

Table S1: Primers used in this study

Oligonucleotide	Sequence, 5' to 3'	gene product
rpoS_F	CAAGCTAATTACTCACGAAGAAG	BB_0771, rpoS: RNA polymerase sigma factor, coding region
rpoS 128R	GTTTTTGGCTTTTGCATTGC	
rpoS-145F	CAAAAAATACTCCCCCTAAAC	BB_0771, rpoS: RNA polymerase sigma factor, long upstream untranslated region
rpoS-59R	CATGCAAAAAGTGTGCCAATT	
rpoS 443F	GATTCAACCTATCTCCTGCTCAG	BB_0771, rpoS: RNA polymerase sigma factor, coding region
rpoS 705R	GGTGCTTTTTTTGGGACTATTG	
ocpC-F	GAAAGAGTTGAAGCTTGC	BB_B19, OspC: Outer surface protein C, coding region
ospC-R	ATTGCATAAGCTCCCGCTAA	
ospC-F4	TGTTAAAGGGCCTAATCTTACAGAAATAA	BB_B19, OspC: Outer surface protein C, coding region
ospC-R4	TACCAATAGCTTTGGTAGCAAGTTCAT	
ospA-F	GCAGCCTTGACGAGAAAAAC	BB_A15, Osp A: Outer surface protein A, coding region
ospA-R	GCCTCAAGTACTCCAGATCC	
flaB-F	TTTCAGGGTCTCAAGCGTCT	BB_0147, flaB, coding region
flaB-R	TGTTGAGCTCCTTCCTGTTG	
rpsO F	TACTGGTTCTGTTGGGGTTCA	BB_0804, rpsO, ribosomal protein S15, coding region
rpsO R	TGGTAATACCGCAATAAACTTCG	
PNPase F	TATGCAGCCGGTAAAATTCC	BB 0805, polynucleotide nucleotidyl-transferase, coding region
PNPase R	AACTGCCGTAAAAGCAGCAT	
rpsO-PNPase F1	AGGGCAAAGGCGAAGTTTAT	Intergenic region between BB_0804 and BB_0805
rpsO-PNPase R1	GCCATAAATCCGGTCTCAAA	
S11BF_Snow	CTTTAGCTTGGGCAAGTGCTGG	BB_0501, rpsK, ribosomal protein S11, coding region
S11BR_Snow	GCAGATTCACAGCCAATGCC	
S13AF_Snow	GCAATAAATCAAGTATTTCTCC	BB_0500, rpsM, ribosomal protein S13, coding region
S13AR_Snow	TGCCTAACGCCCTATAACACG	
AlphaAF_Snow	GCCAAGGTGATGGGTCTTATGG	BB_0502, rpoA, DNA directed RNA polymerase, α subunit, coding region
AlphaAR_Snow	CTTCAGAACTCCAGGAATCAAATC	
S4AF_Snow	GCCGCATCCTCCCGGAATGC	BB_0615, rpsD, ribosomal protein S4, coding region
S4AR_Snow	GTCTCCAGTAACACCGTGATC	
L17AF_Snow	GGAAGTCTAGTCACAGGAGAGCGC	BB_0503, rplQ, ribosomal protein L17, coding region
L17AR_Snow	GCACAGTATCAACTTTTGCCC	

Table S2. mRNA degradation following transcriptional arrest by removal of inducer or addition of actinomycin D. Ct values obtained in qRT-PCR trials. The experiment was performed with two biological samples (n=2; numbers 1 and 2) in duplicate (letters a and b).

time (min)	minus inducer				plus inducer, plus actinomycin D				plus inducer			
	1a	1b	2a	2b	1a	1b	2a	2b	1a	1b	2a	2b
<i>rpoS</i>												
5	21.08	20.1	21.13	20.52	21.33	21.04	21.21	21.19	20.35	19.59	20.45	20.52
10	22.19	21.89	21.15	21.62	21.69	21.49	21.69	21.49	20.34	20.09	20.81	20.14
20	21.92	22.2	22.26	21.27	22.5	19.82	20.33	20.16	20.31	20.95	19.15	18.3
45	23.23	22.92	22.18	21.74	21.45	20.19	21.76	21.58	19.56	19.34	18.62	18.45
240	23.36	23.69	23.68	23.12	24.07	23.61	22.98	22.7	18.94	18.36	19.87	19.75
1260	24.15	23.84	25.15	24.91	25.55	25.75	27.15	26.89	19.67	19.98	19.37	19.66
no template	37.8	36.51	36.53	36.28								
no RT	no data	36.22	29.52	34.4								
<i>flaB</i>												
5	10.82	10.66	11.07	10.5	10.79	11.7	11.79	11.03	10.83	11.34	13.55	11.96
10	11.56	11.54	10.97	10.82	10.33	11.67	11.71	11.77	11.42	11.41	12.3	11.6
20	10.86	11.88	10.79	10.34	10.46	12.01	10.79	10.83	12.26	12.41	13.46	11.02
45	11.54	11.38	10.75	10.44	10.59	no data	11.38	10.74	10.91	11.17	11.91	10.75
240	11.25	11.07	10.71	10.36	13.43	13.55	13.07	12.64	10.26	10.63	12.13	11.81
1260	12.94	13.49	10.75	10.35	14.94	15.81	15.92	15.65	11.11	11.53	10.91	11.27
no template	31.81	32.19	32.23	34.81								
no RT	31.12	29.75	31.29	32.83								

Table S3 mRNA degradation following transcriptional arrest. Ct values obtained from qRT-PCR. The experiment was performed 3 times and most samples were tested in duplicate times with qRT-PCR.

time (min)	<i>rpoS</i> leader region						<i>rpoS</i> coding region					
	1a	1b	2a	2b	3a	3b	1a	1b	2a	2b	3a	3b
0	17.76	17.19	18.48	18.08	18.56	18.59	18.66	19.49	19.08	19.06	19.80	19.90
2	19.96	19.93	20.06	19.96	21.51	20.81	21.16	21.68	20.51	20.69	21.58	21.93
10	20.51	20.26	20.45	20.44	20.87	20.79	21.62	21.73	21.00	21.34	21.87	22.31
45	20.53	20.47	21.08	20.95	21.65	21.80	22.04	22.54	21.68	21.85	22.26	22.95
120	21.08	21.24	22.01	22.37	22.07	22.15	22.51	23.32	22.41	22.61	22.57	23.00
240	21.80	21.71	22.34	23.76	22.52	22.55	23.55	23.95	23.20	23.04	22.61	23.47
1350	24.26	24.17	24.21	24.52	24.70	24.64	25.99	27.06	23.93	24.25	25.04	25.26
240 minus AD	18.41	18.28	18.70	18.94	18.50	18.51	19.31	19.93	18.61	18.85	19.00	19.36
No Template	29.39	38.10	30.02	29.36	34.99	32.62	32.20	35.30	30.69	35.09	37.03	30.67
No RT	33.61	31.77	34.29	29.66	34.00	No Ct	37.74	33.49	43.87	30.36	No Ct	No Ct
	<i>ospA</i>						<i>ospC</i>					
	1a	1b	2a	2b	3a	3b	1a	1b	2a	2b	3a	3b
0	11.34	11.15	12.55	14.63	12.63	12.59	11.24	11.32	9.34	9.25	9.86	9.9
2	11.61	10.7	12.38	13.78	12.44	12.28	11.41	11.47	9.19	9.26	9.33	9.45
10	11.68	11.39	12.72	14.08	12.5	12.32	11.62	11.04	9.18	9.11	9.26	9.41
45	12.71	12.24	13.34	14.84	13.57	13.44	11.61	11.34	9.19	9.47	9.69	9.43
120	14.64	15.73	15.7	16.45	15.28	15.98	12.71	12.67	10.55	10.82	10.56	10.65
240	15.63	15.27	16.35	17.47	16.17	15.5	15.72	15.42	12.23	12.33	13.36	12.66
1350	18.37	18.1	17.48	18.78	18.33	17.71	18.69	18.69	14.31	14.48	15.48	15.45
240 minus AD	11.83	11.73	12.33	13.6	12.84	12.55	11.51	11.17	9.35	9.39	9.66	9.61
No Template	36.47	35.66	36.34	36.13	35.24	31.87	33.67	39.92	28.72	No Ct	30.25	29.23
No RT	35.62	38.27	30.85	35.84	35.06	No Ct	35.62	36.89	40.54	33.33	39.63	No Ct
	<i>rpsO</i> (S15)						<i>pnpase</i>					
	1a	1b	2a	2b	3a	3b	1a	1b	2a	2b	3a	3b
0	13.99	13.67	14.47	14.61	14.37	14.66	13.98	no data	14.51	14.33	14.23	14.81
2	15.02	14.54	15.23	15.02	15.47	15.64	15.01	no data	14.98	14.82	15.34	15.76
10	15.63	15.62	14.99	15.63	15.69	15.69	15.41	no data	14.88	15.08	15.39	16.10
45	15.50	15.50	15.87	16.19	16.04	16.05	15.80	no data	15.26	15.28	15.92	15.97
120	16.66	16.41	17.26	17.47	17.10	16.81	16.37	no data	16.71	16.55	16.74	17.19
240	17.30	17.30	17.86	17.86	17.80	17.17	17.36	no data	17.43	17.28	17.39	17.50
1350	20.18	20.32	19.53	19.29	19.61	19.52	20.28	no data	19.11	18.89	19.59	19.24
240 minus AD	14.25	14.47	14.60	14.56	14.47	14.66	14.49	no data	14.07	13.98	14.55	14.70
No Template	35.79	35.02	35.60	35.00	30.07	31.46	24.67	no data	24.60	35.56	33.66	33.30
No RT	35.03	37.42	32.14	35.93	35.93	36.87	34.53	no data	33.24	36.20	34.96	35.13

	<i>rpsO</i> / <i>pnpase</i> overlap region						<i>flaB</i>					
	1a	1b	2a	2b	3a	3b	1a	1b	2a	2b	3a	3b
0	14.44	14.59	14.96	13.85	15.15	15.42	10.33	10.27	10.11	10.08	10.88	10.83
2	15.50	14.84	15.37	14.10	16.22	16.21	10.36	10.28	9.81	9.95	10.50	10.33
10	16.29	15.79	15.77	14.43	16.22	16.23	10.51	10.06	9.87	9.87	10.51	10.42
45	15.91	16.49	16.05	14.57	16.56	16.65	10.36	10.28	9.78	9.80	10.57	10.23
120	17.05	16.68	17.64	16.16	17.36	17.28	11.48	11.45	11.46	11.67	11.94	11.81
240	17.91	17.60	18.20	16.50	18.11	17.98	12.88	12.56	12.88	13.09	13.41	13.56
1350	20.72	20.39	19.77	18.04	20.09	20.40	15.67	15.82	14.42	14.37	15.51	15.03
240 minus AD	15.03	14.91	15.15	13.40	15.31	15.60	10.40	10.26	9.79	9.88	10.41	10.36
No Template	37.35	38.52	37.38	36.08	33.42	37.37	30.04	33.00	24.91	34.60	34.55	25.96
No RT	31.27	36.00	32.36	No Ct	36.77	36.77	31.82	34.03	33.43	30.83	35.03	33.83

Figure S1: Fraction of mRNA remaining after transcriptional arrest at 22 °C.



