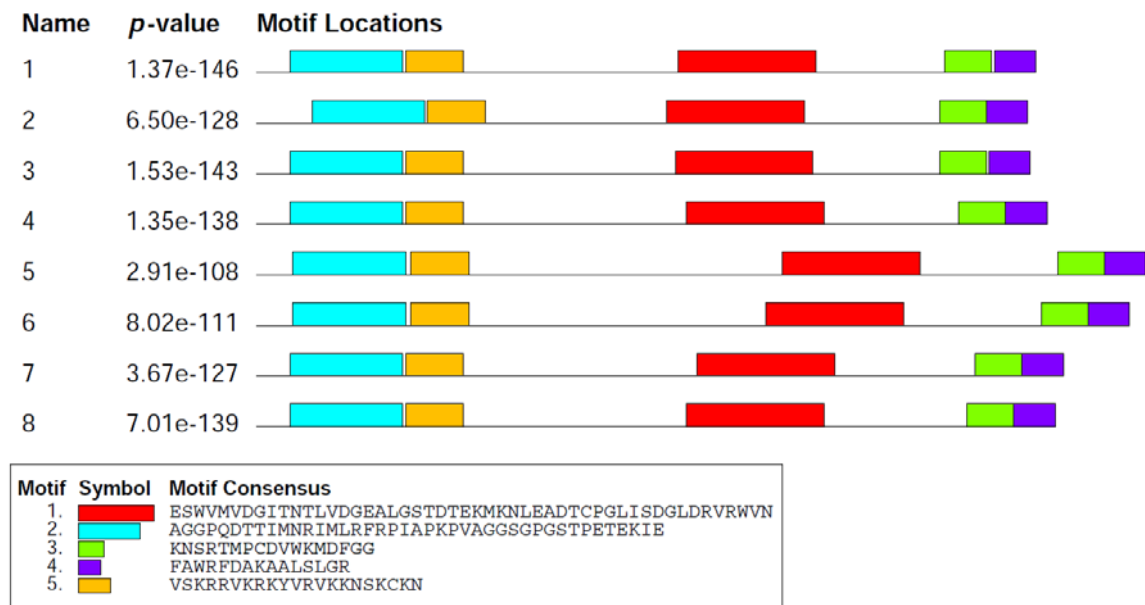


**Figure S1.** Diagram of gene structure of *NtAITRs*.  
Boxes indicate exons, and lines indicate introns.



**Figure S2.** Conserved domains in *NtAITRs*.  
Motif analysis was performed using MEME.

NtA1TR1	-----ATGGACGGTGGAAATGGTTGGCCCGC	26
NtA1TR3	-----ATGGACGGTGGAAATGGTTGGCCAGC	26
NtA1TR2	ATGAGACAGAGCTCTTCAACAGGTATGGATGTTGGGATGGTTGGGCCCTC	50
NtA1TR7	-----ATGGATGTTGAGAAATAGTGGGCCCTC	26
NtA1TR4	-----ATGGACATCGA AAA CAATTGGGCCCG	26
NtA1TR8	-----ATGGACGTCGGAACAATTGGGCCCG	26
NtA1TR5	-----ATGGATGGTAGAGGAGGGTGTGTAT	26
NtA1TR6	-----ATGGATGGTAGAGGAGGGTGTGTAT	26
NtA1TR1	CGCTAGATACGCCGG--TGGACCGCAGGATACGACGATAAAGAACC	73
NtA1TR3	CGCTAGATACGCCGG--TGGACCGCAGGATACAAAGATAATGAACATA	73
NtA1TR2	CGATGGATGCCACGT--TGGACCTTATGATACGACGATAATGAACC	97
NtA1TR7	CTATGGATGCCACGT--TGGACCAAGATAGGATGATAATGAACC	73
NtA1TR4	CCCAAGAACTCAAG--CGCACAAAGATATGACAATAATCAACA	73
NtA1TR8	GTCCTGGCTACCCCGG--TGCACCTAAAGATATGACGATAATCAACA	73
NtA1TR5	TGCTAGGTACGCAAGGGGGTGGTGGTACGATATGTCAAAAGTGGACC	76
NtA1TR6	TGCTAGGTACGCAAGGGGGTGGTGGTGGTACGATATGTCAAAAGTGGACC	76
NtA1TR1	TAATGCTAAGATTCCGACCGATCGCACTTAAACC	123
NtA1TR3	TAATGCTAAGATTCCGACCGATCGCACTTAAACC	123
NtA1TR2	TAATGTTAAGATTCCGGCCGATTGCGCCGAAACCTGTGTGGCCGACGGTTCA	147
NtA1TR7	TAATGTTAAGATTCCGGCCGATTGCAACCGAAACCGTCCGCCGACGGTTCA	123
NtA1TR4	TGATGCTAAGATTCCGGCCGATTGCGCCGAAACCGTCCGCTAATCTTTCA	123
NtA1TR8	TGATGCTAAGATTCCGGCCGATTGCGCCGAAACCGTCCGCTAATCTTTCA	123
NtA1TR5	TTATGCTCAGATTCAAGCCATCGCTCTTAAACCAAGCCGCTGGTGGTCT	124
NtA1TR6	TAATGCTCAGATTCAAGCCATCGCTCTTAAACCAAGCCGCTGGTGGTCT	124
NtA1TR1	TCTCCTGGTTCAACACCGGAAGGAACAAGATAGAA--CTTGTTACCAA	170
NtA1TR3	TCTCCTGGTTCAACACCGGAAGGAACAAGATAGAA--CTTGTTACCAA	170
NtA1TR2	GGTCCCTGGTTCTAAACCGAAGAGTGAAGAGGCTGAA--CCGGTCAAGCAA	194
NtA1TR7	GGTCCGGGTTCTAAACCGGAGAAATGAAGAGGCAAGAA--CCGGTTAGCAG	170
NtA1TR4	GGCTCTGGCTCTACGATCGAGACTCAGAGATTGAA--GTGGTTAGCAA	170
NtA1TR8	GGCTCTGGCTCTACGATCGAGACTCATAAGATTGAA--GTGGTTAGCAA	170
NtA1TR5	GTTTCCGGTGGTCTTCTACTCCGCGACAAAAGACTGAGGTTCTGTTCTGTAC	174
NtA1TR6	GTTTCCGGCGCTTCTACTCCTCCACAAAAGACTGAGGCTCCTGTTCTGTAC	174
NtA1TR1	ACGAAGAGTCAAAAGAAAGTACGTTAGAGTTAAGAAAAA--TAGCA	214
NtA1TR3	ACGAAGAGTCAAAAGAAAGTACGTTAGAGTTAAGAAAAA--TAGCA	214
NtA1TR2	ACGGAGAGGGGAAGAGAAAGTACGTTAGAGTTAAGAAAAAG--TAGGA	238
NtA1TR7	ACGAAGAGGGGAAGAGAAAGTACGTTAGAGTTAAGAAAAA--TAGGA	214
NtA1TR4	AAAGAAGAACAAAGAGAAAGTACGTTAGAGTTAAGAAAAA--TAGCA	214
NtA1TR8	AAAGAAGAACAAAGAGAAAGTACGTTAGAGTTAAGAAAAA--TAGCA	214
NtA1TR5	GGGTCGGTGGAAACGAAGGTACGTTCAAGATAAATAAAAGTAGTACTAGTA	224
NtA1TR6	GGGCCGTTGGAAACGAAGGTACGTTAAGATAAATAAAACACTAGTAGCA	224
NtA1TR1	AGTT--CAAAAG--TAACAAAGAAG--AAGA	235
NtA1TR3	AGTG--CAAAAG--TAACAAAGAAG--AAGG	235
NtA1TR2	AGTGTACTAACAA--TAGTACAGAGA--AAGA	264
NtA1TR7	AGTG--TAAGAA--TAGTGCAGAGA--AAGA	235
NtA1TR4	ACTA--CAAGAA--TAAAAAAGAAG--ACAA	235
NtA1TR8	ATTAA--CAAGAA--TAAAAAAGAAG--ACAG	235
NtA1TR5	GCTCTAACAAAGAGGTCTAGTAGTGGAAGTCGTAGTCCTGCTGGTCAAAAA	274
NtA1TR6	CTTCTAACAAAGAGATCTAGTAGCGGAAGTCGTAGTCCTAGTGGTAGAAAA	274
NtA1TR1	AGGAGAAAA--GGACGGATCCTTACAG--TTTACTGA	272
NtA1TR3	AGAAAAGGA--CGGATCCTTACAG--TTTACTGA	265
NtA1TR2	AGAAAGAAAAATTT--AGATGGATCTTTGAAGAAAGTTTATGA	305
NtA1TR7	AGAAAGAAA--AGATGGATCT--GATAA	263
NtA1TR4	AGAAACAAA--AGATGGATCCTTAGTTT--TTGGATGA	272
NtA1TR8	AGAAA AAAA--AGAAGGATCTTTAGTTT--TTGGATGA	272
NtA1TR5	AGGAAGGCACTTTCCCTGAGGAAATGAGTCCAAACGGTAAGACTGTATC	324
NtA1TR6	AGGAAGGCACTTTCCCTGAGGAAATGAGTCCAAACGGTAAGACTGTATC	324

NtAIR1 TAGTCAA - - - - - A - - - - CTGTTTAAACCCCTTCAGTTGATGC 304  
 NtAIR3 TAGTAAA - - - - - A - - - - CTGTTTAAACCCCTTCAGTTGATGC 301  
 NtAIR2 TAATGGA - - - - - A - - - - GTGTAGTAACCTTCAGCTACTAC 337  
 NtAIR7 TAATGGA - - - - - T - - - - CTATTGTAACCCCTTCAGTTACTTC 295  
 NtAIR4 TCATGGA - - - - - A - - - - CAGTTGTAACACTACAACCTACTGC 304  
 NtAIR8 TCATGGA - - - - - A - - - - CTATTGTAACACTTCAGCTACTGC 304  
 NtAIR5 TGGTGGTACAGTTTCTGGGGGCCAAGCGGTAGTTACCTTACCCTTATTAT 376  
 NtAIR6 TGGTGGG - - - - - CAAGCTGTAGTTACCTTACCCTTATTAT 361

NtAIR1 CTGAAAGC - - - - AGTAGCAGCGTTA - AGAACTCTTTAGAAAAT - - ATCGG 347  
 NtAIR3 CTGAAAGC - - - - AGCAGCAGCGTTA - AGAACTCTCTAGAAAAT - - ATCGG 344  
 NtAIR2 CGGAAAGT - - - - AGCAGCAGCACTA - CTAACCTTCCAGATAATGATCTT 382  
 NtAIR7 CGGAGAGT - - - - AGCAGCAGTGTTA - CAAACCCGACAGATAACGTTTCTT 346  
 NtAIR4 CAGAAAGT - - - - AGTGGAGGAGTTA - AACGCTCACCAGATAACAGATCTT 345  
 NtAIR8 CAGAAACT - - - - AGTGGAGGAGTTA - AAAACTCACCAGAGAACAGATCTT 345  
 NtAIR5 CCGAGTCTCCTGAAAGGAAGGGTTCCTCTGTCGATCATTCAGTAGGTTTT 426  
 NtAIR6 CAGAGTCTCCTGAAAGGAAGGACTCTCCTCTGGCGATCATTCAGTAGGTTTG 411

NtAIR1 ATCTAGA - - - - - CTTTTT - - - - GGATGAATT - - - - - 376  
 NtAIR3 ATCTAGA - - - - - CTTTTT - - - - GGATGAATT - - - - - 367  
 NtAIR2 TTCAAAAGGAAATCACTTTTCTC - TGAGCTAGATC - - - - - 415  
 NtAIR7 TTCAAAAAGAAATCTCTTTCTC - TGAGCTAGATCAACCCCAATGGATGAG 385  
 NtAIR4 TCCCAAAAACCATCAATTTTT - - - - GGATGAATT - - - - - 375  
 NtAIR8 ACCCAAAAACCATCAATTTTT - - - - GGATGAATT - - - - - 375  
 NtAIR5 GTGATAAAAACCGAATAAATATGCTCCGATATGGTTAACTTTGGTAGCCA 476  
 NtAIR6 GTGATAAAAACCGAATAAATATCTCCGATCTGGTTAACTTTGGTAGCCA 461

NtAIR1 - - TTCAGAAACCGGAGAAATAACGATGTTTTAACAGAAAGGATCAGTGGATC 418  
 NtAIR3 - - TTCAGAAATCGGAGAAATAACGATGTTTTAGCCGTAGGATCAGTGGATC 415  
 NtAIR2 - - - - - TGAAGGTGGCTATG - - - - - 415  
 NtAIR7 TTTTCATGAATAATGATAATAATGGTATATCCGCCCTTCAGTTCAACGGATC 435  
 NtAIR4 - - TTGATAAATCTGAGAATACTCGATATTTTATCAATCGGTGCACCGAATC 427  
 NtAIR8 - - TTGATAAATCTGAGAACCAACGATATTTTATCAGTCCGTGCACCGAATC 427  
 NtAIR5 AGGGAATAATAATAATGATAATAGTCTGTTTGCAGGGTTACGGAGGGGTTG 526  
 NtAIR6 AGGGAATAGTAAT - - - GATAATAGTCTCAGTTGCAGGGTTACGGAGGGGTTG 508

NtAIR1 GGATAGATCGGACGGTGGAGATA - - - - - CAGAAAGAAAGGGTTATAGAG 462  
 NtAIR3 AGATAGATCGGACGGTGGAGATG - - - - - CAGAAAGAAAGGGTTATAGAG 455  
 NtAIR2 - - - - - TGAAGGTGGCTATG - - - - - GAGACACCAAAATGGTAGAA 450  
 NtAIR7 GGTTAGATCTGAAGGTGACACCG - - - - - CAGACACCAAGAAATGGTAGAG 483  
 NtAIR4 TGTTAGATCGGACGGCGGAGATG - - - - - CGATCTGCCAAGGTAGTGGAG 471  
 NtAIR8 TGTTAGATCAGACGGTGGAGATG - - - - - CGATCTGCCAAGGTAGTGGAG 471  
 NtAIR5 GTATGGATCGTTTCAGTAGTGTGTTGCCTCAGCCAGTAAGGGTAGTGGGG 576  
 NtAIR6 GTATGGATCGTTTCAGTACTTATGTTGCCTCAGCCAGTAAGGGTAGTGGGG 558

NtAIR1 TCATGGGTGATGGTGGATAAAATGACAAACACGTTGGTAGATGGAGAAGC 512  
 NtAIR3 TCATGGGTGATGGTGGATAAAATGTCAAACACGTTGGTAGATGGAGAAGC 505  
 NtAIR2 TCTTGGGTGATGGTGGAAAGCTATGACAAAATGTTTGTAGATCGAGAAGC 506  
 NtAIR7 TCTTGGGTGATGGTGGATAGAAATAACAAACAATTTGTGGATAGTGAAGC 533  
 NtAIR4 TCATGGGTGATGGTTGATGGTATAACAAACACTTTGGTAGATTTATCAGC 521  
 NtAIR8 TCATGGGTGATGGTTGATGGTATAACAAATACITTTGGTAAGTTTATCAGC 521  
 NtAIR5 TCATGGGTAAAGGTGGAAAGCGTGACTGACGCGTGGCGGAAGGGTATGG 626  
 NtAIR6 TCATGGGTAAAGGTGGAAAGCGTGACTGACGCGTGGGTAGAAGGGTATGG 608

NtAIR1 GTTAGGGAGTACGGACATGGATTAAGATGAAGAATCTGGAAGCTGACACGT 562  
 NtAIR3 GCTAGGGAGTACGGACATGGAGAAGATGAAGAATTGGGAAGCTGACACGT 555  
 NtAIR2 TTTAGGAAGTACAGATACAGAGAAGATGAAGAATCTAGACAAAGACACCT 550  
 NtAIR7 CTTAGGAAGTACGGACATGGAGAAATGAAGAATCTGGAGACGGACACGT 583  
 NtAIR4 CTTAGGAAGTACGGATACGGAGAAGATGAAGAATCTGGAAGCTGACACGT 571  
 NtAIR8 CTTAGGAAATACGGATACGGAGAAGATGAAGAATCTGGAAGCTGACACGT 571  
 NtAIR5 GCTAGGACGTACGGATGAGGACAAACCTGGTGAATCTAGAGCGGACAGCT 676  
 NtAIR6 GCTAGGACGTACAGATGAGGAGAAACCTGGTAAATCTAGAGCTGGACAGCT 658

NtAitr1	GTCCAGGGCTCATATCGGACGGCTTAGATAGGGTTCAGTGGGTGAATCTG	612
NtAitr3	GTCCAGGGCTCATATCAGACGGCTTAGATAGGGTCCGGTGGGTGAATCTG	609
NtAitr2	GTCCAGGGTTGATATCTGATGCCCTAAATAGGGTTCAGTGGGTGAATCCG	600
NtAitr7	ATCCAGGGCTCGTGTCCGATAGCTCAGATAGGGTCCGGTGGGTGAATCCG	633
NtAitr4	GTCCAGGTATGATATCGGACGGCTTAGATAGGGTACAGTGGGTGAATCTA	621
NtAitr8	GTCCAGGAATCATATCGGACGGCTTAGATAGGGTACAGTGGGTGAATCTA	621
NtAitr5	GTCCAGGGTTTGTATCAGACGGTTTAAACAGAGTTAGGTGGGCCAATAGG	726
NtAitr6	GTCCAGGGTTTGTATCAGACGGTTTAAATAGAGTTAGGTGGGCCAATAGG	708
NtAitr1	ACGTATAGGAGATTGGTTGATCCTCTAGAAGGGTCTTGGAAACGCCGCCGGA	662
NtAitr3	GCGTATAGGAGATTGGTTGGATCCTCTAGAAGGGTCTTGGAAACACCGCCGGA	659
NtAitr2	GCAATACCGGAGAATGGTGAATCCTCTAGAAGGCCGGAAGGAGCACCGCCGGA	650
NtAitr7	GCGTACCGGAGAATGGTGAATCCTCTAGAAGACCGAAGGAGTGAACCGCGGA	683
NtAitr4	GCGTATCGGAGAATGATAGATCCGTTAGAAGACCGAAGGAGCGCCCGCGGA	671
NtAitr8	GCGTATCGGAGAATGATAGATCCGTTAGAAGACCGCGGAGAGCCACCGGA	671
NtAitr5	GCGTACAAGGAGATGGTAAAGT-----GAGGGAGGCGTAGCAGAGGGGGA	770
NtAitr6	GCGTACAAGGAGATGGTGAAGC-----GAGGGTGGCGTAGCAGAAAGGAGA	752
NtAitr1	GCTGGTGACGTGGCTGGTATGTAAGGAGAAA--ATAAATTGTGCTTCTTTC	710
NtAitr3	GCTGGTGACGTGGCTGGTTGTGAAGGAGAAA--ATAAATTGTGCTTCTTTC	707
NtAitr2	GATGGTGGTGAGGTGGTTGTGAGGAAGGAG--GAAAAAGTGAAGAGTT	698
NtAitr7	GATGGTGGTGAAAGATGGTTGTGAAGGAGAAA--ATAAGAGAGGAAGAATT	731
NtAitr4	GATGGTGGTGAGGTTAGTTTGTGAAGGAGAAA--AAAAGTGTACGATTAT-	718
NtAitr8	GATGGTGGTGCGGTTAGTTTGTGAAGGAGAAA--AAAAGTGTACCATTTAT	719
NtAitr5	AGTTGTTTGGCTGGTGAATGAAGAAGAGTCTACGGCTGCCGGAAGCA	820
NtAitr6	AGTTGTTTGGCTGGTGAATGAAGAAGAGTCTACGGCTGCCGGAAGCA	802
NtAitr1	TTTTC-----CAGCTTTTGCATGCACTGTAAAGGATACTGTATAT-----	749
NtAitr3	GCC-----AGCTTTTGCATGCACTGTAAAGGATACTGTATAT-----	743
NtAitr2	GCC-----AAATTTTGCATGCACTGTGAGGGTAGTGTATACATTGAAG	741
NtAitr7	ACCTG-----CAGCTTTTGCATGCAATGTGAGGTTAGTGTATACATGGAAG	777
NtAitr4	-----CAGCTTTTGCATGCACTGTGAGAGTTGTTTATACAAATGAAT	759
NtAitr8	ATTATT-ACCAGCTTTTGCATGCACTGTGAGAGTTGTGTATACAAATGAAT	768
NtAitr5	AAAACACGGCGGGCTTACAGTGC CGGGTTAGGGTTATCAAAAGCGGGAAG	870
NtAitr6	AAAACACGGCTGGCTTACAGTGC CAGGTTAGGGTTGATTAGAAGTGGAAG	852
NtAitr1	-----GAAGCACTCACAGACAATGCCGTGTGATGTGTGGAAGATGGATTT	794
NtAitr3	-----GAAGCACTCACCGACAATGCCGTGTGATGTGTGGAAGATGGATTT	788
NtAitr2	AATAAGAA--CTCACAAACAATAACCTGTGTGATGTGTGGAAGATGGAGTT	788
NtAitr7	AATAAGAAAAACTCACGAACAATGCCITGTGATGTGTGGAAGATGGAGTT	827
NtAitr4	AAGGTGAAACAGACAAGGACAATGCCITGTGACGTGTGGAAGATGGATTT	809
NtAitr8	AATGTGAAGCAGACAAGGACAATGCCITGTGACGTGTGGAAGATGGATTT	818
NtAitr5	GA--GAAAACCTCACTGATTCTGCCGTGTGATGTGTGGAAGATGGACGG	917
NtAitr6	GA--GAAAACCTCGCTGATTCTGCCGTGTGATGTGTGGAAGATGGACGG	899
NtAitr1	TGGAGGATTATTTGCATGGAGATTTGATGCTAAAAGCTGCACTTAGTTTGG	844
NtAitr3	TGGAGGATTATTTGCATGGAGATTTGATGCTAAAAGCTGCACTTAGTTTGG	838
NtAitr2	TGGAGGATT--TGCATGGAGGCTTGTATCTAAGACTGTACTTAGATTGG	835
NtAitr7	TGGAGGCTT--TGCATGGAGGTTTGTATCTAAATGCTGCACTTAGCTTGG	874
NtAitr4	TGGAGGATT--TGCATGGAGATTTGATGCTAAGGCTGCACTTAGCTTGG	856
NtAitr8	TGGAGGATT--TGCATGGAGATTTGATGCTAAAAGCTGCACTTAGTTTGG	865
NtAitr5	CGGAGGATA--TGCATGGAGGTTTGATACAAAGGCAGCTCTCTCTTTTGG	964
NtAitr6	TGGCGGATA--TGCATGGAGGTTTGATACAAAGGCAGCTCTCTCTTTTGG	946
NtAitr1	GTCTGTTGA	852
NtAitr3	GTCTGTTGA	846
NtAitr2	GTCTGTTAA	843
NtAitr7	GTCTGTTAA	882
NtAitr4	GGATTTTGA	864
NtAitr8	GGATTTTGA	873
NtAitr5	GCCGGTAG	972
NtAitr6	GCCGGTAG	954

**Figure S3.** CDS sequences alignment of *NtAitr*s.

Sequence alignment was performed using BioEdit. Identical nucleotides were shaded in black.



**Table S1.** Primers used in this study

Primer	Sequence 5'-3'
NtAITR1/3-Nde1F	CAACATATGGACGGTGGAAATGGTTG
NtAITR1/3-Sac1R	CAAGAGCTCAACGACCCAACTAAGTGC
NtAITR5/6-Nde1F	CAACATATGGATGGTAGAGGAGGGTG
NtAITR5/6-Sac1R	CAAGAGCTCCTACCGGCCCAAAGAGAGAG
NtAITR2-Nde1F	CAACATATGGATGTTGGGGATGGTGG
NtAITR2-Sac1R	CAAGAGCTCTTAACAACCCAATCTAAGTACAG
NtAITR4-Nde1F	CAACATATGGACATCGAAAACAATTGG
NtAITR4-Sac1R	CAAGAGCTCAAATCCCCCAAAGTAAGTGC
NtAITR7-Nde1F	CAACATATGGATGTTGAGAATAGTGG
NtAITR7-Sac1R	CAAGAGCTCTTAACGACCCAAGCTAAGTGCAG
NtAITR8-Nde1F	CAACATATGGACGTCGGAAACAATTGG
NtAITR8-Sac1R	CAAGAGCTCAAATCCCCCAACTAAGTGC
NtAITR1-F	GTTTTAACAGAAGGATC
NtAITR2-F	TGAAGAAGTTTAATGATAATGGAAG
NtAITR3-F	CGATGTTTTAGCCGTAG
NtAITR5-R	TTATCATTATTATTATCCCTTG
NtAITR6-R	CAACTGACTATTATCATTACTA
NtPYL7-F	ATGCTTCCCAATAGTCAGA
NtPYL7-R	CGGACTTCACGGAGAGTA
PP2CA-F	GCTGGTGATAATAATCTGTC
PP2CA-R	AGACGATAATCTTCTCGGA
NtGAPHD-F	TGGGTGTCAACGAGAAGGAA
NtGAPHD-R	TCTGGGTGGCAGTAAGGGA
Pps-GGL	TTCAGAggtctcTctcgACTAGTATGGAATCGGCAGCAAAGG
AtU6-1-sgRNA1- gRT-sgRNA1+	CCGGCGACCGGTTTAGGTGCaatcactacttctgt CACCTAAACCGGTCGCCGGgttttagagctagaaat
Pgs-GG2	AGCGTGggtctcGtcaggTCCATCCACTCCAAGCTC
Pps-GG2	TTCAGAggtctcTctgacacTGGAATCGGCAGCAAAGG
AtU6-26-sgRNA2- gRT-sgRNA2+	TCTTCCACACATCACACGGCaatcactacttegactc CCGTGTGATGTGTGGAAGAgtttagagctagaaat
Pgs-GG3	AGCGTGggtctcGtcttcacTCCATCCACTCCAAGCTC
Pps-GG3	TTCAGAggtctcTaagacttTGGAATCGGCAGCAAAGG
AtU6-29-sgRNA3- gRT-sgRNA3+	CCAGCGGCTGTTTTAGGAGCaatctcttagtcgact CTCCTAAACAGCCGCTGGgttttagagctagaaat
Pgs-GG4	AGCGTGggtctcGagtcttTCCATCCACTCCAAGCTC
Pps-GG4	TTCAGAggtctcTgactacaTGGAATCGGCAGCAAAGG
AtU6-1-sgRNA4- gRT-sgRNA4+	TTCTCCACACATCACACGGCaatcactacttctgt CCGTGTGATGTGTGGAGAAgttttagagctagaaat
Pgs-GGR	AGCGTGggtctcGaccgACGCGTATCCATCCACTCCAAGCTC