fermentation

MDPI

Article

The Effect of *E. coli* Uridine-Cytidine Kinase Gene Deletion on Cytidine Synthesis and Transcriptome Analysis

Table S1. Plasmids and strains used in this experiment.

	Description	Source
Strains		
E.coli K12 MG1655	Wild-type,starting strain	Lab stock
E.coli NXBG-11	*E.coli* K12 MG1655,*ΔcddΔpoxB*	Lab stock
E.coli NXBG-12	*E.coli* NXBG-11,*Δudk*	This study
Plasmids		
pCas	repA101(Ts)kan Pcas-cas9 P_{araB}-Red lacI$^{q}P_{trc}$-sgRNA-pMB1	Lab stock
pTargetF	pMB1 aadA sgRNA	Lab stock
pTargetF-*udk*	pMB1 aadA sgRNA-*udk*	This study

Table S2. Primers used in this experiment.

Primer name	Primer sequence (5′ – 3′)	Size （bp）
gRNA-*udk*-S	GTCCTAGGTATAATACTAGTGCCGACACGTTAGTGC-TACTGTTTTAGAGCTAGAAATAGC	60
gRNA-*udk*-A	TTCAAAAAAAGCACCGACTCGG	22
udk-Up-S	CCGAGTCGGTGCTTTTTTTGAAGATGGACGTCGGGAAC-CACAGTG	45
udk-Up-A	AGTCATATATTTAGCGACCTGATTAACCTGGAT	33
udk-Down-S	ATCCAGGTTAATCAGGTCGCTAAATATATGACTGAATAA-GCTTGATAAATTGTGTACCGTTCAGTGA	67
udk-Down-A	ACGCGTCGACGTGACGTGCACCATCAGCCCC	31
Reserved Basic groups	Up 6 bp，Down 6 bp，Total 12 bp	
udk-S	ATCCAGGTTAATCAGGTCG	19
udk-A	ACGCCAATTACGTCAAGG	18

Table S3. Sequencing results after *udk* knockout.

GCGCGCGGCAACGCTATTCGACTGGTATCAGACGGATGAAATCCCTATAATT-GCCGCGTTT-
**GGCGCTTCGTCGCCCCCTTCCTAAC*ATCCAGGTTAATCAGGTCGCTAAATATATG*
*ACT*GAATAAGCTTGATAAATTGTGTACCGTTCAGTGATAACCTAG-**
TATGCCCTTGAC-
GTAATTGGCGTTAAGGGAGTGATGCGCGAAAGGAGAAAATGCCAT·····

Note: The bold part in italics is the primer *udk*-Up-R for amplifying the upstream homologous arm, the curve part is the primer *udk*-Down-F for amplifying the downstream homologous arm, and the box part is the part of *udk* gene that has not been replaced (12 bp).

Table S4. Sequencing data quality control comparison results.

Sample Name	Clean Reads	Clean Bases（bp）	Clean Q20(%)	Clean Q30(%)	Clean Error Rate（%）
E.coli NXBG-11-1	28,838,430	3,778,764,509	98.71	95.84	0.0233
E.coli NXBG-11-2	29,581,342	3,907,767,386	98.69	95.81	0.0234
E.coli NXBG-11-3	28,649,950	3,775,960,309	98.7	95.88	0.0233
E.coli NXBG-12-1	28,908,080	3,774,609,345	98.9	96.25	0.0229
E.coli NXBG-12-2	29,459,504	3,859,114,392	98.87	96.2	0.023
E.coli NXBG-12-3	26,958,152	3,509,871,257	98.86	96.14	0.023

Table S5. Sequencing data quality control comparison results.

Sample Name	Total reads	Genome Mapped reads and Ratio（%）	Uniquely Mapped Reads Ratio(%)
E.coli NXBG-11-1	28,838,430	28,548,836（98.99）	97.9
E.coli NXBG-11-2	29,581,342	29,326,377（99.13）	98.2
E.coli NXBG-11-3	28,649,950	28,396,298（99.11）	98.19
E.coli NXBG-12-1	28,908,080	22,452,908（77.67）	76.35
E.coli NXBG-12-2	29,459,504	22,921,939（77.81）	76.62
E.coli NXBG-12-3	26,958,152	20,962,379（77.76）	76.62

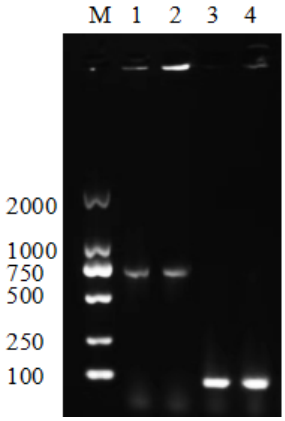

Figure S1. Verification results after the removal of *udk.*

Note: M DNA standard DL2000; Lanes 1-2 are the PCR products before *udk* knockdown (728 bp), and lanes 3-4 are the PCR products after *udk* knockout (86 bp).