

Table S1. Oligonucleotide sequences for generating constructs

| Construct | Forward Oligonucleotides (5' to 3') | Reverse Oligonucleotides (5' to 3') |
|---------------------------|--|---|
| GOF5 | GGCCG <u>AATTC</u> TCTTCAAAATTATAACATTTTCATGTTGTG | GGCCG <u>GATCC</u> TTTTATTGTCGTGCCATTTTGTTTTTATTACG |
| GOF7 | CGCGCG <u>GAATTC</u> AAAAATTACTATGTTTATTTTCGAAATTTAGAAAAACG | GGTCACG <u>AATTC</u> CAAGAAAATTTTGCCTGAAAACTTTTTTTATTG |
| GOF9 | CACAATTCACACATTATACGAGCCGG | TCTAGAG <u>GATCC</u> CCGGGTACCGAGCTCGTGTGGTTTTCTTCGCTTTTCATTAC |
| GOF10 | GTGCCC <u>GAATTC</u> AAGCCTAGAAAAACGAAGAGTTAC | CTAGAG <u>GATCC</u> CCGGGTAC |
| GOF11 | GTGCCC <u>GAATTC</u> AAGCCTAGAAAAACGAAGAGTTAC | TCTAGAG <u>GATCC</u> CCGGGTACCGAGCTCGTTTCTTGATTGTCGTGCCATTTTG |
| GOF12 | GTGCCC <u>GAATTC</u> AAGCCTAGAAAAACGAAGAGTTAC | TCTAGAG <u>GATCC</u> CCGGGTACCGAGCTCGTGTGGTTTTCTTCGCTTTTCATTAC |
| GOF13 | <u>AATTC</u> GAAAAGCGAAGAAAAGCGAAG | <u>GATCC</u> TTTCGCTTTTCTTCGCTTTTCG |
| GOF14 | <u>AATTC</u> GAAAAGCGAAG | <u>GATCC</u> TTTCGCTTTTCG |
| GOF15 | <u>AATTC</u> GAAAAGCGAAGAAAAGCGAAG | <u>GATCC</u> TTTCGCTTTTCTTCGCTTTTCG |
| GOF16 | <u>AATTC</u> GAAAAGCGAAGAAAAGCGAAGAAAAGCGAAGAAAAGCGAAGAAAAGCGAAG | <u>GATCC</u> TTTCGCTTTTCTTCGCTTTTCTTCGCTTTTCTTCGCTTTTCTTCGCTTTTCG |
| pBSG564-662 | GGCCGGATCCAAAGTTTTTCACGCAAAATTTTCTTGG | GGCCTCTAGAGATCAATTCCACAGTTTTTCGCGATC |
| G564 -883/-874 | <u>AATTC</u> TCAAAGCCTATCAAAGCCTAG | <u>GATCC</u> TAGGCTTTGATAGGCTTTGAG |
| G564 -836/-827 | <u>AATTC</u> GAAAACCCACAGAAAACCCACAG | <u>GATCC</u> TGTGGTTTTCTGTGGTTTTTCG |
| G564 -823/-814 | <u>AATTC</u> TAAAAACAAATAAAAACAAAG | <u>GATCC</u> TTTGTTTTTATTGTTTTTTAG |
| GA 20-OXIDASE +222/+213 | <u>AATTC</u> GAAAAGAGAAGGAAAAGAGAAG | <u>GATCC</u> TTCTCTTTCCCTTCTCTTTCCG |
| GA 20-OXIDASE +215/+206 | <u>AATTC</u> GAAAAGAGGAGAAAAGAGGAG | <u>GATCC</u> TCCTCTTTTCTCCTCTTTTCG |
| GA 20-OXIDASE -2498/-2489 | <u>AATTC</u> GAAATAGAGAAGAATAGAGAAG | <u>GATCC</u> TTCTCTATTCTTCTCTATTTCG |
| GA 20-OXIDASE -1410/-1419 | <u>AATTC</u> GAAAAGCAAGGAAAAGCAAGG | <u>GATCC</u> TTTGCTTTTCTTCGCTTTTCG |
| PcWOX9-like +94/+85 | <u>AATTC</u> GAGAAGGGAAGAGAAGGGAAG | <u>GATCC</u> TTCCCTTCTCTTCCCTTCTCG |
| PcWOX9-like +365/+356 | <u>AATTC</u> TAAAAGGGAATAAAAAGGGAAG | <u>GATCC</u> TTCCCTTTTATTCCTTTTAG |
| PcWOX9-like -3186/-3195 | <u>AATTC</u> GAAAAGGGTAGAAAAGGGTAG | <u>GATCC</u> TACCTTTTCTACCTTTTCG |
| PcWOX9-like -2699/-2708 | <u>AATTC</u> GAAAACGACGAAAACGACG | <u>GATCC</u> GTCTTTTTCTGCTTTTCG |
| PcWOX9-like -282/-273 | <u>AATTC</u> GAAAATAGAAGAAAATAGAAG | <u>GATCC</u> TTCTATTTTCTTCTATTTTCG |
| PcWOX9-like -732/-741 | <u>AATTC</u> GAAAAAGAAGAAAAAGAAG | <u>GATCC</u> TTCTTTTTTCTTCTTTTTTCG |
| PtNIP1;1 -814/-805 | <u>AATTC</u> GAAATGCAAAGAATTGCAAAG | <u>GATCC</u> TTTGCAATTCTTTGCAATTTCG |
| PtNIP1;1 -725/-716 | <u>AATTC</u> GTAAATGAAGTAAATGGAAG | <u>GATCC</u> TTCAATTTACTTCAATTTACG |
| PtNIP1;1 -615/-624 | <u>AATTC</u> GTAAAGAGAAGTAAAGAGAAG | <u>GATCC</u> TTCTCTTTACTTCTCTTTACG |
| PtNIP1;1 -528/-537 | <u>AATTC</u> CAATAACGAACAATAACGAAG | <u>GATCC</u> TTCTGTTATTGTTCTGTTATTGG |
| M1 | GGTACCAG <u>AATTC</u> <u>GGCCGCGGGGGGCC</u> CATGTTGTTGTTTGTTCAAAGC | CTAGAG <u>GATCC</u> CCGGGTAC |
| M2 | GTACCAG <u>AATTC</u> AATTTATAACATTTT <u>GGCCGCGGGGGGCC</u> TCAAAGCCTA GAAAAACGAAGAG | CTAGAG <u>GATCC</u> CCGGGTAC |
| M3 5'-fragment | GGTACCAG <u>AATTC</u> AATTTATAACATTTTCATGTTGTTGTTG | CTCTTCGTGGGCCCGCGGCCAACAAACACAACATGAAAATGTTATAA |
| M3 3'-fragment | TGTTTGTGGCCGCGGGGGGCCACGAAGGTTACTATTGGTAATGAAAAG | CTAGAG <u>GATCC</u> CCGGGTAC |
| M4 5'-fragment | GGTACCAG <u>AATTC</u> AATTTATAACATTTTCATGTTGTTGTTG | CATTACCAGGGCCCGCGGCCTTTTCTAGGCTTTGAAACAAAC |

| Construct | Forward Oligonucleotides (5' to 3') | Reverse Oligonucleotides (5' to 3') |
|------------------|---|--|
| M4 3'-fragment | CTAGAAAAGGCCGCGGGGGGCCCTGGTAATGAAAAGCGAAGAAAAC | CTAGAGGATCCCGGGTAC |
| M5 5'-fragment | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | GTTTTCTTGGGCCCGCGGCCATAGTAACTCTTCGTTTTCTAGGCTTTG |
| M5 3'-fragment | GTTACTATGGCCGCGGGGGGCCAAGAAAACACATAATAAAAACAAAATG | CTAGAGGATCCCGGGTAC |
| M6 5'-fragment | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | TGTTTTTAGGGCCCGCGGCCCGCTTTTCATTACCAATAGTAACTC |
| M6 3'-fragment | GAAAAGCGGGCCGCGGGGGGCCATAAAAACAAAATGGCACGACAATCAAG | CTAGAGGATCCCGGGTAC |
| M7 5'-fragment | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | ATTGTCGTGGGCCCGCGGCCCTTATGTGGTTTTCTTCGCTTTTC |
| M7 3'-fragment | CCACATAAGGCCGCGGGGGGCCACGACAATCAAGAAAAGTTTTAC | CTAGAGGATCCCGGGTAC |
| M8 5'-fragment | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | GAAAACCTGGGCCCGCGGCCGCCATTTTGTTTTTATTATGTGG |
| M8 3'-fragment | AAAATGGCGGGCCGCGGGGGGCCAAGTTTTACACAAAACTTTTTC | CTAGAGGATCCCGGGTAC |
| M9 | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | TAGAGGATCCCGGGTACCGAGCTCGAATTTTGAAAAAGTGGGCCCGCGGCC TTTCTTGATTGTCGTGCC |
| M10 | GGTACCAGAATTCAATTATAACATTTTCATGTTGTGTTTG | TAGAGGATCCCGGGTACCGAGCTCGGGGCCCGCGGCCCTTGTGTGAAAACCT TTTCTTGATTG |
| 15-bp NEGATIVE | <u>AATTCGGCCGCGGGGGGCCCGAGCTCGGTACCCGGG</u> | <u>GATCCCGGGTACCGAGCTCGGGGCCCGCGGCCG</u> |
| M11 | AAGCTGGAATTC AAGCCTACGGGGGGCCGAGTTACTATTGGTAATGAAAAG | TCTAGAGGATCCCGGGTACCGAGCTCGTGTG |
| M12 | CACAATTCACACATTATACGAGCCGG | TAGAGGATCCCGGGTACCGAGCTCGTGTGGTTTTCGGGCCCCCGATTACCAATA GTAACCTTCGT |
| M13 | AAGCTGGAATTC AAACCTAGAAAAACGAAGAGTTAC | TCTAGAGGATCCCGGGTACCGAGCTCGTGTG |
| M14 | CACAATTCACACATTATACGAGCCGG | TAGAGGATCCCGGGTACCGAGCTCGTGTGGTTTTCTTCGCTTTTCATTACTAATA GTAACCTTCGTTTTTCTAG |
| M15 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGCCGATCCTTCGCTTTTCGAATTC |
| M15 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCATTAATTAATTAATTTTCATTT ACTTTTTTCC | CCAGTTGCAACCACCTGT |
| M16 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCATATATAACTTTCTGCGCACCAAGA |
| M16 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCAGTTAAATTATTATTATTTCA TTTAAAAATATAAATATT | CCAGTTGCAACCACCTGT |
| M17 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCCTTAAAAATAAAAAGGAAAAAGTAAA TGA |
| M17 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCATATAAAAAATATAACCTTAAT CAAAACAAAGC | CCAGTTGCAACCACCTGT |
| M18 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCCTTAAATAATATTTATATTTTAAATGA AAATAATAATAATT |
| M18 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCCTTACAACTTTTAACCTTAA AATTAACCTT | CCAGTTGCAACCACCTGT |
| M19 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCCTTTAGATTAAGGCTTTGTTTTGATT AA |
| M19 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCCTAGTGTGACAACTAAAAAGTT GTATACAAC | CCAGTTGCAACCACCTGT |
| M20 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCCTCATTTCCTTTTAAAGTTAATTTA AGG |
| M20 3'-fragment | CTGGCATGAACTTCGGTCCGCGGGGGGCCAGAAAATAAATATATAATAAAA GAGTAAATTTGTAATTAATG | CCAGTTGCAACCACCTGT |
| M21 5'-fragment | ACCAGTTTCCTCAAGGGTCC | CGAAGTTCATGCCAGTCCAGCGCCGCGGCCAAACCTATGACAGGGTTGTATACAAC TT |

| Construct | Forward Oligonucleotides (5' to 3') | Reverse Oligonucleotides (5' to 3') |
|------------------|--|--|
| M21 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> CATAAAAAAGTATTAATAAATA ATATTTAGAGTAGTAATATG | CCAGTTGCAACCACCTGT |
| M22 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGGCC</u> ATCATTTAATTACAAATTTACTCTTT ATTATATATATTTATTTT |
| M22 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> CATATAAAAAATGTGGTTGTCC ATATATC | CCAGTTGCAACCACCTGT |
| M23 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGGCC</u> CAACCATATTACTACTCTAAATATTAT TATTTTAATACTTT |
| M23 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> TATCATGACAAATATTTTCACC GAAA | CCAGTTGCAACCACCTGT |
| M24 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGCC</u> TTTTAAAGTGAATAATGATATATGGA CAACC |
| M24 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> CGTGGATAATGGAAAAATAC AA | CCAGTTGCAACCACCTGT |
| M25 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGGCC</u> CTTTTTCGTTCTTTCCATCTTTTCG |
| M25 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> GCATAACATTTTGTATTAGTGA TGAGTTTT | CCAGTTGCAACCACCTGT |
| M26 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGCC</u> AAAGTACTGGAGGGAGATTGCTTG |
| M26 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> CAGAATATAGGAAAATTTTAGAA TCACGTGG | CCAGTTGCAACCACCTGT |
| M27 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGCC</u> AAATATATATGATAAAAACTCATCA CTAATACAA |
| M27 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> TAATATTTTAATTTATAATGTA GTTGATTTTATTG | CCAGTTGCAACCACCTGT |
| M28 5'-fragment | ACCAGTTTCCTCAAGGGTCC | <u>CGAAGTTCATGCCAGTCCAGCGCCGCGCC</u> CTATTATATAGCTATCCACGTGATTC TAAAA |
| M28 3'-fragment | <u>CTGGCATGA</u> <u>ACTTCGGTCCGCGGGGGCC</u> CATACATAAATATGTGTTGATAG TGGGTGA | CCAGTTGCAACCACCTGT |

Underlined nucleotides are incorporated restriction sites.

Nucleotides shown in blue are a part of the 15-bp mutation sequence.

Nucleotides shown in green are a part of the 45-bp mutation sequence.