

Supplementary Table S1 Primers used in this study

Primers	Sequence 5' -3'	Purpose
AaAPK1-qF1	AGGAGCCCGATCAACCTATG	qRT-PCR
AaAPK1-qR1	CAGAGTCAAAATCGTCCAGATC	
AaADS-qF	AATGGGCAAATGAGGGACAC	qRT-PCR
AaADS-qR	TTTCAAGGCTCGATGAACTATG	
AaCYP71AV1-qF	CACCCTCCACTACCCTTG	qRT-PCR
AaCYP71AV1-qR	GACACATCCTTCTCCCAGC	
AaDBR2-qF	CTTGGGTTACAAGCTGTGGCTCAAG	qRT-PCR
AaDBR2-qR	ATATAATCAAACTAGAGGAGTGACC	
AaALDH1-qF	CAGTTTCTGACCCAAATCCAGTTGA	qRT-PCR
AaALDH1-qR	TCGGAGTAGTTGGTCACAT	
Aannua00085S022560-F-cacc	caccATGGATCGATTACCGGGGAT	gateway pEntry cloning
Aannua00085S022560-R	CATAGCATAAACGATTTTAC	
Aannua17791S810490-F-cacc	caccATGGACAACAGATCTATGCT	gateway pEntry cloning
Aannua17791S810490-R	CATAGCGTATACAATCTCCC	
Aannua14947S778390-F-cacc	caccATGGACAACAGATCTATGCTGAC	gateway pEntry cloning
Aannua14947S778390-R	TCGACACTCTGAGTCGGCTG	
Aannua05209S490740-F-cacc	caccATGGACAAGTATGAGGTGGTAAAG	gateway pEntry cloning
Aannua05209S490740-R	ATCATCTTCTTCTGCTCCCC	
Aannua02702S329990-F-cacc	caccATGGAGAAGTATGAGTTAGT	gateway pEntry cloning
Aannua02702S329990-R	TGGGATGGGCGGGATTTCTC	
AaAPK1-F-cacc	caccATGGATCGGAATATGAGTTC	gateway pEntry cloning
AaAPK1-R	GATGGCGTATATGACCTCAC	
AaAPK1-RI-cacc	caccGTGGTTTCTGAAGAACTTAC	gateway pEntry cloning
AaAPK1-RI-R	GGGTCCAGTCTTTTTTCCAA	
AaAPK1-F-EcoRI	GCGAATTCATGGATCGGAATATGAGTTC	Rrotein recombinant
AaAPK1-R-XhoI	GCCTCGAGGATGGCGTATATGACCTCAC	
AabZIP1-F-EcoRI	GCGAATTCATGAACAACAAGAATTTTGG	Rrotein recombinant
AabZIP1-R-XhoI	GCCTCGAGCCATGGACCGAAAGTGTCT	
AaABI1-F-EcoRI	CGGAATTCATGGAAGATATCCCTCCTTCGG	Yeast two hybrid
AaABI1-R-SacI	CGGAGCTCGTCAAGATTTAGTTTTAAACC	
AaSnRK2.2-F-BamHI	GCGGATCCATGGATCGATTACCGGGGAT	Yeast two hybrid
AaSnRK2.2-R-SalI	GCGTCGACCATAGCATAAACGATTTTAC	
AaSnRK2.3-F-SalI	GCGTCGACATGGACAACAGATCTATGCT	Yeast two hybrid
AaSnRK2.3-R-PstI	GCCTGCAGCATAGCGTATACAATCTCCC	
AaSnRK2.4-F-SalI	GCGTCGACATGGACAACAGATCTATGCTGA	Yeast two hybrid
AaSnRK2.4-R-PstI	GCCTGCAGTCGACACTCTGAGTCGGCTG	
AaSnRK2.5-F-SalI	GCGTCGACATGGACAAGTATGAGGTGGTAA	Yeast two hybrid
AaSnRK2.5-R-PstI	GCCTGCAGATCATCTTCTTCTGCTCCCC	
AaSnRK2.6-F-SalI	GCGTCGACATGGAGAAGTATGAGTTAGT	Yeast two hybrid
AaSnRK2.6-R-PstI	GCCTGCAGTGGGATGGGCGGGATTTCTC	
AaAPK1-F-PstI	GCCTGCAGATGGATCGGAATATGAGTTC	Overexpression
AaAPK1-R-BclI	GCTGATCAGATGGCGTATATGACCTCAC	

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AcSnRK2_7 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
AcSnRK2_2 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 68
AcSnRK2_3 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 87
Ammu149475778390 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 89
AaFAK1 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 86
AcSnRK2_6 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 84
Ammu00805022560 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 87
Ammu17915810490 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 89
OsSAPK9 .....MAAAGAGAGAPF.AALTVGF.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 98
AcSnRK2_1 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK9 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 87
OsSAPK10 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 88
AcSnRK2_8 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK1 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK2 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK3 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 70
AcSnRK2_9 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK5 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK4 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK6 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
OsSAPK7 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
AcSnRK2_5 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
AcSnRK2_4 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
AcSnRK2_10 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
Ammu027025329990 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 83
Ammu052095490740 .....MNRSLMTLVG.GMCMFIMHDSRVLVDKSGNFG.ARMRRCTNLEL.ARMRRCTNLEL.VRELNHR.HFHPNIRPFDVLT 69
Consensus
y g nqf a l a k i t q id v rei nhr l hpl r f e t

AcSnRK2_7 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
AcSnRK2_2 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK.....V 168
AcSnRK2_3 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 166
Ammu149475778390 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 161
AaFAK1 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 165
AcSnRK2_6 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 165
Ammu00805022560 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 166
Ammu17915810490 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 168
OsSAPK9 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 177
AcSnRK2_1 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK9 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 166
AcSnRK2_8 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 167
OsSAPK1 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK2 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK3 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 149
AcSnRK2_9 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK5 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK4 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK6 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
OsSAPK7 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
AcSnRK2_5 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
AcSnRK2_4 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 156
AcSnRK2_10 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
Ammu052095490740 .....FHHAIWDAAGGELIRGNSGASGSD.....PREFQISGVYCSMCHRDLEL.LDGSFAFFKICDFGYSK..... 148
Consensus
h se a ggel i r f e e f f q l gv h chrdklen ldgs kicdfgysk

AcSnRK2_7 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
AcSnRK2_2 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 268
AcSnRK2_3 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 260
Ammu149475778390 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 281
AaFAK1 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 259
AcSnRK2_6 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 259
Ammu00805022560 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 260
Ammu17915810490 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 262
OsSAPK9 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 271
AcSnRK2_1 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 260
OsSAPK9 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 260
OsSAPK10 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 261
AcSnRK2_8 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK1 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK2 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 243
OsSAPK3 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 243
AcSnRK2_9 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK5 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK4 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK6 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
OsSAPK7 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
AcSnRK2_5 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
AcSnRK2_4 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 250
AcSnRK2_10 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
Ammu027025329990 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 256
Ammu052095490740 .....S.LHSPFSSVGTGFANAPPVLLRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 242
Consensus
s l h s p f s s v g t g f a n a p p v l l r q e m g s d v w v s c g v l y v l m v y v p e f i d g f r f r f q i a g l w v s g e y v h i s p c g d r s r i f v

AcSnRK2_7 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 327
AcSnRK2_2 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 347
AcSnRK2_3 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 339
Ammu149475778390 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 355
AaFAK1 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 332
AcSnRK2_6 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 338
Ammu00805022560 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 338
Ammu17915810490 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 340
OsSAPK9 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 349
AcSnRK2_1 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 320
OsSAPK9 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 339
OsSAPK10 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 340
AcSnRK2_8 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 318
OsSAPK1 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 323
OsSAPK2 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 322
OsSAPK3 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 312
AcSnRK2_9 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 323
OsSAPK5 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 336
OsSAPK4 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 321
OsSAPK6 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 324
OsSAPK7 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 324
AcSnRK2_5 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 322
AcSnRK2_4 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 330
AcSnRK2_10 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 322
Ammu027025329990 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 336
Ammu052095490740 .....ADGKRIVIEELKFWELRQEMGSDVWVSCGVLYVLMVYVPEFIDGFRFRFQIAGLWVSGEYVHISPCGDRSRIFV 320
Consensus
e d l l s d c c l d i s s g e i v y a l

AcSnRK2_7 .....EDLSDCCLDISSGEIVYAL..... 350
AcSnRK2_2 .....EDLSDCCLDISSGEIVYAL..... 369
AcSnRK2_3 .....EDLSDCCLDISSGEIVYAL..... 361
Ammu149475778390 .....EDLSDCCLDISSGEIVYAL..... 357
AaFAK1 .....EDLSDCCLDISSGEIVYAL..... 355
AcSnRK2_6 .....EDLSDCCLDISSGEIVYAL..... 362
Ammu00805022560 .....EDLSDCCLDISSGEIVYAL..... 361
Ammu17915810490 .....EDLSDCCLDISSGEIVYAL..... 363
OsSAPK9 .....EDLSDCCLDISSGEIVYAL..... 371
AcSnRK2_1 .....EDLSDCCLDISSGEIVYAL..... 362
OsSAPK9 .....EDLSDCCLDISSGEIVYAL..... 361
OsSAPK10 .....EDLSDCCLDISSGEIVYAL..... 362
AcSnRK2_8 .....EDLSDCCLDISSGEIVYAL..... 343
OsSAPK1 .....EDLSDCCLDISSGEIVYAL..... 339
OsSAPK2 .....EDLSDCCLDISSGEIVYAL..... 339
OsSAPK3 .....EDLSDCCLDISSGEIVYAL..... 334
AcSnRK2_9 .....EDLSDCCLDISSGEIVYAL..... 339
OsSAPK5 .....EDLSDCCLDISSGEIVYAL..... 370
OsSAPK4 .....EDLSDCCLDISSGEIVYAL..... 360
OsSAPK6 .....EDLSDCCLDISSGEIVYAL..... 365
OsSAPK7 .....EDLSDCCLDISSGEIVYAL..... 359
AcSnRK2_5 .....EDLSDCCLDISSGEIVYAL..... 365
AcSnRK2_4 .....EDLSDCCLDISSGEIVYAL..... 361
AcSnRK2_10 .....EDLSDCCLDISSGEIVYAL..... 374
Ammu027025329990 .....EDLSDCCLDISSGEIVYAL..... 361
Ammu052095490740 .....EDLSDCCLDISSGEIVYAL..... 370
Consensus
e d l s d c c l d i s s g e i v y a l

```

Fig. S1 Alignment of six SnRK2s kinase family candidates with SnRK2S family members from *Arabidopsis* and Rice.

		ATP binding loop	
AaAPK1		MDNM...SSPGMDFIMHSDRYDQVVDIGSGNFGVARLMDQTEELVAVKYIERGSKIDENVREIINHRSLRHFNIV	78
AtSnRK2.2		MDPAINSPIMEDDFIMHSDRYDQVVDIGSGNFGVARLMDQTEELVAVKYIERGSKIDENVREIINHRSLRHFNIV	80
AtSnRK2.3		MDPAP.VITGDFDFIMHSDRYDQVVDIGSGNFGVARLMDQTEELVAVKYIERGSKIDENVREIINHRSLRHFNIV	79
AtSnRK2.6_(OST1)		MDREA..VSGEMDFIMHSDRYDQVVDIGSGNFGVARLMDQTEELVAVKYIERGSKIDENVREIINHRSLRHFNIV	78
Consensus			
AaAPK1		RFEEILTFHHLAIMMEYASGGELFERICNAGRFDEARFFFQQLISGVSYCHMCHROLKIENTLLDGSFAPRLKI	158
AtSnRK2.2		RFEEILTFHHLAIMMEYASGGELFERICNAGRFDEARFFFQQLISGVSYCHMCHROLKIENTLLDGSFAPRLKI	160
AtSnRK2.3		RFEEILTFHHLAIMMEYASGGELFERICNAGRFDEARFFFQQLISGVSYCHMCHROLKIENTLLDGSFAPRLKI	159
AtSnRK2.6_(OST1)		RFEEILTFHHLAIMMEYASGGELFERICNAGRFDEARFFFQQLISGVSYCHMCHROLKIENTLLDGSFAPRLKI	158
Consensus			
		Activation loop	
AaAPK1		CDFGYS.....KSSVLHSQFRSTVGTPAVIAPPELLRGEYDGRADVWSCGVTLVYVLMGAYFFEDPEERDVRKTIH	231
AtSnRK2.2		CDFGYSKVLFIISKSSVLHSQFRSTVGTPAVIAPPELLRGEYDGRADVWSCGVTLVYVLMGAYFFEDPEERDVRKTIQ	240
AtSnRK2.3		CDFGYS.....KSSVLHSQFRSTVGTPAVIAPPELLRGEYDGRADVWSCGVTLVYVLMGAYFFEDPEERDVRKTIQ	232
AtSnRK2.6_(OST1)		CDFGYS.....KSSVLHSQFRSTVGTPAVIAPPELLRGEYDGRADVWSCGVTLVYVLMGAYFFEDPEERDVRKTIH	231
Consensus			
AaAPK1		RILNVCYPIEDENICISPECHLISRIFVDEPARITLREITSDQWFLKNLHGLMDENRNGS.QFQEPQEQSLDTIMQ	311
AtSnRK2.2		RILNVCYPIEDENICISPECHLISRIFVDEPARITLREITSDQWFLKNLHGLMDENRNGS.QFQEPQEQSLDTIMQ	319
AtSnRK2.3		RILNVCYPIEDENICISPECHLISRIFVDEPARITLREITSDQWFLKNLHGLMDENRNGS.QFQEPQEQSLDTIMQ	311
AtSnRK2.6_(OST1)		RILNVCYPIEDENICISPECHLISRIFVDEPARITLREITSDQWFLKNLHGLMDENRNGS.QFQEPQEQSLDTIMQ	310
Consensus			
AaAPK1		IIEEATVPEWGLYD.....DMDDDLIDDESDEIDNDSSGEIVYA	354
AtSnRK2.2		IIEEATVETWRNRGDDDFMADNIDLDD.MDDDESE.SEIDNDSSGEIVYA	368
AtSnRK2.3		IIEEATVPEWRNRGDDDFMADNIDLDD.MDDDESE.SEIDNDSSGEIVYA	360
AtSnRK2.6_(OST1)		IIEEATVPEAGIQNHLYLGSIDDDMEEDDESDDDDNDSSGEIVYA	361
Consensus			
		ABA box	



PP2C interface residues

Fig. S2 Alignment AaAPK1 with SnRK2.2/2.3/2.6 from *Arabidopsis*. The under the red line represented the conserved ATP binding loop in SnRK2s family; the sequences under the purple line represented the activation loop in SnRK2s family; the sequences in the red box represented the amino acid residues for PP2C interface; the sequences in the blue box represented the domain for ABA response.

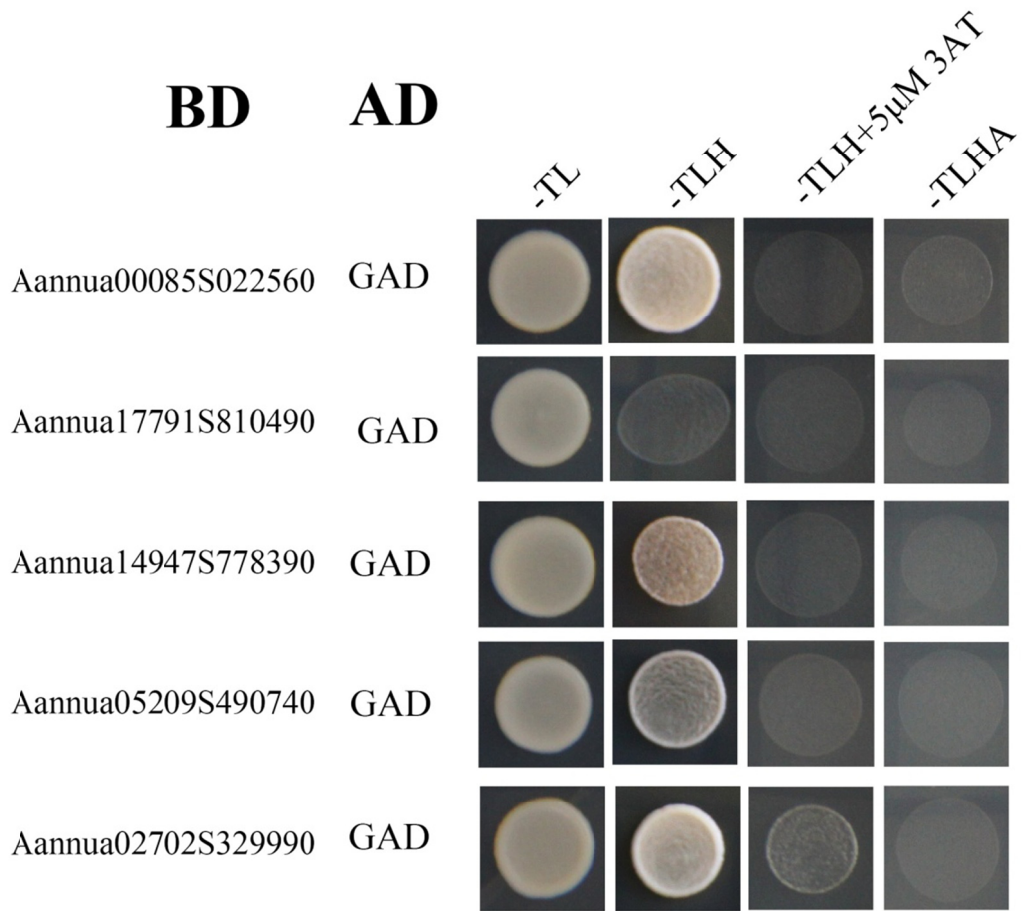


Fig. S3 The self-activation test of six kinase candidates in Y2H assay. The BD represented the candidate genes cloned into pGBKT7 vector, while the GAD represented the empty pGADT7 vector. -TL: synthetic medium dropout threonine and histidine; -TLH: synthetic medium drop out threonine, leucine and histidine; -TLHA: synthetic medium dropout threonine, leucine, histidine and adenosine.

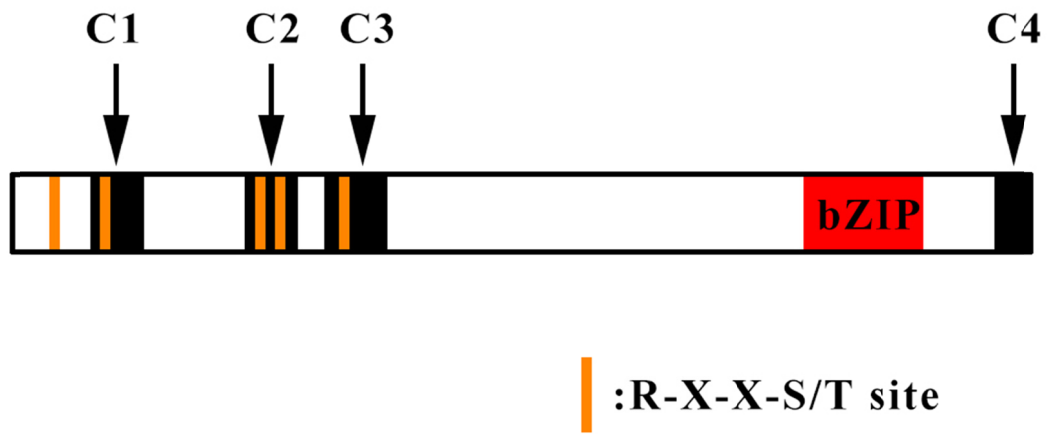


Fig. S4 The Schemes of putative SnRk2 type kinase target in AabZIP1. The yellow histogram represent the R-X-X-S/T site in AabZIP1.

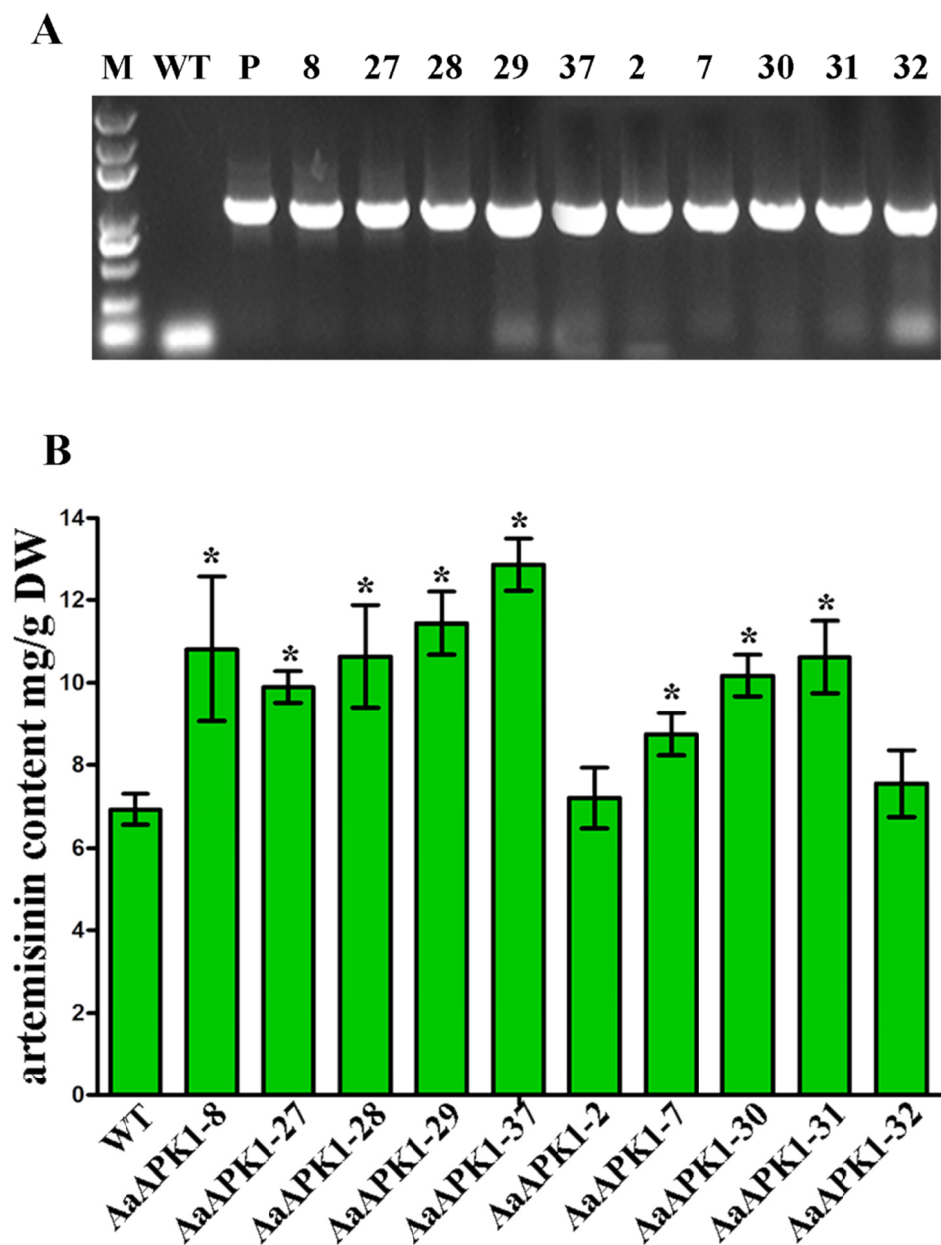


Fig. S5 The PCR detection of positive *AaAPK1* overexpression *Artemisia* and artemisinin contents analysis of 10 independent transgenic *Artemisia*. A, The PCR detection of positive transgenic *Artemisia* using genomic DNA. M: marker; WT: wild type *Artemisia*, used as negative control; P: PHB-*AaAPK1* plasmid, used as positive control. B: the artemisinin contents in *AaAPK1*-overexpressing and wild type *Artemisia*. WT: wild-type *A. annua* plants. *: significant difference at the level of $p < 0.05$ given by t-test. Error bars represent \pm SD (n=3).

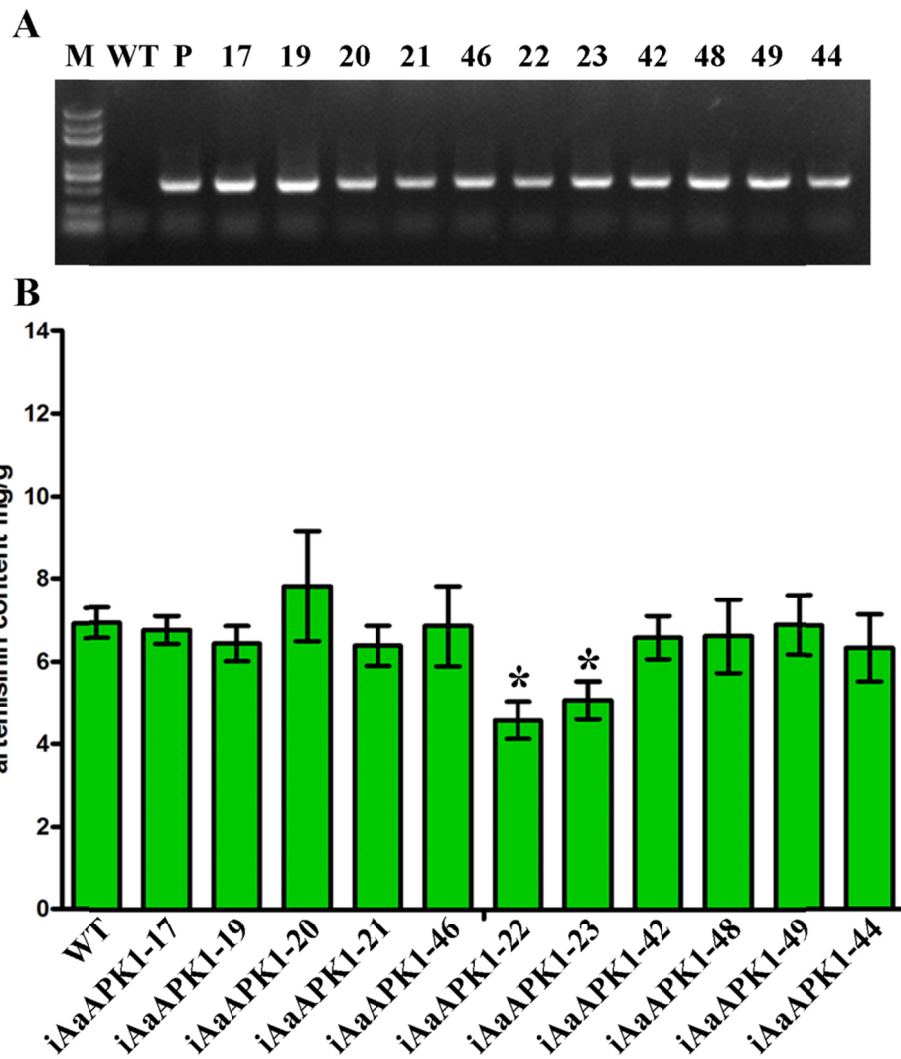


Fig. S6 The PCR detection of positive AaAPK1-RNAi *Artemisia* and artemisinin contents analysis of 10 independent AaAPK1-RNAi *Artemisia*. A, The PCR detection of positive transgenic *Artemisia* using genomic DNA. M: marker; WT: wild type *Artemisia*, used as negative control; P: pHELLSGATE-iAaAPK1 plasmid, used as positive control. B: the artemisinin contents in AaAPK1-RNAi and wild type *Artemisia*. WT: wild-type *A. annua* plants. *: significant difference at the level of $p < 0.05$ given by t-test. Error bars represent \pm SD (n=3).

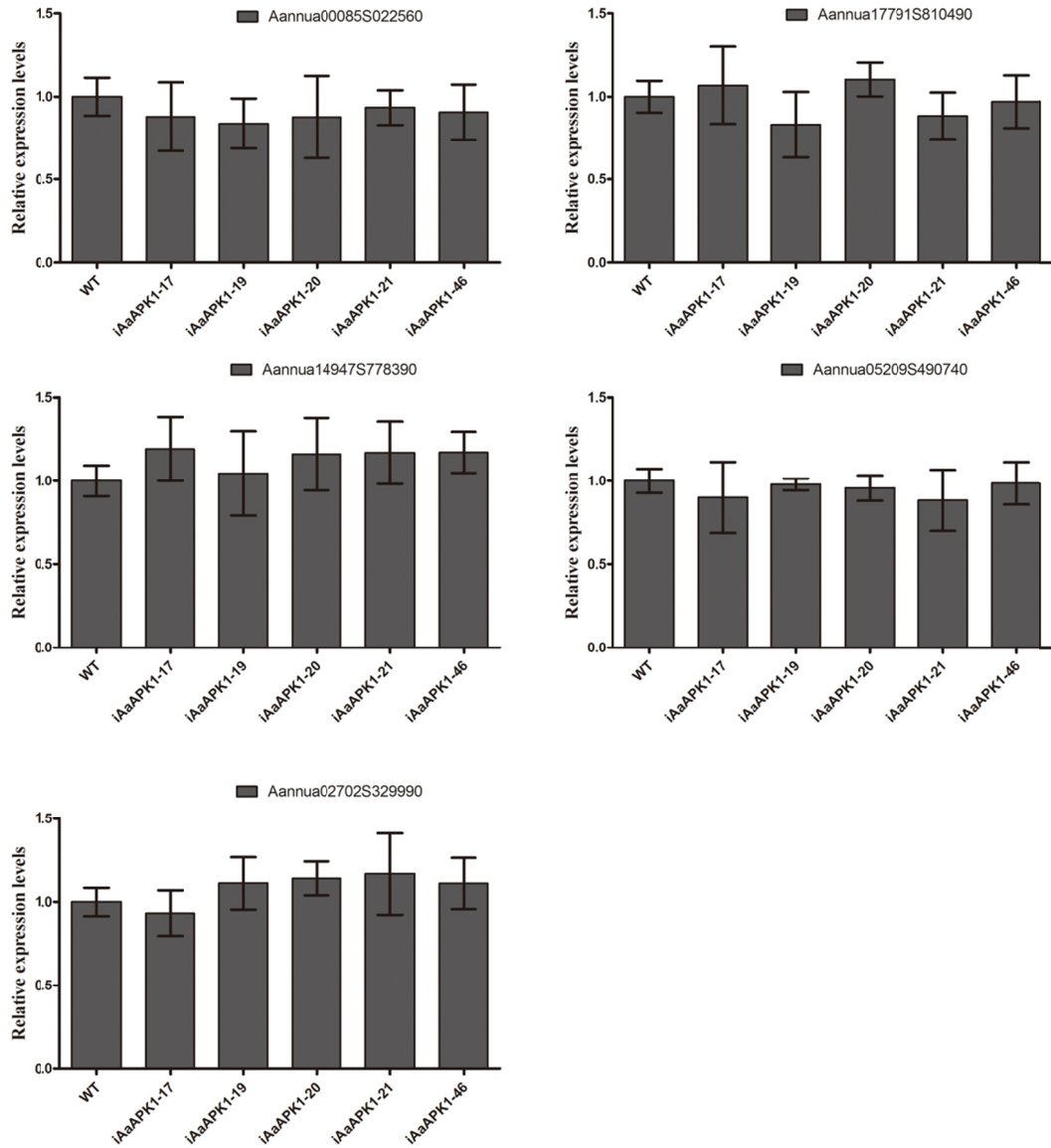


Fig. S7 The relative expression levels of *Aannua00085S022560*, *Aannua17791S810490*, *Aannua14947S778390*, *Aannua05209S490740* and *Aannua02702S329990* in AaAPK1-RNAi transgenic *Artemisia* and wild type *Artemisia*. WT: wild-type *A. annua* plants.