

Supplementary information

Table S1. Strains used in this work

Strain	Genotype	Description
NCM3722	wild-type <i>E. coli</i> K-12 strain	wild-type <i>E. coli</i> K12 strain
CY325	$\Delta gcvB$	<i>gcvB</i> deletion in NCM3722
CY713	wild-type <i>E. coli</i> K-12 strain	repaired NCM3722 with wild-type <i>fliC</i>
CY1027	$\Delta gcvB::cat$	<i>gcvB</i> deletion in CY713
CY1038	$\Delta oxyR::cat$	<i>oxyR</i> deletion in CY713
CY454	<i>oxyR-myc-stop codon-kan</i>	<i>oxyR-myc</i> constructed in NCM3722
CY455	<i>oxyR-myc-stop codon-kan</i> $\Delta gcvB$	<i>oxyR-myc</i> constructed in CY325
CY1042	$\Delta gcvB oxyR::cat$	<i>oxyR</i> and <i>gcvB</i> double deletion strain
CY1037	<i>kan::P1oxyR-lacZ</i> $\Delta oxyR::cat$	P1 <i>oxyR-lacZ</i> translational fusion constructed in the <i>gcvB</i> wild-type background CY1057
CY1041	<i>kan::P1oxyR-lacZ</i> $\Delta oxyR::cat$ $\Delta gcvB$	P1 <i>oxyR-lacZ</i> translational fusion constructed in the <i>gcvB</i> knockout background CY1042
CY1047	<i>kan::P3oxyR-lacZ</i> $\Delta gcvB$ $\Delta oxyR::cat$	P3 <i>oxyR-lacZ</i> transcriptional fusion constructed in the <i>gcvB</i> knockout background CY1042
CY1052	<i>kan::P3oxyR-lacZ</i> $\Delta oxyR::cat$	P3 <i>oxyR-lacZ</i> transcriptional fusion constructed in the <i>gcvB</i> wild-type background CY1057
CY1057	$\Delta oxyR::cat$	<i>oxyR</i> deletion in NCM3722 background
CY1059	<i>kan::P2oxyR-lacZ</i> $\Delta oxyR::cat$	P2 <i>oxyR-lacZ</i> translational fusion constructed in the <i>gcvB</i> wild-type background CY1057
CY1060	<i>kan::P2oxyR-lacZ</i> $\Delta oxyR::cat$ $\Delta gcvB$	P2 <i>oxyR-lacZ</i> translational fusion constructed in <i>gcvB</i> knockout background CY1042

Table S2. Primers used for RT-qPCR

Primers	Sequences
<i>flu</i> -F	AACCGGGACAGTGATGAGAG
<i>flu</i> -R	AGACGGACGCTGTTGTTTTTC
<i>yeeR</i> -F	TCATGAAACTGCCGGAAACC
<i>yeeR</i> -R	GGATTTCTGTTCCGCTGACC
<i>oxyR</i> -F	CTGATGCTGGAAGATGGTCA
<i>oxyR</i> -R	AGCGCTGGCAGTAAAGTGAT
<i>recA</i> -F	GTGCGTTTATCGATGCTGAAC
<i>recA</i> -R	CACAGATTTCCAGTGCCTGCT

Table S3. DEGs identified between the *gcvB* knockout and wild-type strains.

ID	Symbol	EXP _{WT}	EXP _{CY325}	Log2(FC)	<i>q</i> -value (FDR)
AA953_RS06745	<i>fhuC</i>	329.9075	142.12	-1.23433	7.49E-08
AA953_RS06750	<i>fhuD</i>	304.025	134.6325	-1.2105	1.04E-07
AA953_RS06755	<i>fhuB</i>	156.0425	77.0725	-1.05673	0.000417
AA953_RS16720	<i>flu</i>	44.44	2769.188	5.985994	2.09E-46
AA953_RS16725	<i>yeeR</i>	23.0725	104.1275	2.201021	7.12E-06

DEGs: differentially expressed genes
EXP_{WT} and EXP_{CY325} respectively indicate gene expression (FPKM) in wild-type NCM3722 and the *gcvB* deletion strain CY325.
FC: Fold change.

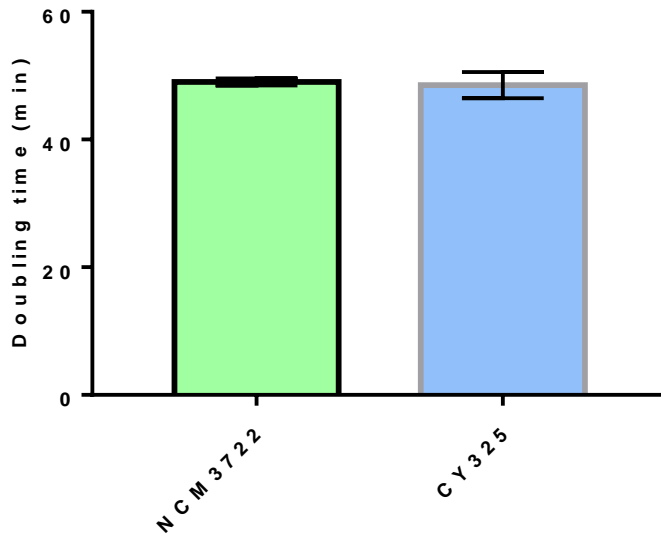
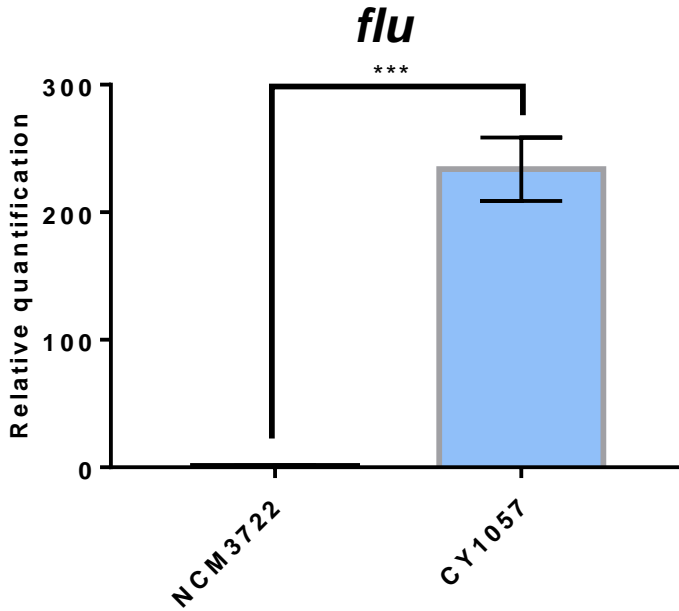


Figure S1. Doubling time of NCM3722 (WT) and CY325 ($\Delta gcvB$) grown in glucose minimal medium.

Doubling time of each strain is expressed as average \pm S.D. of three independent cultures.

(A)



(B)

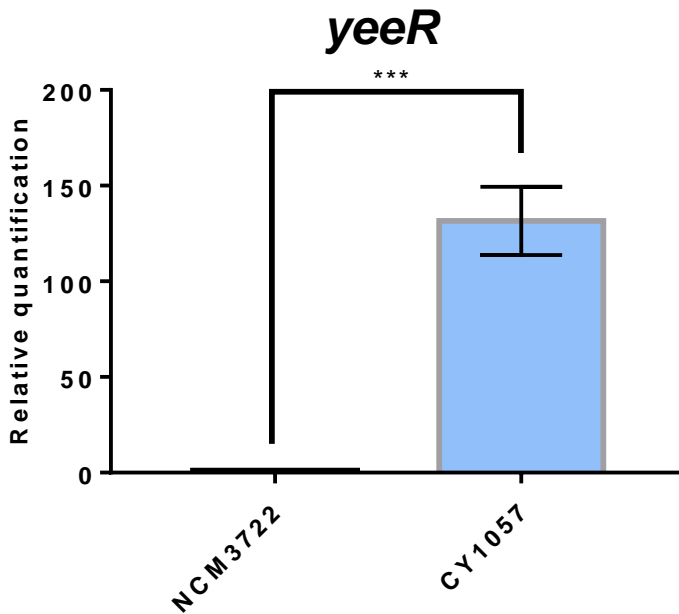


Figure S2. Gene expression of *flu* and *yeeR* in the *oxyR* wild-type and knockout strains.
A-B. Gene expression of *flu* and *yeeR* detected by RT-qPCR in the *oxyR* knockout strain CY1057 and in the wild-type strain NCM3722 grown in glucose minimal medium. The mRNA level of each gene in NCM3722 was normalized to 1 and that in CY1057 was determined relative to this value. The relative expression was shown as the average \pm S.D. of three independent experiments. *** $P < 0.001$ by student t-test.

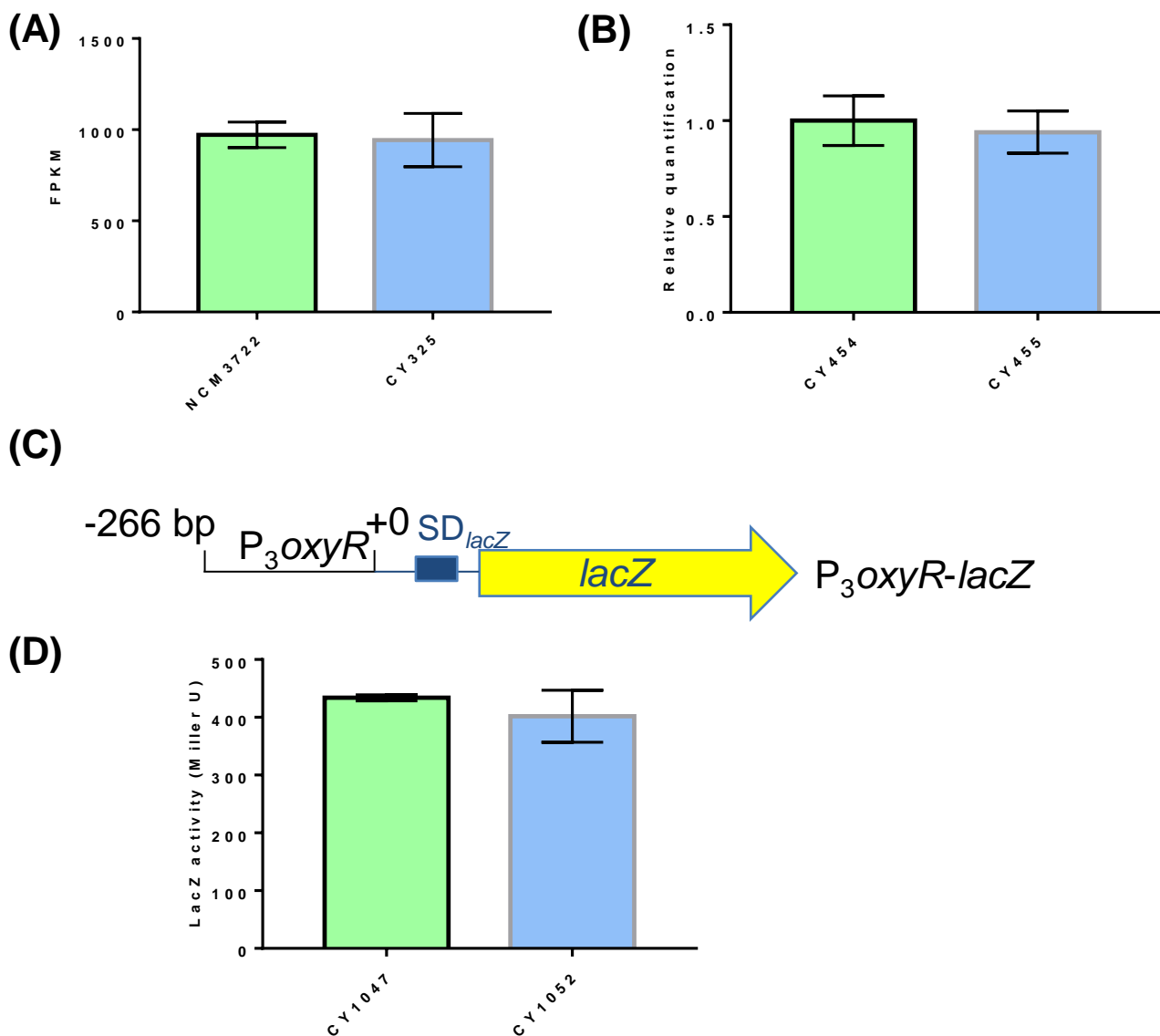


Figure S3. Transcriptional expression of *oxyR*.

A. The FPKM values of *oxyR* expression in the wild-type strain NCM3722 and in the *gcvB* knockout strain CY325 obtained by RNAseq. The FPKM values are shown as the average \pm S.D. of two RNAseq assays. **B.** Gene expression of *oxyR* detected by RT-qPCR in the *gcvB* knockout (CY455) and wild-type (CY454) strains grown in glucose minimal medium. The mRNA level of each gene in CY454 was normalized to 1 and that in CY455 was determined relative to this value. The relative expression was shown as the average \pm S.D. of three independent experiments. **C.** Composition diagram of the promoter of *oxyR* with *lacZ* transcriptional fusion. P_3oxyR covers the DNA region from -266 bp to 0 bp relative to *oxyR* translational start point. SD_{lacZ} indicates the ribosome binding site of *lacZ*. Yellow arrow indicates the entire coding region of *lacZ*. **D.** β -galactosidase activities of $P_3oxyR-lacZ$ fusion in the *gcvB* wild-type (CY1052) and knockout strains (CY1047). The LacZ activity was shown as the average \pm S.D. of three independent experiments.