

S3 Table. Plasmid list

Plasmid	Relevant characteristics	Reference
pUC18	Cloning vector; Ap ^r	[4]
pBAD2- <i>gfp</i>	<i>gfp</i> reporter gene vector, Ap ^r , Gen ^r , <i>araC</i> , P _{BAD} promoter	[5]
pBAD2- <i>bgaB</i> -His	<i>bgaB</i> reporter gene vector, Ap ^r , <i>araC</i> , P _{BAD} promoter, His-Tag at the C-terminal of BgaB	[6]
pFU53	<i>luxCDABE</i> reporter gene vector, Ap ^r ; pSC101*	[7]
pJNS02	Ap ^r , pSC101*, promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from ATG of <i>cnfY</i>) fused to <i>luxCDABE</i> operon, transcriptional fusion	[2]
pJNS10	<i>cnfY</i> complementation vector; promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus coding region of <i>cnfY</i> , Ap ^r , pSC101*	[2]
pJNS11	empty vector (<i>cnfY</i> complementation), Ap ^r , pSC101*	[2]
pBO3146	pBAD2- <i>bgaB</i> -His; ICR between pYV0075(<i>yscW</i>) and pYV0076(<i>lcrF</i>) plus 9 bp of <i>lcrF</i> coding region (-123 to +9 bp from <i>lcrF</i> ATG)	[6]
pBO3190	pUC18; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant TT48,49AA	[6]
pBO3192	pBAD2- <i>bgaB</i> -His; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG)	[6]
pBO4449	pBAD2- <i>bgaB</i> -His; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R1+2 ATCAG29-33TCCT	This study
pBO4465	pUC18; YPK_2615 (<i>cnfY</i>) RNAT plus coding region (-82 to +80 bp from <i>cnfY</i> ATG); runoff plasmid for structure probing and primer extension inhibition	This study
pBO4466	pUC18; YPK_2615 (<i>cnfY</i>) 5' UTR plus coding region (-82 to +80 bp from <i>cnfY</i> ATG), mutant R1+2 ATCAG29-33TCCT; runoff plasmid for structure probing and primer extension inhibition	This study
pBO4477	pBAD2- <i>gfp</i> ; ICR between pYV0075(<i>yscW</i>) and pYV0076(<i>lcrF</i>) plus 9 bp of <i>lcrF</i> coding region (-123 to +9 bp from <i>lcrF</i> ATG)	This study
pBO4478	pBAD2- <i>gfp</i> ; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant TT48,49AA	This study
pBO4481	pBAD2- <i>gfp</i> ; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG)	This study
pBO4493	pEX-K168 (Eurofins Genomics, Ebersberg, Germany); promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus <i>cnfY</i> coding region (-82 to +117 bp from <i>cnfY</i> ATG), mutant R1 AG32	This study
pBO4494	pEX-K168 (Eurofins Genomics, Ebersberg, Germany); promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus <i>cnfY</i> coding region (-82 to +117 bp from <i>cnfY</i> ATG), mutant R1+2 ATCAG29-33TCCT	This study
pBO4499	pJNS10; exchange of promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus plus <i>cnfY</i> coding region (-82 to +117 bp from <i>cnfY</i> ATG) in pJNS10 against Gen ^R cassette	This study
pBO4610	pBAD2- <i>bgaB</i> -His; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R1 AG32 33CT	[6]
pBO4611	pBAD2- <i>bgaB</i> -His; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R2 A29Δ	[6]
pBO6500	pFU53; promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from ATG of <i>cnfY</i>); translational fusion	This study
pBO6501	pFU53; promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from ATG of <i>cnfY</i>), mutant R1 AG32; translational fusion	This study
pBO6502	pFU53; promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from ATG of <i>cnfY</i>), mutant R1+2 ATCAG29-33TCCT; translational fusion	This study
pBO6503	pJNS10-R1; exchange of Gen ^R cassette in pBO4499 against promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus <i>cnfY</i> coding region (-82 to +117 bp from <i>cnfY</i> ATG), mutant R1 AG32	This study
pBO6504	pJNS10-R1+2; exchange of Gen ^R cassette in pBO4499 against promoter region of YPK_2615 (<i>cnfY</i>) plus 5' UTR of <i>cnfY</i> plus <i>cnfY</i> coding region (-82 to +117 bp from <i>cnfY</i> ATG), mutant R1+2 ATCAG29-33TCCT	This study

pBO6505	pBAD2- <i>gfp</i> ; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R1 AG32 33CT	This study
pBO6506	pBAD2- <i>gfp</i> ; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R2 A29Δ	This study
pBO6507	pBAD2- <i>gfp</i> ; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant R1+2 ATCAG29-33TCCT	This study
pBO6523	pBAD2- <i>bgaB</i> -His; YPK_2615 (<i>cnfY</i>) RNAT plus 30 bp of <i>cnfY</i> coding region (-82 to +30 bp from <i>cnfY</i> ATG), mutant T26C	This study
pBO6524	<i>EcoRI</i> (GAATTC) -> <i>SacI</i> (GAGCTC) replacement in pBAD2- <i>bgaB</i> -His	This study
pBO6527	pBO6524; 5'-UTR of YPK_2615 (<i>cnfY</i>) plus 30 bp of <i>cnfY</i> coding region (-266 to +30 bp from <i>cnfY</i> ATG)	This study
pBO6528	pBAD2- <i>bgaB</i> -His; 5'-UTR of YPK_2615 (<i>cnfY</i>) plus 30 bp of <i>cnfY</i> coding region (-266 to +30 bp from <i>cnfY</i> ATG)	This study