Table S2 VIGS silencing fragment sequences used in this study

Name	**Silencing fragment sequence (5′→3′, 300 bp)**
VIGS: *NbDOX1*	AAAACTGCTAGCGAGGAGAAATTTCGTGGACACAGGGAAACAATTTAACA TGATCGCTGCTTCTTGGATACAGTTTATGGTTCATGATTGGATCGATCACTT GGAAGATACTCAACAGATTGAGCTTCATGCACCTAAAGAAGTTGCAAGTC AGTGTCCTCTCAAGTCCTTTAAGTTTAACAAAACCAAGGAAACTCCAACA AACTTTTATGAAATCAAAACTGGTCACTTGAACAGGCGTACCCCATGGTGG GATGGAAGCGTTATATATGGGAGCAATGCAGAGGTTTTGAAGAAAGT
VIGS: *NbRBOHC*	ATAGGTATGAATAAGGAGTCTAAGGAATTTGCTGTAGAGCTATATGATGCGC TAGCTCGGAGGAGAAACATTACAACTGATTCCATTAACAAAGCACAGCTC AAAGAGTTCTGGGATCAAGTGGCTGACCAAAGTTTTGATTCTCGCCTTCA AACTTTCTTTGACATGGTTGATAAAGATGCTGATGGTAGAATCACAGAAGA AGAAGTCAGAGAGATTATAGGCCTTAGCGCGTCTGCCAACAGGCTGTCAA CAATCCAGAAACAAGCTGATGAATACGCAGCA ATGATCATGGAAGAG
VIGS: *NbPER52*	ATGGCTTTTCGTTTGAGTCATTTGAGCCTTGCCCTGAGCCTTTTGGCTCTTG CACTTGCAGGTGTTGCCATATATAGGAACACTTATGAAGCCATGAGTAAGG GTTTCCAAACACTTTCTCCAGAGTTGGATCTGCTGGAGTCAGCGGCCAGC ATTTTAACCCTAAATAATAATAATGCTGAGAAAAATTCAGAGAGCAAGTTA ACCCAACCATTATCTCCAACGGCATGCATCTTCTCCGCTGTTCAGGGAGTT GTGAACAGTGCAATTGATAGAGAAAGGCGCATGGGAGCTTCTCTC
VIGS: *NbPEX19*	CTTAGGGATGATGTTGCCCGATAGGAATGCTAAGAAAAAGGGGAAGCAAA CGGCTTCCGGTGAGTCAAAAGACTCGCACGTAGCTGAAGCTCTTGATAGG CTTAGGGAGCAGACTAGAGAGGCTGTTAAAGGATTGGAATCAGTGGCCGG GCCGAGACCTGGCTTAGATAACTTGGGGAATGATGCAATGATGGAGGAGT GGGTTAAGCAGTTTGAGGAGCTTTCTGGATCTCAGGACATGGAGTCGATA GTAGAGACCATGATGCAACAGCTTTTGTCAAAGGAAATCCTTCATGAACC
VIGS: *NbMIJ24.8*	ATGGGGCAATCTTCATCTGCGGAGCAAGTGTCGCCGGAGCAAAGAGAGGC AGAATCTTTGGCAGCTTCAACTGGAGCTCTTCCTTCTCTACAAAAAGCTTT CTCTCTCCTTTCTGATCCTCAAACTCACTCCATTCCCCTCCCTTCTCTTCAG AAATGTTTTGGGTTCTCCTTTGAGGGATCAACAAGTGAAGAATCGACAGT GCCGAAGGAAATTCCAGTTTTGTTGAGTCATTTGAGTTCTTCAATAGTTGA CTTGTTTTTCTTGTCTGAAAAAGGAGGTGTTAGTTGGGTTGAGTTC
VIGS: *NbMZN14.5*	CCAAAAATTTAAAAATTCAAAAGATTATTATGCCAAGATTGGTAAGGCGTG GAAGCGTGGTTATCTTCTTTATGGTCCTCCCGGGACAGCGGTTAAGGACAA TACCGAGCTAAGAAAGTTATTGATAGACACTACAAGTAAATCTATAATTGTA

	ATAGAAGACATCGATTGTTCCCTTGACCTTACCGGTCAAAGAGAGGAGAA GAAGAAAAAAGACGAGGAAGATAAAGAAAAAGATGAGAAAGATGCCATT ATGAAAAAGATGAAAAAAGGAGAGGTGAAAGAGAAAAGTGAAGTAAC
VIGS: *NbF6F22.26*	GTGCCTCCAAATGACTTGCTGAATGGATTCGGTAGTTTACAGAAAGCCGGT AGCATCCATGAAGACCCTCCTCATTCTGAAGCTGCAGATGTGAGAACTCCA CTTGATCACGGTAATAGGCCTAATGCATCTCCAAATATCCTAGAGCAGAATG CGAGATCCTCACTGAGGACCCAAAACTTTAACTCTGCACATGGTGGTGGC AGAGGCATAACACCATCTTCTAATTATCATCATGGAGTTGGTCCTTCAGGGT TTAGAGATGAAGGGTTGGAAGGAGAACAA TCATTTCCTGCAGAT
VIGS: *NbF23M19.10*	ATGGATTCTTTCTTCAGCAAAGGTTTCAAAGCTGCTAAATGTAAAACCCTA TTGAAATTGACGATTCCTCGTATAAAACTACTGAGGAATCGTAGGGAGATG CAGCTGAAGCAGATGAGAAAAGAAATTGCTAAGCTACTAGAGACTGGTCA GGAAGCTACTGCTCGGATTCGGGTAGAGCATATAATAAGAGAAGAGAAAA TGATGGCAGCACAGGAGATAGTCGAGCTATTCTGCGAGCTTATATCTGTTC GTCTTCCAATTATTGAAGCACAAAGGGAATGTCCTCTAGATCTGAAA
VIGS: *NbPALY*	AGAGAATACTTGTTCGCCTACGCTGATGATCCTTGCAGTTGCAACTACCCT TTAATGCAGAAACTGAGACAAGTACTTGTTGATCATGCAATGAAGAATGGT GAAAGTGAGAAGAATGTGAACAGCTCAATCTTCCAAAAGATTGGAGCTTT CGAAGACGAATTGAAGGCTGTTTTACCTAAAGAAGTTGAGAGTGCAAGAG CTGCATTGGAAAGTGGCAACCCTGCTATTCCTAACAGGATTACAGAATGCA GATCGTATCCATTGTACAGGTTTGTGAGAAAGGAGCTTGGAACAGAA
VIGS: *NbPAL2*	AACTCCTTGGGCTTAATCTCAGCTAGAAAAACAGCTGAAGCCGTGGACAT CTTAAAGCTAATGTCATCCACATATCTAGTCGCACTTTGCCAAGCGATAGAC TTGAGGCATTTGGAAGAAAATCTGAGGAATGCAGTCAAGAACACGGTGAG CCAAGTCGCTAAGAGAACCTTGACGATGGGTGCCAATGGAGAACTTCATC CATCAAGATTCTGCGAAAAGGACTTGCTTCGAGTCGTGGACAGGGAATAC GTCTTTGCATACGCTGATGACGCCTGCAGCGCTAACTACCCACTGATG
VIGS: *NbPAL4*	GTCATCCACATATCTAGTTGCACTCTGCCAAGCGATAGACTTGAGGCATTT GGAAGAAAATCTGAGGAATGCAGTCAAGAACACGGTGAGCCAAGTCGCT AAGAGAACCTTGACAATGGGTGCCAATGGAGAACTTCATCCATCAAGATT CTGCGAAAAGGACTTGCTTCGAGTCGTGGACAGGGAATATGTCTTTGCATA CGCTGATGACGCCTGCAGCGCCAACTACCCACTGATGCAGAAACTGAGGC AAGTACTCGTCGACCACGCCTTACAAAATGGCGAAAATGAGAAGAACAC
VIGS: *NbTBC5A*	ATCCTGAGCATGGTAGCTATTTCCAGACTCCTGGATGCCAAGCCATGTTGA GGAGAATTCTACTACTTTGGTGCCTTAGACATCCAGAGTATGGTTACAGAC

	AAGGGATGCATGAACTGTTGGCCCCACTTCTCTATGTCCTTCAAGCTGATA CGGAGCAGCTTTCTGAAGTTAGGAATCTTTACGAGGATCATTTTGCTGACA AATTTGATGGGTTCTCATTTCATGAAAATGACTTGACATATAAATTTGACTT TAAAAAATTCTCGGAATCTGTGGAAGATGATAA TGGATCTCAGA
VIGS: *NbF6N7.6*	CATCTCAACTTTTTCGTGAAGCTCAGGGAGATGGTTTCGTTCCTAATGACA GGAGGAAGCAAGACCAAAAAACAAATGATTATCCTCGCATTGCTGAATCT AATGATGTTCAGAAGTTGCCTGAAGATGTTCAAGTGCCTGCAGATCCCTTG GAGTTTGACAAATTGTCACTAGTATGGGGAAAACCAAGGCAGCCTCCACT GGGAACAGAAGAGTGGTCCACTTTCCTGGACTGTGAAGGTAGAGTCACA GACTCGGAAGCAGTAAGAAAGAGGATATTTTATGGAGGAGTCGAACAAG
VIGS: *NbRIN4*	CACAACATTGCTAAATCGCCAATTCATCCAAATTCTCAGCAGGCGAAGATA TCAGGACGAGTAGCTGCTTCGCCTCAGCCTGATAGAGGAGCTGTAGTTCC AAAATTTGGCGAATGGGATGATAACGATCCTCAATCTGCAGAAAACTATTC TGAGGTTTTTAACAGAGTGCGAAATGAAAGGAATGAAAGGAACAGAGGC CCTGGAAATGTGCTAGGCACACCTGGTAGAACATCTTACAGTACCGAAAG GCATCAACGAAACGAAAAGCAAAAGAGCTGC TGCTTTCCTTTGTGGTGA
VIGS: *NbPRPX1*	AGATCTATATTTTTACGAGGATTCGCGATTGAAATCCTACATGTTTATTCAGG ACCACCAGAAATAGTGTACAAGTTTAGGCATTGGGGTTACATGGAAGGTCC ATTTAAAGGACATGCTGCTACTGGTGGACTTGTAGAGCTCTTTGGGATTGG CATTTTTGAATTGGACAAAGAGAGTAACAAGATCGTTAAGGCAGAGATGT TCTTTGATAGAGGAGAATTGCTTGGAGGCCTTGTGAAAGGAGAAAGCAAT GATGAATTGGAATTGGCTGCTTCAAAATGTCCT TTCATGAAATAA
VIGS: *NbPRPX2*	ATGGTCCACAAGACAGATCCTAATGACTTCAAAACTGTTGATCCAAAAATA TTCACAAAGAGTGTCAATGGCAGGAAAGGGTTGACACCAGAAGAAAATG CAAAACTTGGTGGTGGCTACAATACATTCCTTCAAACGTCATTGCCAGAGA GTGTTCGAGTCTACAACCCTGATGAGGAGACATTTGAATCATCACAGAAA GTTTTCAGATCCATATTTTTACGAGGATTCGCCATTGAAATCCTTCATGTTTA TTCAGGACCACCAGAAATTGTGTACAAATTTAGGCATTGGGGTCAC
VIGS: *NbDRB4*	ATGGATATTTTTCAGCAAAGACAGAATAACGTTGGACAACCTTCTCGTGTC AATGGAACTCCATTGGCTGGTTGGGAAGCCAATACCTCGAAAGGGATGCT TCATCTATACAAGAATCGACTACAACAGTATGCCCAAAAGCAAAATCTCAC TTTACCCGTGTATTCTTCTGAACTTGATGGCCCTCCGCACGCCCATCAGTTT AGGTCAAAAGTGACTATTGATGGAAAAACTTATGAAACTCAGGAGTTCTT CTCTACATTGAAGGAAGCTGAACATGCAGCTGCAAAAGTTGCTTTT
VIGS:	ATGTCGAAATGTGATGGTGATTTGGTTGATGGATTGGTGAATCCTAACAATA

NbRIHA	ACTCTTTTGCTATGCAACGTGAAAAGATCATCATTGATACTGATCCTGGCAT TGATGACAGTATGGCAATACTAATGGCATTTCAGACACCGGGAGTTGAGAT CGTAGGCTTGACTACGATCTTTGGCAATGTTACTACAAAAGACGCTACACG TAATGCATTACTTTTGTGTGAAGCTGCAGGATATCCGGATGTTCCAGTCGCC GAGGGCAGCCCTGAACCTCTGAAGGGAGGGGAGCCACGTGTT
VIGS: *NbVAD1*	TTTCCCATTCTTATAGTGATCACCATTGCTGTGATCCTGCTCTTAATGCAGAT GAGCATACTTGTGTTATTAGGTCGACCTCAGCACGTCCACGTGATACCTCA AGGGGACTGCACAGGTAGCATGTATCGACTGGGAGATAGGGGTATAGACA CACTAGCTTTTCTGGATAAACAGATTAGTCATCTCAAAGAGGAGATGGTTA TGGTCGAAACACTGCTCGGCAAAATGCAGCAGGAGCATACACTTCTAAAC ACGAAATTGAAAGAGTTTGAGCGCCTACGGA AGCACCAGAAAGGA
VIGS: *NbACO*	GAGGTGATCACCAATGGGAAATACAAGAGTGTAATGCACAGAGTGATTAC ACAAACAGACGGGACTCGGATGTCATTAGCTTCGTTTTATAATCCAGGAGG TGATGCAGTAATATTTCCAGCACCAGCTTTGGTTGAGAAAGACGCAGAGG AAAGCAAAGCAGTTTATCCAAAGTTTGTGTTTGATGATTATATGAAGTTATA TGCTGGACTCAAGTTTCAAGCCAAAGAGCCAAGGTTTGAAGCCATGATCA AGGCCATGGAAACTGGTGTGAAATGTGATCCTATTGCAACTGCTTAA
VIGS: *NbDNAJ*	TCCCTTTCCCGCAATGTAATTTGCTCCAAGTGCAGTGGTAAAGGATCCAAG TCTGGTGCTTCAATGAAGTGTTCTGGTTGTAAAGGTAGTGGTATGAAGGTT TCAATTAGACAACTTGGCCCGTCAATGATCCAGCAAATGCAGCACCCTTGT AATGAATGCAAGGGTACTGGAGAGACTATTGACGATAAGGATCGGTGCCC TCAATGCAAAGGTGAAAAAGTGGTTCAGGAGAAGAAAGTCCTAGAAGTT CATGTTGAAAAAGGCATGCAAAATGGACAGA AAATTACATTCCCCGGA
VIGS: *GmSRC7*	ATGGCTGCAACAACACGTTCCCTTCCATTCATCTATGATGTGTTCCTCAGCT TCAGAGGGGAAGACACACGCTATGGTTTCACTGGCAATCTATACAGGGCT CTCTGTGAGAAGGGAATTCATACCTTCTTTGATGAAGAGAAGCTTCACGGT GGAGATGAAATAACACCTGCACTTTCGAAGGCAATTCAAGAGTCCAGGAT TGCTATTACTGTGCTTTCTCAAAACTATGCTTTTTCCTCATTTTGTTTAGATG AACTTGTAACCATCCTTCACTGCAAGAGTGAAGGGCTGTTGGTT