Supplemental Table S1

Sequences of oligonucleotide primers used in this study.

Primer names	Primers sequences (5’-3’)
pHIS2-NRS1-D0-F	5’-AATTCCCCTTAGTTTCGGGCCCTTAGTTTCGGGCCCTTAGTTTCGGGGAGCT-3’
pHIS2-NRS1-D0-R	5’-CCCCGAAACTAAGGGCCCGAAACTAAGGGCCCGAAACTAAGGGG-3’
pHIS2-NRS1-D1-F	5’-AATTCCCTTAGTTTCGGCCTTAGTTTCGGCCTTAGTTTCGGGAGCT-3’
pHIS2-NRS1-D1-R	5’-CCCTTAGTTTCGGCCTTAGTTTCGGCCTTAGTTTCGGG-3’
pHIS2-NRS1-D2-F	5’-AATTCCTTAGTTTCGCTTAGTTTCGCTTAGTTTCGGAGCT-3’
pHIS2-NRS1-D2-R	5’-CCTTAGTTTCGCTTAGTTTCGCTTAGTTTCGG-3’
pHIS2-NRS1-D3-F	5’-AATTCTTAGTTTCTTAGTTTCTTAGTTTCGAGCT-3’
pHIS2-NRS1-D3-R	5’-CGAAACTAAGAAACTAAGAAACTAA-3’
pHIS2-NRS1-D4-F	5’-AATTCTAGTTTTAGTTTTAGTTTGAGCT-3’
pHIS2-NRS1-D4-R	5’-CAAACTAAAACTAAAACTAG-3’
pHIS2-NRS1-D5-F	5’-AATTCAGTTTAGTTTAGTTTGAGCT-3’
pHIS2-NRS1-D5-R	5’-CAAACTAAACTAAACTG-3’
pHIS2-NRS1-D6-F	5’-AATTCTAGTTTAGTTTAGTTGAGCT-3’
pHIS2-NRS1-D6-R	5’-CAACTAAACTAAACTAG-3’
pHIS2-NRS1-D7-F	5’-AATTCAGTTAGTTAGTTGAGCT-3’
pHIS2-NRS1-D7-R	5’-CAACTAACTAACTG-3’
pHIS2-NRS1-D8-F	5’-AATTCTAGTTAGTTAGTGAGCT-3’
pHIS2-NRS1-D8-R	5’-CACTAACTAACTAG-3’
pHIS2-NRS2-D0-F	5’-AATTCCCCTGAATCTCGGGCCCTGAATCTCGGGCCCTGAATCTCGGGGAGCT-3’
pHIS2-NRS2-D0-F	5’-CCCCGAGATTCAGGGCCCGAGATTCAGGGCCCGAGATTCAGGGG-3

pHIS2-NRS2-D1-F	5’-AATTCCCTGAATCTCGGCCTGAATCTCGGCCTGAATCTCGGGAGCT-3’
pHIS2-NRS2-D1-R	5’-CCCGAGATTCAGGCCGAGATTCAGGCCGAGATTCAGGG-3’
pHIS2-NRS2-D2-F	5’-AATTCCTGAATCTCGCTGAATCTCGCTGAATCTCGGAGCT-3’
pHIS2-NRS2-D2-R	5’-CCGAGATTCAGCGAGATTCAGCGAGATTCAGG-3’
pHIS2-NRS2-D3-F	5’-AATTCTGAATCTCTGAATCTCTGAATCTCGAGCT-3’
pHIS2-NRS2-D3-R	5’-CGAGATTCAGAGATTCAGAGATTCAG-3’
pHIS2-NRS2-D4-F	5’-AATTCGAATCTGAATCTGAATCTGAGCT-3’
pHIS2-NRS2-D4-R	5’-CAGATTCAGATTCAGATTCG-3’
pHIS2-NRS2-D5-F	5’-AATTCAATCAATCAATCGAGCT-3’
pHIS2-NRS2-D5-R	5’-CGATTGATTGATTG-3’
pHIS2-NRS2-D6-F	5’-AATTCGAATCGAATCGAATCGAGCT-3’
pHIS2-NRS2-D6-R	5’-CGATTCGATTCGATTCG-3’
pHIS2-NRS2-D7-F	5’-AATTCAATCTAATCTAATCTGAGCT-3’
pHIS2-NRS2-D7-R	5’-CAGATTAGATTAGATTG-3’
pHIS2-NRS2-D8-F	5’-AATTCGAATGAATGAATGAGCT-3’
pHIS2-NRS2-D8-R	5’-CATTCATTCATTCG-3’
pHIS2-NRS1-M1-F	5’-AATTCGCGTTGCGTTGCGTTGAGCT-3’
pHIS2-NRS1-M1-R	5’-CAACGCAACGCAACGCG-3’
pHIS2-NRS1-M2-F	5’-AATTCTAGGGTAGGGTAGGGGAGCT-3’
pHIS2-NRS1-M2-F	5’-CCCCTACCCTACCCTAG-3’
pHIS2-NRS1-M3-F	5’-AATTCGGGGGGGGGGGGGGGAGCT-3’
pHIS2-NRS1-M3-R	5’-CCCCCCCCCCCCCCCCG-3’
pHIS2-NRS2-M1-F	5’-AATTCTCATCTCATCTCATCGAGCT-3’
pHIS2-NRS2-M1-R	5’-CGATGAGATGAGATGAG-3’

pHIS2-NRS2-M2-F	5’-AATTCGACGCGACGCGACGCGAGCT-3’
pHIS2-NRS2-M2-R	5’-CGCGTCGCGTCGCGTCG-3’
pHIS2-NRS2-M3-F	5’-AATTCTCCGATCCGATCCGAGAGCT-3’
pHIS2-NRS2-M3-R	5’-CTCGGATCGGATCGGAG-3’
pHIS2-MYB-F	5’-AATTCGGATAGGATAGGATAGAGCT-3’
pHIS2-MYB-R	5’-CTATCCTATCCTATCCG-3’
pHIS2-MYB-M1-F	5’-AATTCTTATATTATATTATAGAGCT-3’
pHIS2-MYB-M1-R	5’-CTATAATATAATATAAG-3’
pHIS2-MYB-M2-F	5’-AATTCGTCGAGTCGAGTCGAGAGCT-3’
pHIS2-MYB-M2-R	5’-CTCGACTCGACTCGACG-3’
pHIS2-MYB-M3-F	5’-AATTCTTCGCTTCGCTTCGCGAGCT-3’
pHIS2-MYB-M3-R	5’-CGCGAAGCGAAGCGAAG-3’
pCAM-NRS1-F	5’-AGCTTTAGTTTAGTTTAGTTACCCTTCCTCTATATAAGGAAGT TCATTTCATTTGGAGAGAACACGGC-3’
pCAM-NRS1-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGTAACTAAACTAAACTAA-3’
pCAM-NRS1-M3-F	5’-AGCTTGCTGGGCTGGGCTGGACCCTTCCTCTATATAAGGAAG TTCATTTCATTTGGAGAGAACACGGC-3’
pCAM-NRS1-M3-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGTCCAGCCCAGCCCAGC-A-3’
pCAM-NRS2-F	5’-AGCTTGAATCGAATCGAATCACCCTTCCTCTATATAAGGAAGT TCATTTCATTTGGAGAGAACACGGC-3’
pCAM-NRS2-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGT-GATTCGATTCGATTCA-3’
pCAM-NRS2-M3-F	5’-AGCTTTCCGATCCGATCCGAACCCTTCCTCTATATAAGGAAGT TCATTTCATTTGGAGAGAACACGGC-3’
pCAM-NRS2-M3-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGT-TCGGATCGGATCGGAA-3’
pCAM-MYB-F	5’-AGCTTGGATAGGATAGGATAACCCTTCCTCTATATAAGGAAGT TCATTTCATTTGGAGAGAACACGGC-3’
pCAM-MYB-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGT-TATCCTATCCTATCCA-3’
pCAM-MYB-M3-F	5’-AGCTTTTCGCTTCGCTTCGCACCCTTCCTCTATATAAGGAAGT TCATTTCATTTGGAGAGAACACGGC-3’

pCAM-MYB-M3-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAG AGGAAGGGTGCGAAGCGAAGCGAAA-3’
pROK-ANAC074-F	5’-CACGGGTACCATGGGTTTGAAAGATATTGG-3’
pROK-ANAC074-R	5’-CCCGAGCTCTCATTGGAAAGCGAGGATATTTTC-3’
pHIS2-NRS1p+-F	5’-ATCGGAATTCTAGTTTAGCTCACATGACGGGG-3’
pHIS2-NRS1p+-R	5’-ACCGAGCTCAACTACAAATATATATTATGAC-3’
pHIS2-NRS1p--F	5’-ATCGGAATTCTAGCTCACATGACGGGGTTTTT-3’
pHIS2-NRS1p--R	5’-ACCGAGCTCCAAATATATATTATGACTCCTTA-3’
pHIS2-NRS1pm-F	5’-ATCGGAATTCGCTGGTAGCTCACATGACGGGGTTTTT-3’
pHIS2-NRS1pm-R	5’-ACCGAGCTCCCAGCCAAATATATATTATGACTCCTTA-3’
pHIS2-NRS2p+-F	5’-ATCGGAATTCGAATCTAAGGGAGACTGTTCTTAC-3’
pHIS2-NRS2p+-R	5’-ACCGAGCTCGATTCGTAGAAGAAGAAAGGTG-3’
pHIS2-NRS2p--F	5’-ATCGGAATTCTAAGGGAGACTGTTCTTACACAAG-3’
pHIS2-NRS2p--R	5’-ACCGAGCTCGTAGAAGAAGAAAGGTGGAACC-3’
pHIS2-NRS2pm-F	5’-ATCGGAATTCTCCGAAAGGGAGACTGTTCTTAC-3
pHIS2-NRS2pm-R	5’-ACCGAGCTCTCGGAGTAGAAGAAGAAAGGTG-3’
pHIS2-MYBp+-F	5’-ATCGGAATTCGGATATTTTTTTTTGTCATCGTG-3’
pHIS2-MYBp+-R	5’-ACCGAGCTCTATCCGTTCAAATTATAGAACATG-3’
pHIS2-MYBp--F	5’-ATCGGAATTCTTTTTTTTTGTCATCGTGACGATA-3’
pHIS2-MYBp--R	5’-ACCGAGCTCGTTCAAATTATAGAACATGCG-3’
pHIS2-MYBpm-F	5’-ATCGGAATTCTTCGCTTTTTTTTTGTCATCGTG-3’
pHIS2-MYBpm-R	5’-ACCGAGCTCGCGAAGTTCAAATTATAGAACATG-3’
pCAM-NRS1p+-F	5’-ATCGAAGCTTAGTTTAGCTCACATGACGGGG-3’
pCAM-NRS1p+-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTAT ATAGAGGAAGGGTAACTACAAATATATATTATGAC-3’
pCAM-NRS1p--F	5’-ATCGAAGCTTTAGCTCACATGACGGGGTTTTTTT-3’

pCAM-NRS1p--R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCAAATATATATTATGACTCCTTAATG-3’
pCAM-NRS1pm-F	5’-ATCGAAGCTTGCTGGTAGCTCACATGACGGGGTTTTTTT-3’
pCAM-NRS1pm-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCCAGCCAAATATATATTATGACTCCTTAATG-3’
pCAM-NRS2p+-F	5’-ATCGAAGCTTGAATCTAAGGGAGACTGTTCTTAC-3’
pCAM-NRS2p+-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTGATTCGTAGAAGAAGAAAGGTG-3’
pCAM-NRS2p--F	5’-ATCGAAGCTTTAAGGGAGACTGTTCTTACACAAG-3’
pCAM-NRS2p--R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTGTAGAAGAAGAAAGGTGGAACC-3’
pCAM-NRS2pm-F	5’-ATCGAAGCTTTCCGATAAGGGAGACTGTTCTTAC-3’
pCAM-NRS2pm-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTTCGGAGTAGAAGAAGAAAGGTGGAACCA-3’
pCAM-MYBp+-F	5’-ATCGAAGCTTGGATATTTTTTTTTGTCATCGTG-3’
pCAM-MYBp+-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTTATCCGTTCAAATTATAGAACATG-3’
pCAM-MYBp--F	5’-ATCGAAGCTTTTTTTTTTTGTCATCGTGACGATA-3’
pCAM-MYBp--R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTGTTCAAATTATAGAACATGCGA-3’
pCAM-MYBpm-F	5’-ATCGAAGCTTTTCGCTTTTTTTTTGTCATCGTGACG-3’
pCAM-MYBpm-R	5’-ACCCCATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTGCGAAGTTCAAATTATAGAACATG-3’
pCAM-NACRS-F	5’-AGCTTTCTTCTGTAACACGCATGTGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGAACACGGC-3’
pCAM-NACRS-R	5’-CATGGCCGTGTTCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCACATGCGTGTTACAGAAGAA-3’
ChIP-AT2G21320-F1	5’-TCAGCTTAGCAAAAGTACAC-3’
ChIP-AT2G21320-R1	5’-ACATTTTTAGGAATATGTT-3’
ChIP-AT2G21320-F2	5’-GAGAGATTTAGTGAGAGCTT-3’
ChIP-AT2G21320-R2	5’-GCAGTGTCAAAAATGGTCTC-3’
ChIP-AT2G21320-F3	5’-CTGGGTTAACATTTGCTTG-3’

ChIP-AT2G21320-R3	5’-CTGAAGTATCAATTGGAGC-3’
ChIP-AT2G31880-F1	5’-GTACAATTTAGCCCATTTCAC-3’
ChIP-AT2G31880-R1	5’-ACTGAATTCTTACATAAGAT-3’
ChIP-AT2G31880-F2	5’-CATCCTCGTTAGCTATCTGG-3’
ChIP-AT2G31880-R2	5’-GTTCCATAGTGAGCCACCG-3’
ChIP-AT2G31880-F3	5’-CCGGTTTTGTAGAACCGGG-3’
ChIP-AT2G31880-R3	5’-GTTATGTTACACACACCTTC-3’
ChIP-AT3G13470-F1	5’-CTAAAAGCAAATCATTAAG-3’
ChIP-AT3G13470-R1	5’-TTAGAACTCTCTAGAACGT-3’
ChIP-AT3G13470-F2	5’-TTTCTTCTATAAATTTACC-3’
ChIP-AT3G13470-R2	5’-CGATCTTAAAATGTTTTTAT-3’
ChIP-AT3G13470-F3	5’-GAAGACTATAGACCGTGTG-3’
ChIP-AT3G13470-R3	5’-TTTTTAAAGATATTTCAATG-3’
pGAD-ANAC074-F	5’-CAGAGTGGCCATTATGGCCC-ATGGGTTTGAAAGATATTG-3’
pGAD-ANAC074-R	5’-GAGGCCGAGGCGGCCGACATG-TCATTGGAAAGCGAGGATA-3’
pGAD-AT3G44350-F	5’-CAGAGTGGCCATTATGGCCC-ATGGGAGAAGAGCTTTCTG-3’
pGAD-AT3G44350-R	5’-GAGGCCGAGGCGGCCGACATG-TTAAGACCAATTCATTTG-3’
pGAD-AT2G33480-F	5’-CAGAGTGGCCATTATGGCCC-ATGGAGAAGAGGAGCTC-3’
pGAD-AT2G33480-R	5’-GAGGCCGAGGCGGCCGACATG-CTATAGAAACAAACAAAAC-3’
pGAD-AT3G56520-F	5’-CAGAGTGGCCATTATGGCCC-ATGGAGCCAACACACAG-3’
pGAD-AT3G56520-R	5’-GAGGCCGAGGCGGCCGACATG-CTATTCGGATTCGGAATC-3’
pGAD-AT3G04420-F	5’-CAGAGTGGCCATTATGGCCC-ATGGAGAATCCGGTGGG-3’
pGAD-AT3G04420-R	5’-GAGGCCGAGGCGGCCGACATG-TTATGTTCTTGAGATAGAAG-3’
pGAD-AT4G01540-F	5’-CAGAGTGGCCATTATGGCCC-ATGATGAAAGGTCTGATTGG-3’

pGAD-AT4G01540-R	5’-GAGGCCGAGGCGGCCGACATG-TCATAACTTCTTCACCGG-3’
pGAD-AT2G43000-F	5’-CAGAGTGGCCATTATGGCCC-ATGAGTGGCGAAGGTAAC-3’
pGAD-AT2G43000-R	5’-GAGGCCGAGGCGGCCGACATG-CTAGGGTTTAGTGTTGCC-3’
pGAD-AT5G50820-F	5’-CAGAGTGGCCATTATGGCCC-ATGGACATTTCTGCGCAG-3’
pGAD-AT5G50820-R	5’-GAGGCCGAGGCGGCCGACATG-TCACCGGCTTTGAATAAC-3’
pGAD-AT1G69490-F	5’-CAGAGTGGCCATTATGGCCC-ATGGAAGTAACTTCCCAATC-3’
pGAD-AT1G69490-R	5’-GAGGCCGAGGCGGCCGACATG-CTAAAACTTAAACATCGCTTG-3’
pGAD-AT1G77450-F	5’-CAGAGTGGCCATTATGGCCC-ATGATGAAATCTGGGGCTG-3’
pGAD-AT1G77450-R	5’-GAGGCCGAGGCGGCCGACATG-TCAGAAAGTTCCCTGCC-3’
pGAD-AT4G28500-F	5’-CAGAGTGGCCATTATGGCCC-ATGACTTGGTGCAATGAC-3’
pGAD-AT4G28500-R	5’-GAGGCCGAGGCGGCCGACATG-TTAAGGGATAAAAGGTTG-3’