs. <i>Prupe.4G126800.1</i>	0.012	0.035	0.352	1.16
<i>PsNAC57</i> vs. <i>Prupe.4G123700.2</i>	0.031	0.093	0.335	3.11
<i>PsNAC58</i> vs. <i>Prupe.4G106100.1</i>	0.022	0.041	0.535	1.38
<i>PsNAC59</i> vs. <i>Prupe.4G053300.1</i>	0.003	0.033	0.082	1.11
<i>PsNAC60</i> vs. <i>Prupe.4G040900.1</i>	0.012	0.033	0.367	1.09
<i>PsNAC61</i> vs. <i>Prupe.2G278100.1</i>	0.000	0.047	0.000	1.56
<i>PsNAC62</i> vs. <i>Prupe.5G006200.1</i>	0.015	0.035	0.422	1.18
<i>PsNAC63</i> vs. <i>Prupe.5G076100.1</i>	0.005	0.035	0.134	1.17
<i>PsNAC64</i> vs. <i>Prupe.2G196600.1</i>	0.301	2.465	0.122	82.18
<i>PsNAC64</i> vs. <i>Prupe.5G131900.1</i>	0.000	0.032	0.000	1.06
<i>PsNAC65</i> vs. <i>Prupe.2G320600.1</i>	0.513	2.637	0.194	87.90
<i>PsNAC65</i> vs. <i>Prupe.5G135400.1</i>	0.017	0.046	0.368	1.53
<i>PsNAC66</i> vs. <i>Prupe.1G220400.1</i>	0.266	1.092	0.244	36.41
<i>PsNAC66</i> vs. <i>Prupe.3G310600.1</i>	0.616	3.010	0.205	100.32
<i>PsNAC66</i> vs. <i>Prupe.5G146100.1</i>	0.010	0.061	0.160	2.05
<i>PsNAC67</i> vs. <i>Prupe.3G264600.1</i>	0.227	1.330	0.170	44.32
<i>PsNAC67</i> vs. <i>Prupe.5G196000.1</i>	0.018	0.042	0.428	1.41
<i>PsNAC68</i> vs. <i>Prupe.5G203200.1</i>	0.081	0.093	0.864	3.11
<i>PsNAC69</i> vs. <i>Prupe.5G221600.1</i>	0.007	0.030	0.240	1.01
<i>PsNAC70</i> vs. <i>Prupe.5G241300.1</i>	0.002	0.053	0.031	1.77
<i>PsNAC71</i> vs. <i>Prupe.6G057300.1</i>	0.040	0.041	0.970	1.36
<i>PsNAC72</i> vs. <i>Prupe.6G092100.1</i>	0.029	0.041	0.689	1.38
<i>PsNAC73</i> vs. <i>Prupe.6G098300.1</i>	0.204	0.423	0.482	14.09
<i>PsNAC75</i> vs. <i>Prupe.6G098600.1</i>	0.022	0.053	0.404	1.78
<i>PsNAC75</i> vs. <i>Prupe.6G238600.1</i>	0.434	1.706	0.254	56.88
<i>PsNAC76</i> vs. <i>Prupe.6G103600.1</i>	0.089	0.228	0.391	7.59
<i>PsNAC79</i> vs. <i>Prupe.6G112000.1</i>	0.021	0.023	0.922	0.76
<i>PsNAC81</i> vs. <i>Prupe.6G134400.1</i>	0.151	0.180	0.837	6.00
<i>PsNAC81</i> vs. <i>Prupe.7G102000.1</i>	0.540	1.521	0.355	50.71
<i>PsNAC82</i> vs. <i>Prupe.6G138100.1</i>	0.010	0.035	0.291	1.15
<i>PsNAC83</i> vs. <i>Prupe.6G238600.1</i>	0.014	0.047	0.297	1.56
<i>PsNAC83</i> vs. <i>Prupe.6G098600.1</i>	0.455	1.747	0.260	58.23
<i>PsNAC84</i> vs. <i>Prupe.7G217000.2</i>	0.001	0.033	0.026	1.11
<i>PsNAC85</i> vs. <i>Prupe.7G166300.1</i>	0.000	0.039	0.000	1.30
<i>PsNAC86</i> vs. <i>Prupe.6G134400.1</i>	0.406	2.753	0.148	91.77
<i>PsNAC86</i> vs. <i>Prupe.7G102000.1</i>	0.093	0.116	0.805	3.85
<i>PsNAC87</i> vs. <i>Prupe.7G092400.2</i>	0.028	0.084	0.328	2.81

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Supplemental Table 6. (Continued)

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC88</i> vs. <i>Prupe.7G061900.1</i>	0.718	1.849	0.388	61.63
<i>PsNAC88</i> vs. <i>Prupe.7G064900.1</i>	0.502	0.793	0.633	26.44
<i>PsNAC90</i> vs. <i>Prupe.7G065000.1</i>	0.746	NaN	NaN	NaN
<i>PsNAC90</i> vs. <i>Prupe.7G061900.1</i>	0.038	0.080	0.478	2.66
<i>PsNAC91</i> vs. <i>Prupe.7G013900.1</i>	0.096	0.098	0.974	3.27
<i>PsNAC92</i> vs. <i>Prupe.7G001200.1</i>	0.010	0.052	0.194	1.75
<i>PsNAC93</i> vs. <i>Prupe.8G221900.1</i>	0.018	0.058	0.314	1.93
<i>PsNAC94</i> vs. <i>Prupe.8G174800.1</i>	0.016	0.043	0.375	1.45
<i>PsNAC95</i> vs. <i>Prupe.8G097100.1</i>	0.026	0.049	0.534	1.64
<i>PsNAC95</i> vs. <i>Prupe.8G095200.1</i>	0.042	0.111	0.374	3.71
<i>PsNAC96</i> vs. <i>Prupe.8G074800.1</i>	0.084	0.138	0.608	4.61
<i>PsNAC97</i> vs. <i>Prupe.8G058100.1</i>	0.010	0.043	0.224	1.44
<i>PsNAC98</i> vs. <i>Prupe.8G045800.1</i>	0.012	0.034	0.354	1.13
<i>PsNAC99</i> vs. <i>Prupe.8G035300.1</i>	0.267	0.476	0.560	15.87
<i>PsNAC102</i> vs. <i>Prupe.8G002500.1</i>	0.006	0.067	0.084	2.24

^zMillion years ago.

Supplemental Table 7. Estimated non-synonymous (Ka) to synonymous (Ks) substitution ratios and divergence times of the syntenic gene pairs of NAC between siberian apricot and japanese apricot.

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC2</i> vs. <i>Pm008481</i>	NaN	NaN	NaN	NaN
<i>PsNAC4</i> vs. <i>Pm007070</i>	0.005	0.018	0.284	0.59
<i>PsNAC4</i> vs. <i>Pm016114</i>	0.482	1.696	0.284	56.55
<i>PsNAC4</i> vs. <i>Pm024558</i>	0.271	1.219	0.222	40.63
<i>PsNAC5</i> vs. <i>Pm006506</i>	0.004	0.019	0.234	0.63
<i>PsNAC5</i> vs. <i>Pm015876</i>	0.330	1.360	0.243	45.34
<i>PsNAC6</i> vs. <i>Pm006470</i>	0.004	0.017	0.267	0.55
<i>PsNAC7</i> vs. <i>Pm006394</i>	0.248	0.351	0.706	11.71
<i>PsNAC9</i> vs. <i>Pm029010</i>	0.006	0.019	0.318	0.62
<i>PsNAC10</i> vs. <i>Pm005783</i>	0.009	0.028	0.322	0.94
<i>PsNAC11</i> vs. <i>Pm005306</i>	0.103	0.138	0.743	4.61
<i>PsNAC12</i> vs. <i>Pm005091</i>	0.003	0.022	0.116	0.72
<i>PsNAC13</i> vs. <i>Pm004758</i>	0.009	0.121	0.073	4.02
<i>PsNAC14</i> vs. <i>Pm004078</i>	0.006	0.028	0.226	0.95
<i>PsNAC18</i> vs. <i>Pm018292</i>	0.005	0.019	0.275	0.65
<i>PsNAC21</i> vs. <i>Pm028718</i>	0.360	0.487	0.739	16.22
<i>PsNAC30</i> vs. <i>Pm028713</i>	0.023	0.042	0.540	1.41
<i>PsNAC32</i> vs. <i>Pm028710</i>	0.014	0.015	0.912	0.50
<i>PsNAC33</i> vs. <i>Pm018442</i>	0.162	0.208	0.781	6.92
<i>PsNAC36</i> vs. <i>Pm019488</i>	0.049	0.093	0.531	3.09
<i>PsNAC37</i> vs. <i>Pm019659</i>	0.012	0.036	0.348	1.19
<i>PsNAC38</i> vs. <i>Pm007070</i>	0.454	2.417	0.188	80.58
<i>PsNAC38</i> vs. <i>Pm016114</i>	0.007	0.019	0.380	0.64
<i>PsNAC38</i> vs. <i>Pm024558</i>	0.640	2.461	0.260	82.04
<i>PsNAC40</i> vs. <i>Pm006506</i>	0.306	1.178	0.260	39.27
<i>PsNAC40</i> vs. <i>Pm015876</i>	0.010	0.016	0.614	0.53
<i>PsNAC41</i> vs. <i>Pm015914</i>	0.010	0.013	0.729	0.45
<i>PsNAC42</i> vs. <i>Pm014764</i>	0.006	0.010	0.546	0.34
<i>PsNAC45</i> vs. <i>Pm013492</i>	0.011	0.013	0.886	0.42
<i>PsNAC46</i> vs. <i>Pm012630</i>	0.001	0.011	0.135	0.36

(Continued on next page)

Supplemental Table 7. (Continued)

Duplication gene pairs	Ka	Ks	Ka/Ks	Divergence time (Mya) ^z
<i>PsNAC47</i> vs. <i>Pm012336</i>	0.038	0.058	0.645	1.94
<i>PsNAC48</i> vs. <i>Pm011991</i>	0.566	1.600	0.354	53.33
<i>PsNAC50</i> vs. <i>Pm009954</i>	0.451	1.626	0.277	54.21
<i>PsNAC50</i> vs. <i>Pm011604</i>	0.009	0.016	0.583	0.53
<i>PsNAC51</i> vs. <i>Pm009955</i>	0.296	1.782	0.166	59.40
<i>PsNAC51</i> vs. <i>Pm011603</i>	0.007	0.012	0.605	0.41
<i>PsNAC52</i> vs. <i>Pm011397</i>	0.000	0.030	0.000	1.00
<i>PsNAC54</i> vs. <i>Pm011146</i>	0.005	0.018	0.285	0.59
<i>PsNAC55</i> vs. <i>Pm011037</i>	0.008	0.036	0.224	1.18
<i>PsNAC56</i> vs. <i>Pm010926</i>	0.005	0.017	0.285	0.57
<i>PsNAC57</i> vs. <i>Pm010886</i>	0.016	0.058	0.282	1.94
<i>PsNAC58</i> vs. <i>Pm010673</i>	0.003	0.015	0.184	0.51
<i>PsNAC59</i> vs. <i>Pm010104</i>	0.000	0.024	0.000	0.79
<i>PsNAC60</i> vs. <i>Pm009954</i>	0.011	0.018	0.612	0.59
<i>PsNAC61</i> vs. <i>Pm019488</i>	0.010	0.047	0.213	1.56
<i>PsNAC62</i> vs. <i>Pm022916</i>	0.002	0.032	0.062	1.06
<i>PsNAC63</i> vs. <i>Pm023559</i>	0.012	0.042	0.297	1.39
<i>PsNAC64</i> vs. <i>Pm018292</i>	0.325	2.033	0.160	67.77
<i>PsNAC64</i> vs. <i>Pm024260</i>	0.001	0.024	0.045	0.79
<i>PsNAC65</i> vs. <i>Pm019659</i>	0.529	3.259	0.162	108.65
<i>PsNAC66</i> vs. <i>Pm007070</i>	0.271	1.263	0.215	42.11
<i>PsNAC66</i> vs. <i>Pm016114</i>	0.627	2.637	0.238	87.91
<i>PsNAC66</i> vs. <i>Pm024558</i>	0.011	0.054	0.205	1.80
<i>PsNAC67</i> vs. <i>Pm015914</i>	0.233	1.235	0.189	41.16
<i>PsNAC67</i> vs. <i>Pm024887</i>	0.011	0.021	0.521	0.69
<i>PsNAC68</i> vs. <i>Pm024976</i>	0.086	0.091	0.950	3.03
<i>PsNAC69</i> vs. <i>Pm025184</i>	0.203	0.389	0.521	12.97
<i>PsNAC70</i> vs. <i>Pm025250</i>	0.069	0.136	0.506	4.54
<i>PsNAC71</i> vs. <i>Pm000566</i>	0.063	0.107	0.589	3.57
<i>PsNAC72</i> vs. <i>Pm000962</i>	0.062	0.119	0.524	3.97
<i>PsNAC73</i> vs. <i>Pm000998</i>	0.019	0.037	0.529	1.22
<i>PsNAC75</i> vs. <i>Pm001001</i>	0.010	0.020	0.505	0.66
<i>PsNAC76</i> vs. <i>Pm001039</i>	0.078	0.131	0.596	4.37
<i>PsNAC78</i> vs. <i>Pm001136</i>	0.073	0.114	0.640	3.79
<i>PsNAC79</i> vs. <i>Pm001146</i>	0.031	0.031	0.991	1.03
<i>PsNAC80</i> vs. <i>Pm001157</i>	0.025	0.027	0.922	0.91
<i>PsNAC81</i> vs. <i>Pm001403</i>	0.136	0.167	0.815	5.56
<i>PsNAC81</i> vs. <i>Pm028056</i>	0.571	1.668	0.342	55.60
<i>PsNAC82</i> vs. <i>Pm001467</i>	0.007	0.017	0.386	0.57
<i>PsNAC83</i> vs. <i>Pm001001</i>	0.520	1.618	0.321	53.92
<i>PsNAC83</i> vs. <i>Pm030099</i>	0.013	0.024	0.525	0.80
<i>PsNAC84</i> vs. <i>Pm027280</i>	0.002	0.033	0.052	1.11
<i>PsNAC85</i> vs. <i>Pm026735</i>	0.003	0.029	0.087	0.97
<i>PsNAC86</i> vs. <i>Pm001403</i>	0.402	2.303	0.175	76.77
<i>PsNAC86</i> vs. <i>Pm028056</i>	0.107	0.113	0.945	3.78
<i>PsNAC87</i> vs. <i>Pm026045</i>	0.012	0.026	0.480	0.86
<i>PsNAC88</i> vs. <i>Pm025886</i>	0.017	0.019	0.927	0.62
<i>PsNAC91</i> vs. <i>Pm028678</i>	0.039	0.061	0.641	2.04
<i>PsNAC92</i> vs. <i>Pm025312</i>	0.006	0.044	0.127	1.47
<i>PsNAC93</i> vs. <i>Pm020580</i>	0.009	0.064	0.141	2.14
<i>PsNAC94</i> vs. <i>Pm020961</i>	0.004	0.005	0.828	0.18
<i>PsNAC95</i> vs. <i>Pm021768</i>	0.012	0.040	0.295	1.34
<i>PsNAC95</i> vs. <i>Pm021749</i>	0.007	0.017	0.437	0.56
<i>PsNAC96</i> vs. <i>Pm021945</i>	0.072	0.073	0.982	2.44
<i>PsNAC99</i> vs. <i>Pm022529</i>	0.007	0.010	0.734	0.32
<i>PsNAC102</i> vs. <i>Pm022820</i>	0.003	0.004	0.847	0.13

^zMillion years ago.

Supplemental Fig. 2. Expression analysis of *PsNACs* during siberian apricot fruit and kernel development by RNA-sequencing (RNA-Seq) data and quantitative real-time polymerase chain reaction (qRT-PCR). (A-K) *PsNACs* of fruit development; and (L-O) *PsNACs* of kernel development. Data were normalized to Ubiquitin-conjugating enzyme (*UBC*) gene and vertical bars indicate standard deviation. QRT-PCR value were given as means $\pm$ SD of three independent biological replicates. Column and line in the chart represented qRT-PCR and RNA-seq, respectively.