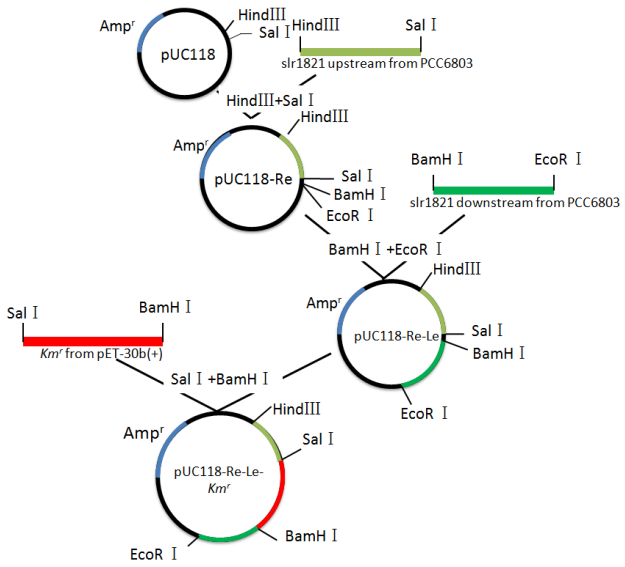
Supplemental Table S1. Statistics result of RNA sequencing data.

Sample_ ID	Raw Data Total_Reads	Raw Data Total_Bases	Clean Data Total_Reads	Clean Data Total_Bases	Error%	Q20%	Q30%	GC%
M-1	19019678	2.87E+09	18885526	2.73E+09	0.0109	98.78	96.62	49.23
M-2	20045072	3.03E+09	19596762	2.81E+09	0.0119	98.43	95.42	49.15
M-3	20440760	3.09E+09	20012366	2.86E+09	0.0118	98.48	95.55	49.49
MA-1	24578712	3.71E+09	24028760	3.45E+09	0.0119	98.41	95.38	49.12
MA-2	22051244	3.33E+09	21507562	3.08E+09	0.0122	98.3	95.11	49.01
MA-3	23445508	3.54E+09	22897854	3.28E+09	0.012	98.37	95.29	49.35
WT-1	15365482	2.32E+09	15167632	2.13E+09	0.0106	99.05	96.98	52.42
WT-2	20409760	3.08E+09	20153882	2.85E+09	0.0106	99.06	97	51.36
WT-3	19982788	3.02E+09	19445352	2.78E+09	0.0124	98.22	94.86	51
WTA-1	24030246	3.63E+09	23478232	3.37E+09	0.0121	98.36	95.23	50.85
WTA-2	24443248	3.69E+09	23900728	3.43E+09	0.012	98.4	95.31	51.26
WTA-3	24981840	3.77E+09	24438662	3.51E+09	0.0119	98.42	95.37	50.78

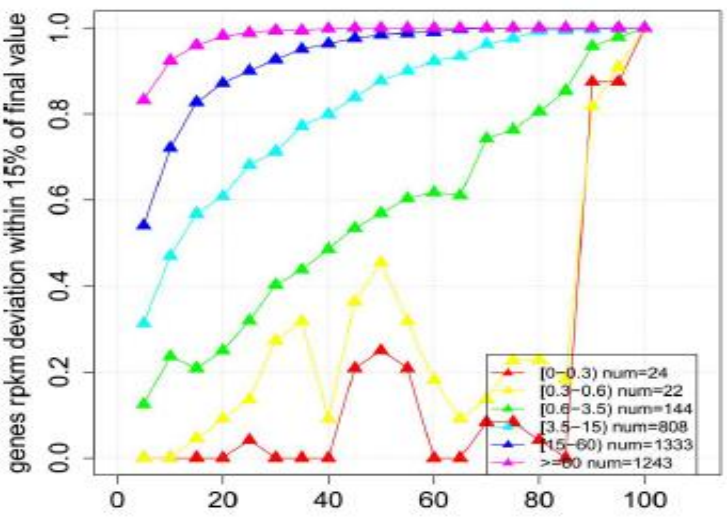
Supplemental Table S10. Sequences of primers using in RT-qPCR.

Name	Sequences of primers
rnpB-S	GAGTTAGGGAGGGAGTTGC
rnpB-A	GTGCAGGATGACGGAGAAA
sll1017-S	TGCTGCGGACAGAGTGGT
sll1017-A	GTGGGCTGGTATGGCTTT
slr1201-S	AAGTCACCGTCCTGGCTCT
slr1201-A	CCCTGGTTTCATCGTCCC
slr0901-S	TTATTTCTGCCCAAGAGT
slr0901-A	ACCGATTATGCCTCCACA
sll0783-S	TAACACCGGGACCATAGA
sll0783-A	TACAGTGGCGTTTGAAGG
sll1327-S	GAGCCACTAGGGAATCGG
sll1327-A	GGCAGTAAAGCCAAGCAAT
slr1291-S	ACCTACGACCGTACCCAC
slr1291-A	AAAGAAGCCATAGCACCC
slr0851-S	CGGTGTTGACTGAAAGAATG
slr0851-A	GAGGCTAGAAGCCCTGAC
slr0952-S	ATATCCGCATTCCCAACC
slr0952-A	CGGGCAGTGTAACCTTCG
sll1590-S	GTGTCATTGCGGTAAACATC
sll1590-A	CCCTTAATGCCTTCCAAGC
slr1728-S	AGAAGTGCGCTTTGGTTG
slr1728-A	GGAATAGGTCCGATAGGGT



Supplemental Figure S1. Construction of the plasmid for homologous recombination to knockout *slr1821* gene.

A



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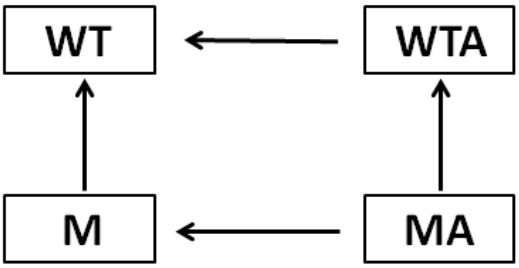

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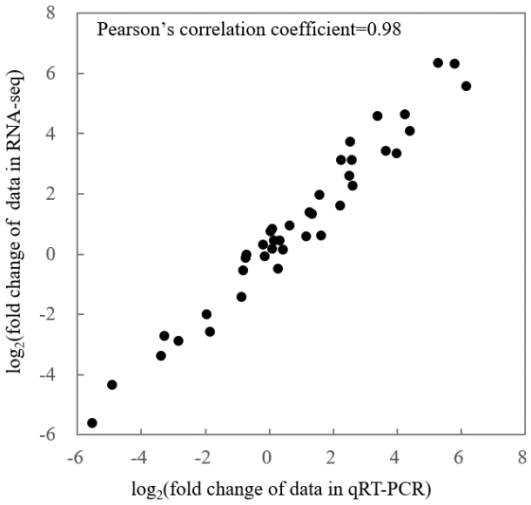
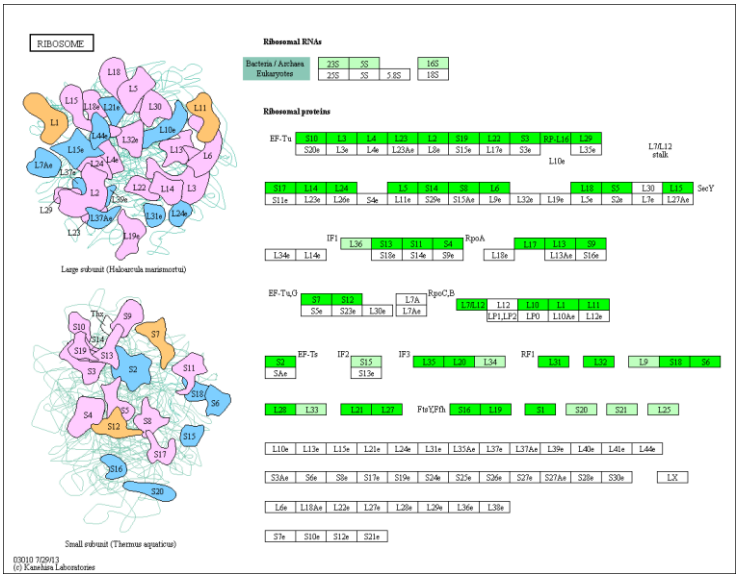


Supplemental Figure S2. RNA sequencing data analysis and validation. (A) Representative saturation curve of sample M1. (B) Comparison scheme of differential expressed genes between each two samples pairs indicated as arrow. WT: wild type in Na_2SO_4; M: ⊿*slr1821* knockout mutant in Na_2SO_4; WTA: wild type in $(NH_4)_2SO_4$; MA: ⊿*slr1821* knockout mutant in $(NH_4)_2SO_4$. The arrow indicated comparison direction, for example, MA/M. (C) Validation of sequencing data by quantitative RT-PCR for representative genes.

A



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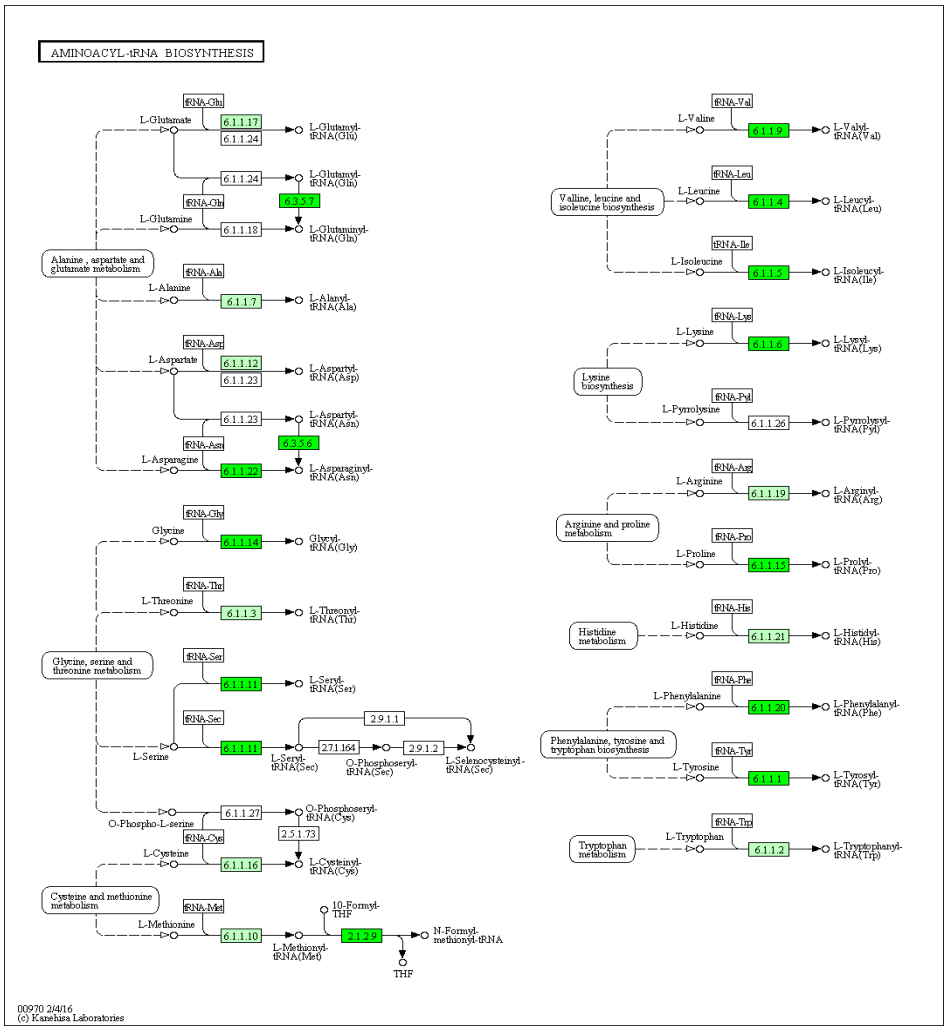
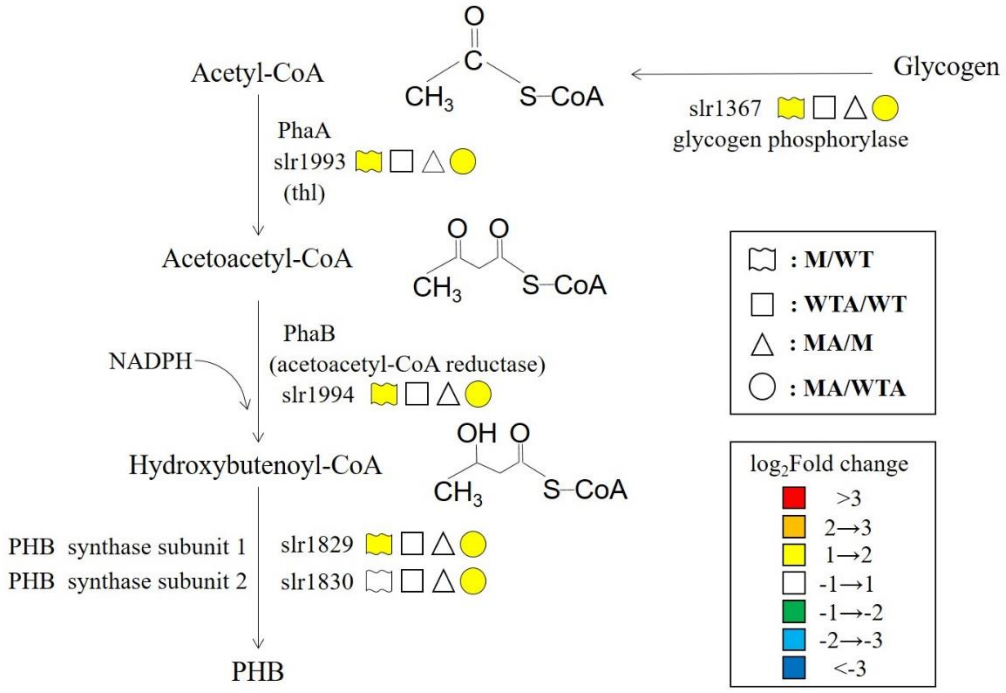


Supplemental Figure S3. Suppressed expression of translational machinery in *⊿slr1821* vs WT upon NH_4^+ stress. (A) Ribosomal proteins in ribosome large and small subunit. (B) Synthetase involved in aminoacyl-tRNA biosynthesis. Dark green highlights the suppressed gene, light green is the component without significant regulation. White ones were components not available in Synechocystis 6803.



Supplemental Figure S4. Knockout of *slr1821* resulted in higher expression of PHB synthesis genes. The comparison pair and fold changes are indicated in different shapes and colors respectively. WT and WTA are wild type without and with NH_4^+ stress. M and MA are Δ*slr1821* knockout mutant without and with NH_4^+ stress.