

Suppl. figure S2

Amino acid sequence alignment of the 18 putative quinoa MAPKs with all 20 Arabidopsis MAPKs.

The quinoa genome database (<http://quinoa.kazusa.or.jp/>) was screened for genes annotated as MAPKs, and the corresponding translation products were retrieved. Highly (red; 80%) and moderately (blue; 40%) conserved residues are shown in colour. The alignment was generated using the MultAlin tool. See also phylogenetic tree in figure 3.

Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

 10 20 30 40 50
ATMPK11_B	-----	-----	-----	-----	-----
ATMPK13_B	-----	-----	-----	-----	-----
ATMPK6_A	-----	-----	-----	-----	-----
ATMPK10_A	-----	-----	-----	-----	-----
Cqu_c04092_1_g0	-----MGEA	SPPGAYATVA	AS-----W	LGATT-TAWP	SRLGAS---H
Cqu_c06022_1_g0	MVVADATAES	VAAIQYVLSH	AMQDNDDLIL	MHVTQPTKKS	HLLIKSFFRR
Cqu_c03819_1_g0	-----	-----	-----	-----	-----
Cqu_c04159_1_g0	-----	-----	-----	-----	-----
ATMPK3_A	-----	-----	-----	-----	-----
Cqu_c03402_1_g0	-----	-----	-----	-----	-----
Cqu_c03736_1_g0	-----	-----	-----	-----	-----
ATMPK12_B	-----	-----	-----	-----	-----
ATMPK4_B	-----	-----	-----	-----	-----
ATMPK5_B	-----	-----	-----	-----	-----
Cqu_c17078_1_g0	-----	-----	-----	-----	-----
ATMPK1_C	-----	-----	-----	-----	-----
Cqu_c02858_1_g0	-----	-----	-----	-----	-----
ATMPK7_C	-----	-----	-----	-----	-----
ATMPK2_C	-----	-----	-----	-----	-----
ATMPK14_C	-----	-----	-----	-----	-----
ATMPK8_D	-----	-----	-----	MGG-----	G GNLVDGVERRW
Cqu_c08055_1_g0	-----	-----	-----	MGN-----	G -TLVDGVERR-
ATMPK15_D	-----	-----	-----	MGG-----	G GNLVDGVERRW
ATMPK9_D	-----	-----	-----	-----	-----
ATMPK18_D	-----	-----	-----	-----	-----
ATMPK20_D	-----	-----	-----	-----	-----
ATMPK19_D	-----	-----	-----	-----	-----
Cqu_c06169_1_g0	-----	-----	-----	-----	-----
Cqu_c03735_1_g0	-----	-----	-----	-----	-----
ATMPK16_D	-----	-----	-----	-----	-----
Cqu_c07086_1_g0	-----	-----	-----	-----	-----
Cqu_c09059_1_g0	-----	-----	-----	-----	-----
ATMPK17_D	-----	-----	-----	-----	-----
Cqu_c04094_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	MG-----	N GTLVDGVERRW
Cqu_c14619_1_g0	-----	-----	-----	-----	-----
Cqu_c03126_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	-----	-----
Consistency	0000000000	0000000000	0000000000	0000000000	0000000000
 60 70 80 90 100
ATMPK11_B	-----	-----	-----	-----	-----
ATMPK13_B	-----	-----	-----	-----	-----
ATMPK6_A	-----	-----	-----	-----	-----
ATMPK10_A	-----	-----	-----	-----	-----
Cqu_c04092_1_g0	H-----	-FVLT-----	-----	IRYEPR-----	-FP-----A
Cqu_c06022_1_g0	HSDPGLAGIS	NFDPTADVGE	GGGGSGGKDF	LEV MKRACKG	TFPNSRVWVE
Cqu_c03819_1_g0	-----	-----	-----	-----	-----
Cqu_c04159_1_g0	-----	-----	-----	-----	-----
ATMPK3_A	-----	-----	-----	-----	-----
Cqu_c03402_1_g0	-----	-----	-----	-----	-----
Cqu_c03736_1_g0	-----	-----	-----	-----	-----
ATMPK12_B	-----	-----	-----	-----	-----
ATMPK4_B	-----	-----	-----	-----	-----
ATMPK5_B	-----	-----	-----	-----	-----
Cqu_c17078_1_g0	-----	-----	-----	-----	-----
ATMPK1_C	-----	-----	-----	-----	-----
Cqu_c02858_1_g0	-----	-----	-----	-----	-----
ATMPK7_C	-----	-----	-----	-----	-----
ATMPK2_C	-----	-----	-----	-----	-----
ATMPK14_C	-----	-----	-----	-----	-----
ATMPK8_D	-L-----	-FQRPS-----	-----	SSS SSSSSNNNNN	NHEQPIFNSS
Cqu_c08055_1_g0	-W-----	-FSRRG-----	-----	GVV ANNSYKLD	ES INNNSSNSS
ATMPK15_D	-LF-----	-FQRRP-----	-----	SSS SSSNNHDQIQ	NP-----

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ATMPK9_D -----
ATMPK18_D -----
ATMPK20_D -----
ATMPK19_D -----
Cqu_c06169_1_g0 -----
Cqu_c03735_1_g0 -----
ATMPK16_D -----
Cqu_c07086_1_g0 -----
Cqu_c09059_1_g0 -----
ATMPK17_D -----
Cqu_c04094_1_g0 -----
Cqu_c01012_1_g0 ----- FSRRG ----- VVV ANNSYKLD ES INNNNSSNSS
Cqu_c14619_1_g0 -----
Cqu_c03126_1_g0 -----
Cqu_c01012_1_g0 -----
Consistency 0000000000 0000000000 0000000000 0000000000 0000000000

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..... 110..... 120..... 130..... 140..... 150

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ATMPK11_B -----
ATMPK13_B -----
ATMPK6_A ----- MDG G SGQPAADT
ATMPK10_A ----- ME ----- PTNDA
Cqu_c04092_1_g0 TMA ----- TLRCIS PPTTSLRVSE SSDTHTIMDA S AAQPSDT
Cqu_c06022_1_g0 KVEQGSLDNK GAVILLRCKE LMVDLLVVGQ RRHLVSVLLG PRRSFSTGST
Cqu_c03819_1_g0 -----
Cqu_c04159_1_g0 -----
ATMPK3_A -----
Cqu_c03402_1_g0 -----
Cqu_c03736_1_g0 -----
ATMPK12_B -----
ATMPK4_B -----
ATMPK5_B -----
Cqu_c17078_1_g0 -----
ATMPK1_C -----
Cqu_c02858_1_g0 -----
ATMPK7_C -----
ATMPK2_C -----
ATMPK14_C -----
ATMPK8_D SF ----- SSS SNPNHSANSG ELIIEEDLDF S ----- GL
Cqu_c08055_1_g0 SSRQVSVISE FSGNQINNHS SSKQQEGEEQ ELNIEFDFDL S ----- GL
ATMPK15_D ----- PTVSNPND DEDLKKLTPD S ----- KL
ATMPK9_D -----
ATMPK18_D -----
ATMPK20_D -----
ATMPK19_D -----
Cqu_c06169_1_g0 -----
Cqu_c03735_1_g0 -----
ATMPK16_D -----
Cqu_c07086_1_g0 -----
Cqu_c09059_1_g0 -----
ATMPK17_D -----
Cqu_c04094_1_g0 ----- MDASAAQPS DTDMMDAAGA PPENHPPPSS
Cqu_c01012_1_g0 SSR ----- QVSVISEF SGKQINNHS SKQQGEEEEQ Q EFNIEFDF
Cqu_c14619_1_g0 -----
Cqu_c03126_1_g0 -----
Cqu_c01012_1_g0 -----
Consistency 0000000000 0000000000 0000000000 0000000000 0000000000

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..... 160..... 170..... 180..... 190..... 200

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ATMPK11_B MSIEKPF ----- FGDDSNRGV SINGGRYVQY
ATMPK13_B ----- MEKREDGGI LTYDGRYVMY
ATMPK6_A EMTEAPGGFP AAA ----- PSPQ MPGIENIPAT LSHGGRFIQY
ATMPK10_A ETLETQGEVT TAIWP ----- SSQI LKTTIDIPGT LSHDGRYIQY
Cqu_c04092_1_g0 DMMDAAGAPP ENHPP PSSD QSOPPOQPPQ QQQQVSIPAT LSHGGKFIQY
Cqu_c06022_1_g0 VLRGGAPKSV DMVEYLIENS PCTCVAVQKK GQNSGYILNS KTHRNFWLLY
Cqu_c03819_1_g0 MSEFPMAAA ----- AGG GGQFPEFPAV YTHGGQFIQY
Cqu_c04159_1_g0 MSEFPMAAA ----- AGG GGQFPEFPAV YTHGGQFIQY
ATMPK3_A ----- MNTG GGQYDFPAV ETHGGQFISY
Cqu_c03402_1_g0 ----- ME N SAKSKEVRGI PTYGGTYTMY
Cqu_c03736_1_g0 ----- MEQNLRGV PTHGGRYVQY
ATMPK12_B MSGESSS ----- GSTEHC IKVV PTHGGRYVQY
ATMPK4_B MSAESC FG ----- S SGDQSSSKGV ATHGGSYVQY
ATMPK5_B MAKEIESA ----- T DLGDTNIKGV LVHGGRYFQY
Cqu_c17078_1_g0 ----- MEN SAKSKEVRGI PTYGGTYILY
ATMPK1_C ----- MATLVDPPNG IRNEGK HYF

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Cqu_c02858_1_g0	-----	-----	-----	MATQVEPPNG	VRC	PGK	-HYY
ATMPK7_C	-----	-----	-----	MAMLVEPPNG	IKQ	QGK	-HYY
ATMPK2_C	-----	-----	-----	MATPVDPPNG	IRN	QGK	-HYF
ATMPK14_C	-----	-----	-----	MAMLVDPPNG	IRQ	EGK	-HYY
ATMPK8_D	FLINVPKR	---	---	---	NHLPMD	PHK	---KGE
Cqu_c08055_1_g0	KPIKVPKR	---	---	---	APTSRFPLP	MDPHKKS	SALE
ATMPK15_D	RQIKVQQR	---	---	---	NHLPME	KKG	---IPN
ATMPK9_D	---	---	---	---	MDPH	KKV	---ALE
ATMPK18_D	---	M	---	---	QONQV	KKG	---TKE
ATMPK20_D	---	M	---	---	QDNR	KKN	---NLE
ATMPK19_D	---	M	---	---	QKTQE	KKN	---MKE
Cqu_c06169_1_g0	---	M	---	---	QDQR	KKA	---VKE
Cqu_c03735_1_g0	MEQNLRG	---	---	---	TPTHG	GRY	---VOY
ATMPK16_D	---	M	---	---	QPDHR	KKS	---SVE
Cqu_c07086_1_g0	---	M	---	---	QDQR	KKT	---SVD
Cqu_c09059_1_g0	---	---	---	---	MQDQR	KKA	---VKE
ATMPK17_D	---	---	---	---	---	---	---MLE
Cqu_c04094_1_g0	DQSQPPQQP	---	---	PQ	QQQVSIPAT	LSHGGKFIQY	
Cqu_c01012_1_g0	DLSGLKPIK	---	---	VPK	RAPTSRFPLP	MDPHKKS	SALE
Cqu_c14619_1_g0	---	---	---	---	---	---	---
Cqu_c03126_1_g0	---	---	---	---	---	---	---
Cqu_c01012_1_g0	---	---	---	---	---	---	---
Consistency	0000001000	0000000000	0000000000	1111132332	3431221434		

	210.....	220.....	230.....	240.....	250
ATMPK11_B	NVYGNLFEVS	KKYVPLRPI	GRGASGIVCA	AWNSETGEEV	AIKKIGNAFG	
ATMPK13_B	NVLGNIFELS	SKYIPPIEPI	GRGAYGIVCC	ATNSETNEEV	AIKKIANAFD	
ATMPK6_A	NIFGNIFEVT	AKYKPPIMPI	GKGAYGIVCS	AMNSETNESV	AIKKIANAFD	
ATMPK10_A	NLFGHIFELP	AKYKPIRPI	GRGACGIVCS	AVDSETNEKV	AIKKITQVFD	
Cqu_c04092_1_g0	NIFGNIFEVT	AKYKPPIMPI	GKGAYGIVCS	SLNSDTNEHV	AIKKIANAFD	
Cqu_c06022_1_g0	NVHGSLEFEVS	SKYVPIRPI	GRGASGLVCA	AVNSDTHHEV	AIKKIGNAFD	
Cqu_c03819_1_g0	NIFGNLFEVT	AKYRPPIMPI	GRGAYGIVCS	VLNTETKEMV	ALKKIANAFD	
Cqu_c04159_1_g0	NIFGNLFEVT	AKYRPPIMPI	GRGAYGIVCS	VLNTETKEMV	ALKKIANAFD	
ATMPK3_A	DIFGSLFEIT	SKYRPIPI	GRGAYGIVCS	VLDTETNELV	AMKKIANAFD	
Cqu_c03402_1_g0	NILGTLFEVS	SKYAPPIQPV	GRGAYGIVCC	ARNSETNEDV	AIKKIADAFN	
Cqu_c03736_1_g0	NLYGNLFEVS	SKYVPLRPV	GRGAYGIVCA	AVNSETQEEV	AIKKVSNAFH	
ATMPK12_B	NVYGQLFEVS	RKYVPIRPI	GRGACGIVCA	AVNSVTGEKV	AIKKIGNAFD	
ATMPK4_B	NVYGNLFEVS	RKYVPLRPI	GRGAYGIVCA	ATNSETGEEV	AIKKIGNAFD	
ATMPK5_B	NVYGNLFEVS	NKYVPIRPI	GRGAYGFVCA	AVDSETHEEI	AIKKIGKAFD	
Cqu_c17078_1_g0	NIFGSLFEVA	SKYAPPIQPV	GRGAYGIVCC	ARNSETNEDV	AIKKIADAFN	
ATMPK1_C	SMWQTLFEID	TKYM-PIKPI	GRGAYGVVCS	SVNSDTNEKV	AIKKIHNVYE	
Cqu_c02858_1_g0	SMWQALFEID	TKYV-PIKPI	GRGAYGIVCS	SXNKETNERV	AIKKIHNAFE	
ATMPK7_C	SMWQTLFEID	TKYV-PIKPI	GRGAYGVVCS	SINRETNERV	AIKKIHNVFE	
ATMPK2_C	SMWQTLFEID	TKYV-PIKPI	GRGAYGVVCS	SVNRESNERV	AIKKIHNVFE	
ATMPK14_C	TMWQTLFEID	TKYV-PIKPI	GRGAYGVVCS	SINSETNERV	AIKKIHNVFE	
ATMPK8_D	TEFFTEYGEA	NRYQ-IQEVV	GKGSYGVVAS	AVDSHTGERV	AIKKINDVFE	
Cqu_c08055_1_g0	NDFFTYGEA	SRYQ-VQEII	GKGSYGIVGS	AVDTHTGEXV	AIKKINDVFE	
ATMPK15_D	AEFFTEYGEA	NRYQ-IQEVV	GKGSYGVVGS	AIDTHTGERV	AIKKINDVFD	
ATMPK9_D	TEFFTEYGEA	SRYQ-IQEVI	GKGSYGVVAS	AIDTHSGEKV	AIKKINDVFE	
ATMPK18_D	MEFFTEYGDA	NRYR-ILEVI	GKGSYGVVCA	AIDTHTGEKV	AIKKINDVFE	
ATMPK20_D	MEFFSDYGDA	NRFK-VQEVI	GKGSYGVVCS	AIDTLTGEKV	AIKKIHDIFE	
ATMPK19_D	MEFFTEYGDA	NRYR-ILEVI	GKGSYGVVCA	AIDTQTGEKV	AIKKINDVFE	
Cqu_c06169_1_g0	PEFFTDYGEA	NRYK-ILEVI	GKGSYGVVCA	AIDTHTGEKV	AIKKINDIYE	
Cqu_c03735_1_g0	NLYGNVFEVS	SKYVPLRPV	GRGAYGIVCA	AVNSETQEEV	AIKKVSNAFH	
ATMPK16_D	VDFFTYGEA	SRYR-IEEVI	GKGSYGVVCS	AYDTHTGEXV	AIKKINDIFE	
Cqu_c07086_1_g0	VDFFTYGEA	NRYK-IEEVI	GKGSYGVVCS	AYDTHVGEKV	AXKKINDIFE	
Cqu_c09059_1_g0	PEFFTDYGEA	NRYK-ILEVI	GKGSYGVVCA	AIDTHTGEKV	AIKKINDXYE	
ATMPK17_D	KEFFTEYGEA	SQYQ-IQEVV	GKGSYGVVAS	AECPTHGKGV	AIKKMTNVFE	
Cqu_c04094_1_g0	NIFGNIFEVT	AKYKPPIMPI	GKGAYGIVCS	SLNSDTNEHV	AIKKIANAFD	
Cqu_c01012_1_g0	NDFFTYGEA	SRYQ-VQEII	GKGSYGIVGS	AVDTHTGEXV	AIKKINDVFE	
Cqu_c14619_1_g0	---	---	---	---	---	---
Cqu_c03126_1_g0	---	---	---	---	---	---
Cqu_c01012_1_g0	---	---	---	---	---	MDWYP
Consistency	4453547544	5684145458	8786687866	6555474748	8788846686	

	260.....	270.....	280.....	290.....	300
ATMPK11_B	NIIDAKRTL	EIKLLKHMDH	-DNVIAI	-ID	IIRPPQPDF	NDVHIVYELM
ATMPK13_B	NRVDAKRTL	EIKLLSHMDH	-DNVIKI	-KD	IIELPEKERF	EDVYIVYELM
ATMPK6_A	NKIDAKRTL	EIKLLRHMDH	-ENIVAI	-RD	IIPPLRNAF	NDVYIAYELM
ATMPK10_A	NTIEAKRTL	EIKLLRHFDH	-ENIVAI	-RD	VILPPQRDSF	EDVYIVNELM
Cqu_c04092_1_g0	NKVDKRTL	EIKLLRHMDH	-ENVVAI	-RD	IIPPRREAF	NDVYXAYELM
Cqu_c06022_1_g0	NIVDAKRTL	EIKLLRHMDH	-ENIIAI	-KD	IIRPPKKEAF	NDVYIVYELM
Cqu_c03819_1_g0	NYMDAKRTL	EIKILRHFDH	-ENIIVL	-RD	VIPPPVRREF	TDVYVATELM
Cqu_c04159_1_g0	NYMDAKRTL	EIKILRHFDH	-ENIIVL	-RD	VIPPPVRREF	TDVYVATELM
ATMPK3_A	NHMDAKRTL	EIKLLRHLDH	-ENIIAI	-RD	VVPPPLRRQF	SDVYISTELM

Cqu_c03402_1_g0	NRIDAKRTLRL	EIKLLCHMDH	-DNVIKI-KD	IIRPPERENF	NDVYIVYELL
Cqu_c03736_1_g0	NRIDAKRILRL	EIKLLRHMDH	-DNVISI-RD	IIRPPQKENF	NDVYIMVHEL
ATMPK12_B	NIIDAKRTLRL	EIKLLRHMDH	-ENVITI-KD	IVRPPQORDIF	NDVYIVYELM
ATMPK4_B	NIIDAKRTLRL	EIKLLKHMDH	-ENVIIV-KD	IIRPPQRENF	NDVYIVYELM
ATMPK5_B	NKVDAKRTLRL	EIKLLRHLEH	-ENVVVI-KD	IIRPPKKEDF	VDVYIVFELM
Cqu_c17078_1_g0	NRIDAKRTLRL	EIKLLCHMDH	-DNVIKI-KD	IIRPPERENF	NDVYIVYELL
ATMPK1_C	NRIDALRTLRL	ELKLLRHRLRH	-ENVIAL-KD	VMMPIHKMSF	KDVYLVYELM
Cqu_c02858_1_g0	NRVDALRTLRL	ELKLLRHRLRH	-DNVIAL-KD	VMLPAHPKNF	KDVYLVYELM
ATMPK7_C	NRVDALRTLRL	ELKLLRHVRH	-ENVIAL-KD	VMLPANRSSF	KDVYLVYELM
ATMPK2_C	NRIDALRTLRL	ELKLLRHRLRH	-ENVVAL-KD	VMMANHKRSF	KDVYLVYELM
ATMPK14_C	NRIDALRTLRL	ELKLLRHVRH	-ENVISL-KD	VMLPTHRYSF	RDVYLVYELM
ATMPK8_D	HVSDATRILRL	EIKLLRLLRH	-PDVVEI-KH	IMLPPSRREF	RDIYVVFELM
Cqu_c08055_1_g0	HVSDATRILRL	EIKLLRLLRH	-PDVVEI-KH	IMLPPSRREF	KDIYVVFELM
ATMPK15_D	HISDATRILRL	EIKLLRLLRH	-PDVVEI-KH	IMLPPSRREF	RDVYVVFELM
ATMPK9_D	HVSDATRILRL	EIKLLRLLRH	-PDIVEI-KH	VMLPPSRREF	RDIYVVFELM
ATMPK18_D	HISDALRILRL	EVKLLRLLRH	-PDIVEI-KS	IMLPPSKREF	KDIYVVFELM
ATMPK20_D	HISDAARILRL	EIKLLRLLRH	-PDIVEI-KH	IMLPPSRREF	KDIYVVFELM
ATMPK19_D	HVSDALRILRL	EVKLLRLLRH	-PDIVEI-KS	IMLPPSKREF	KDIYVVFELM
Cqu_c06169_1_g0	HISDAIRILRL	EVKLLRLLRH	-PDIVEI-KR	IMXPPSKRDF	RDIYVVFELM
Cqu_c03735_1_g0	NRIDAKRILRL	EIKLLRHMDH	-DNVISI-RD	IIRPPQKENF	NDVYIMVHELM
ATMPK16_D	HVSDATRILRL	EIKLLRLLRH	-PDIVEI-KH	ILLPPSRREF	RDIYVVFELM
Cqu_c07086_1_g0	HVSDATRILRL	EIKLLRLLRH	-PDIVEI-KH	ILLPPSRREF	KDIYVVFELM
Cqu_c09059_1_g0	HISDAIXILRL	EVKLLRLLRH	-PDIVEI-KR	IMLPPSKRDF	RDIYVVLLELM
ATMPK17_D	HVSDAIRILRL	EIKLLRLLRH	-PDIVEI-KH	IMLPPCRKEF	KDIYVVFELM
Cqu_c04094_1_g0	NKVDAKRTLRL	EIKLLRHMDH	-ENVVAI-RD	IIPPPRREAF	NDVYIAYELM
Cqu_c01012_1_g0	HVSDATRILRL	EIKLLRLLHF	-AHET		
Cqu_c14619_1_g0					
Cqu_c03126_1_g0					
Cqu_c01012_1_g0	GHGVDRFKRQ	FAHLEEHGK	GEKSTPLSRQ	HASLPRERVP	APKTDANENN
Consistency	6458848588	8788875648	0567747065	7637636447	4877665887

		310	320	330	340	350
ATMPK11_B	DTDLHHIIRS	NQPLTDDHSR	FFLYQLLRGL	KYVHSANVLH	RDLKPSNLLL	
ATMPK13_B	DTDLHQIIRS	TQTLTDDHCQ	YFLYQILRGL	KYIHSANVLH	RDLKPSNLVL	
ATMPK6_A	DTDLHQIIRS	NQALSEEHCQ	YFLYQILRGL	KYIHSANVLH	RDLKPSNLLL	
ATMPK10_A	EFDLYRTLKS	DQELTKDHGM	YFMYQILRGL	KYIHSANVLH	RDLKPSNLLL	
Cqu_c04092_1_g0	DTDLHQIIRS	NQGLSEEHCQ	YFLYQXLRGL	KYIHSANVLH	RDLKPSNLLL	
Cqu_c06022_1_g0	DTDLHQIIRS	SQALTDDHCQ	YFLYQLLRGL	KYVHSAKVLH	RDLKPSNLLL	
Cqu_c03819_1_g0	DTDLHQIIRS	HQSLSEEHCQ	YFLYQILRGL	KYIHSANVIH	RDLKPSNLLI	
Cqu_c04159_1_g0	DTDLHQIIRS	HQSLSEEHCQ	YFLYQILRGL	KYIHSANVIH	RDLKPSNLLI	
ATMPK3_A	DTDLHQIIRS	NQSLSEEHCQ	YFLYQLLRGL	KYIHSANIIH	RDLKPSNLLL	
Cqu_c03402_1_g0	DTDLHQIIRS	TQELTEDHCQ	YFLYQILRGL	KYIHSANVLH	RDLKPSNLLL	
Cqu_c03736_1_g0	DTDLHQIIRS	NQQLTDDHCR	YFLYQILRGL	KYIHSAGVLH	RDLKPSNLLM	
ATMPK12_B	DTDLQRIIRS	NQTLTSDQCR	FLVYQLLRGL	KYVHSANILH	RDLRPSNVLL	
ATMPK4_B	DTDLHQIIRS	NQPLTDDHCR	FFLYQLLRGL	KYVHSANVLH	RDLKPSNLLL	
ATMPK5_B	DTDLHQIIRS	NQSLNDDHCQ	YFLYQILRGL	KYIHSANVLH	RDLKPSNLLL	
Cqu_c17078_1_g0	DTDLHQIIRS	TQELTEDHCQ	YFLYQILRGL	KYIHSANVLH	RDLKPSNLLL	
ATMPK1_C	DTDLHQIIRS	SQVLSNDHCQ	YFLFQLLRGL	KYIHSANILH	RDLKPGNLLV	
Cqu_c02858_1_g0	DTDLHQIIRS	SQALSNDHCQ	YFLFQLLRGL	KYLHSANILH	RDLKPGNLLI	
ATMPK7_C	DTDLHQIIRS	SQSLSDDHCQ	YFLFQLLRGL	KYLHSANILH	RDLKPGNLLV	
ATMPK2_C	DTDLHQIIRS	SQVLSNDHCQ	YFLFQLLRGL	KYIHSANILH	RDLKPGNLLV	
ATMPK14_C	DSDLNQIIRS	SQSLSDDHCQ	YFLFQLLRGL	KYLHSANILH	RDLKPGNLLV	
ATMPK8_D	ESDLHQVIKA	NDDLTPPEHYQ	FFLYQLLRGL	KYVHAANVFH	RDLKPKNILA	
Cqu_c08055_1_g0	ESDLHQVIKA	NDDXTPEHYQ	FFLYQLLRGL	KYVHTANVFH	RDLKPKNILA	
ATMPK15_D	ESDLHQVIKA	NDDLTPPEHQ	FFLYQLLRGL	KYVHAANVFH	RDLKPKNILA	
ATMPK9_D	ESDLHQVIKA	NDDLTPPEHYQ	FFLYQLLRGL	KFIHTANVFH	RDLKPKNILA	
ATMPK18_D	ESDLHQVIKA	NDDLTPPEHQ	FFLYQMLRAL	KFMHTANVYH	RDLKPKNILA	
ATMPK20_D	ESDLHQVIKA	NDDLTPPEHYQ	FFLYQLLRGL	KYIHTANVYH	RDLKPKNILA	
ATMPK19_D	ESDLHQVIKA	NDDLTPPEHQ	FFLYQMLRAL	KYMHTANVYH	RDLKPKNILA	
Cqu_c06169_1_g0	ESDLHQVIKA	NDDLTPPEHQ	FFLYQMLRAL	KYMHTANVYH	RDLKPKNILA	
Cqu_c03735_1_g0	DTDLHQIIRS	NQQLTDDHCR	YFLYQILRGL	KYIHSAGVLH	RDLKPSNLLM	
ATMPK16_D	ESDLHQVIKA	NDDLTPPEHYQ	FFLYQLLRGL	KYIHTANVFH	RDLKPKNILA	
Cqu_c07086_1_g0	ESDXHQVIKA	NDDLTPPEHYQ	FFLYQLLRGL	KYIHTANVFH	RDLKPKNILA	
Cqu_c09059_1_g0	ESDLHQVIKA	NDDLTPPEHQ	FFLYQMLRAL	KYMHTANVYH	RDLKPKNILA	
ATMPK17_D	ESDLHHVLKV	NDDLTPQHHQ	FFLYQLLRGL	KFMHSAHVFH	RDLKPKNILA	
Cqu_c04094_1_g0	DTDLHQIIRS	NQGLSEEHCQ	YFLYQILRGL	KYNIFCQCSY	RDLKPSNLCL	
Cqu_c01012_1_g0		RPCS	VALTTDDQIF	SSSYAANVFH	RDLKPKNILA	
Cqu_c14619_1_g0						
Cqu_c03126_1_g0						
Cqu_c01012_1_g0	DMENRAVART	ALE-SPPKSN	ADGSENEVPQ	NGQNKGNYS	RSLKKSASIS	
Consistency	6687777776	5547646746	6787868868	8768687758	8888858785	

		360	370	380	390	400
ATMPK11_B	NANCDLKIGD	FGLARTK---	SETDFMTEY	VVTRWYRAPE	LLLNC-SEYT	
ATMPK13_B	NTNCDLKICD	FGLARTS---	NETEIMTEY	VVTRWYRAPE	LLLNS-SEYT	

ATMPK6_A	NANCDLKICD	FGLARVT	---	SE	SDFMTEY	VVTRWYRAPE	LLNS	SDYT								
ATMPK10_A	STQCDLKICD	FGLARAT	---	PES	NLMTEY	VVTRWYRAPE	LLGS	SDYT								
Cqu_c04092_1_g0	NANCDLKICD	FGLARVT	---	SET	SDFMTEY	VVTRWYRAPE	LLNS	SDYT								
Cqu_c06022_1_g0	NANCDLKIGD	FGLARTT	---	TET	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
Cqu_c03819_1_g0	NANCDLKICD	FGLARPT	---	SENE	HMTTEY	VVTRWYRAPE	LLNS	SDYT								
Cqu_c04159_1_g0	NANCDLKICD	FGLARPT	---	SENE	HMTTEY	VVTRWYRAPE	LLNS	SDYT								
ATMPK3_A	NANCDLKICD	FGLARPT	---	SEN	SDFMTEY	VVTRWYRAPE	LLNS	SDYT								
Cqu_c03402_1_g0	NANCDLKICD	FGLARTT	---	AET	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
Cqu_c03736_1_g0	NANCDLKIGD	FGLARTT	---	SET	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
ATMPK12_B	NSKNELKIGD	FGLARTT	---	SDT	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
ATMPK4_B	NANCDLKLGD	FGLARTK	---	SET	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
ATMPK5_B	NSNCDLKITD	FGLARTT	---	SET	EYMTTEY	VVTRWYRAPE	LLNS	SEYT								
Cqu_c17078_1_g0	NANCDLKICD	FGLARTT	---	AET	SDFMTEY	VVTRWYRAPE	LLNC	SEYT								
ATMPK1_C	NANCDLKICD	FGLARAS	---	NTK	GQFMTEY	VVTRWYRAPE	LLCC	DNYG								
Cqu_c02858_1_g0	NANCDLKICD	FGLARTS	---	SGK	GQFMTEY	VVTRWYRAPE	LLCC	DKYG								
ATMPK7_C	NANCDLKICD	FGLARTS	---	QGN	EQFMTEY	VVTRWYRAPE	LLCC	DNYG								
ATMPK2_C	NANCDLKICD	FGLARTS	---	NTK	GQFMTEY	VVTRWYRAPE	LLCC	DNYG								
ATMPK14_C	NANCDLKICD	FGLART	---	YE	QFMTEY	VVTRWYRAPE	LLCC	DNYG								
ATMPK8_D	NADCKLKICD	FGLARVSFND	APT	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c08055_1_g0	NADCKLKICD	FGLARVSFND	APS	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK15_D	NADCKLKICD	FGLARVSFND	APT	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK9_D	NSDCKLKICD	FGLARVSFND	APS	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK18_D	NANCKLKVCD	FGLARVAFND	TPT	TVFWDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK20_D	NANCKLKVCD	FGLARVAFND	TPT	TVFWDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK19_D	NANCKLKVCD	FGLARVSFND	TPT	TVFWDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c06169_1_g0	NANCKLKVCD	FGLARVAFND	TPT	TVFWDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c03735_1_g0	NANCDLKIGD	FGLART	---	TSET	SDFMTEY	VVTRWYRAPE	LLN	CSEYT								
ATMPK16_D	NADCKLKICD	FGLARVAFND	TPT	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c07086_1_g0	NADCKLKICD	FGLARVAFND	TPT	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c09059_1_g0	NANCKLKVCD	FGLARVAFND	TPT	TVFWDY	VATR	WYRAPE	LCGSFF	SKYT								
ATMPK17_D	NADCKIKICD	LGLARVSFTD	SPS	AVFWDY	VATR	WYRAPE	LCGSFF	SNYT								
Cqu_c04094_1_g0	-----	-----	-----	-----	-----	MPTR	WYRAPE	LLN								
Cqu_c01012_1_g0	NADCKLKICD	FGLARVSFND	APS	AIFWTDY	VATR	WYRAPE	LCGSFF	SKYT								
Cqu_c14619_1_g0	-----	-----	-----	-----	-----	-----	-----	YT								
Cqu_c03126_1_g0	-----	MLYFHT	---	TG	ESFLTDY	VVMR	WYKEPE	L								
Cqu_c01012_1_g0	GSKC	IGV	---	---	---	QSRK	DPEEE	PIAE								
Consistency	7768	5888	57	7888	855	111	1444	375	868	868	999	889	99	9545	30	6486

ATMPK11_B	AAIDIWSVGC	ILGEIMT	---	RE	PLFPGR	DYVQQLRLIT	ELIGSP	DDSS
ATMPK13_B	GAIDIWSVGC	IFMEILR	---	RE	TLFPGR	DYVQQLKLIT	ELIGSP	DDSD
ATMPK6_A	AAIDVWSVGC	IFMELMD	---	RK	PLFPGR	DHVHQLRLLM	ELIGTP	SEEE
ATMPK10_A	AAIDVWSVGC	IFMEIMN	---	RE	PLFPGR	DQVNQLRLLL	ELIGTP	SEEE
Cqu_c04092_1_g0	AAIDVWSVGC	IFMELMD	---	RK	PLFPGR	DHVHQLRLLM	ELIGTP	SEHE
Cqu_c06022_1_g0	AAIDVWSVGC	IFGEIMT	---	RE	PLFPGR	DYVHQLRLIT	ELIGSP	DDSS
Cqu_c03819_1_g0	ASIDLWSVGC	IFMELMN	---	RR	PLFPGR	DHVHQMRLLT	ELLGTP	TEAD
Cqu_c04159_1_g0	ASIDLWSVGC	IFMELMN	---	RK	PLFPGR	DHVHQMRLLT	ELLGTP	TEAD
ATMPK3_A	AAIDVWSVGC	IFMELMN	---	RK	PLFPGR	DHVHQMRLLT	ELLGTP	TESD
Cqu_c03402_1_g0	AAIDMWSVGC	IMMEI IK	---	RE	PLFPGR	DYLOQLQLIN	ELLGSP	PEDSD
Cqu_c03736_1_g0	AAIDTWSVGC	ILGEIMT	---	RE	PLFPGR	DYVHQLKLV	ELIGSP	DDSS
ATMPK12_B	AAIDIWSVGC	ILGEIMT	---	GQ	PLFPGR	DYVHQLRLIT	ELVGSP	DNSS
ATMPK4_B	AAIDIWSVGC	ILGETMT	---	RE	PLFPGR	DYVHQLRLIT	ELIGSP	DDSS
ATMPK5_B	SAIDVWSVGC	IFAEIMT	---	RE	PLFPGR	DYVHQLKLIT	ELIGSP	DGAS
Cqu_c17078_1_g0	AAIDMWSVGC	IMMEI IK	---	KE	PLFPGR	DYLOQLQLIN	ELLGSP	PEDSD
ATMPK1_C	TSIDVWSVGC	IFAEILG	---	RK	PIFQGT	ECLNQLKLIV	NILGSQ	REED
Cqu_c02858_1_g0	TSIDVWSVGC	IFAEILG	---	RK	PLFPGT	ECLNQLKLIV	NILGSQ	RDAD
ATMPK7_C	TSIDVWSVGC	IFAEILG	---	RK	PIFPGT	ECLNQLKLII	NVGSQ	QESD
ATMPK2_C	TSIDVWSVGC	IFAEILG	---	RK	PVFPGT	ECLNQIKLII	NILGSQ	REED
ATMPK14_C	TSIDVWSVGC	IFAEILG	---	RK	PIFPGT	ECLNQLKLII	NVGSQ	QDWD
ATMPK8_D	PAIDIWSVGC	IFAEMLL	---	GK	PLFPGR	NVVHQLDLMT	DFLGTP	PPES
Cqu_c08055_1_g0	PAIDIWSIGC	IFAEMLT	---	GK	PLFPGR	NVVHQLDLMT	DLMGTP	PPPEA
ATMPK15_D	PAIDIWSVGC	IFAEMLL	---	GK	PLFPGR	NVVHQLDIMT	DFLGTP	PPPEA
ATMPK9_D	PAIDIWSIGC	IFAEMLT	---	GK	PLFPGR	NVVHQLDIMT	DLLGTP	PPPEA
ATMPK18_D	PAIDVWSIGC	IFAEVLT	---	GK	PLFPGR	SVVHQLLELIT	DLLGTP	PKSET
ATMPK20_D	PAIDIWSIGC	IFAEVLM	---	GK	PLFPGR	NVVHQLDLMT	DLLGTP	PSLDT
ATMPK19_D	PAIDIWSIGC	IFAEVLT	---	GK	PLFPGR	SVVHQLDLIT	DLLGTP	PKSET
Cqu_c06169_1_g0	PAIDIWSIGC	IFAEVLT	---	GK	PLFPGR	SVVHQLDIIT	DLLGTP	PSHDV
Cqu_c03735_1_g0	AAIDIWSVGC	ILGEIMT	---	RE	PLFPGR	DYVHQLKLV	ELIGSP	DDSS
ATMPK16_D	PAIDIWSIGC	IFAEMLT	---	GK	PLFPGR	NVVHQLDLMT	DMLGTP	PSAEA
Cqu_c07086_1_g0	PAIDIWSIGC	IFAEMLT	---	GK	PLFPGR	NVVHQLDLMT	ELLGTP	SPDA
Cqu_c09059_1_g0	PAIDIWSIGC	IFAEVLT	---	GK	PLFPGR	SVVHQLDIIT	DLLGTP	PSHDV
ATMPK17_D	PAIDMWSVGC	IFAEMLT	---	GK	PLFPGR	NVVHQLLELVT	DLLGTP	SPIT
Cqu_c04094_1_g0	SSDLQLLSM	YVEDALA	---	HH	YLSLH	DISDEPICMS	-----	PFC
Cqu_c01012_1_g0	PAIDIWSIGV	YLOKCSLENH	YS	WKKCGASV	GPMDR	-----	SYGD	STP
Cqu_c14619_1_g0	PAIDIWSIGC	IFAEMLT	---	GK	PLFPGR	NVVHQLDLMT	ELLGTP	SPDA

Cqu_c03126_1_g0 ---QIKF IINFL--- ---GSPSESD
 Cqu_c01012_1_g0 NEEAVDELTK KATALAT---
 Consistency 4789789988 8758774000 0046788786 5376874765 5668674444

..... 460..... 470..... 480..... 490..... 500

ATMPK11_B LGFLRSDNAR RYVRQLPQYP RQNFAARFPN MSVNAVDLLQ KMLVFDPNRR
 ATMPK13_B LDFLRSDNAR KYVKQLPHVQ KQSFREKFPN ISPMALDLAE KMLVFDPSKR
 ATMPK6_A LEFL-NENAK RYIRQLPPYP RQSITDKFPT VHPLAIDLIE KMLTFDPRRR
 ATMPK10_A LGSL-SEYAK RYIRQLPTLP RQSFTEKFPN VPPLAIDLVE KMLTFDPKQR
 Cqu_c04092_1_g0 LGFL-NENAK RYIRQLPPFR RQSLSEKFPX VHPAAIDLIE KMLTFDPRQR
 Cqu_c06022_1_g0 LGFLRSNHAR RYVKQLPQYP KQQFSARFPN MSPAATDLE KMLVFDPNKR
 Cqu_c03819_1_g0 LGFLHNEDAR RYIRQLPPQP RQQLRQVFPN VNPLAIDLIE KMLTFDPTRR
 Cqu_c04159_1_g0 LGFLHNEDAR RYIRQLPPQP RQQLRQLFPH VNPLAIDLIE RMLTFDPTRR
 ATMPK3_A LGFTHNEDAK RYIRQLPNFP RQPLAKLFVH VNPMAIDLVD RMLTFDPNRR
 Cqu_c03402_1_g0 LGFLRSENAK KYIKQLPHVP KQPF SHKFPS VSPLVLDLAE KMLVFDPSKR
 Cqu_c03736_1_g0 IAFLOSENAK RYVRQLPQYP RQQFSVKFPN ASPLAIDLLE KMLVFDPSKR
 ATMPK12_B LGFLRSDNAR RYVRQLPRYP KQQFAARFPK MPTTAIDLLE RMLVFDPNRR
 ATMPK4_B LGFLRSDNAR RYVRQLPQYP RQNFAARFPN MSAGAVDLE KMLVFDPSRR
 ATMPK5_B LEFLRSANAR KYVKELPKFP RQNF SARFPS MNSTAILLE KMLVFDPVKR
 Cqu_c17078_1_g0 LGFLRSENAK KYIKQLPHVP KQPF SHKFPS VSPLVLDLAE KMLVFDPSKR
 ATMPK1_C LEFIDNPKAK RYIRSLPYS GMSLSRLYPG AHVLAIDLLO KMLVFDPSKR
 Cqu_c02858_1_g0 LEFIDNPKAK RFIKSLPYS TASLSRLYPT ANPLAIDLLO KMLVFDPTKR
 ATMPK7_C IRFIDNPKAR RFIKSLPYSR GTHLSNLYPQ ANPLAIDLLO RMLVFDPTKR
 ATMPK2_C LEFIDNPKAK RYIESLPYS GISFSRLYPG ANVLAIDLLO KMLVLDPSKR
 ATMPK14_C LQFIDNQKAR RFIKSLPFSK GTHFSHIYPH ANPLAIDLLO RMLVFDPTKR
 ATMPK8_D ISRIRNEKAR RYLSMRKKQ PVPF SHKFPK ADPLALRLE RLLAFDPKDR
 Cqu_c08055_1_g0 ISRIRNEKAR RYLSXMRKKP PIPFSQKFPN VDPLALRLE RLLAFDPKDR
 ATMPK15_D ISKIRNDKAR RYLGMRKKQ PVPFSKKFPK ADPSALRLE RLLAFDPKDR
 ATMPK9_D IARIRNEKAR RYLGMRKKP PVPFTHKFPH VDPLALRLLH RLLAFDPKDR
 ATMPK18_D ISGVRNDKAR KYLTEMRKKN PVTFSQKFSK ADPLALRLLQ RLLAFDPKDR
 ATMPK20_D ISVRNEKAR RYLTSMRKKP PIPFAQKFPN ADPLSLKLE RLLAFDPKDR
 ATMPK19_D IAGVRNEKAR KYLNEMRKKN LVPFSQKFPN ADPLALRLLQ RLLAFDPKDR
 Cqu_c06169_1_g0 ISGVRNDKAR KYLDMRKKQ PVPF SHKFSN ADPLALRLLQ RLLSFDPKDR
 Cqu_c03735_1_g0 IAFLOSENAK RYVRQLPQYP RQQFSVKFPN ASPLAIDLLE KMLVFDPSKR
 ATMPK16_D IGRVRNEKAR RYLSMRKKK PIPF SHKFPH TDPLALRLE KMLSFEPKDR
 Cqu_c07086_1_g0 IARIRNEXAR RYLSMRKKK PIPFTHKFPN ADPLALRLE RMLAFEPKDR
 Cqu_c09059_1_g0 ISGVRNDKAR KYLDMRKKQ PVPF SHKFSN ADPLALRLLQ RLLSFDPKDR
 ATMPK17_D LSRIRNEKAR KYLGMRKKD PVPFTHKFPN IDPVALKLLQ RLLAFDPKDR
 Cqu_c04094_1_g0 FDFEQHALSE EQMRELIYRE ALAFNPEFQQ E-----
 Cqu_c01012_1_g0 -----
 Cqu_c14619_1_g0 IAPG-LSRSS PIISIMRKKK AYSFHHKFPN ADPLAFVCWN EMLAVEPKDR
 Cqu_c03126_1_g0 LAFIKNQNVV KFIEGMPYSN GVRLEDEYLW ANPLALDLLR RMLVLNPTKR
 Cqu_c01012_1_g0 -----
 Consistency 7446465586 7774575344 3447535874 5465765866 6785778448

..... 510..... 520..... 530..... 540..... 550

ATMPK11_B ITVDEALCHP YLAPLHEYNE -----EPV C--VRPFHFD F-EQPSLTEE
 ATMPK13_B ITVDEALKQP YLASLHEINE -----EPT C--PTPFSFD F-EETALDEQ
 ATMPK6_A ITVDALAHF YLNSLHDISD -----EPE C--TIPFNFD F-ENHALSEE
 ATMPK10_A ISVKEALAHF YLSSFHDITD -----EPE C--SEPFNFD L-DEHPFSEE
 Cqu_c04092_1_g0 ITVEDALAHF YLNSLHDISD -----EPI C--MSPFCFD F-EQHALSEE
 Cqu_c06022_1_g0 VTVDEALCHP YLASLHDIND -----EPI C--SAPFRFD F-EQSSLTEE
 Cqu_c03819_1_g0 ITVEEALAHF YLARLHDIAD -----EPV C--QEPFSFD F-ENQALTEE
 Cqu_c04159_1_g0 ITVEEALAHF YLARLHDIAD -----EPV C--QEPFSFD F-ENQALTEE
 ATMPK3_A ITVEQALNHQ YLAKLHDPND -----EPI C--QKPFSE F-EQOPLDEE
 Cqu_c03402_1_g0 ITVDEALNHP YLSSLHEINE -----EPT C--PKPFQFD F-EQSTLDEE
 Cqu_c03736_1_g0 ITVHEALCHP YLAPLHDINE -----EPV C--PQPFSFD F-EQPSFTEE
 ATMPK12_B ISVDEALGHA YLSPHHDVAK -----EPV C--STPFSFD F-EHPSCTEE
 ATMPK4_B ITVDEALCHP YLAPLHDINE -----EPV C--VRPFNFD F-EQPTLTEE
 ATMPK5_B ITVEEALCYP YLSALHDIND -----EPV C--SNHFSFH F-EDPSSTEE
 Cqu_c17078_1_g0 ITVDEALNHP YLSSLHEINE -----EPT C--PKPFQFD F-EQSTLDEE
 ATMPK1_C ISVSEALQHP YMAPLYDPNA -----NPP A--QVPIDLD V-DED-LREE
 Cqu_c02858_1_g0 ISVTEALQHP YMSPLYDPRA -----NPP A--QFPIDLE I-DED-LXEE
 ATMPK7_C ISVTDALHHP YMAGLFDPGS -----NPP A--HVPISLD I-DEN-MEEP
 ATMPK2_C ISVTEALQHP YMAPLYDPSA -----NPP A--QVPIDLD VDEDEDLGAE
 ATMPK14_C ISVSDALLHP YMEGLLEPEC -----NPS E--NVPVSSL E-IDENMEGD
 ATMPK8_D ASAEDALADP YFSGLSNSER -----EPT TQPIISKLEFD F-ERKKLVKD
 Cqu_c08055_1_g0 PSAAEALADP YFYGLSSADR -----EPC TTPISKLEFE F-ERRKLAKD
 ATMPK15_D PSAAEALADP YFNGLSSKVR -----EPS TQPIISKLEFE F-ERKKLTKD
 ATMPK9_D PSAAEALADP YFYGLANVDR -----EPS TQPIPKLEFE F-ERRKITKE
 ATMPK18_D PTPAEALADP YFKGLSKIER -----EPS SQQISKMEFE F-ERRRLTKD
 ATMPK20_D PTAAEALADP YFKGLAKVER -----EPS CQPIITKMEFE F-ERRKVTKD
 ATMPK19_D PTAAEALADP YFKCLAKVER -----EPS CQPIISKMEFE F-ERRRLTKD
 Cqu_c06169_1_g0 PTAAEALADP YFKGLSRVER -----EPA CQPIISKLEFE F-ERRRVTKE
 Cqu_c03735_1_g0 ITVHEALCHP YLAPLHDINE -----EPV C--PQPFSFD F-EQPSFTEE


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ATMPK16_D  P T A E E A L A D V Y F K G L A K V E R ----- E P S A Q P V T K L E F E F - E R R R I T K E
Cqu_c07086_1_g0 P S A E E A L A D P Y F K G L A K V E R ----- E P S A Q P V T K M E F E F - E R R R M T K E
Cqu_c09059_1_g0 P T A E E L L - K D Y M N G N E G S N Y ----- I Y P S A - - I G Q F K K Q F - A H L E E N A G
ATMPK17_D  P S A E E A L A D P Y F Q G L A N V D Y ----- E P S R Q P I S K L E F E F - E R R K L T R D
Cqu_c04094_1_g0 -----
Cqu_c01012_1_g0 -----
Cqu_c14619_1_g0 P S A E E A L A D P Y F K G L A K F A Y L E E H Y K N G S T G P P I D R Q H A S L - P R A C V L Y S
Cqu_c03126_1_g0 I T V T E A L R H S Y M A D L H I P T E ----- Y P P P - - Q R S L D I D I - - E A D V G E S
Cqu_c01012_1_g0 -----
Consistency 4 6 6 4 7 8 8 3 5 6 8 5 4 3 7 4 4 4 4 3 0 0 0 0 0 0 6 8 3 4 0 0 3 3 5 5 4 6 6 6 0 6 4 3 3 5 4 5 6
    
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..... 560..... 570..... 580..... 590..... 600
ATMPK11_B  N I K E L I Y R E S V K F N P -----
ATMPK13_B  D I K E L V W R E S L H F K N M -----
ATMPK6_A   Q M K E L I Y R E A L A F N P E Y Q Q -----
ATMPK10_A  Q F R E L I Y C E A L A F N P E T S N D -----
Cqu_c04092_1_g0 Q M R E L I Y R E A L A F N P E F Q Q E -----
Cqu_c06022_1_g0 N V K E L I W K E S V K F N P D P A H -----
Cqu_c03819_1_g0 Q M K D M I H Q E A L A L N P G Y I -----
Cqu_c04159_1_g0 Q M K D M I H Q E A L A L N P G Y I -----
ATMPK3_A   Q I K E M I Y Q E A I A L N P T Y G -----
Cqu_c03402_1_g0 D I K E L V W R E T L K F N P D K M I E -----
Cqu_c03736_1_g0 N I K E L I W R E S V S F N P D P L I G -----
ATMPK12_B  H I K E L I Y K E S V K F N P D H -----
ATMPK4_B   N I K E L I Y R E T V K F N P Q D S V -----
ATMPK5_B   E I K E L V W L E S V K F N P L P S I -----
Cqu_c17078_1_g0 D I K E L V W R E T L K F N P D K M I E -----
ATMPK1_C   M I R E M M W N E M L H Y H P Q A S T L - N T - - - E L - - - - -
Cqu_c02858_1_g0 M I R E S M W Q E I M H Y H P E A I N Q - N M - - - E L C G - - - - -
ATMPK7_C   V I R E M M W N E M L Y Y H P E A E I S - N A - - - - - - - - -
ATMPK2_C   M I R E L M W K E M I H Y H P E A A T I N N N - - - E V S E F - - - - -
ATMPK14_C  M I R E M M W E E M L H Y L P R A -----
ATMPK8_D   D V R E L I Y R E I L E Y H P Q M L E E Y L R G - G - D Q L S F M Y P S G V D R F K - - - R Q F A
Cqu_c08055_1_g0 D V R E L I Y R E I L E Y H P Q M L Q E Y L R G - G Q D Q T S F M Y P S G V D R F K - - - R Q F A
ATMPK15_D  D I R E L I Y R E I L E Y H P Q M L E E Y L R G - G - N Q L S F M Y P S G V D R F R - - - R Q F A
ATMPK9_D   D V R E L I Y R E I L E Y H P Q M L Q E Y L R G - G - E Q T S F M Y P S G V D R F K - - - R Q F A
ATMPK18_D  D I R E L I Y R E I L E Y H P Q L L K D Y M S G - - - S E G S N F V Y P S A I G H L R - - - Q Q F T
ATMPK20_D  D I R E L I S R E I L E Y H P Q L L K D H M N G - - - A D K A S F L Y P S A V D Q F R - - - R Q F A
ATMPK19_D  D I R E L I Y R E I L E Y H P Q L L K D Y M N S - - - E G S S F L Y P S A I G H L R - - - K Q F A
Cqu_c06169_1_g0 D V R E L I Y R E I L E Y H P Q L L K D Y M N G - - - N E G S N Y I Y P S A I G Q F K - - - K Q F A
Cqu_c03735_1_g0 N I K E L I W R E S V S E Q H Q F L M H F L D R H P L E S L P V A A P - R L P H F K T L C T S E I Q
ATMPK16_D  D V R E L I Y R E S L E Y H P K M L K E Y L D G - - - S E P T N F M Y P S A V E H F K - - - K Q F A
Cqu_c07086_1_g0 D V R E L I Y R E I L E Y H P K M L K E F L D G - - - S E P T N F M Y P S A V D H F K - - - K Q F A
Cqu_c09059_1_g0 R S G P V I P L E R K H - - - I S L P R S T V H - - - S S T I P P K P L A S S H - - - - - K D H Q
ATMPK17_D  D V R E L M Y R E I L E Y H P Q M L Q E Y L Q G E E N I N S H F L Y P S G V D Q F K - - - Q E F A
Cqu_c04094_1_g0 -----
Cqu_c01012_1_g0 -----
Cqu_c14619_1_g0 D N S V H G S T E V T E D L S K C R I K E V ----- E K A H
Cqu_c03126_1_g0 Y L R E L I W R E M V F -----
Cqu_c01012_1_g0 -----
Consistency 4 6 6 7 6 6 5 5 8 4 6 4 5 4 6 4 2 3 2 1 0 1 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0
    
```

```

..... 610..... 620..... 630..... 640..... 650
ATMPK11_B  -----
ATMPK13_B  -----
ATMPK6_A   -----
ATMPK10_A  -----
Cqu_c04092_1_g0 -----
Cqu_c06022_1_g0 -----
Cqu_c03819_1_g0 -----
Cqu_c04159_1_g0 -----
ATMPK3_A   -----
Cqu_c03402_1_g0 -----
Cqu_c03736_1_g0 -----
ATMPK12_B  -----
ATMPK4_B   -----
ATMPK5_B   -----
Cqu_c17078_1_g0 -----
ATMPK1_C   -----
Cqu_c02858_1_g0 -----
ATMPK7_C   -----
ATMPK2_C   -----
ATMPK14_C  -----
ATMPK8_D   H L E E N Q G K P G A A G G G R S T A - - - L H R H H A S L P R E R V P A P N G - - -
Cqu_c08055_1_g0 H L E E H L G K - - - - - G E K S T P - - - L S R Q H A S L P R E R V P A P K T - - -
    
```

```

ATMPK15_D HLEENQGP --- GGRSNA --- LQRQHAS LPRERVPASK N-----
ATMPK9_D HLEENYGK --- GEKGSF --- LQRQHAS LPRERVPAPK K-----
ATMPK18_D YLEENSSRN --- G-PVIP --- LERKHAS LPRSTVHSTV VHSTS-----
ATMPK20_D HLEENSGKT --- G-PVAP --- LERKHAS LPRSTVIHST AVARG-----
ATMPK19_D YLEENSGKS --- G-PVIP --- PDRKHAS LPRSAVHSSA VNSNA-----
Cqu_c06169_1_g0 HLEENAGRS --- G-PVIP --- LERKHIS LPRSTVHSST IPPKP-----
Cqu_c03735_1_g0 IMKNSYGLV --- Y-PSIPS RAGPKRRNSF MRGITCTSSS NSAFFLPNIP
ATMPK16_D YLEEHYKNG --- TSHNPP --- ERQHAS LPRACVLYSD NNHPV-----
Cqu_c07086_1_g0 YLEEHYKNG --- S-TGPP --- IDRQHAS LPRACVLYSD NSV-----
Cqu_c09059_1_g0 AKEE --- --- --- --- MRPSESYG-----
ATMPK17_D RLEEHNDDEE --- EHNSPP --- HQRKYTS LPRERVCSS E-----
Cqu_c04094_1_g0 -----
Cqu_c01012_1_g0 -----
Cqu_c14619_1_g0 VDRNG --- AIP --- MTRLPLQ VPQN-----
Cqu_c03126_1_g0 -----
Cqu_c01012_1_g0 -----
Consistency 0011000000 0000000000 0000010000 0110000000 0000000000

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..... 660..... 670..... 680..... 690..... 700

```

ATMPK11_B -----
ATMPK13_B -----
ATMPK6_A -----
ATMPK10_A -----
Cqu_c04092_1_g0 -----
Cqu_c06022_1_g0 -----
Cqu_c03819_1_g0 -----
Cqu_c04159_1_g0 -----
ATMPK3_A -----
Cqu_c03402_1_g0 -----
Cqu_c03736_1_g0 -----
ATMPK12_B -----
ATMPK4_B -----
ATMPK5_B -----
Cqu_c17078_1_g0 -----
ATMPK1_C -----
Cqu_c02858_1_g0 -----
ATMPK7_C -----
ATMPK2_C -----
ATMPK14_C -----
ATMPK8_D -ETAEESSDV ERRAAAASVAS T----- L
Cqu_c08055_1_g0 -DANENNDME NRAVARTALE S----- P
ATMPK15_D -ETVEERSND IERRTTAAVA S----- T
ATMPK9_D -ENGSHNHDI ENRSIASLVT T----- L
ATMPK18_D -QPNLGATDS RRVSEFESKN GASSAGHPST SAYPTKSIGP PPRVPP---S
ATMPK20_D -GQPKLMNNT NTLNPETTQN IP---FNHA TIQA---Q QRNLS---A
ATMPK19_D -QPSLNASDS RRVSEIEPSRN GV---VPST SAYSTKPLGP PPRVP---S
Cqu_c06169_1_g0 -LASSHKDHQ AKEEMRPSES YG---NLSS SIR---Q PPRVPP---A
Cqu_c03735_1_g0 -GI IALLEDLN LLINGDPQMI PSLGKHIPVQ EAGNQTKVFG YYRFPPLNQR
ATMPK16_D -AQQSSAEVT DGLSKCSIRD ERPRGADRNA QMPMSRIPIN VPQTIQGA AV
Cqu_c07086_1_g0 --HGSTEVT EDLSKCRICE VEKAHVDRNG AIPMTRLPLQ VPQNVO---GAA
Cqu_c09059_1_g0 -NLSSSIRQP PRVPP----- A
ATMPK17_D -DEGSDSVHA QSSASVVFT P----- P
Cqu_c04094_1_g0 -----
Cqu_c01012_1_g0 -----
Cqu_c14619_1_g0 -VOGAAARPG RF-----
Cqu_c03126_1_g0 -----
Cqu_c01012_1_g0 -----
Consistency 0000000000 0000000000 0000000000 0000000000 0000000000

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..... 710..... 720..... 730..... 740..... 750

```

ATMPK11_B -----
ATMPK13_B -----
ATMPK6_A -----
ATMPK10_A -----
Cqu_c04092_1_g0 -----
Cqu_c06022_1_g0 -----
Cqu_c03819_1_g0 -----
Cqu_c04159_1_g0 -----
ATMPK3_A -----
Cqu_c03402_1_g0 -----
Cqu_c03736_1_g0 -----
ATMPK12_B -----
ATMPK4_B -----
ATMPK5_B -----
Cqu_c17078_1_g0 -----

```

ATMPK1_C	-----	-----	-----	-----	-----
Cqu_c02858_1_g0	-----	-----	-----	-----	-----
ATMPK7_C	-----	-----	-----	-----	-----
ATMPK2_C	-----	-----	-----	-----	-----
ATMPK14_C	-----	-----	-----	-----	-----
ATMPK8_D	ESEE	AD	NGGGYS	ARNLMKSASI	SGSKCIG
Cqu_c08055_1_g0	PKSN	ADGSENEVP	QNGQNKGNYS	ARSLKKSASI	SGSKCIG
ATMPK15_D	LDSP	KASQQAE	TENGGGGYS	ARNLMKSSSI	SGSKCIG
ATMPK9_D	ESPP	TSQHEGSDY	RNGTSQTGYS	ARSLKKSASI	SASKCIG
ATMPK18_D	GRPGRVV	ESSVSYENG	RNLKEAYFRS	AVSSPHCYF	RPNTMTNPEN
ATMPK20_D	AKPSTFM	GPVAPFDNG	RISRDAYDP	RSFIRSTNL	PFSQQSAATV
ATMPK19_D	GKPGRVV	ESSVTYEND	RNLKESSYDA	RTSYRSTVL	PPQTVSPNCY
Cqu_c06169_1_g0	ARPGRVV	GPVVAYESG	RSMKDG YDA	RVSLQNAVI	PPQTASPQYY
Cqu_c03735_1_g0	SDFEKYALCS	PGLQYAFEAD	KCLNKSFADS	YHNFDFPPTH	ANDNLRPIAN
ATMPK16_D	ARPGKVV	GSVLRYNNC	GAATGVEAL	EQQRRMVRN	PAAASQYPKR
Cqu_c07086_1_g0	ARPGKVV	GNLMRYNNC	GVAATAEVT	DRRPRNPSI	PASQFPTPSS
Cqu_c09059_1_g0	ARPGRVV	GPVAYESG	RSMKDG YD	ARVSLQNAVI	PPQTASPQYY
ATMPK17_D	QTPNTAT	GLSSQKASQ	VDKAATPVKR	SACLMRSDSI	CASRCVG
Cqu_c04094_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	-----	-----
Cqu_c14619_1_g0	-----	-----	-----	-----	SETLCVI
Cqu_c03126_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	-----	-----
Consistency	0000000000	0000000000	0000000000	0000000000	0000000000

. 760 770 780 790 800

ATMPK11_B	-----	-----	-----	-----	-----
ATMPK13_B	-----	-----	-----	-----	-----
ATMPK6_A	-----	-----	-----	-----	-----
ATMPK10_A	-----	-----	-----	-----	-----
Cqu_c04092_1_g0	-----	-----	-----	-----	-----
Cqu_c06022_1_g0	-----	-----	-----	-----	-----
Cqu_c03819_1_g0	-----	-----	-----	-----	-----
Cqu_c04159_1_g0	-----	-----	-----	-----	-----
ATMPK3_A	-----	-----	-----	-----	-----
Cqu_c03402_1_g0	-----	-----	-----	-----	-----
Cqu_c03736_1_g0	-----	-----	-----	-----	-----
ATMPK12_B	-----	-----	-----	-----	-----
ATMPK4_B	-----	-----	-----	-----	-----
ATMPK5_B	-----	-----	-----	-----	-----
Cqu_c17078_1_g0	-----	-----	-----	-----	-----
ATMPK1_C	-----	-----	-----	-----	-----
Cqu_c02858_1_g0	-----	-----	-----	-----	-----
ATMPK7_C	-----	-----	-----	-----	-----
ATMPK2_C	-----	-----	-----	-----	-----
ATMPK14_C	-----	-----	-----	-----	-----
ATMPK8_D	VQSKTDKEDT	IAEEEDNETV	AELTDKVASL	HNS	-----
Cqu_c08055_1_g0	VQSRKDPEEE	PIAENEEAV	DELTKKATAL	AT	-----
ATMPK15_D	VQSKTNIED	SIVEEQD	ETVAVKVASL	HNS	-----
ATMPK9_D	MKPRNKSEYG	ESNNDTV	DALSQKVAAL	HT	-----
ATMPK18_D	RNIEASSFPP	KPQNPVHQ	FSPTEPP	AATTNQADVE	TMNHPNPYFQ
ATMPK20_D	AMGKQQERRT	TMEPE	KQARQIS	QYNRYAPDVA	INIDNNPFIM
ATMPK19_D	FLPNTMNQEK	RSGTEAAS	QPKPQFV	PTQCNSAKP	AELNPNPYVQ
Cqu_c06169_1_g0	IRPNIQPAQS	KPGLGAGNEQ	GHVSWAKQQQ	LPVQPTHEVT	IDINTNPHYH
Cqu_c03735_1_g0	FLHMNNSMAW	FHQVKAVAAT	VAKYFTGPLL	PRRSLLATQL	IREFFFPLLS
ATMPK16_D	TQPCKSNRGD	EDCATAAEGP	SRLKPN	QYIPQKVSAA	QDTAMSRWY
Cqu_c07086_1_g0	SYPKRNPCK	NERGEDDSME	GSNGLQPK	QYLARKVAAA	QAGPGSQWY
Cqu_c09059_1_g0	IRPNIQPAQS	KPGLGAGNEQ	GHVSWAKQQQ	LPVQPTHEVT	IDINTNPHYH
ATMPK17_D	VSSAVS	-----	-----	-----	-----
Cqu_c04094_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	-----	-----
Cqu_c14619_1_g0	NNCGVAATAE	VTDRRPGEIH	RYLPLNSLHL	PKPQYLARKV	AAAQAGP
Cqu_c03126_1_g0	-----	-----	-----	-----	-----
Cqu_c01012_1_g0	-----	-----	-----	-----	-----
Consistency	0000000000	0000000000	0000000000	0000000000	0000000000

. 810 820 830 840 850

ATMPK11_B	-----	-----	-----	-----	-----
ATMPK13_B	-----	-----	-----	-----	-----
ATMPK6_A	-----	-----	-----	-----	-----
ATMPK10_A	-----	-----	-----	-----	-----
Cqu_c04092_1_g0	-----	-----	-----	-----	-----
Cqu_c06022_1_g0	-----	-----	-----	-----	-----
Cqu_c03819_1_g0	-----	-----	-----	-----	-----
Cqu_c04159_1_g0	-----	-----	-----	-----	-----

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ATMPK3_A -----
Cqu_c03402_1_g0-----
Cqu_c03736_1_g0-----
ATMPK12_B -----
ATMPK4_B -----
ATMPK5_B -----
Cqu_c17078_1_g0-----
ATMPK1_C -----
Cqu_c02858_1_g0-----
ATMPK7_C -----
ATMPK2_C -----
ATMPK14_C -----
ATMPK8_D -----
Cqu_c08055_1_g0-----
ATMPK15_D -----
ATMPK9_D -----
ATMPK18_D PQLPKTDQLN NNTHMAIDAK LLQAQ-----SQFG-PAG AA---AVAVA
ATMPK20_D ARTGMNKAEN ISDRIIDTN LLQAT-----AGIG-VAA AAAAAAPGGS
ATMPK19_D SQH-----KVGIDAK LLHAQ-----SQYG-PAG AA---AVAVA
Cqu_c06169_1_g0PQPKSDQ---YSSRVALDAK IMQAQ-----S-QFS AT---AVAMS
Cqu_c03735_1_g0ASPPVTNPNT HTEALAAALAQ THIQMFIGHP YLSQFGHPVG SGPFWAFRPI
ATMPK16_D -----
Cqu_c07086_1_g0-----
Cqu_c09059_1_g0PQPKSDQ---YSSRVALDAK IMQAQS-----QFS AT---AVAMS
ATMPK17_D -----
Cqu_c04094_1_g0-----
Cqu_c01012_1_g0-----
Cqu_c14619_1_g0-----GSQGTKCT YLQFW-----
Cqu_c03126_1_g0-----
Cqu_c01012_1_g0-----
Consistency 0000000000 0000000000 0000000000 0000000000 0000000000

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..... 860..... 870.....

```

ATMPK11_B -----
ATMPK13_B -----
ATMPK6_A -----
ATMPK10_A -----
Cqu_c04092_1_g0-----
Cqu_c06022_1_g0-----
Cqu_c03819_1_g0-----
Cqu_c04159_1_g0-----
ATMPK3_A -----
Cqu_c03402_1_g0-----
Cqu_c03736_1_g0-----
ATMPK12_B -----
ATMPK4_B -----
ATMPK5_B -----
Cqu_c17078_1_g0-----
ATMPK1_C -----
Cqu_c02858_1_g0-----
ATMPK7_C -----
ATMPK2_C -----
ATMPK14_C -----
ATMPK8_D -----
Cqu_c08055_1_g0-----
ATMPK15_D -----
ATMPK9_D -----
ATMPK18_D AHRNIGTISY -SAAS-----
ATMPK20_D AHRKVGAVRY -GMSKMY-----
ATMPK19_D AHRNIGAVGY -GMS-----
Cqu_c06169_1_g0AHRNVGTVQY -GMS-----
Cqu_c03735_1_g0AKSEVDDSSY LSLSRCVKRL MKYKE
ATMPK16_D -----
Cqu_c07086_1_g0-----
Cqu_c09059_1_g0AHRNVGTVQY -GMS-----
ATMPK17_D -----
Cqu_c04094_1_g0-----
Cqu_c01012_1_g0-----
Cqu_c14619_1_g0-----QTR LPIHSLLGRL WLRTG
Cqu_c03126_1_g0-----
Cqu_c01012_1_g0-----
Consistency 0000000000 0000000000 000000

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Additional supplemental data

GyrA, *CheA* sequences of quinoa endophytic bacteria

>*GyrA* partial sequence

```
AGCGTTATCGTATCCCGGGCGCTTCCGGATGTGCGTGACGGTCTGAAGCCGGTTCACAGA
CGGATTTTTGTACGCGATGAATGATTTAGGCATGACCAGTGACAAACCATATAAAAAATCT
GCCCCGTATCGTCGGTGAAGTTATCGGTAAGTACCACCCGCACGGTGACTCAGCGGTTTAC
GAATCAATGGTCAGAATGGCGCAGGATTTTAAACAACCGCTACATGCTTGTTGACGGACAC
GGCAACTTCGGTTCGGTTGACGGCGACTCAGCGGCCGCGATGCGTTACACAGAAGCGAGA
ATGTCAAAAATCGCAATGGAAATCCTCCGGGACATTACGAAAGATACGATTGATTATCAA
GATAACTATGACGGCGCAGAAAGAGAACCTGTCTCATGCCTTCGAGATTTCCGAATCTG
CTCGTCAACGGAGCTGCCGGTATCGCGGCCGGAATGGCGACAAATATTCTCCGCATCAG
CTTGGGGAAGTCATTGAAGGGCGTGCTTGCCGTAAG
```

>*CheA* partial sequence

```
GGAAGGAGATGGTGCAGTCCATTATTGACGGAGGAGACGGCAAACGTGATATTTCTGAAG
TGAGTGCGAAGCTCGACGTAAATGCGGTGCATGAGACTGCGGCTTCAGCCGAAACAGCAG
AACCGCCGGCTTCAAAAACAACAGGCTTCAACTGAATGGAATTATGATGAGTTCGAACGGA
CTGTTATTGAAGAGGCGGAAGAGCAAGGATTCAGCCGCTATGAAATAACGGTTTCCCTGA
ATGAAAGCTGCATGCTCAAAGCCGTGCGCGTGTACATGATATTTGAAAAGCTGAATGAAG
CCGGGGAAGTCGAAAAACGATACCCGCCGCGGAAGTGCTTGAGACGGAAGATTTTCGAA
CGGATTTTTCAGGTGTGTTTCTTAACAAAGC
```

List of primers used in colony PCRs

Flg_fo	ATGAGAATTAACCACAATAT	(Asano et al. 2001)
Flg_re	GTTGGTTTGCTTGAGCAAGC	
PeBA1_fo	ATGGCTAACCAGAAGAAGAAAAC	(Wang et al. 2016).
PeBA1_re	TTATCCGTTTACGATGGTGTC	
BmyD_fo	GCTCTTGATGACCTTCTCTGCG	(Xu et al. 2013)
BmyD_re	ATTTTGTGCGATTGGTTCTGTT	
GyrA_fo	CAGTCAGGAAATGCGTACGTCCCTT	(Reva et al. 2004)
GyrA_re	CAAGGTAATGCTCCAGGCATTGCT	
CheA_fo	AGGGCTGCCCATACATTAAGGAATGAGC	
CheA_re	AGTTTCAACCGGGACCATTCTCATATTCAG	

Asano Y, Onishi H, Tajima K, Shinozawa T (2001) Flagellin as a biomarker for *Bacillus subtilis* strains; Application to the DB9011 strain and the study of interspecific diversity in amino-acid sequences. *Biosci Biotech Bioch* 65: 1218-1222. doi: DOI 10.1271/bbb.65.1218.

Reva ON, Dixelius C, Meijer J, Priest FG (2004) Taxonomic characterization and plant colonizing abilities of some bacteria related to *Bacillus amyloliquefaciens* and *Bacillus subtilis*. *FEMS microbiology ecology* 48: 249-259. doi: 10.1016/j.femsec.2004.02.003.

Wang N, Liu M, Guo L, Yang X, Qiu D (2016) A Novel Protein Elicitor (PeBA1) from *Bacillus amyloliquefaciens* NC6 Induces Systemic Resistance in Tobacco. *International Journal of Biological Sciences* 12: 757-767. doi: 10.7150/ijbs.14333.

Xu Z, Shao J, Li B, Yan X, Shen Q, Zhang R (2013) Contribution of bacillomycin D in *Bacillus amyloliquefaciens* SQR9 to antifungal activity and biofilm formation. *Applied and environmental microbiology* 79: 808-815. doi: 10.1128/AEM.02645-12.

