

# Identification and Analysis of the SAURs in *Prunus sibirica*

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## Article

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## Abstract

In present study, we identified the members of small auxin-up RNA (*SAUR*) gene family in *Prunus sibirica* (*P. sibirica*) and analyzed their localization, phylogeny, duplication, cis-elements in the promoter, and expression patterns. In total, 57 *PsSAURs* were identified, randomly distributed along eight chromosomes. Among them, eight and ten pairs of segmentally duplicated genes and tandem duplication genes were found in 13 and 21 *PsSAURs*, respectively. Phylogenetic analysis indicated that the *PsSAURs* were divided into five groups (Group A-E). Light-responsive cis-elements, methyl jasmonate, abscisic acid, salicylic acid, and gibberellin, as well as low-temperature responsiveness, and defense and stress responsiveness were identified by analyzing *PsSAURs* promoter sequences. Expression pattern analysis showed that *PsSAURs* had different tissue and stage expression patterns. This study provided a foundation for further investigations for the functional analyses of *SAURs* in *P. sibirica*.

## 1 Introduction

Auxin plays an important role in plant growth, development, and stress response. Early auxin-induced genes are divided into three major categories: Auxin/indole-3-acetic acid (*Aux/IAA*), Gretchen Hagen 3 (*GH3*), and small auxin upregulated RNA (*SAUR*) [1]. *SAUR* was first identified in the hypocotyl elongation zone of soybean (*Glycine max* L.) [2]. Subsequently, *SAURs* were identified in *Arabidopsis* [1], corn (*Zea mays* L.) [3], wheat (*Triticum aestivum* L.) [4], apple (*Malus pumila* Mill.) [5], grape (*Vitis vinifera* L.) [6], and citrus (*Citrus reticulata* Blanco) [5]. *SAURs* are major response genes in the auxin pathway that can respond to auxin family of genes within 2–5 minutes [7]. Currently, functional studies on *SAUR* in plant growth and development have been reported. For example, *AtSAUR63* promotes the elongation of cells in *Arabidopsis* [8], *AtSAUR19-24* plays a major regulatory role in hypocotyl elongation and increases the leaf size in *Arabidopsis* [9], and *AtSAUR36* is a positive regulator that mediates auxin-induced leaf senescence [10]. The *SAURs* not only participate in the regulation of plant growth and development but also play an important role in the response to environmental stress. For example, *AtSAUR41* plays an important role in abiotic stress resistance, which could increase the resistance to salt stress in transgenic plants [11]. However, research on *SAURs* in non-model plants remains limited, and the expression and function of *SAURs* are lacking.

*P. sibirica* is an ecological and economic tree species in Asia, which is broadly distributed in northern China, eastern Mongolia, eastern Siberia and the coastal areas of Russia [12]. *P. sibirica* kernel is rich in nutrition, fat and protein and it is widely used in industry, food, cosmetics, medicine and other aspects. It can be fried and salted, and can also be used to make a variety of food and beverages [13]. In addition, *P. sibirica* is drought and cold resistant that can adapt to various harsh environmental conditions. It is a pioneer tree species for afforestation on arid and semi-arid mountainous areas [14]. Therefore, *P. sibirica* has a very broad development and utilization potential.

Studies have shown that *SAURs* plays an important role in plant growth, development and stress resistance, but the research related to *SAUR* of *P. sibirica* has not been reported. The completion of genome sequencing for the *P. sibirica* provides valuable data for systematic analysis of the *PsSAUR* family. This study aims to use bioinformatics to identify *PsSAUR* family members and conduct a systematic analysis at the whole-genome level. The results of the study will provide a reference for the study the function of *PsSAUR* and provide technical support for the subsequent improvement of *P. sibirica* varieties and germplasm resources.

## 2 Results

### 2.1 Whole-genome identification and characteristics of *PsSAURs*

A total of 57 *PsSAURs* were identified in *P. sibirica* genome, which were randomly distributed on eight chromosomes (Fig. 1). Among them, the highest number (24) of *PsSAURs* was chromosome 8, with several genes forming clusters, and the other seven chromosomes each containing 1–10 *PsSAURs*. The *PsSAURs* were named *PsSAUR1*–*PsSAUR57* according to their position on chromosome. The length *PsSAURs* were ranged from 70 to 236 amino acid (aa), the Mw and PIs ranging from 8.05 (*PsSAUR53*) to 27.03 (*PsSAUR17*) kDa and 5.11 (*PsSAUR33*) to 10.46 (*PsSAUR19*), respectively (Table 1). A total of forty-nine and 8 *PsSAURs* were hydrophilic and hydrophobic proteins. Protein instability index analysis showed that 17 *PsSAURs* were stable with an instability index less than 40. In addition, the protein subcellular localization prediction showed that *PsSAURs* were primarily located in the cytoplasm, nucleus, and mitochondria.

Table 1  
Information related to *PsSAURs* in *P. sibirica*

| Gene name       | Accession            | Chromosome location      | Strand | Number of amino acids/aa | Molecular weight/kD | Theoretical pI | Instability index | Aliphatic index | Grand average of hydropathicity (GRAVY) |
|-----------------|----------------------|--------------------------|--------|--------------------------|---------------------|----------------|-------------------|-----------------|-----------------------------------------|
| <i>PsSAUR1</i>  | PaF106G0100000780.01 | Chr1: 4851261–4851947    | +      | 166                      | 18.68785            | 9.9            | 59.13             | 90.42           | -0.005                                  |
| <i>PsSAUR2</i>  | PaF106G0100002700.01 | Chr1: 20203785–20204276  | +      | 163                      | 18.46055            | 9.37           | 56.43             | 69.26           | -0.452                                  |
| <i>PsSAUR3</i>  | PaF106G0100004332.01 | Chr1: 29206302–29206619  | +      | 105                      | 12.08995            | 7.83           | 61.56             | 87.24           | -0.355                                  |
| <i>PsSAUR4</i>  | PaF106G0100004336.01 | Chr1: 29228506–29229489  | -      | 150                      | 17.0335             | 9.79           | 62.65             | 82.53           | -0.28                                   |
| <i>PsSAUR5</i>  | PaF106G0100005296.01 | Chr1: 33845860–33846426  | +      | 188                      | 21.21526            | 8.74           | 56.44             | 74.15           | -0.414                                  |
| <i>PsSAUR6</i>  | PaF106G0200006771.01 | Chr2 : 110636–111793     | +      | 133                      | 14.77948            | 5.17           | 44.96             | 57.22           | -0.714                                  |
| <i>PsSAUR7</i>  | PaF106G0200006772.01 | Chr2 : 116535–116960     | +      | 141                      | 15.90597            | 6.9            | 40.75             | 73.97           | -0.671                                  |
| <i>PsSAUR8</i>  | PaF106G0200008604.01 | Chr2: 15878329–15879323  | +      | 172                      | 19.42461            | 10.45          | 29.56             | 71.4            | -0.49                                   |
| <i>PsSAUR9</i>  | PaF106G0200009291.01 | Chr2 : 19915629–19916397 | +      | 124                      | 14.43145            | 7.89           | 27.07             | 75.32           | -0.673                                  |
| <i>PsSAUR10</i> | PaF106G0200009494.01 | Chr2: 21116519–21116899  | +      | 126                      | 14.75434            | 8.75           | 34.76             | 88.17           | -0.107                                  |
| <i>PsSAUR11</i> | PaF106G0200010737.01 | Chr2: 27010514–27011408  | +      | 132                      | 15.73591            | 7.12           | 29.14             | 70.76           | -0.742                                  |
| <i>PsSAUR12</i> | PaF106G0300014330.01 | Chr3: 1769202–1769762    | +      | 186                      | 21.06221            | 9.22           | 40.42             | 78.06           | -0.409                                  |
| <i>PsSAUR13</i> | PaF106G0300014329.01 | Chr3: 1770375–1771793    | -      | 177                      | 20.16526            | 6.79           | 60.88             | 86.5            | -0.288                                  |
| <i>PsSAUR14</i> | PaF106G0300014203.01 | Chr3: 2666558–2667170    | +      | 117                      | 13.1601             | 6.06           | 37.09             | 96.5            | -0.099                                  |
| <i>PsSAUR15</i> | PaF106G0400018086.01 | Chr4: 1700338–1701561    | +      | 117                      | 12.85694            | 5.7            | 55.59             | 90              | 0.104                                   |
| <i>PsSAUR16</i> | PaF106G0400016888.01 | Chr4 : 8162844–8163143   | +      | 99                       | 11.12376            | 6.02           | 42.29             | 90.51           | -0.153                                  |
| <i>PsSAUR17</i> | PaF106G0400016886.01 | Chr4: 8164068–8166793    | -      | 236                      | 27.02566            | 7.65           | 40.32             | 75.59           | -0.398                                  |
| <i>PsSAUR18</i> | PaF106G0400016640.01 | Chr4 : 9687821–9688240   | -      | 139                      | 15.99332            | 9.38           | 80.52             | 95.25           | -0.408                                  |
| <i>PsSAUR19</i> | PaF106G0500019384.01 | Chr5 : 7321462–7322312   | +      | 166                      | 19.46583            | 10.46          | 33.43             | 77.47           | -0.627                                  |
| <i>PsSAUR20</i> | PaF106G0600022654.01 | Chr6: 7496390–7497064    | +      | 128                      | 14.52475            | 6.9            | 43.44             | 88.28           | -0.501                                  |

| Gene name       | Accession            | Chromosome location      | Strand | Number of amino acids/aa | Molecular weight/kD | Theoretical pI | Instability index | Aliphatic index | Grand average of hydropathicity (GRAVY) |
|-----------------|----------------------|--------------------------|--------|--------------------------|---------------------|----------------|-------------------|-----------------|-----------------------------------------|
| <i>PsSAUR21</i> | PaF106G0600022655.01 | Chr6 : 7500637–7501071   | +      | 144                      | 15.97596            | 5.65           | 51.05             | 68.4            | -0.583                                  |
| <i>PsSAUR22</i> | PaF106G0600022656.01 | Chr6 : 7505887–7506315   | +      | 142                      | 16.00309            | 6.9            | 41.36             | 73.45           | -0.677                                  |
| <i>PsSAUR23</i> | PaF106G0600024333.01 | Chr6: 22092133–22092647  | +      | 170                      | 19.37449            | 8.76           | 54.84             | 85.35           | -0.106                                  |
| <i>PsSAUR24</i> | PaF106G0700028558.01 | Chr7:7344400–7344855     | -      | 151                      | 17.02373            | 9.55           | 63.49             | 92.98           | -0.142                                  |
| <i>PsSAUR25</i> | PaF106G0700028555.01 | Chr7: 7361195–7361650    | -      | 151                      | 17.03777            | 9.55           | 69.5              | 90.4            | -0.165                                  |
| <i>PsSAUR26</i> | PaF106G0700028553.01 | Chr7 : 7377830–7378284   | -      | 135                      | 15.23753            | 7.81           | 73.42             | 87.41           | -0.11                                   |
| <i>PsSAUR27</i> | PaF106G0700028551.01 | Chr7 : 7383579–7383929   | -      | 116                      | 12.98013            | 5.7            | 51.53             | 99.14           | 0.241                                   |
| <i>PsSAUR28</i> | PaF106G0700028552.01 | Chr7: 7383579–7384040    | -      | 153                      | 17.24314            | 9.58           | 52.95             | 91.76           | -0.092                                  |
| <i>PsSAUR29</i> | PaF106G0700028547.01 | Chr7 : 7429270–7429728   | -      | 152                      | 17.14089            | 9.3            | 59.34             | 92.43           | -0.148                                  |
| <i>PsSAUR30</i> | PaF106G0700027893.01 | Chr7: 12353407–12353796  | -      | 129                      | 14.30748            | 6.83           | 39.07             | 76.28           | -0.188                                  |
| <i>PsSAUR31</i> | PaF106G0700027703.01 | Chr7 : 13383893–13384288 | -      | 125                      | 14.04426            | 8.78           | 53.76             | 87.36           | -0.3                                    |
| <i>PsSAUR32</i> | PaF106G0700027134.01 | Chr7 : 16479544–16480270 | -      | 106                      | 12.08287            | 8.6            | 53.09             | 77.26           | -0.446                                  |
| <i>PsSAUR33</i> | PaF106G0700026812.01 | Chr7 : 18024373–18025218 | +      | 125                      | 14.02486            | 5.11           | 59.04             | 82.56           | -0.371                                  |
| <i>PsSAUR34</i> | PaF106G0800031625.01 | Chr8 : 11282676–11284223 | +      | 158                      | 17.77833            | 8.61           | 50.16             | 78.29           | -0.266                                  |
| <i>PsSAUR35</i> | PaF106G0800031622.01 | Chr8 : 11300070–11300537 | +      | 155                      | 17.7714             | 6.88           | 45.6              | 84.26           | 0.059                                   |
| <i>PsSAUR36</i> | PaF106G0800031620.01 | Chr8 : 11310028–11310553 | +      | 109                      | 12.31222            | 6.07           | 36.93             | 89.36           | -0.143                                  |
| <i>PsSAUR37</i> | PaF106G0800031618.01 | Chr8 : 11335417–11335943 | +      | 145                      | 16.30579            | 8.47           | 36.42             | 87.38           | -0.254                                  |
| <i>PsSAUR38</i> | PaF106G0800031616.01 | Chr8 : 11349134–11349529 | +      | 97                       | 10.62313            | 6.71           | 36.13             | 76.29           | -0.228                                  |
| <i>PsSAUR39</i> | PaF106G0800031609.01 | Chr8 : 11404246–11406526 | -      | 120                      | 13.21033            | 6.71           | 39.09             | 102.33          | 0.235                                   |
| <i>PsSAUR40</i> | PaF106G0800031605.01 | Chr8: 11432471–11433969  | +      | 158                      | 17.76854            | 9.2            | 31.21             | 83.86           | -0.046                                  |
| <i>PsSAUR41</i> | PaF106G0800031604.01 | Chr8 : 11436254–11436994 | +      | 91                       | 10.21372            | 6.55           | 39.31             | 85.71           | -0.202                                  |

| Gene name       | Accession            | Chromosome location      | Strand | Number of amino acids/aa | Molecular weight/kD | Theoretical pI | Instability index | Aliphatic index | Grand average of hydropathicity (GRAVY) |
|-----------------|----------------------|--------------------------|--------|--------------------------|---------------------|----------------|-------------------|-----------------|-----------------------------------------|
| <i>PsSAUR42</i> | PaF106G0800031608.01 | Chr8: 11404246–11438414  | -      | 186                      | 20.61977            | 6.42           | 31.52             | 90.65           | -0.068                                  |
| <i>PsSAUR43</i> | PaF106G0800031599.01 | Chr8 : 11491197–11498191 | -      | 186                      | 20.49061            | 6.9            | 32.59             | 88.55           | -0.062                                  |
| <i>PsSAUR44</i> | PaF106G0800031596.01 | Chr8 : 11506866–11507486 | -      | 156                      | 17.59013            | 5.94           | 49.6              | 90.58           | -0.315                                  |
| <i>PsSAUR45</i> | PaF106G0800031595.01 | Chr8 : 11508605–11508910 | +      | 101                      | 11.33027            | 8.71           | 40.39             | 94.65           | 0.051                                   |
| <i>PsSAUR46</i> | PaF106G0800031594.01 | Chr8 : 11513969–11514385 | +      | 101                      | 11.25811            | 8.93           | 65.03             | 90.79           | -0.023                                  |
| <i>PsSAUR47</i> | PaF106G0800031591.01 | Chr8 : 11521494–11522770 | +      | 101                      | 11.31822            | 9.36           | 64.39             | 88.91           | -0.027                                  |
| <i>PsSAUR48</i> | PaF106G0800031590.01 | Chr8: 11524532–11524816  | +      | 94                       | 10.64937            | 8.85           | 53.16             | 99.47           | 0.055                                   |
| <i>PsSAUR49</i> | PaF106G0800031588.01 | Chr8 : 11542778–11543299 | +      | 171                      | 19.52165            | 9.64           | 58.7              | 77.49           | -0.587                                  |
| <i>PsSAUR50</i> | PaF106G0800031587.01 | Chr8 : 11565588–11566287 | -      | 150                      | 16.86448            | 9.21           | 66.27             | 93.6            | -0.157                                  |
| <i>PsSAUR51</i> | PaF106G0800030701.01 | Chr8 : 16931768–16932043 | -      | 91                       | 10.14858            | 8.66           | 58.21             | 76.15           | -0.297                                  |
| <i>PsSAUR52</i> | PaF106G0800030700.01 | Chr8: 16933274–16933676  | +      | 94                       | 10.49326            | 8.54           | 64.09             | 88.09           | 0.121                                   |
| <i>PsSAUR53</i> | PaF106G0800030699.01 | Chr8: 16934478–16934909  | -      | 70                       | 8.05333             | 7.99           | 50.22             | 83.57           | -0.056                                  |
| <i>PsSAUR54</i> | PaF106G0800030698.01 | Chr8 : 16936378–16936848 | +      | 94                       | 10.59748            | 8.52           | 61.73             | 89.15           | 0.122                                   |
| <i>PsSAUR55</i> | PaF106G0800030697.01 | Chr8 : 16938188–16938499 | +      | 103                      | 11.42508            | 7.79           | 16.37             | 81.46           | -0.237                                  |
| <i>PsSAUR56</i> | PaF106G0800030696.01 | Chr8 : 16940616–16940909 | +      | 97                       | 11.22181            | 7.06           | 38.9              | 75.36           | -0.497                                  |
| <i>PsSAUR57</i> | PaF106G0800030695.01 | Chr8: 16942827–16943126  | +      | 99                       | 11.17022            | 9.87           | 45.24             | 83.54           | -0.242                                  |

## 2.2 Phylogenetic of the *PsSAURs*

To study the phylogenetic relationships among *PsSAURs*, 78 *AtSAUR* protein sequences in *Arabidopsis* and 57 *PsSAUR* protein sequences in *P. sibirica* were used to construct a phylogenetic tree (Fig. 2). The *PsSAURs* were divided into five groups (Groups A-E). Among them, Group E had the largest number of *PsSAURs*, which contained 24 *PsSAUR* members, followed by Group A, which contained 14 *PsSAUR* members, Group B, Group C, and Group D consisted 9, 7, and 3 *PsSAUR* members, respectively. Most of *PsSAURs* with similar locations were distributed in the same group as follows: *PsSAUR24*, *PsSAUR25*, *PsSAUR26*, *PsSAUR27*, *PsSAUR28*, and *PsSAUR29* from Group A were located on chromosome 7; *PsSAUR6*, *PsSAUR7*, *PsSAUR8*, *PsSAUR9*, and *PsSAUR11* from Group B were located on chromosome 2; *PsSAUR34*, *PsSAUR35*, *PsSAUR36*, *PsSAUR37*, *PsSAUR38*, *PsSAUR39*, *PsSAUR40*, *PsSAUR41*, *PsSAUR42*, *PsSAUR43*, *PsSAUR44*, *PsSAUR45*, *PsSAUR46*, *PsSAUR47*, *PsSAUR48*, *PsSAUR51*, *PsSAUR52*, *PsSAUR53*, *PsSAUR54*, *PsSAUR55*, and *PsSAUR56* from Group E were located on chromosome 8.

## 2.3 Gene structure and conserved motifs in *PsSAURs*

The exon-intron structure of *PsSAURs* and their conserved motifs were analyzed to understand their sequence characteristics (Fig. 3). Totally, 73.68% (42/57) of *PsSAURs* are none intron, ten *PsSAURs* contained one intron, only four *PsSAURs* including *PsSAUR13*, *PsSAUR15*, *PsSAUR17*, and *PsSAUR23*, contained two introns, and *PsSAUR49* contained three introns. MEME was used to analyze the conserved motifs of 57 *PsSAUR* proteins. A total of five conserved motifs were obtained (Fig. 3), including Motif1 (RFVVPISYLNHPLFQDLLSQAEFEFGFDHPMG), motif2 (SSKSLDVPKGHFVYVGESQK), motif3 (JTIPCSEETFE), motif4 (MGFRLPGIVHAKKNL), and motif5 (MNKIRSIVRLKQILKKWQKSA), at lengths of 32, 21, 11, 15, and 21 aa, respectively. 16 *PsSAURs* contained motif1, motif2, motif3, and motif4, 14 *PsSAURs* contained motif1, motif2, motif3, and motif5, and 19 contained motif1, motif2, and motif3. However, two *PsSAURs* (*PsSAUR36*, *PsSAUR37*) contained motif1, motif2 and motif4, two *PsSAURs* (*PsSAUR28*, *PsSAUR29*) contained motif1, motif3, and motif5, and *PsSAUR33* contained motif2, motif3, and motif5. Generally, some *PsSAURs* in the same group had similar conserved structures. For example, *PsSAURs* in Group D contained motif1, motif2, motif3, and motif5, and most *PsSAURs* in Group E contained motif1, motif2, motif3, and motif4.

## 2.4 Gene duplication in *PsSAURs*

The gene duplication of *PsSAURs* was analyzed, and even segmental duplications and ten tandem duplications of *PsSAURs* were obtained (Table 2). These include 21 *PsSAURs* located on chromosomes 1, 3, 4, 6, 7, and 8, respectively. Taken together with the phylogenetic relationship of *PsSAURs*, the result showed that most of the gene pairs for segmental duplication (6/7) and tandem duplication (9/10) were located in the same group, including the segmental duplication *PsSAUR3/PsSAUR46* and the tandem duplication *PsSAUR12/PsSAUR13*.

Table 2  
*PsSAUR* gene duplication of in *P. siberia*

| Type                  | Chromosome | Gene ID                           |
|-----------------------|------------|-----------------------------------|
| Segmental duplication | Chr1&Chr7  | <i>PsSAUR3/PsSAUR32</i>           |
|                       | Chr1&Chr8  | <i>PsSAUR3/PsSAUR46</i>           |
|                       | Chr1&Chr8  | <i>PsSAUR4/PsSAUR50</i>           |
|                       | Chr2&Chr6  | <i>PsSAUR6/PsSAUR20</i>           |
|                       | Chr2&Chr2  | <i>PsSAUR9/PsSAUR11</i>           |
|                       | Chr2&Chr6  | <i>PsSAUR10/PsSAUR23</i>          |
|                       | Chr3&Chr7  | <i>PsSAUR14/PsSAUR33</i>          |
| Tandem duplication    | Chr1       | <i>PsSAUR6/PsSAUR7</i>            |
|                       | Chr3       | <i>PsSAUR12/PsSAUR13</i>          |
|                       | Chr4       | <i>PsSAUR16/PsSAUR17</i>          |
|                       | Chr6       | <i>PsSAUR20/PsSAUR21/PsSAUR22</i> |
|                       | Chr7       | <i>PsSAUR27/PsSAUR28</i>          |
|                       | Chr8       | <i>PsSAUR39/PsSAUR42</i>          |
|                       | Chr8       | <i>PsSAUR40/PsSAUR41</i>          |
|                       | Chr8       | <i>PsSAUR45/PsSAUR46</i>          |
|                       | Chr8       | <i>PsSAUR47/PsSAUR48</i>          |
|                       | Chr8       | <i>PsSAUR55/PsSAUR56</i>          |

## 2.5 Promoter analysis of *PsSAURs*

The cis-acting elements of promoter regions (1,000 bp from the start codon) were analyzed (Fig. 4). The results revealed that the promoters of the 11 *PsSAURs* contain the auxin signaling transduction related cis-elements, including *PsSAUR6*, *PsSAUR15*, *PsSAUR30*, *PsSAUR36*, *PsSAUR37*, *PsSAUR38*, *PsSAUR39*, *PsSAUR44*, *PsSAUR45*, *PsSAUR48*, and *PsSAUR49*. and 11 *PsSAURs*, including *PsSAUR9*, *PsSAUR11*, *PsSAUR17*, *PsSAUR29*, *PsSAUR33*, *PsSAUR34*, *PsSAUR57*, and *PsSAUR55*, contain cis-acting element involved in defense and stress responsiveness. Cis-responsive elements were also involved in hormonal response, and primarily included 84 methyl jasmonate (MeJA), 25 zein, 65 abscisic acid (ABA), 17 salicylic acid (SA), and 8 gibberellin (GA) responsive elements. In addition, *PsSAUR* promoters also contained 11 low-temperature responsiveness elements, six endosperm expression cis-responsive elements, and two wound-responsive elements.

## 2.6 Expression patterns of *PsSAURs* in different floral organs

The expression patterns of *PsSAURs* in pistil, stamen, petal, and sepal were analyzed (Fig. 5). A total of 34 *PsSAURs* had an average expression level of FPKM > 1, which were used in subsequent analyses. *PsSAUR4*, *PsSAUR8*, *PsSAUR19*, and *PsSAUR22* were highly expressed in pistil, *PsSAUR13* was highly expressed in stamen, *PsSAUR30*, *PsSAUR32*, *PsSAUR33*, *PsSAUR38*, *PsSAUR41*, *PsSAUR42*, *PsSAUR43*, *PsSAUR44*, *PsSAUR45*, *PsSAUR46*, *PsSAUR48*, *PsSAUR51*, and *PsSAUR52* were highly expressed in petal, *PsSAUR9* and *PsSAUR11* were highly expressed in sepal.

## 2.7 Expression patterns of *PsSAURs* in kernels at different developmental stages

To analyze the function of *PsSAURs* in kernel development, the expression patterns of *PsSAURs* in kernel during six different developmental stages (S1-S6) were analyzed (Fig. 6). The results showed that the average expression level of 17 *PsSAURs* revealed an FPKM of  $> 1$ , and the expression patterns of *PsSAURs* in kernel were differences during different developmental stages, such as *PsSAUR49* was downregulation during the development. *PsSAUR9* and *PsSAUR11*, *PsSAUR5* and *PsSAUR14*, and *PsSAUR42* and *PsSAUR43* were high expressed at S1, S2, and S3 respectively, which were the rapidly growth stage, whereas the expression of *PsSAUR8* was higher at the S5 and S6, which were the mature stage.

### 3 Discussion

*SAURs* are major class of early auxin-induced genes in plants. With the increasing number of plant genomes sequenced, whole-genome identification and analysis of *SAUR* family have been completed in many plants, the analysis of the *SAURs* was unclear in *Prunus sibirica*, thus, we identified and analyzed the *PsSAURs* in current study.

Fifty-seven *PsSAURs*, distributing across eight chromosomes of *P. sibirica* genome, were identified. Compared with the number of *SAURs* (70) in apple, there were fewer *SAURs* in *P. sibirica*. This may be because only one whole-genome duplication event in *P. sibirica*, whereas the apple genome has experienced two whole-genome duplication events [15].

Understanding the structure of genes is essential for elucidating their function. Studies have shown that the *SAURs* generally have no introns and are usually distributed in clusters [16]. Analysis of *PsSAURs* showed that 85% of these have no introns, which was associated with the previous reports, such as cucumber (67/73) (*Cucumis sativus* L.) [17], grape (59/64) [6], tomato (90/99) (*Lycopersicon esculentum* Miller), potato (131/134) (*Solanum tuberosum* L.) [18], and apple (44/70) [5]. In addition, chromosome location analysis revealed that *PsSAURs* were distributed in clusters on chromosomes 1, 4, 6, 7, and 8, which might be result from the gene duplication. Analysis of the phylogeny and conserved structures of the 57 *PsSAURs* showed that this family is divided into five different groups. Several differences in the conserved domains among different groups were found, indicating functional diversity in the *PsSAURs* during the evolution.

This current study analyzed the *PsSAURs* through genomics and bioinformatics, providing a theoretical basis for further studies on the functions of the *PsSAURs* and serving as an important reference for future studies on the regulatory roles of the *PsSAURs* in Rosaceae.

## 4 Materials And Methods

### 4.1 Identification of *PsSAURs*

To identify *SAURs* in *P. sibirica* genome, 78 *SAURs* in *Arabidopsis* (Phytozome 12 database) were used as a reference sequence to search against the *P. sibirica* genome (<https://www.rosaceae.org>, tfGDR1049) by using BLAST (a minimum amino acid identity of  $\geq 50$ , E-value  $< 1e-5$ ). The *SAURs* structural domain sequence PF02519 was downloaded from the pfam database (<http://pfam.xfam.org/>), and Hidden Markov Model (HMM) was used to screen candidate sequences containing the *SAURs* structural domain. In addition, Conserved Domain Search (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>) and the SMART website (<http://smart.embl-heidelberg.de/>) were used to confirm the presence of conserved structural domains. ExPASy ProtParam (<https://web.expasy.org/protparam/>) [19] was used to predict the physical and chemical parameters, including the number of amino acids, molecular weights (Mw), putative isoelectric points (PIs), grand average of hydropathicity, aliphatic index, and instability index. CELLO (<http://cello.life.nctu.edu.tw/>) was used to predict the subcellular location of the *SAURs*.

### 4.2 *PsSAUR* phylogenetic tree construction

Phylogenetic tree was conducted on the identified full-length protein sequences of *SAURs* from *P. sibirica* and *A. thaliana*. The sequence alignment of 135 *SAURs* by using the Clustal X [20]. The phylogenetic tree was constructed in MEGA X [21] based on the maximum likelihood method, the JTT + F model, and bootstrap values were calculated for 1000 replicates. Evolview was used to display the phylogenetic tree [22].

### 4.3 Structure, conserved motifs, and gene duplication analysis of *PsSAURs*

GSDS 2.0 (<http://gsds.cbi.pku.edu.cn/index.php>) [23] was used to analyze the exon and intron composition of *PsSAURs*. MEME (<http://meme-suite.org/tools/meme>) [24] was used to predict the conserved domains of *PsSAURs* with five different sequence motifs and a sequence motif width of 6–50 aa. Tbtools [25] was used to perform collinearity and gene duplication analysis of *PsSAURs*.

### 4.4 Gene duplication and evolutionary analysis of *PsSAURs*

The chromosomal location of *PsSAURs* were from *P. sibirica* genome annotation files. BLASTP was used to search collinearity for each of *PsSAURs* (e-value  $< 1e^{-5}$ , the top 5 matches). Then, the replication events were examined by MCScanX in TBtools [25].

### 4.5 Analysis of cis-acting elements in *PsSAUR* promoters

To analyze the cis-acting elements in promoter sequences, the sequences 1,000 bp upstream of the coding regions of the identified *PsSAURs* were extracted. The PlantCARE (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) [26] database was used for predicting the cis-acting elements in the promoters, and the results were visualized by TBtools [25].

### 4.6 Expression analysis of *PsSAUR*

The gene expression patterns of *PsSAURs* in pistil, stamen, petal, sepal, and kernels of different developmental stages were analyzed. The expression levels of *PsSAURs* were measured as fragments per kilobase million (FPKM). The gene expressed of average FPKM value was  $> 1$  for further analysis. TBtools [25] was used to displayed the heatmaps of *PsSAURs* expressions.

# Declarations

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## Availability statement

The datasets analysed during the current study are available in supplementary information file.

## Author contributions

D, J. H., and W. B. designed project. W. B. analyzed data and wrote the paper. S. R., S. Z., J. C., and Y. L. helped with the data analysis. B.W., Y. B., and T.W. took the lead on revising the manuscript. All authors read and approved to publish the manuscript.

## Additional Information (including a Competing Interests Statement)

### Competing interests

The authors declare no competing interests.

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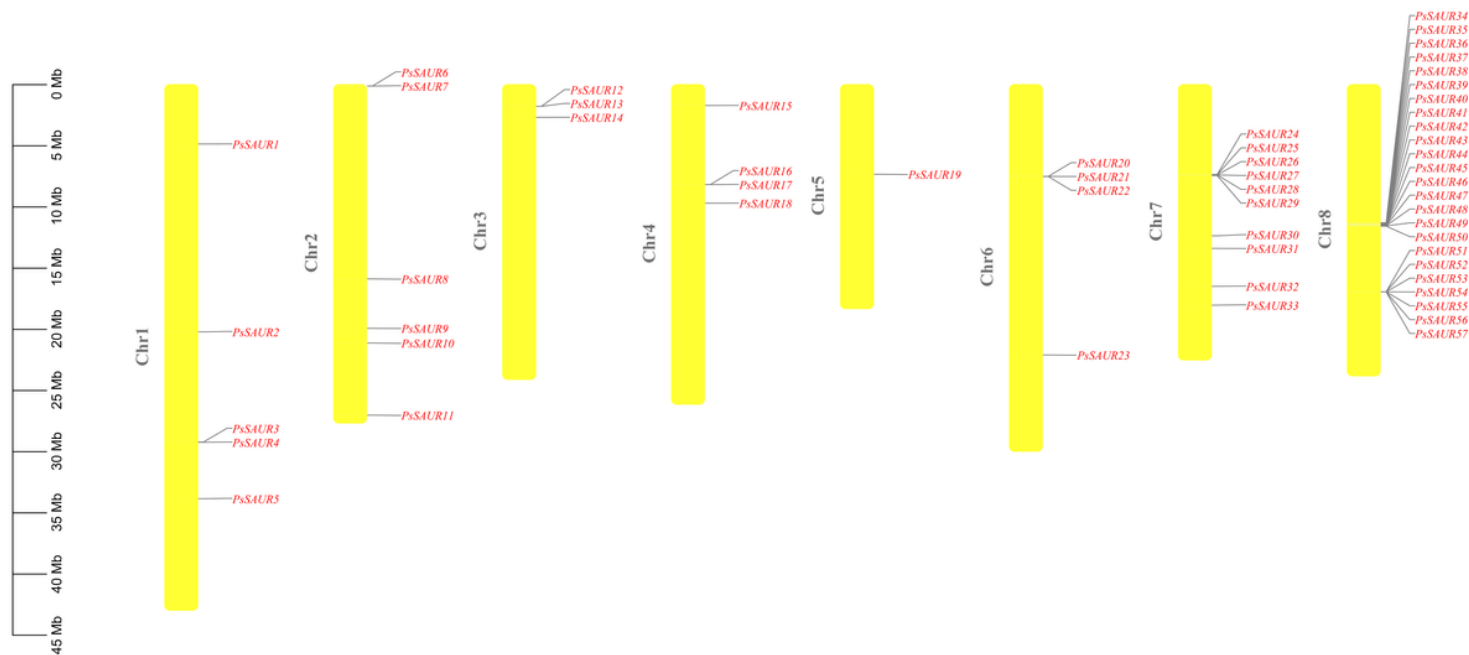
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## Figures



**Figure 1**

Chromosome distribution of *PsSAURs*

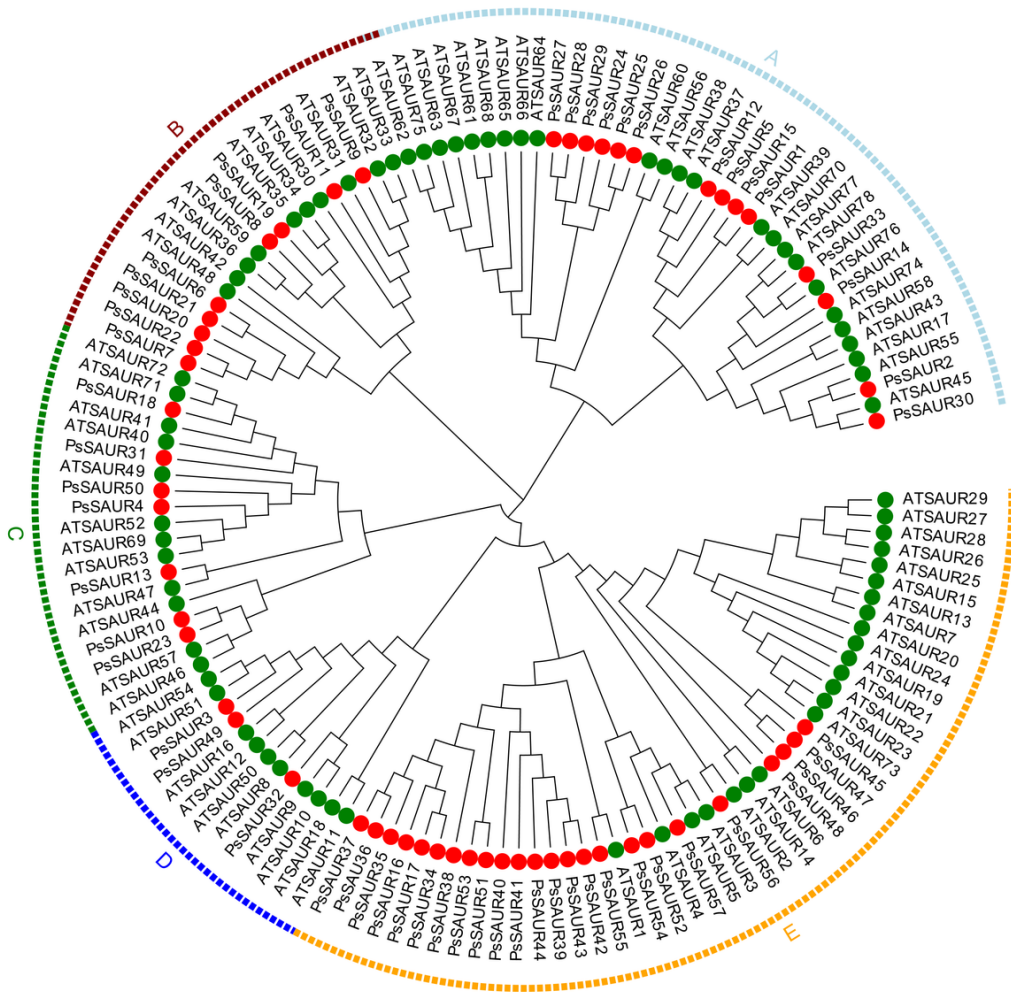
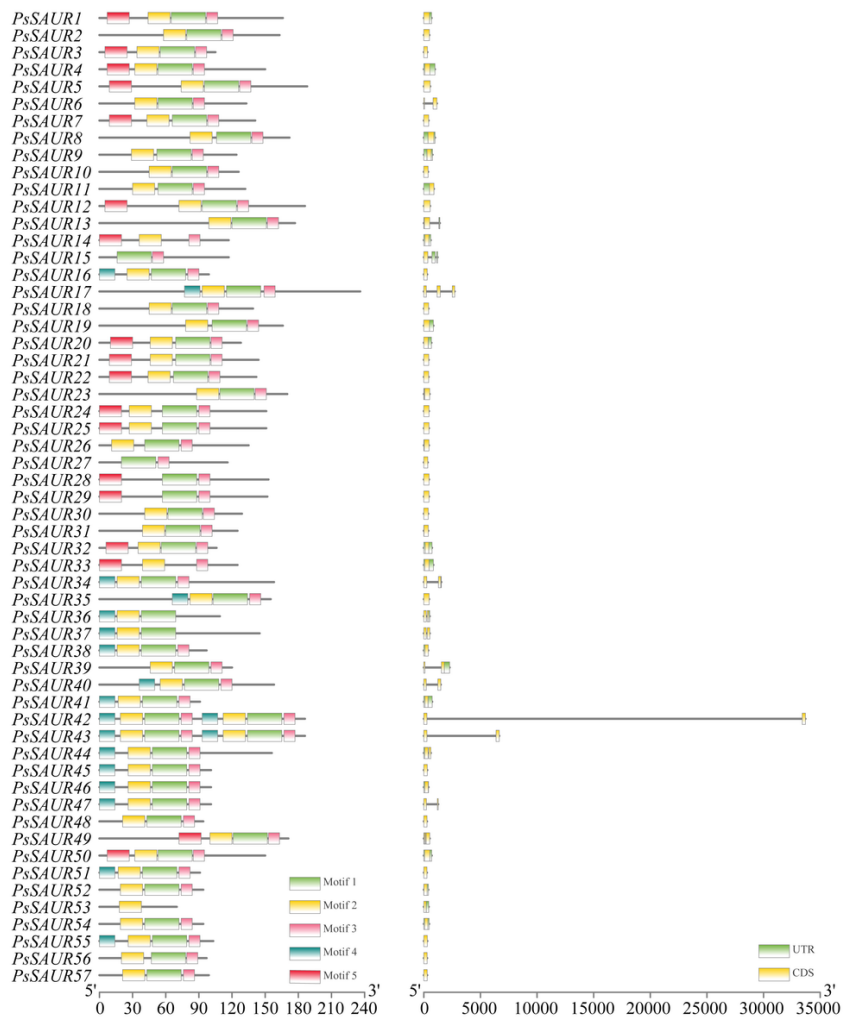


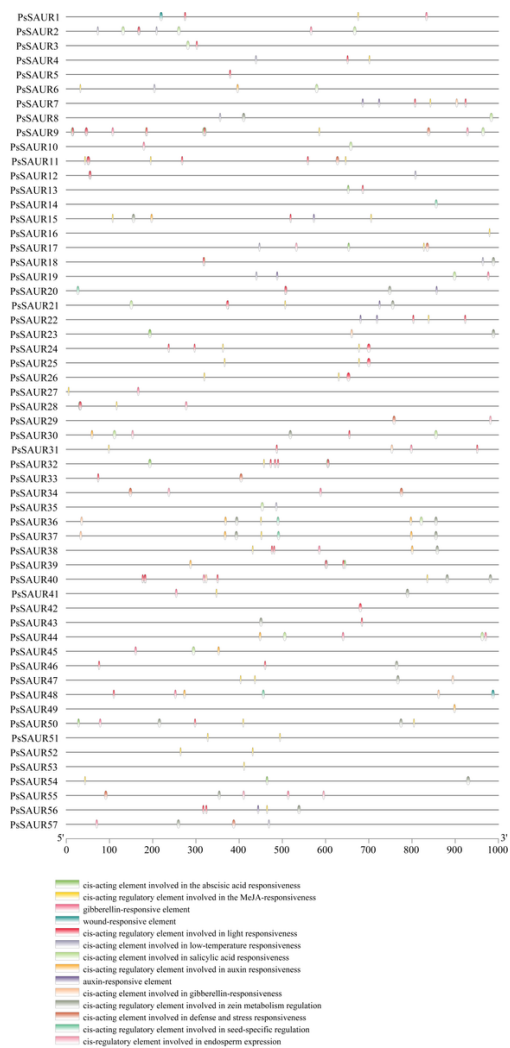
Figure 2

Phylogenetic relationship of *PsSAURs*



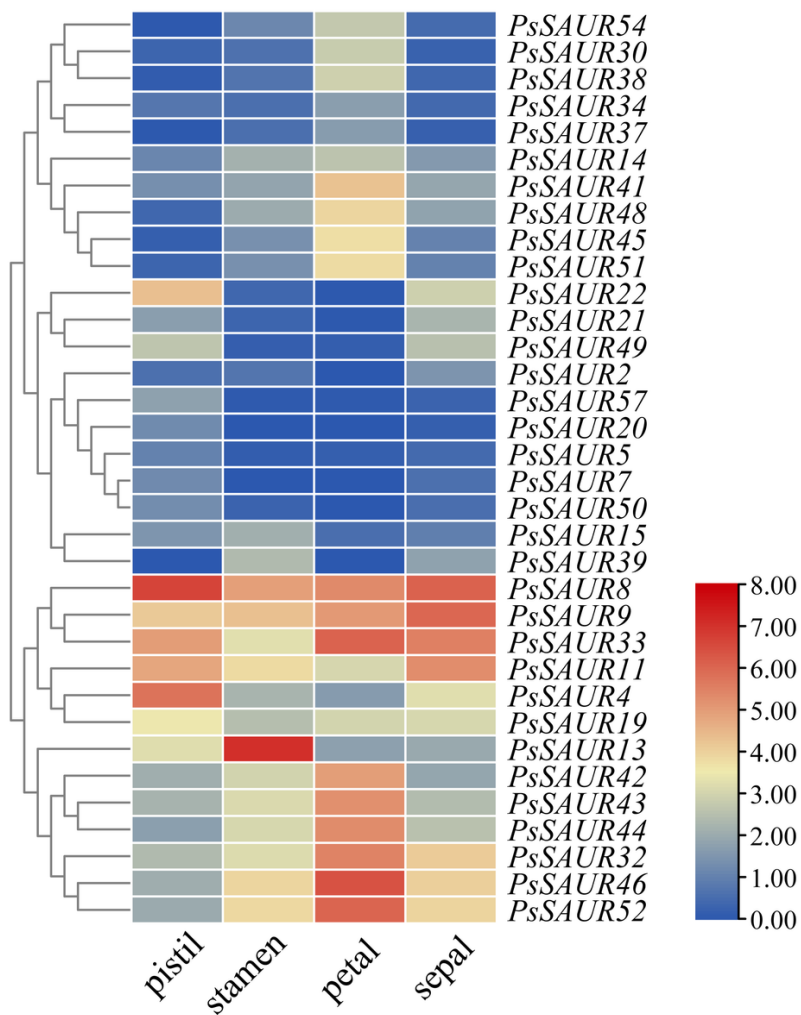
**Figure 3**

The Conserved motifs and gene structure of *PsSAUR*



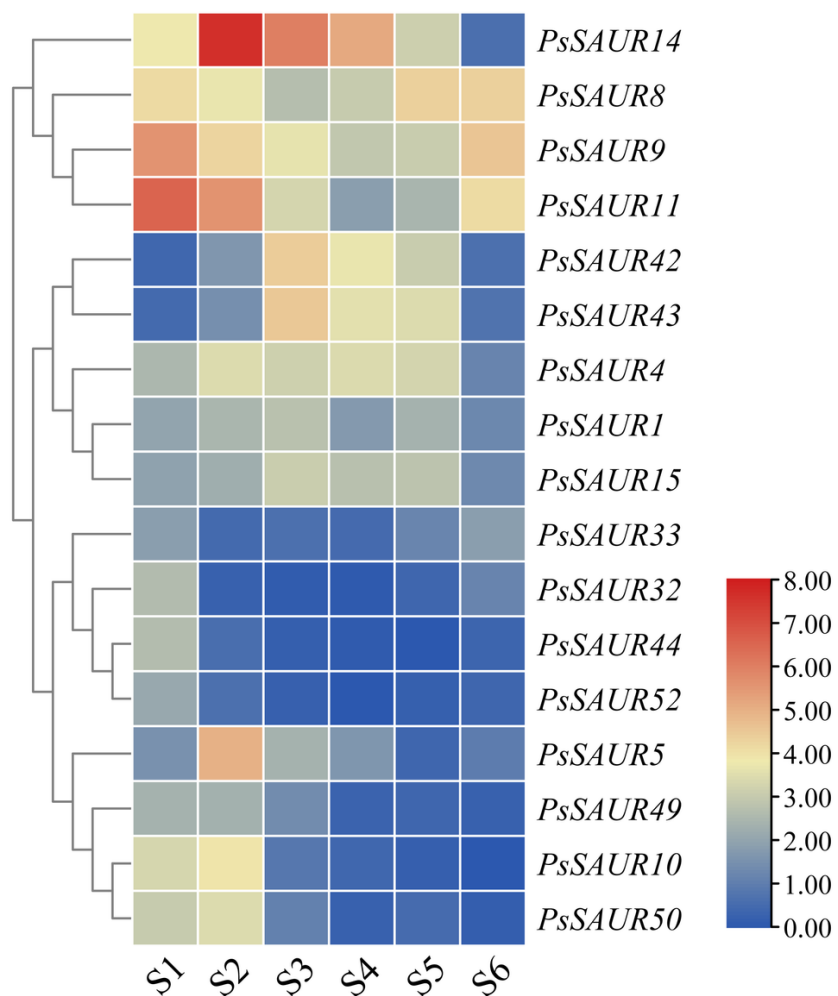
**Figure 4**

Distribution of major cis-elements in promoter of *PsSAURs*



**Figure 5**

The expression profile of *PsSAURs* in different floral organs



**Figure 6**

The expression profile of *PsSAURs* in kernels at different developmental stages

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [SupplementarymaterialSAURrawdata.zip](#)