

Supplementary Table S1. Primers used in this study.

Primers name	DNA Sequences (5' to 3')	Application
16s rRNA-F	GCACGTAATGGTGGGAATC	qRT-PCR
16S rRNA-R	CTCCAATCCGGACTACGACA	qRT-PCR
YZ- <i>pdeR</i> -F	TTGCCAATAACATCCTGCTCTT	qRT-PCR
YZ- <i>pdeR</i> -R	GCCTATGCCGATACTGAATC	qRT-PCR
YZ- <i>yihX</i> -F	CCGAGTGGTGGTGCTATCTA	qRT-PCR
YZ- <i>yihX</i> -R	GATTCTGGCTTCAGGTTTGC	qRT-PCR
YZ- <i>rpsN</i> -F	ACCCGAACTTCCGCAAGA	qRT-PCR
YZ- <i>rpsN</i> -R	GTGTGAACATCATCCGACGAA	qRT-PCR
YZ- <i>rpoA</i> -F	CGGCAACTATCTTGGCTGAAC	qRT-PCR
YZ- <i>rpoA</i> -R	CAGTTAGCAGAGCGGACAGT	qRT-PCR
YZ- <i>trmD</i> -F	GGCAATCCAGCAATCCATCA	qRT-PCR
YZ- <i>trmD</i> -R	GGTCGGTACGAAGGAGTTGA	qRT-PCR
YZ- <i>dhaK</i> -F	AAGTCGCACTGATGTCTGGT	qRT-PCR
YZ- <i>dhaK</i> -R	GGCTTGACCGCATTCATACA	qRT-PCR
YZ- <i>gntT</i> -F	CCTCTCCTATGCCGAGTTCT	qRT-PCR
YZ- <i>gntT</i> -R	TGTGTCCATCACCGATTCCA	qRT-PCR
YZ- <i>YE_RS15980</i> -F	GCTTCCAACAAGTGCTATCAGA	qRT-PCR
YZ- <i>YE_RS15980</i> -R	CAAACATTCTTACCGCCACAAC	qRT-PCR
YZ- <i>dusB</i> -F	GTCTGCCGAACACCGTAACT	qRT-PCR
YZ- <i>dusB</i> -R	CGTATTCGCCCTCGCCATTA	qRT-PCR
YZ- <i>corA</i> -F	GGTAACTCAACGGTGGCATT	qRT-PCR
YZ- <i>corA</i> -R	GTCCAGCAGCAACTCATAGG	qRT-PCR
YZ- <i>epmA</i> -F	CGCAGCAATAATGGCAGAGA	qRT-PCR
YZ- <i>epmA</i> -R	AATGGATGTCCGTCACTGTC	qRT-PCR
YZ- <i>trmL</i> -F	CGGCTTACCCTCCAATGTTTC	qRT-PCR
YZ- <i>trmL</i> -R	CAGGCTTCGTACACCACAAC	qRT-PCR
YZ- <i>fliE</i> -F	ACCAGCAAACAGCCCGTA	qRT-PCR
YZ- <i>fliE</i> -R	CGTCTTGATAAGCCGCTACTAA	qRT-PCR
YZ- <i>flgC</i> -F	GTTGATGTGACCGGCGAGAT	qRT-PCR
YZ- <i>flgC</i> -R	AGTGTCAGCGTCTTGAGCAT	qRT-PCR
YZ- <i>alaC</i> -F	GCCGTGGTGAAGACATCATT	qRT-PCR
YZ- <i>alaC</i> -R	CGAGGTTGAATAGCCGTGAG	qRT-PCR
YZ- <i>fyuA</i> -F	TGGCAGCAGCAGCATTATTC	qRT-PCR
YZ- <i>fyuA</i> -R	CATTGTCGGCATGTCGTAGG	qRT-PCR
YZ- <i>hypE</i> -F	CGCCACTACGCCATATTACC	qRT-PCR
YZ- <i>hypE</i> -R	TCCGCTTCGTTGATTTCAT	qRT-PCR
YZ- <i>lsrD</i> -F	TGCCTGTTGTATGCCTTGAC	qRT-PCR
YZ- <i>lsrD</i> -R	GAGCCGTACCGAGAATGGA	qRT-PCR
YZ- <i>hisJ</i> -F	ACAAGGCTCGACTCAGGAAG	qRT-PCR
YZ- <i>hisJ</i> -R	CTCACTGCCAGCGACTTCAT	qRT-PCR
<i>dkkA</i> -F	TAAGCCGCCGATCTGCTGAAT	To identify <i>ΔdkkA</i>

<i>dkkA</i> -R	GAAGTCAAGTCGGTTACCTT	To identify $\Delta dkkA$
<i>relA</i> -F	AACAGCAAATCCCCCAATTC	To identify $\Delta relA\Delta spoT$ and $\Delta dkkA\Delta relA\Delta spoT$
<i>relA</i> -R	GGTGCTCAGGCTATAGCAT	To identify $\Delta relA\Delta spoT$ and $\Delta dkkA\Delta relA\Delta spoT$

Supplementary Table S2. Statistical analysis of RNA-Seq data in the WT and mutant strains.

Sample Name	Raw Reads	Raw Bases (bp)	Clean Reads	Clean Bases (bp)	Genome Mapped Reads	Genome Mapped Ratio (%)	Unique Mapped Reads	Unique Mapped Reads Ratio (%)
WT-1	23676006	3575076906	23309948	3050093381	22844598	98.00	21828056	93.64
WT-2	24703604	3730244204	24303912	3160428673	23818997	98.00	22818158	93.89
WT-3	23510642	3550106942	23131770	3056330141	22691768	98.10	21665010	93.66
$\Delta dkkA$ -1	25354062	3828463362	24970570	3325072720	24401701	97.72	23580072	94.43
$\Delta dkkA$ -2	28460700	4297565700	28065896	3752245167	27506717	98.01	26545712	94.58
$\Delta dkkA$ -3	24358918	3678196618	24038218	3222763611	23548300	97.96	22576128	93.92
$\Delta relA\Delta spoT$ -1	28023310	4231519810	27317700	3393662150	26738618	97.88	25971514	95.07
$\Delta relA\Delta spoT$ -2	24525074	3703286174	24244748	3158094318	23764932	98.02	22970646	94.74
$\Delta relA\Delta spoT$ -3	23932950	3613875450	23658478	3110151493	23193469	98.03	22583891	95.46
$\Delta dkkA\Delta relA\Delta spoT$ -1	23258634	3512053734	22960764	3002781309	22519203	98.08	22025031	95.92
$\Delta dkkA\Delta relA\Delta spoT$ -2	26148594	3948437694	25842156	3328877730	25365103	98.15	24723192	95.67
$\Delta dkkA\Delta relA\Delta spoT$ -3	27424488	4141097688	27166778	3537542759	26584190	97.86	25769114	94.86

Supplementary Table S3. Statistical analysis of ribosome proteins biosynthesis in mutant strains compared to WT.

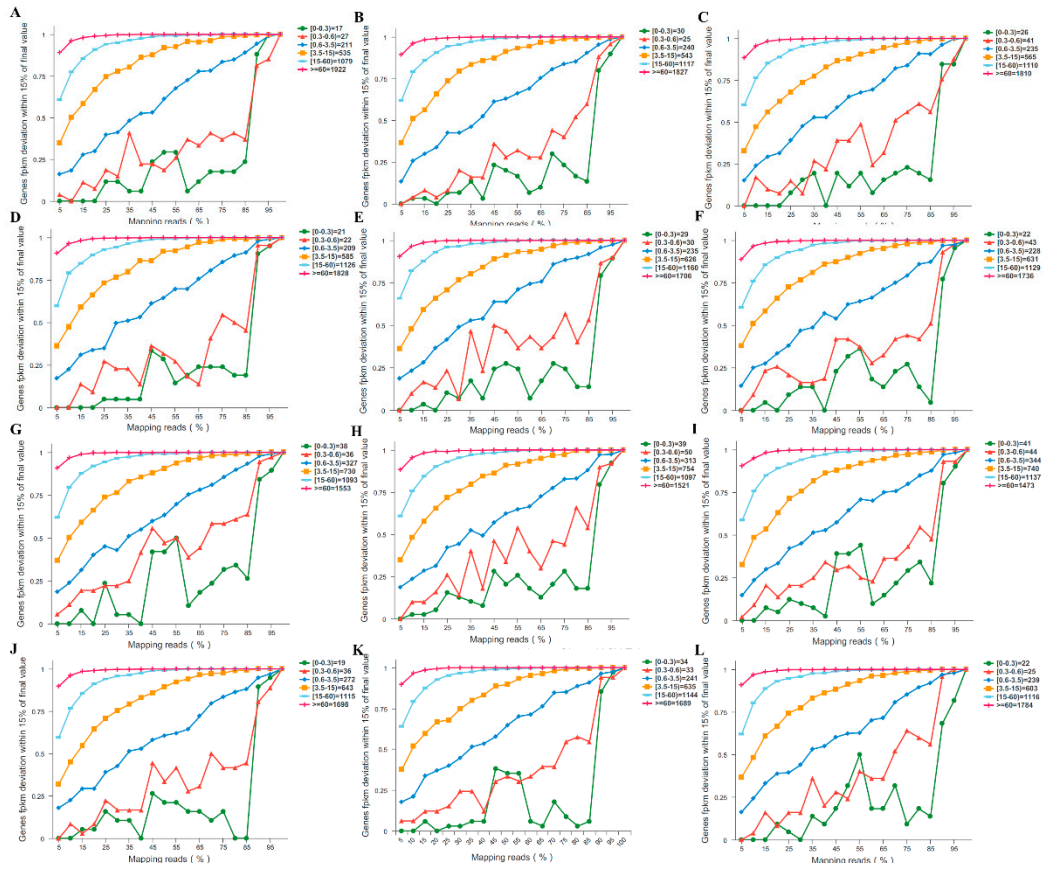
Gene ID	Gene Name	Description	FC <i>AdkkA</i> /WT	P value <i>AdkkA</i> /WT	FC <i>AreLAAspoT</i> /WT	P value <i>AreLAAspoT</i> /WT	FC <i>AdkkAArelAAspoT</i> /WT	P value <i>AdkkAArelAAspoT</i> /WT
YE_RS03125	<i>rpsT</i>	30S ribosomal protein S20	2.016	2.82E-05	5.674	4.32E-20	2.578	2.33E-08
YE_RS20925	<i>rpmH</i>	50S ribosomal protein L34	2.032	0.002101	6.358	3.43E-15	2.41	0.000259
YE_RS18770	<i>rplM</i>	50S ribosomal protein L13	2.937	3.23E-07	3.573	1.56E-12	3.147	3.23E-10
YE_RS04275	<i>rplS</i>	50S ribosomal protein L19	NS	NS	2.541	6.17E-13	NS	NS
YE_RS19585	<i>rpmD</i>	50S ribosomal protein L30	2.207	5.63E-08	2.587	5.10E-13	NS	NS
YE_RS18470	<i>rpsU</i>	30S ribosomal protein S21	2.204	0.008421	2.568	0.001224	2.063	0.011729
YE_RS19645	<i>rpsC</i>	30S ribosomal protein S3	2.027	1.79E-05	2.995	1.70E-10	NS	NS
YE_RS19635	<i>rpmC</i>	50S ribosomal protein L29	NS	NS	2.418	2.14E-08	NS	NS
YE_RS19630	<i>rpsQ</i>	30S ribosomal protein S17	NS	NS	2.044	0.000564	NS	NS
YE_RS00325	<i>rpmB</i>	50S ribosomal protein L28	2.311	0.000153	3.544	4.13E-08	2.03	0.002088
YE_RS00550	<i>rpmE</i>	50S ribosomal protein L31	NS	NS	3.809	5.32E-15	2.267	3.11E-08
YE_RS19545	<i>rplQ</i>	50S ribosomal protein L17	3.194	2.95E-12	3.114	4.28E-10	2.497	9.71E-08
YE_RS19605	<i>rpsH</i>	30S ribosomal protein S8	2.217	9.95E-08	4.844	6.50E-22	2.307	8.56E-10
YE_RS19600	<i>rplF</i>	50S ribosomal protein L6	2.403	9.81E-15	3.56	2.50E-24	NS	NS
YE_RS09610	<i>rplT</i>	50S ribosomal protein L20	2.037	2.60E-05	2.138	1.08E-05	NS	NS
YE_RS19650	<i>rplV</i>	50S ribosomal protein L22	2.123	2.12E-12	3.243	3.59E-17	NS	NS
YE_RS19655	<i>rpsS</i>	30S ribosomal protein S19	2.048	1.98E-07	2.416	4.02E-09	NS	NS
YE_RS01490	<i>rplL</i>	50S ribosomal protein L7/L12	NS	NS	2.68	1.29E-11	NS	NS

YE_RS02280	<i>rpsO</i>	30S ribosomal protein S15	2.4	2.19E-05	5.133	3.04E-12	2.292	0.000277
YE_RS02045	<i>rpsF</i>	30S ribosomal protein S6	2.523	1.73E-10	3.05	3.35E-09	2.406	8.76E-09
YE_RS16465	<i>rpsB</i>	30S ribosomal protein S2	2.505	1.10E-08	4.681	7.39E-17	2.774	6.66E-10
YE_RS08205	<i>rpmF</i>	50S ribosomal protein L32	NS	NS	2.705	6.74E-06	NS	NS
YE_RS19570	<i>rpmJ</i>	50S ribosomal protein L36	2.346	3.14E-05	2.86	2.01E-05	0.219	8.03E-05
YE_RS19615	<i>rplE</i>	50S ribosomal protein L5	2.199	9.20E-13	3.503	7.15E-19	NS	NS
YE_RS19610	<i>rpsN</i>	30S ribosomal protein S14	2.457	5.75E-11	5.006	1.75E-20	2.373	2.35E-09
YE_RS19680	<i>rpsJ</i>	30S ribosomal protein S10	3.235	1.45E-14	6.795	2.35E-36	3.962	4.46E-17
YE_RS02175	<i>rplU</i>	50S ribosomal protein L21	2.396	6.61E-05	2.945	3.85E-06	2.051	0.001674
YE_RS19665	<i>rplW</i>	50S ribosomal protein L23	2.458	3.58E-10	4.269	5.34E-27	2.432	9.85E-12
YE_RS19660	<i>rplB</i>	50S ribosomal protein L2	2.039	4.33E-07	3.18	3.34E-16	NS	NS
YE_RS01480	<i>rplA</i>	50S ribosomal protein L1	2.384	2.81E-10	4.441	6.94E-25	NS	NS
YE_RS01485	<i>rplJ</i>	50S ribosomal protein L10	NS	NS	3.823	5.51E-19	NS	NS
YE_RS02055	<i>rpsR</i>	30S ribosomal protein S18	2.129	2.35E-06	3.445	3.62E-07	2.357	4.01E-07
YE_RS19710	<i>rpsL</i>	30S ribosomal protein S12	2.662	5.04E-08	5.235	2.63E-17	2.879	8.99E-09
YE_RS18765	<i>rpsI</i>	30S ribosomal protein S9	2.631	2.49E-06	2.333	9.39E-05	2.02	0.000994
YE_RS04260	<i>rpsP</i>	30S ribosomal protein S16	2.06	0.000151	4.307	1.74E-13	2.333	1.24E-05
YE_RS19640	<i>rplP</i>	50S ribosomal protein L16	NS	NS	3.297	2.24E-12	NS	NS
YE_RS19595	<i>rplR</i>	50S ribosomal protein L18	2.412	6.16E-17	4.697	6.46E-36	2.517	2.80E-14
YE_RS19580	<i>rplO</i>	50S ribosomal protein L15	2.253	9.31E-18	NS	NS	NS	NS
YE_RS19590	<i>rpsE</i>	30S ribosomal protein S5	2.508	5.55E-12	3.492	1.61E-18	NS	NS
YE_RS19560	<i>rpsK</i>	30S ribosomal protein S11	2.782	3.92E-11	2.802	1.01E-13	2.051	5.98E-11
YE_RS19565	<i>rpsM</i>	30S ribosomal protein S13	2.844	6.46E-14	3.076	9.10E-13	2.354	5.31E-13
YE_RS07755	<i>rpsA</i>	30S ribosomal protein S1	NS	NS	2.885	1.72E-05	NS	NS
YE_RS01475	<i>rplK</i>	50S ribosomal protein L11	2.378	8.97E-13	7.685	4.76E-30	3.066	1.90E-16
YE_RS19620	<i>rplX</i>	50S ribosomal protein L24	2.545	2.01E-09	3.76	5.02E-16	2.085	4.02E-06
YE_RS19625	<i>rplN</i>	50S ribosomal protein L14	2.266	3.25E-12	6.21	1.32E-31	3.291	3.80E-23
YE_RS00330	<i>rpmG</i>	50S ribosomal protein L33	2.253	2.45E-06	2.664	6.69E-07	NS	NS
YE_RS19555	<i>rpsD</i>	30S ribosomal protein S4	3.07	7.26E-20	6.41	3.30E-33	4.723	3.01E-39
YE_RS19670	<i>rplD</i>	50S ribosomal protein L4	2.494	1.07E-11	4.296	6.52E-38	2.49	2.36E-14
YE_RS19675	<i>rplC</i>	50S ribosomal protein L3	2.894	1.65E-22	5.91	1.89E-29	3.735	2.95E-15
YE_RS02180	<i>rpmA</i>	50S ribosomal protein L27	2.117	6.85E-05	2.174	8.77E-05	NS	NS
YE_RS19705	<i>rpsG</i>	30S ribosomal protein S7	2.803	2.97E-11	6.297	9.41E-25	3.56	4.08E-17
YE_RS02180	<i>rpmA</i>	50S ribosomal protein L27	2.117	6.85E-05	NS	NS	NS	NS

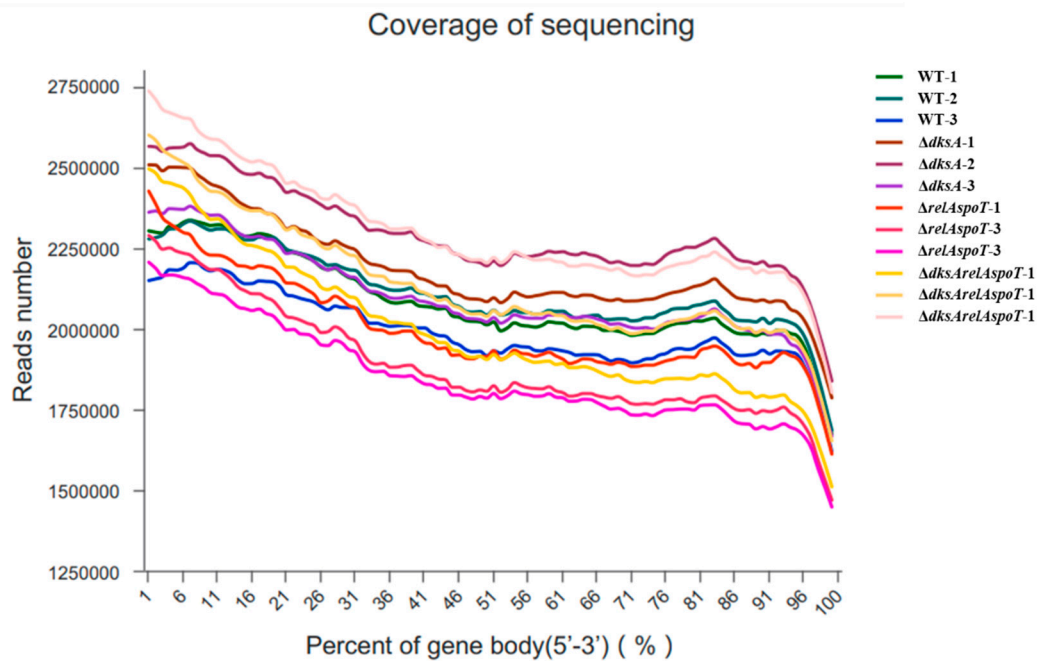
Supplementary Table S4. The growth gap of mutant strain compared with WT in medium at 30 h.

Strains	LBNS	LBNS+R	LBNS+Cys-Cys	LBNS+H	LBNS+REH	LBNS+REHCys-Cys
<i>ΔdksA</i>	17.61%	15.53%	11.79%	13.71%	13.34%	11.87%
<i>ΔrelAΔspoT</i>	33.50%	9.11%	10.21%	11.59%	14.79%	18.19%
<i>ΔdksAΔrelAΔspoT</i>	32.97%	12.95%	12.98%	12.15%	24.61%	21.11%
<i>ΔdksA(dksA)</i>	10.02%	4.73%	2.05%	-2.48%	-0.18%	-1.92%
<i>ΔrelAΔspoT(spoT)</i>	16.29%	10.08%	0.88%	2.94%	3.34%	6.90%

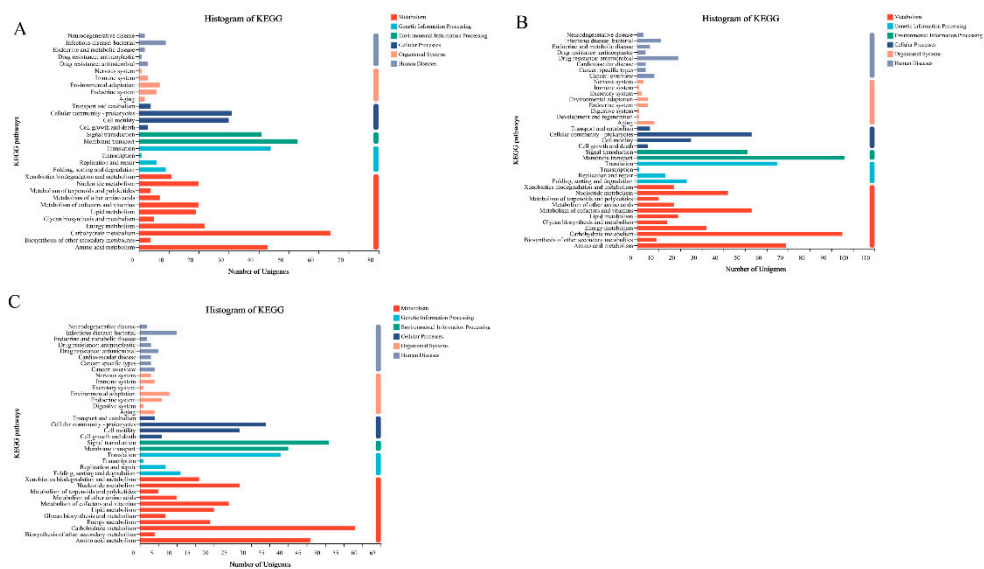
R, Arginine; Cys-Cys, Cystine; H, Histidine; E, Glutamic acid



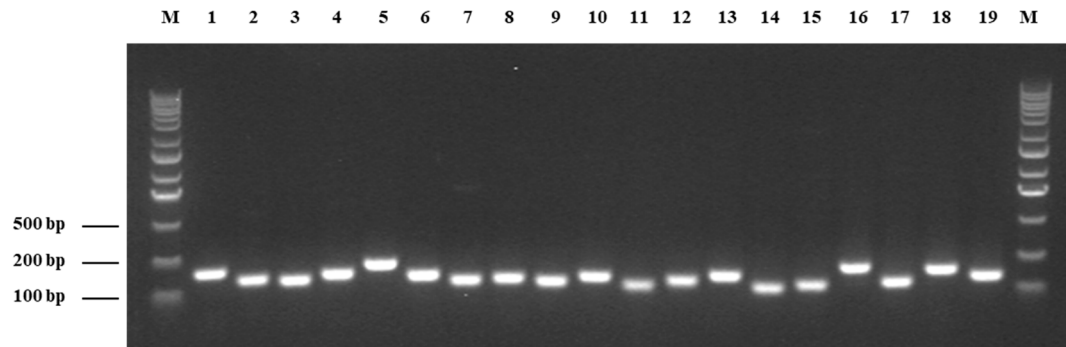
Supplementary Figure S1. Saturation curve of RNA sequencing. (A)-(C) saturation curve of three WT samples; (D)-(F) saturation curve of three $\Delta dksA$ samples; (G)-(H) saturation curve of three $\Delta relA\Delta spoT$ samples; (J)-(K) saturation curve of three $\Delta dksA\Delta relA\Delta spoT$ samples.



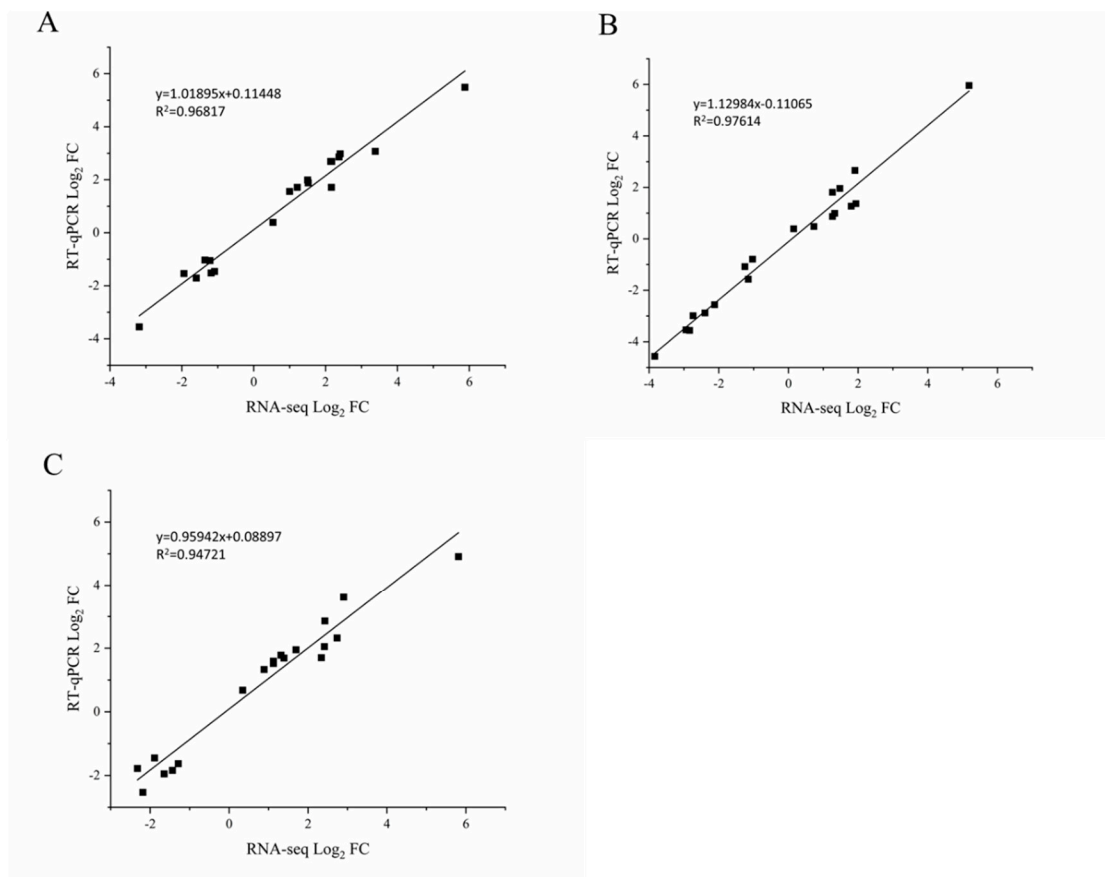
Supplementary Figure S2. The map of sequencing gene coverage.



Supplementary Figure S3. Annotation of sequencing results based on KEGG database. (A) *ΔdksA*; (B) *ΔrelAspoT*; (C) *ΔdksAΔrelAspoT*.



Supplementary Figure S4. Agarose electrophoresis of DNA amplified with the primers used for RT-qPCR. 1-19 represents *pdeR*, *yihX*, *rpsN*, *rpoA*, *trmD*, *dhaK*, *gntT*, *YE_RS15980*, *dusB*, *corA*, *epmA*, *trmL*, *fliE*, *flgC*, *alaC*, *fyuA*, *hypE*, *lsrD*, *hisJ*, respectively.



Supplementary Figure S5. Comparison results between RNA-Seq data (X axis) and RT-qPCR data (Y axis). (A) $\Delta dksA$; (B) $\Delta relA\Delta spoT$; (C) $\Delta dksA\Delta relA\Delta spoT$. Data are means and SEM from three independent RT-qPCRs.