Supplementary Table S1

Table S1 Percent identities of the studied genes against NCBI database (nucleotide BLAST)

Gene	Most identical gene	Max score	Percentage of gene identity
C-glycosyltransferase (*CGT1*)	MK616593.1 *Phyllostachys prominens* C-glycosyltransferase (CGT1) mRNA, complete cds	307	97
Flavanone 2-hydroxylase (*F2H*)	MK628906 *Phyllostachys edulis* flavanone 2-hydroxylase (F2H) mRNA, complete cds	287	99.37
Sucrose nonfermenting 1-related protein kinase 1 (*SnRK1*)	KR611568 *Triticum aestivum* sucrose non-fermenting-1-related protein kinase alpha subunit mRNA, complete cds	294	88.57
Serine/threonine protein 2 (*PP2A*)	XM_006657013 PREDICTED: Oryza brachyantha serine/threonine-protein phosphatase PP2A-1 catalytic subunit (LOC102722026), mRNA	161	87.94

Source of data: https://blast.ncbi.nlm.nih.gov/Blast.cgi (Access date: 31 May 2024)

Sequencing results from PCR products (The yellow color indicates the primer sequences)

1. Sequences of *CGT1* gene (181 bp)

5′CTTGTGGGTGGTGAAGAGCACTGTCGTGGACAGAGACGACTCAGCCGAGCTCAGCGAGCTGCTCGGCGAGG
GGTTCTTGGAGCGGGTGCAGGGGCGGGGGCTCGTGACCAAGGCGTGGGTGGAGCAAGAAGAGGTCCTGAAGC
ACGAATCCATCGGGCTGTTCATCAGCCACTGTGGTTGG3′

```
Phyllostachys prominens C-glycosyltransferase (CGT1) mRNA, complete cds
Sequence ID: MK616593.1Length: 1419Number of Matches: 1
Range 1: 915 to 1095GenBankGraphicsNext MatchPrevious Match
 Alignment statistics for match #1
 Score                 Expect   Identities      Gaps            Strand
 307 bits(166)         6e-79    176/181(97%)    0/181(0%)       Plus/Plus
Query  1     CTTGTGGGTGGTGAAGAGCACTGTCGTGGACAGAGACGACTCAGCCGAGCTCAGCGAGCT  60
             ||||||||||||||||||||| |||||||||||||||||||| |||||||| ||||||||
Sbjct  915   CTTGTGGGTGGTGAAGAGCACCGTCGTGGACAGAGACGACTCCGCCGAGCTTAGCGAGCT  974

Query  61    GCTCGGCGAGGGGTTCTTGGAGCGGGTGCAGGGGCGGGGGCTCGTGACCAAGGCGTGGGT  120
             ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  975   GCTCGACGAAGGGTTCTTGGAGCGGGTGCAGGGGCGGGGGCTCGTGACCAAGGCGTGGGT  1034

Query  121   GGAGCAAGAAGAGGTCCTGAAGCACGAATCCATCGGGCTGTTCATCAGCCACTGTGGTTG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1035  GGAGCAAGAAGAGGTCCTGAAGCACGAATCCATCGGGCTGTTCATCAGCCACTGTGGTTG  1094

Query  181   G  181
             |
Sbjct  1095  G  1095
```

2. Sequences of *F2H* gene (158 bp)

5’GACATCCTCATGGACGTGGCGGAGGACGAGGCCGCCGAGGTCAGGCTCAGCAGGGAGAACATCAAGGCCTTCGTCCTCGACATCTTCACCGCGGGGTCTGACACGACGGCCACCAGCGTCGAGTGGATGCTGGCGGAGCTGATCAACCACCCGGCCTA 3’

Phyllostachys edulis flavanone 2-hydroxylase (F2H) mRNA, complete cds

Sequence ID: MK628906.1Length: 1554Number of Matches: 1

Range 1: 826 to 983GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

```
 Score                Expect     Identities      Gaps          Strand
 287 bits(155)        7e-73      157/158(99%)    0/158(0%)     Plus/Plus
Query  1    GACATCCTCATGGACGTGGCGGAGGACGAGGCCGCCGAGGTCAGGCTCAGCAGGGAGAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  826  GACATCCTCATGGACGTGGCGGAGGACGAGGCCGCCGAGGTCAGGCTCACCAGGGAGAAC  885

Query  61   ATCAAGGCCTTCGTCCTCGACATCTTCACCGCGGGGTCTGACACGACGGCCACCAGCGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  886  ATCAAGGCCTTCGTCCTCGACATCTTCACCGCGGGGTCTGACACGACGGCCACCAGCGTC  945

Query  121  GAGTGGATGCTGGCGGAGCTGATCAACCACCCGGCCTA  158
            ||||||||||||||||||||||||||||||||||||||
Sbjct  946  GAGTGGATGCTGGCGGAGCTGATCAACCACCCGGCCTA  983
```

3. Sequences of *SnRK1*gene (248 bp)

5′AGCTCGACGATGAAACCCTTAATGATGTTATCAAGATGGGGTTTGACAAGAATCAGCTAATTGAATCTATTCAAAATAGATTGCAAAATGAGGCGACGGTTGCATATTATTTACTCTTGGACAATAAGCTTCGTACAATCAGTGGCTACCTTGGTGCTGAGTACCAAGAATCTATGGACCCTTTCTCTCAAACTTCAGCTGAAACACCAAGTTCTGCATCTGAACCTAGGCAGTACGGTTCTATGGAA3′

Triticum aestivum sucrose non-fermenting-1-related protein kinase alpha subunit mRNA, complete cds

Sequence ID: KR611568.1Length: 1503Number of Matches: 1

Related Information

Gene-associated gene details

Range 1: 860 to 1104GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

```
 Score                Expect     Identities      Gaps       Strand
 294 bits(159)        7e-75      217/245(89%)    3/245(1%)  Plus/Plus
Query  1     AGCTCGACGATGAAACCCTTAATGATGTTATCAAGATGGGGTTTGACAAGAATCAGCTAA  60
             |||| || ||||| || || |||||||||||||| ||||| ||||||||||||||||| |
Sbjct  860   AGCTTGATGATGAGACTCTGAATGATGTTATCAAAATGGGATTTGACAAGAATCAGCTCA  919

Query  61    TTGAATCTATTCAAAATAGATTGCAAAATGAGGCGACGGTTGCATATTATTTACTCTTGG  120
              ||||||| ||||||| |||||||||||||||||||| ||||||||||||||||||||||
Sbjct  920   CTGAATCTCTTCAAAAGAGATTGCAAAATGAGGCGACAGTTGCATATTATTTACTCTTGG  979

Query  121   ACAATAAGCTTCGTACAATCAGTGGCTACCTTGGTGCTGAGTACCAAGAATCTATGGAC-  179
             |||||||||||||||||| ||||||||||||||| |||||||| ||||| || ||||||
Sbjct  980   ACAATAAGCTTCGTACAACCAGTGGCTACCTTGGAGCTGAGTATCAAGAGTCAATGGACT  1039

Query  180   C--CTTTCTCTCAAACTTCAGCTGAAACACCAAGTTCTGCATCTGAACCTAGGCAGTACG  237
             |  ||||||| |||  |||| |||||||||||||||| ||||||||| || ||||||| |
Sbjct  1040  CATCTTTCTCCCAAGTTTCACCTGAAACACCAAGTTCAGCATCTGAAGCTCGGCAGTATG  1099

Query  238   GTTCT  242
             |||||
Sbjct  1100  GTTCT  1104
```

4. Sequences of *PP2A* gene (141 bp)

5′ACGCCCCCCGACACCAACTACCTATTCATGGGCGAGTACGTCGACCGAGCTACTATTCAGTGGAGACTGTTA
CACAGTTAGTGGTTTGAAAGTTAGTAAGGAACCAGAATCACAATATTGAGAGGAAATCATGAGAGCAGA3′

PREDICTED: Oryza brachyantha serine/threonine-protein phosphatase PP2A-1 catalytic subunit (LOC102722026), mRNA

Sequence ID: XM_006657013.2Length: 1389Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 426 to 565GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

```
 Score           Expect      Identities      Gaps        Strand
 161 bits(87)    4e-35       124/141(88%)    5/141(3%)   Plus/Plus
Query  5    CCCCCGACACCAACTACCTATTCATGGGCGAGTACGTCGACCG-AGCTACTATTCAGTGG  63
            |||| |||||||||||||| ||||||||||| |||||||||||  |||||||||||||||
Sbjct  426  CCCCTGACACCAACTACCTCTTCATGGGCGACTACGTCGACCGTGGCTACTATTCAGTGG  485

Query  64   AGACTGTTACACAGTTAGTGG-TTTGAAAGTTAGT-A-AGGAACCAGAATCACAATATTG  120
            |||||||||||   ||||||| | | |||||| || | ||  | ||||||||||||||||
Sbjct  486  AGACTGTTACATTATTAGTGGCTCTTAAAGTTCGTTATAGAGA-CAGAATCACAATATTG  544

Query  121  AGAGGAAATCATGAGAGCAGA  141
            |||||||||||||||||||||
Sbjct  545  AGAGGAAATCATGAGAGCAGA  565
```