Table S1. Oligonucleotides used in this study

CC132	GACGTAACTCGTTACCGTGAGT
CC133	TTTGACGCCGTGACAGTCACCGTAT
CC175	atatggatccGCGATTAAAGAAGCGAGCGGAGACCTC
CC546	ATTTATATCATATGTACGAGTTTAAAGATTATTATCAGAATACTG
CC768	GCGCTGATAGACGGAAAACTG
CC770	GACTGCTAGTTCTTTGCCGTTTGC
CC772	CTTGTTACTAGTTAAGCAACAACCAAGTTCATAGC
CC773	CTTGTTGGATCCCTTGAAAATTCCTTGCCGTC
CC1010	GGTTTTAGTCCACTCTCAACTCCTGATC
CC1090	CCACGAAAAGTCTTCCTCAATCTCCGTATACTATTTG
CC1091	GGAGGGACTGGCTAATGCTGCGTAAATTAAG
CC1092	ccgaagtatttttttcactttattaatttgttcgtatgtattcatACCGCTCATAACTCCAATACTTTAAAATTTTCG
CC1093	CGAAAATTTTAAAGTATTGGAGTTATGAGCGGTatgaatacatacgaacaaattaataaagtgaaaaaaatacttcgg
CC1094	ctatttaaataacagattaaaaaaattataaCATTATGGAGGTTTAAAAAAAGAGGCACTCCCTAAG
CC1095	CTTAGGGAGTGCCTCTTTTTTTAAACCTCCATAATGttataatttttttaatctgttatttaaatag
CC1096	GGATTCAAGAGCGGAGCGATTGCCACAACC
CC1114	CAATTCCGGTGATATTCTCATTTTAGCcatACCGCTCATAACTCCAATACTTTAAAATTTTCG
CC1115	CGAAAATTTTAAAGTATTGGAGTTATGAGCGGTatgGCTAAAATGAGAATATCACCGGAATTG
CC1116	TAAAATATTATATTTTACTGGATGAATTGTTTtagCATTATGGAGGTTTAAAAAAAGAGGCACTCCCTAAG
CC1117	CTTAGGGAGTGCCTCTTTTTTTAAACCTCCATAATGctaAAACAATTCATCCAGTAAAATATAATATTTTA
HP279	GCATCGGCATAACCACCACGC

Non-hybridising sequences are shown in lower case letters

Table S2. Fold-changes in sporulation and competence related transcripts in RNase J1 or RNase Y depletion strains compared to wild-type in (Durand et al., 2012a).

Gene	RNase J1↓	RNase Y↓	Profile J1/Y
Sporulation genes			
spo0A	2.9	2.4	UU
spo0B	2.3	1.1	U-
spo0E	6.3	1.4	U-
spoIID	4.5	3.7	UU
spoIIE	5.0	2.3	UU
spoIIIAE	1.0	2.1	-U
spoIIIC	5.1	3.7	UU
spoIIIE	2.4	2.1	UU
spoIIP	2.9	1.9	U-
spoIIR	1.2	2.0	-U
spoIISA	2.0	8.6	UU
spoIISB	5.1	8.5	UU
spoIVFA	2.2	2.5	UU
spoIVFB	3.0	3.2	UU
spoVAEA	1.3	2.4	-U
spoVAF	1.3	2.4	-U
spoVB	1.1	2.2	-U
spoVE	3.1	1.0	U-
spoVFA	1.3	2.1	-U
spoVG	0.2	0.3	DD
spoVID	1.0	2.3	-U
spoVM	2.2	1.0	U-
spoVR	1.7	3.3	-U
Competence genes			
comEB	2.3	2.8	UU
comEC	1.4	2.1	-U
comER	1.2	3.2	-U
comK	2.6	1.0	U-
comN	0.5	0.5	-D
comQ	0.4	0.7	D-
comS	0.4	0.6	D-
comZ	1.5	2.1	-U

(U) up-regulated, (D) is down-regulated, (-) unchanged.

Table S3. Fold-changes in cell envelope biosynthesis related transcripts in RNase J1 or RNase Y depletion strains compared to wild-type in (Durand et al., 2012a).

Name	RNase J1↓	RNase Y↓	Profile J1/Y
Biosynthesis of peptidoglycan			
gcaD	1.1	0.4	-D
glmS	2.2	0.7	U-
murAA	2.4	3.0	UU
murB	2.5	4.9	UU
murG	2.5	5.8	UU
racE	2.3	1.3	U-
spoVB	1.1	2.2	-U
spoVE	3.1	1.0	U-
yabM	2.7	3.9	UU
ykuD (ldt)	4.2	8.6	UU
ytgP	2.1	3.7	UU
yycJ (walJ)	3.4	2.4	UU
Biosynthesis of lipoteichoic acid			
dgkA	1.9	2.1	-U
ltaSA	1.0	3.6	-U
yqgS	3.0	1.7	U-
yvgJ	1.5	2.1	-U
Biosynthesis of teichoic acid			
dltA	2.3	3.1	UU
dltB	2.3	2.7	UU
dltC	2.4	2.6	UU
dltD	2.4	2.8	UU
dltE	3.1	2.8	UU
ggaB	1.1	0.4	-D
mnaA	2.0	0.9	U-
pgcA (gtaC)	2.1	1.7	U-
tagA	1.9	2.7	-U
tagB	1.2	2.1	-U
tagO	1.4	2.9	-U
Biosynthesis of teichuronic acid			
tuaA	1.0	4.5	-U
tuaA	1.1	6.0	-U
tuaB	1.6	5.5	-U
tuaC	1.4	4.3	-U
tuaD	1.4	3.9	-U
tuaE	1.2	3.1	-U
tuaF	1.2	2.6	-U
tuaG	1.3	2.6	-U
tuaH	1.2	2.5	-U

Penicillin binding proteins			
dacB	2.4	2.2	UU
dacC	0.5	0.6	D-
pbpA	1.0	2.1	-U
pbpC	0.7	0.2	-D
pbpE	0.4	0.5	D-
pbpG	1.6	3.8	-U
pbpH	3.0	1.0	U-
pbpI	1.4	4.5	-U
pbpX	1.4	2.4	-U
ponA	1.5	2.4	-U
Export of anionic polymers and attachment to peptidoglycan			
lytR (tagU)	3.1	0.5	U-
tagG	0.8	4.0	-U
tagH	1.1	3.7	-U
yvhJ (tagV)	3.0	1.3	U-
ywtF (tag T)	2.4	4.7	UU

(U) up-regulated, (D) is down-regulated, (-) unchanged.

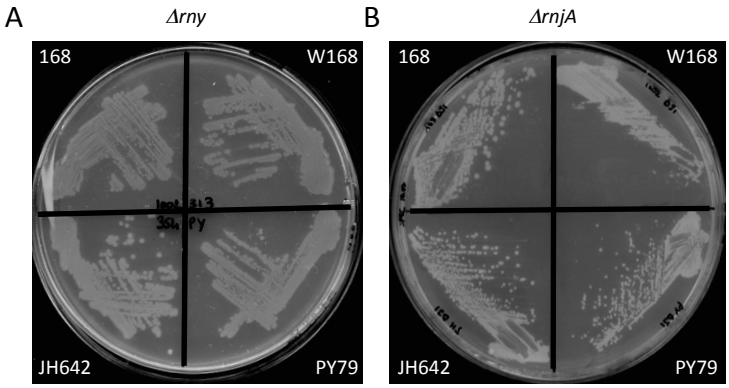

Figure S1. Deletion mutants of RNase Y and J1 are viable in four commonly used *B. subtilis* genetic backgrounds. Luria Bertani (LB) plates showing growth of (A) *Δrny* and (B) *ΔrnjA* mutants in strains 168 *trpC2*, W168 *trp*$^{+}$, JH642 *trpC2 pheA1* and PY79 *ΔSPβ*.

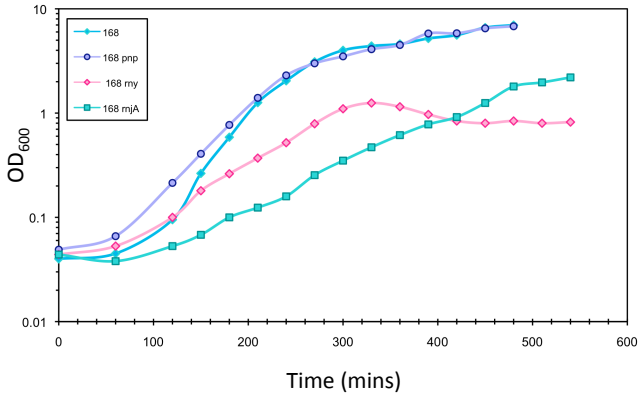

Figure S2. Growth curves of RNase mutant strains in liquid medium. Cells were grown in 2xYT medium in Erlenmeyer flasks with orbital shaking at 200 rpm and an air/liquid ratio of 10.

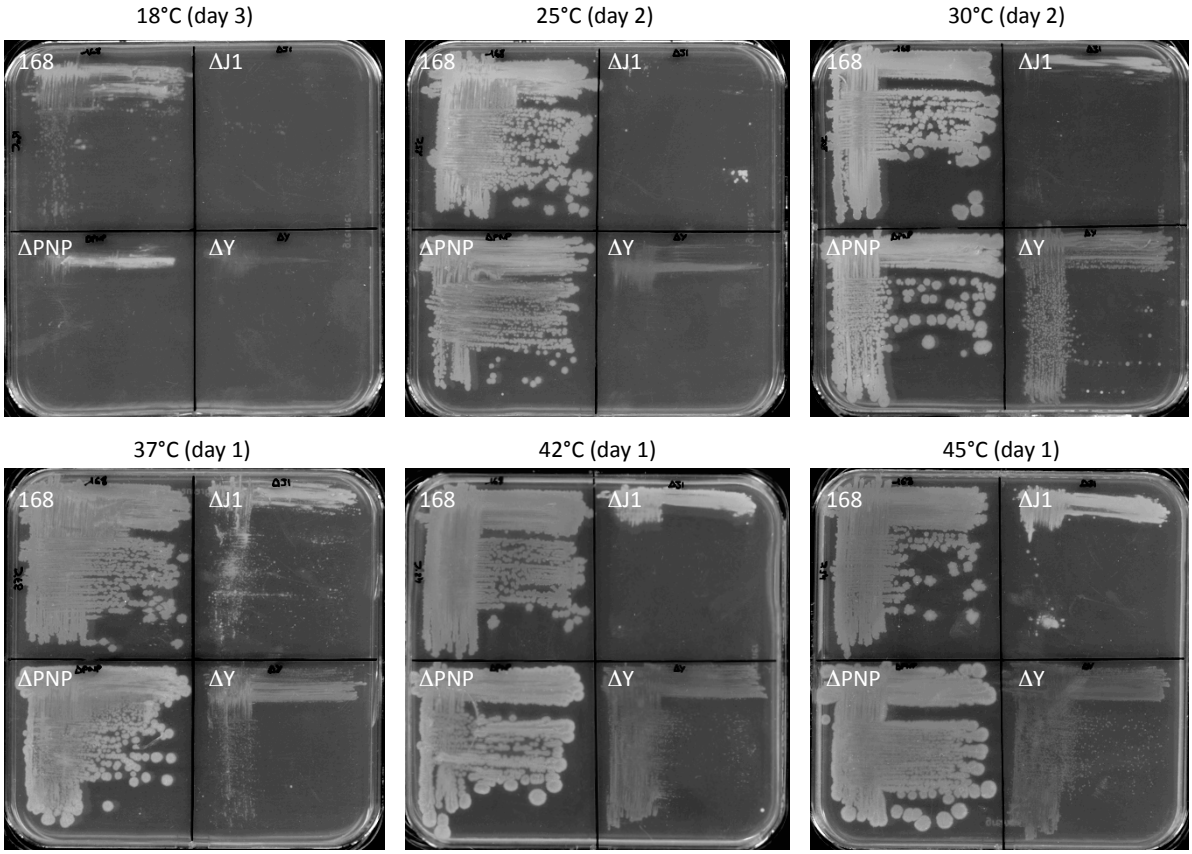

Figure S3. Effect of temperature on RNase mutants. Cells were streaked out on LB plates and incubated at the temperatures indicated for the times shown.

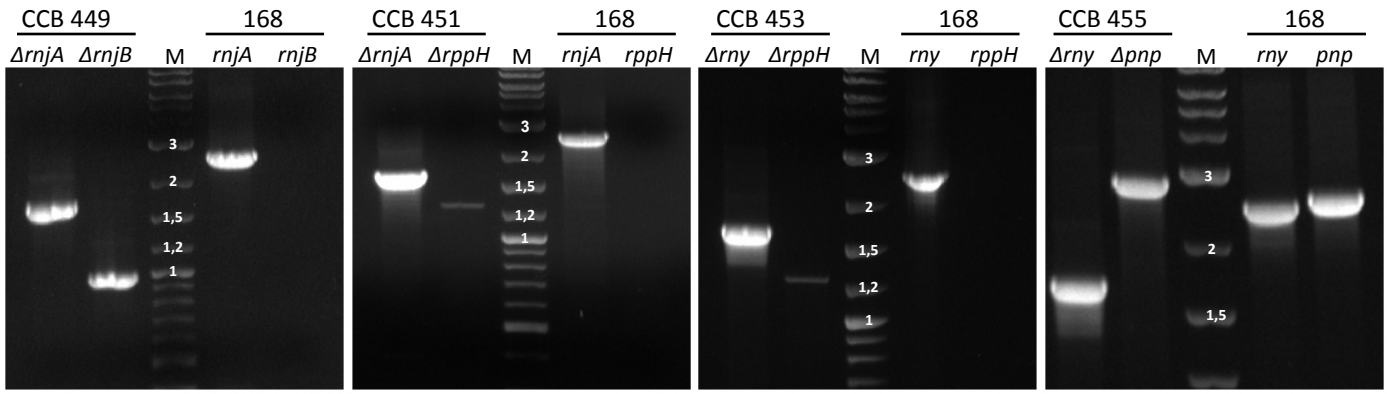

Figure S4. Confirmation of double mutants by PCR. Deletions were verified by colony PCR using the following oligonucleotide pairs: *rnjA* (CC1090/1096); *rny* (CC768/770); *pnp* (CC132/133); *rnjB* (CC175/1010); *rppH* (HP279/CC546). For *rppH* and *rnjB*, the lower oligonucleotide hybridizes to the antibiotic resistance cassette and therefore only yields a product in the mutant strain. A DNA marker (M) is shown in the middle of the gel. Expected sizes were as follows: *rnjA* (WT/mutant: 2.57 vs 1.66 bp), *rny* (WT/mutant: 2.54 vs 1.73 bp), *pnp* (WT/mutant: 2.59 vs 2.8 kb), *rnjB* (WT/mutant: no product vs 996 bp); *rppH* (WT/mutant: no product vs 1.30 kb).