

## Supplementary File

**Table S1** Primers sequences of all genes for qRT-PCR.

<b>Primer Name</b>	<b>Forward Primer (5'-3')</b>	<b>Reverse Primer (5'-3')</b>
<i>liYUCCA1</i>	CCTCGTACACGGTCCCATAA	ATGGAGTTTGAGTCGGTCGT
<i>liYUCCA2</i>	CCTTCCCTTCAAGCTACCC	CGGGAAACATACTCCGTTGT
<i>liYUCCA3</i>	AGACAGTCCAGTCAGCGAAA	ACTCAAACCTCGCAAGAACCG
<i>liYUCCA4</i>	AGAAGCAGGGCATAGTCGAA	GGAACGCCACGGTTTGATAA
<i>liYUCCA5-1</i>	GACAAGGTCTTCTTCTTCTCCTCC	GCAAGAGTGGATCACCTCG
<i>liYUCCA6-1</i>	CTGGAGGAGAGAGATGGAAGG	CTTTCAGACAAGCCGCCGT
<i>liYUCCA7</i>	GACGTCGGAGCCTTCTCTAA	AAGTCGTTCTCCTTGAGCCA
<i>liYUCCA8</i>	GAGCTCTAGCGAAGATCCGA	TGCGATAACCAGTAGCGAGT
<i>liYUCCA9</i>	GATATTTATCAGACCGTCGGTGT	TTGTTGGGTATTACAGGGTAGTGA
<i>liYUCCA10</i>	CGGGTTTAGCAACATCGGTT	TGGGCATAAAGGTGGGAACA
<i>liYUCCA11</i>	CATTCCCTCCCAACACTCCT	ATACGCCGATTTGACGTTCC
<i>lielF2</i>	TACCAGTGGCTCGCTTGAC	CAACCAAAGCAAATGACGTACTC
<i>liPP2A-4</i>	GAATGCCTGCGAAAGTATGG	TCCTAATGTTGTCAAGGGTCTC
<i>liRPL15</i>	GGGCGAAGAGGAAAGGTAG	CGGAAGACGGCGATAAAGAG
<i>CaMV35S</i>	ACAGAACTCGCCGTAAAGAC	GAAGGGTCTTGCGAAGGATA
<i>NbActin</i>	CGTTATGGTTGGAATGGGACAGAA	AAGAACAGGGTGCTCCTCGTGG
<i>NbIAA8</i>	ACCCTGCCAAAGATAGTGCT	GTGGTTGAACACGTGAGGTC
<i>NbIAA16</i>	TTGGCCACCAGTGAGATCAT	CTCCGTCCACGCTAACTTTC
<i>NbGH3.1</i>	TATGTACGCAGCTTCCGAGT	CACGGGATGAGTTAGGGTCA
<i>NbGH3.6</i>	CGTGTTTGCCTCAGGCTTTA	ACTGCCTCTCTCACTGAAGG
<i>NbSAG12</i>	CGTTATGGTTGGAATGGGACAGAA	AAGAA CAGGGTGCTCCTCGTGG

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10      20      30      40      50      60
1      ATGGATTCTGCTGGAGGAGAGATGGAAGGTAAGTACACATGACTTGTCTGCTCC
1      M D F C W R R E M E G K L A H D Y L S S

70      80      90      100     110     120
61     GCAAAGAGCCATCACGGCGTGATGACGTCACGGCGCGCTCTGCGTCCACGGGACCG
21     A K S H H G V M T S P R R V C V V T G P

130     140     150     160     170     180
121    GTGATCGTAGGCGCGGACCGTCCGGACTAGCGACGGCGCTTGTCTGAAAGAGAAAGGA
41     V I V G A G P S G L A T A A C L K E K G

190     200     210     220     230     240
181    ATAACTTCGGTACTACTCGAGAGATCAAAGTGCATAGCTTCACTATGGCAGCTTAAGACT
61     I T S V L L E R S N C I A S L W Q L K K T

250     260     270     280     290     300
241    TAGCAGCGGCTCCATCTCCACCTTCTAAGCAATCTGTGAAGTCCGCTCATACCCTTT
81     Y D R L H L H L P K Q F C E L P L I P F

310     320     330     340     350     360
301    CCCGCGGATTTCCAATTATCCGACGAAGCAGCTTCATCGAGTACCTCGAGGACTAC
101    P A D F P T Y P T K Q Q F I E Y L E D Y

370     380     390     400     410     420
361    GCGCGGAGGTTTCGATATACGGCCGGAGTTTGGTCAGACGGTTGAGTCGGCGGAGTTTGT
121    A R R F D I R P E F G Q T V E S A E F D

430     440     450     460     470     480
421    GAGAACCTCGGATGTGGCCGTGACGAGCGTGGTGAAGAGGCGACGAGTACGTT
141    E N L G M W R V T S V G E E G T T E Y V

490     500     510     520     530     540
481    TGCCGGTGGTTGGTGGCTGCGACGGGGAGAATCGCGAGCCGGTTCGCCAGGTTTGTAG
161    C R W L V A A T G E N A E P V V P R F E

550     560     570     580     590     600
541    GGTATGGAGAAGTTTGAAGCCACCGGATAGTTAAGCACAGGATCATTATAAGACCGGC
181    G M E K F E A T G I V K H T S H Y K T G

610     620     630     640     650     660
601    GGAGATTCGCGGAAAAGGGTTTGGTCTCGGATGTGAAACTCCGGCATGGAGGTT
201    G D F A G K R V L V V G C G N S G M E V

670     680     690     700     710     720
661    TGTITGGACTCTGCAATTTCCGGTCTCAGCCTTCTCTGTTGTCAGAGACGCTGTGCAC
221    C L D L C N F G A Q P S L V V R D A V H

730     740     750     760     770     780
721    GTCCTACCACGAGAGATGTGGGTACTTCGACTTTTGGCTGTCCATGTGCTACTTAAA
241    V L P R E M L G T S T F G L S M L L L K

790     800     810     820     830     840
781    TGGTTCGCCATCCGGCTCGTTGACCGTTTCTCTTGGTTGTTCCCGGTCATCCTCCGG
261    W L P I R L V D R F L L V V S R F I L G

850     860     870     880     890     900
841    GATACCACCTGTTAGGTCTTAACCGTCCCGTTTAGGCCCACTAGAGCTCAAAAATCTC
281    D T T L L G L N R P R L G P L E L K N L

910     920     930     940     950     960
901    ACCGGAAAACCGCGTTCTCGACGTCGGGACGCTTCCCAAGATCAAACCGGAGATATC
301    T G K T P V L D V G T L A K I K T G D I

970     980     990     1000    1010    1020
961    AAGGTGTGTTCCGGGATAAGAAGGTTCAAACGGCATGAAGTTGAGTTCGATAACGGGAAA
321    K V C S G I R R F K R H E V E F D N G K

1030    1040    1050    1060    1070    1080
1021   ACAGAGAGATTTGAGCCATAAATATGGCACTGGCTACAAAAGCAACGTACCCCTTGG
341   T E R F D A I I L A T G Y K S N V P S W

1090    1100    1110    1120    1130    1140
1081   CTAAGGAGAATAAAATGTTTAGTAAGAAAGATGATTCCCAATACAAGATTTCCGGAG
361   L K E N K M F S K K D G F P I Q E F P E

1150    1160    1170    1180    1190    1200
1141   GGATGGAGAGGGGAATGTGGCTATATGCTGCGGATTCACAAAACGTGAATTTTCGGA
381   G W R G E C G L Y A V G F T K R G I F G

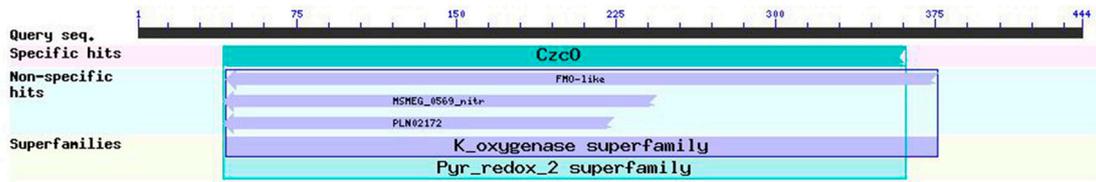
1210    1220    1230    1240    1250    1260
1201   GCATCAATGGATGCAAGAAAATACCTCAAGACATATACGAGTGTCTCAAGAAAATCTGAT
401   A S M D A K K I A Q D I Y E C S R K S D

1270    1280    1290    1300    1310    1320
1261   CAAGCCATAGACATATACAAGTGTTCATGTCAAGAAAACCTGATCAAGCCATAGTAGA
421   Q A H R H I Q V F M S R K P D Q A Y S R

1330
1321   TTAGTACGCGTTGA
441   L L D G *

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**Figure S1.** The nucleic acid and amino acid sequences of *liYUCCA6-1*.



**Figure S2.** The conserved domain of IiYUCCA6-1.



**Figure S3.** The predicted protein tertiary structure of IiYUCCA6.

Species/Abbrv	Group Name	Sequence
1. 5-1(cDNA)		...T G T T G C T G T G G T G G C C T C C T C T G C C T G T G C G C G C T T G C T G T G C T G C T G C C T G C C T G G C T G T T T T G G C G T T T G G C T T G G C C G G C
2. 5-2(cDNA)		...T G T T G C T G T G G T G G C C T C C T C T G C C T G T G C G C G C T T G C T G T G C T G C T G C C T G C C T G G C T G T T T T G G C G T T T G G C T T G G C C G G C
3. 5-1(gDNA)		...T G T T G C T G T G G T G G C C T C C T C T G C C T G T G C G C G C T T G C T G T G C T G C T G C C T G C C T G G C T G T T T T G G C G T T T G G C T T G G C C G G C
4. 5-2(gDNA)(2)		...T G T T G C T G T G G T G G C C T C C T C T G C C T G T G C G C G C T T G C T G T G C T G C T G C C T G C C T G G C T G T T T T G G C G T T T G G C T T G G C C G G C

**Figure S4.** The sequence comparison of *IiYUCCA5-1* and *IiYUCCA5-2* based on *I. indigotica* genome data.