

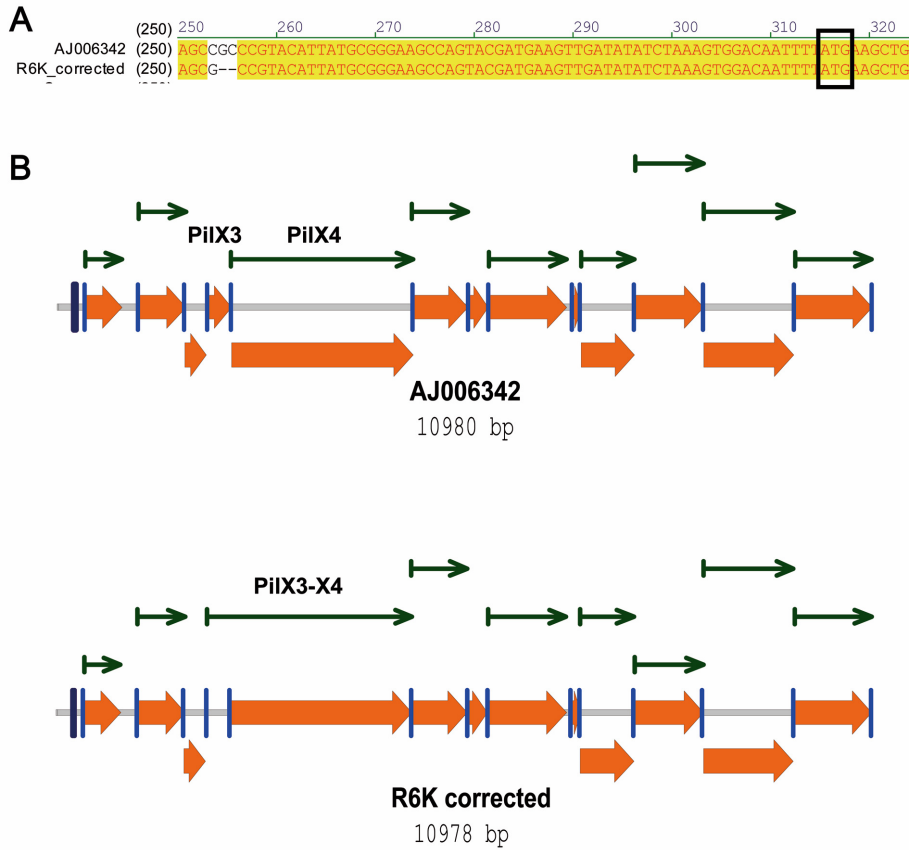
SUPPLEMENTARY DATA

Supplementary Figure 1

A	1	MGAIESRKLL	ASET	PVGQFI	PYSH	HVTDTI	ISTK	NAEYLS	VWKIDGRSHQ		
	51	SASEADVFQW	IRELNNTLRG	ISSAN	LSLWT	HIVRRR	VYEY	PDAEFDNVFC			
	101	RQLDEKYRES	FTGYNLMVND	LYLTVVYRPV	SDKVLSFFAK	RERET	PDQKK				
	151	HRQES	CIKAL	EDINR	TILGQS	FKRYG	AELLS	VYEKGGHAFS	APLEFLARLV		
	201	NGEHIPMPIC	RDRFSDYMAV	NRPMF	SKWGE	VGELR	SLTGL	RRFG	MLEIRE		
	251	YDDATE	PGQL	NVLLES	DYEF	VLTHS	FSVLS	RPAAKE	YLQR	HQKN	LIDARD
	301	VATDQIEEID	EALNQLISGH	FVMGE	HHCTL	TVYGETVQOV	RDNLAHASAA				
	351	MLDVA	VLPKP	VDLAL	EAGYW	AQLPA	NWQWR	PRPAP	ITSLN	FLSFS	PFHNF
	401	MSGK	PTGNPW	GPAVT	IILK	TV	SGTPLYFNFH	ASKEEEDATD	KRLLGNTMLI		
	451	GQSSSGKTVL	LGFLLAQAQK	FKPTIVAFDK	DRGMEISIRA	MGGRYLPLKT					
	501	GEP	SGFNPFQ	LPPT	HANLIF	LKQFVKKLAA	AGGEVTHRDE	EEIDQAITAM			
	551	MSDSIDKSLR	RLSLLLQFLP	NPRSDDMDAR	PTVHARLVKW	CEGGDYGWLF					
	601	DNPTDALDLS	THQIYGF	DIT	EFLDNPEART	PVMYLLYRT	ESMIDGRRFM				
	651	YVFDE	FWKPL	QDEYF	FEDLAK	NKQKT	IRKQN	GIFVF	FATQEP	SDALE	SNIAK
	701	TLIQQC	ATYI	FLANPKADYE	DYTQGFKLTD	SEFELVRGLG	EFSRRFLIKQ				
	751	GDQSALAEMN	LGKFR	TIVDG	ETVERDFDDE	LLVLSGTPDN	AEIAESIIAE				
801	VGDDP	AVWLP	IFLDR	VKAER	SDV						
B	1	MGAIESRKLL	ASET	PVGQFI	PYSH	HVTDTI	ISTK	NAEYLS	VWKIDGRSHQ		
	51	SASEADVFQW	IRELNNTLRG	ISSANLSLWT	HIVRRRVY EY	PDAEFDNVFC					
	101	RQLDEKYRES	FTGYNLMVND	LYLTVVYRPV	SDKVLSFFAK	RERETPDQKK					
	151	HRQESCIKAL	EDINRNLGQS	FKRYGAELLS	VYEKGGHAFS	APLEFLARLV					
	201	NGEHIPMPIC	RDRFSDYMAV	NRPMF	SKWGE	VGELR	SLTGL	RRFG	MLEIRE		
	251	YDDATEPGQL	NVLLES	DYEF	VLTHS	FSVLS	RPAAKE	YLQR	HQKN	LIDARD	
	301	VATDQIEEID	EALNQLISGH	FVMGEHHCTL	TVYGETVQOV	RDNLAHASAA					
	351	MLDVA	VLPKP	VDLAL	EAGYW	AQLPA	NWQWR	PRPAP	ITSLN	FLSFS	PFHNF
	401	MSGKPTGNPW	GPAVTIILK	TV	SGTPLYFNFH	ASKEEEDATD	KRLLGNTMLI				
	451	GQSSSGKTVL	LGFLLAQAQK	FKPTIVAFDK	DRGMEISIRA	MGGRYLPLKT					
	501	GEP	SGFNPFQ	LPPT	HANLIF	LKQFVKKLAA	AGGEVTHRDE	EEIDQAITAM			
	551	MSDSIDKSLR	RLSLLLQFLP	NPRSDDMDAR	PTVHARLVKW	CEGGDYGWLF					
	601	DNPTDALDLS	THQIYGF	DIT	EFLDNPEART	PVMYLLYRT	ESMIDGRRFM				
	651	YVFDEFWKPL	QDEYFEDLAK	NKQKTIRKQN	GIFVFATQEP	SDALESNIAK					
	701	TLIQQC	ATYI	FLANPKADYE	DYTQGFKLTD	SEFELVRGLG	EFSRRFLIKQ				
	751	GDQSALAEMN	LGKFR	TIVDG	ETVERDFDDE	LLVLSGTPDN	AEIAESIIAE				
801	VGDDP	AVWLP	IFLDR	VKAER	SDV						

Supplementary Figure 1. Tandem Mass Spectrometry of TrwK. Selected protein bands were excised manually from the gel and subjected to in-gel digestion with trypsin and analyzed by LC-MS/MS. Obtained spectra were processed using ProteinLynx Global Server and searched against NCBI databases using MASCOT search engine. Amino acid sequences of the bands with MW_{app} 94 kDa (Panel A) and MW_{app} of 80 kDa (Panel B) in the SDS-PAGE (Fig.1) were identified by peptide fragment fingerprinting as *E. coli* TrwK. Comparison of sequence coverage in Panels A and B shows that fragment B is missing peptides in its N-terminus, suggesting a cleavage site of the protein in aac. 173.

Supplementary Figure 2



Supplementary Figure 2. PilX3-PilX4 gene fusion in R6K. The intergenic region between PilX3 and PilX4 in R6K (accession number AJ006342) was sequenced. An error was found resulting in a bad annotation of the R6K genome (*Panel A*). As a result two genes were annotated instead of only one (*Panel B*). The ATG codon (boxed in Panel A) indicates the N-terminus of PilX4 in previous annotations.