

Supplementary Material

The long 5'UTR of *nrdAB* modulates transcription, mRNA stability, and virulence in *Pseudomonas aeruginosa*

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Table S1. Plasmids and strains.

Name	Reference name	Description	Source
Plasmids			
pJET1.2/blunt	pJET1.2	Blunt-end vector; Amp ^R	Thermo Scientific
pETS130-GFP	pETS130	Broad host range, promoterless GFP; Gm ^R	1
pETS134	pETS130-PA	pETS130 derivative carrying <i>nrdA</i> promoter; Gm ^R	2
pETS257	pETS-PA- Δ5'UTR	pETS130 derivative carrying <i>nrdA</i> promoter without 5'UTR; Gm ^R	This work
pETS258	pETS130-PA:: <i>gfp</i>	pETS130 derivative carrying <i>nrdA</i> promoter translationally fused to <i>gfp</i> ; Gm ^R	This work
pETS259	pETS130-PA-Δ5'UTR:: <i>gfp</i>	pETS130 derivative carrying <i>nrdA</i> promoter without Δ5'UTR translationally fused to <i>gfp</i> ; Gm ^R	This work
pJN105	pJN105	Expression vector with <i>araBAD</i> promoter. Gm ^R	3
pJN106	pJN-5'UTRfor	pJN105 derivative carrying 5'UTR forward strand. Gm ^R	This work
pJN107	pJN-5'UTRrev	pJN105 derivative carrying 5'UTR reverse strand. Gm ^R	This work
pSH624-ssr	pSH624	Plasmid that expresses the gen coding for the Ssr recombinase from <i>Pseudomonas putida</i> DOT-T1E. Gm ^R	Gift from Susanne Häußler (Addgene plasmid # 199241) ⁴
pS148-CsR	pS148	Plasmid that expresses <i>Streptococcus pyogenes</i> ' Cas9 and a tailored sgRNA for counterselection in gram-negative bacteria. Cb ^R	Gift from Susanne Häußler (Addgene plasmid # 197858) ⁴
pS149	pS148-Δ5'UTR	pS148-CsR derivative carrying sgRNA for 5'UTR mutant. Cb ^R	This work
Strains			
<i>E. coli</i>			
DH5a	DH5a	<i>recA1 endA1 hsdR17 supE44 thi-1 relA1 Δ(lacZYA-argF) U169 deoR Φ80dlacZM15</i>	Laboratory
<i>P. aeruginosa</i>			
PAO1	PAO1 WT	Wild-type (ATCC 15692 / CECT 4122) - Spanish Type Culture Collection	Laboratory
PW9311	PAO1 Δ <i>rnr</i>	<i>P. aeruginosa</i> PAO1 <i>rnr</i> :: <i>ISphoA</i> /hah; TcR	5
PW7510	PAO1 Δ <i>rhl</i>	<i>P. aeruginosa</i> PAO1 <i>rhl</i> :: <i>ISphoA</i> /hah; TcR	5
PW5993	PAO1 Δ <i>rne</i>	<i>P. aeruginosa</i> PAO1 <i>rne</i> :: <i>ISphoA</i> /hah; TcR	5
PAO1 Δ5'UTR	PAO1 Δ5'UTR	<i>P. aeruginosa</i> PAO1 5'UTR deletion mutant by CRISPR-cas9	This work

Table S2. Oligonucleotides.

Primer number	Name	Sequence (5' → 3')	Application
1	Pnrda_GFP_up	AGGATCCGAATTCTTGCTCCACACAGCC TC	<i>Pnrda</i> promoter cloning/Sequencing
2	Pnrda_GFP_low	ACCCGGGTTCTCGCGTGTGGTGTCTG	<i>Pnrda</i> promoter cloning/Sequencing
3	Pnrda_UTR_5'_low	TAGCGGGCATCAGAGTGGTCCGTGCG	<i>Pnrda</i> -Δ5'UTR promoter cloning/Sequencing
4	Pnrda_UTR 3' up	ACTCTGATGCCCGCTAGCAAAACCATTA	<i>Pnrda</i> -Δ5'UTR promoter cloning/Sequencing and DNA absence test
5	Pnrda_SmaI_Rv	AAACCCGGGCTCGCGTGTGGTGTCTG	<i>Pnrda</i> promoter cloning/Sequencing
7	GFP_SmaI_Fw	AAACCCGGGAGTAAAGGAGAAGAACTT TTCACGTG	GFP cloning
8	GFP_KpnI_Rv	AAGGTACCCCCCTCGAAGCTTGCAT	GFP cloning
9	pJN105_UTR_EcoRI_Fw	GAATTCCTCCCATTAGCGCATTATCTTG	pJN105 cloning 5'UTR fw
10	pJN105_UTR_PstI_Rv	CTGCAGTGGGTATCTCCACGTTCTC	pJN105 cloning 5'UTR fw
11	pJN105_UTR_PstI_Fw	CTGCAGCCCCATTAGCGCATTATCTTG	pJN105 cloning 5'UTR Rv
12	pJN105_UTR_EcoRI_Rv	GAATTCGTGGGTATCTCCACGTTCTC	pJN105 cloning 5'UTR Rv
13	putORF-UTR up	TGACGTTGGAAGACGGTAC	pJN105 cloning check
14	putORF-UTR low	CGAATGCTGAGGGTGGGGAC	pJN105 cloning check
15	aaSSR-1F	TGAGCCAAGTAGCCAGGGTCG	Ssr amplification, curation plasmid test
16	aaSSR-1R	GATTTGTAGACGTTGGCAGCGCAG	Ssr amplification, curation plasmid test
17	aaCas9-1F	AAGCACAAGTGTCTGGACAAGG	Cas9 amplification, curation plasmid test
18	aaCas9-1R	TCACTCAAACCTCCACGTTCCAGC	Cas9 amplification, curation plasmid test
19	SEVA-T0-F	GAACGCTCGGTTGCCGCC	Check guide cloning
20	5'UTR_PAO1(+)-Rec	GAGCGCACGAACGGCTACAACGGAACC AACCAGCGCACGGACCACTCTGATGCCC GCTAGCAAAACCATTACGAGAACGTGG AGATACCCACCATGCATA	Recombineering oligonucleotide CRISPR-cas9
21	sgRNA_UTR_Fw	gcgcgCCGTCGAACACAATACCTAG	Single guide cloning CRISPR-cas9
22	sgRNA_UTR_Rv	aaacCTAGGTATTGTGTTTCGACGGc	Single guide cloning and check cloning CRISPR-cas9
23	Pnrda up	CTACGGACGCTTCCTAGG	UTR mutant PCR testing CRISPR-cas9
24	PA +1 low	GGTATGCATGGGTGGGTATC	UTR mutant PCR testing CRISPR-cas9 and SP2 in <i>nrdA</i> 5'RACE
25	PE1-nrdA	TCCTTGCGATGAGCGCCGTCG	Primer extension
26	PE2-nrdA	CAGCCGGCCTCGCGGCGGC	Primer extension
27	27f	AGAGTTTGATCMTGGCTCAG	Calibration curve 16S amplification
28	16sRNA 1306R	TTCACGCAGTCGAGTTGCA	Calibration curve 16S amplification
29	nrdAqM2-low	TGTTTCATGTCGTGGGTACG	Calibration curve <i>nrdA</i> amplification
30	qRTgreen_IVT_PAO-nrdA_fw	TCCCTACACCGATGACAAG	Calibration curve <i>nrdA</i> amplification
31	qRTgreen_IVT_PAO-nrdJA_fw	CTCAAGAGCAAGGACGGTAC	Calibration curve <i>nrdJ</i> amplification
32	nrdJBamHIlow	GGATCCCGGCAGGCCGTTGATTTC	Calibration curve <i>nrdJ</i> amplification
33	T7 promoter	TAATACGACTCACTATAGGG	Calibration curve <i>cat</i> amplification
34	GFP mut3 Rv	GAATTGGGACAACCTCCAGTG	Calibration curve <i>cat</i> amplification
35	greenQRT_PAO-nrdA_fw	ACCTGGAGAAACTGGGCAAG	qRT-PCR <i>nrdA</i>
36	greenQRT_PAO-nrdA_rv	TGTGGATGAAGTAGCGGTCTG	qRT-PCR <i>nrdA</i>
37	greenQRT_PAO-nrdJA_fw	CGAATTCATCCGCGCCAAG	qRT-PCR <i>nrdJA</i>
38	greenQRT_PAO-nrdJA_rv	TCCACCGCCTGCATGAAC	qRT-PCR <i>nrdJA</i>
39	16S RNA qRT-PCR fw	TGCCTGGTAGTGGGGGATAA	qRT-PCR 16S
40	16S RNA qRT-PCR Rv	TCTGATAGCGTGAGGTCCGA	qRT-PCR 16S

41	qPCR_pETS130_cat_rv	AGCACAAGTTTTATCCGGCC	qRT-PCR <i>cat</i>
42	qPCR_pETS130_cat_FW	CATATCACCAGCTCACCGTC	qRT-PCR <i>cat</i>
43	IVT_PAO-nrdA_rv	ACCTGGTCCTGGATCTCTTC	DNA absence test
44	TSS_PAO_nrdA Rv	CTGGCCTGCGGGTTCTC	SP1 in <i>nrdA</i> 5'RACE
45	Oligo dT	GACCACGCGTATCGATGTCGACTTTTTTTT TTTTTTTTT	PCR1 in 5'RACE
46	PCR Anchor Primer	GACCACGCGTATCGATGTCGAC	PCR2 in 5'RACE
47	TSS_PAO_UTRnrdA_rv	CGAATGCTGAGGGTGGGGAC	SP3 in <i>nrdA</i> 5'RACE
48	pJET 1.2 Fw	CGACTCACTATAGGGAGAGCGGC	Check cloning/Sequencing
49	pJET 1.2 Rv	AAGAACATCGATTTTCCATGGCAG	Check cloning/Sequencing
50	pUCP20T-up	CCTCTTCGCTATTACGCCAG	Check cloning/Sequencing

Figure S1. Riboswitch analysis. Results retrieved in 2021 by Riboswitch Scanner Software ^{6,7}

Targeted riboswitch family: Cobalamin

MAIN STRAND (5'-3') :

No	Score	E-value	Region from	Region to
1	6.1	0.00058	249	378

COMPLEMENTARY STRAND (3'-5') :

No such riboswitch found

RIBOSWITCH SEQUENCES :

>seq: 249-378

ATGACGTTGGAAAAGCGGTACGGGTGTTGCAACGGACGCTGTAAACAGACAGTCAACACC
ACTAGGTATTGTGTTTCGACGGCAAAACGCCACGAACCCGCCAGGGCCAGGGAGGCACTCA
CAGTCCCCAC

Figure S2. *nrdA* expression with and without the 5'UTR in PAO1 WT and RNA-processing mutants. (a) Transcriptional expression of *nrdA* in *P. aeruginosa* PAO1 WT pETS130-GFP derivative strains compared to chromosomal mutants in RNA-processing related genes. (b) Transcriptional expression of *nrdA* lacking the 5'UTR in PAO1 WT pETS130-GFP derivatives compared to RNA-processing related gene chromosomal mutants.

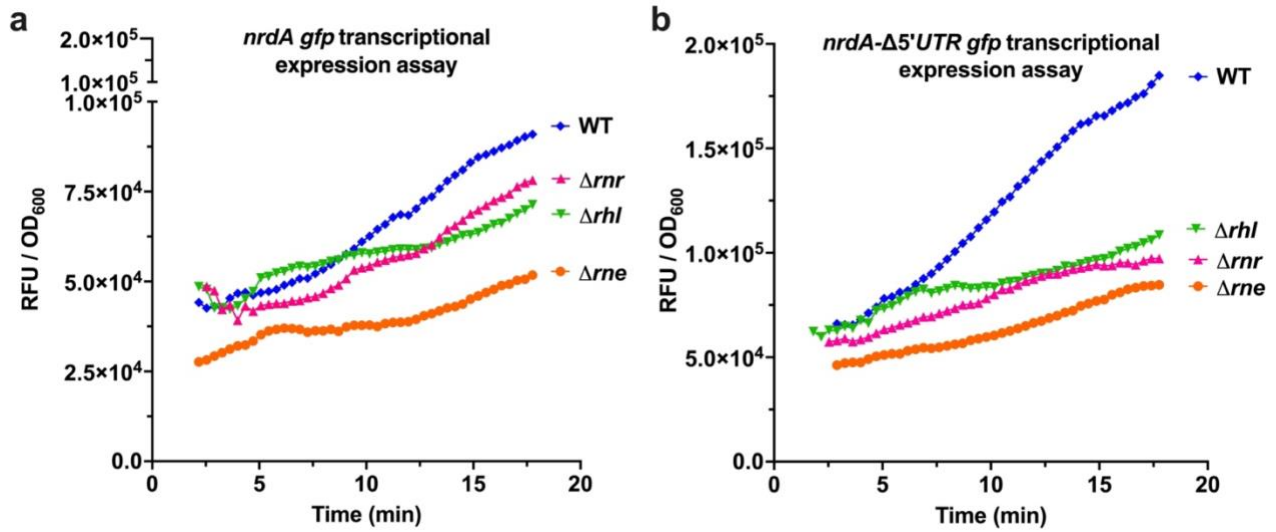


Figure S3. *nrdJ* expression under aerobic and anaerobic conditions. (a) Fold Change values of *nrdJ* expression measured by RT-qPCR in PAO1 $\Delta 5'$ UTR (*nrdA*) (chromosomically deleted) compared to PAO1 WT, under both aerobic and anaerobic conditions during exponential and stationary growth phases. Significance: p -value <0.0001 (****). **(b)** Fold Change values of *nrdJ* expression measured by RT-qPCR comparing PAO1 WT and PAO1 $\Delta 5'$ UTR (*nrdA*) during *Galleria mellonella* infection **(c)** Western blot analysis of NrdJ protein levels in PAO1 WT and PAO1 $\Delta 5'$ UTR (*nrdA*) during exponential and stationary growth under aerobic and anaerobic conditions. The cropped version is shown; the full-length and cropped blot is presented below in this Supplementary Figure S4 and is also available at <https://doi.org/10.34810/data2361>.

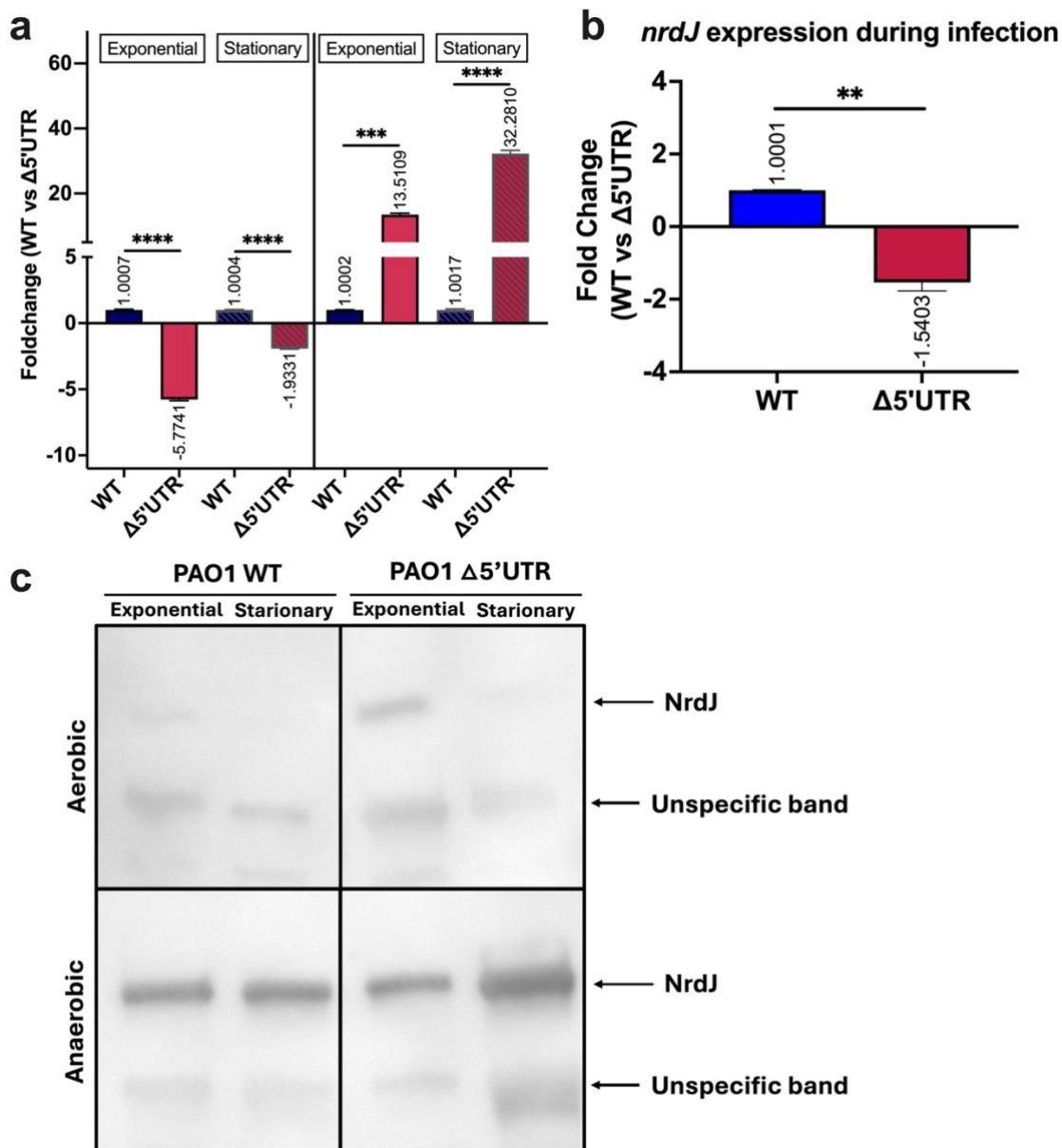
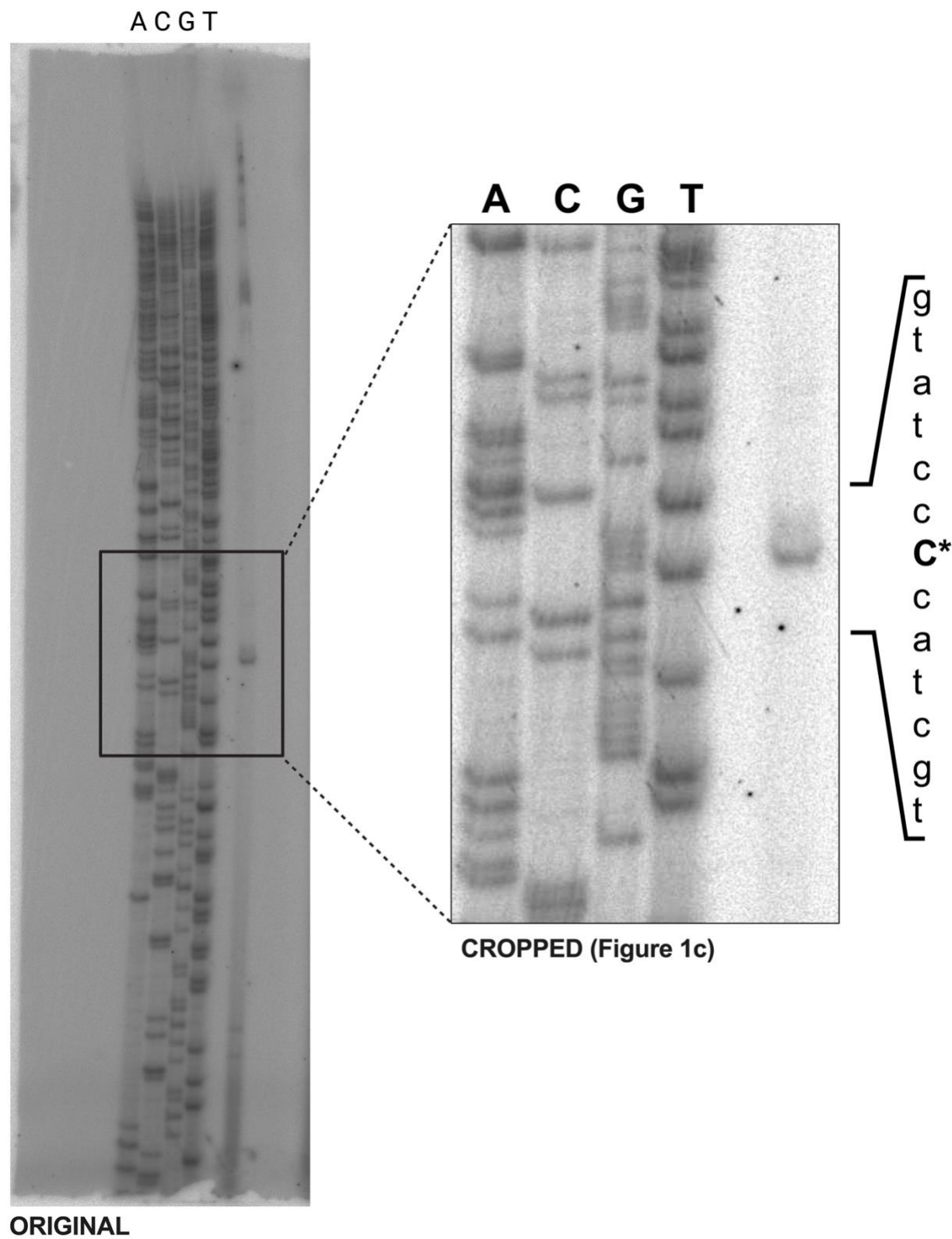
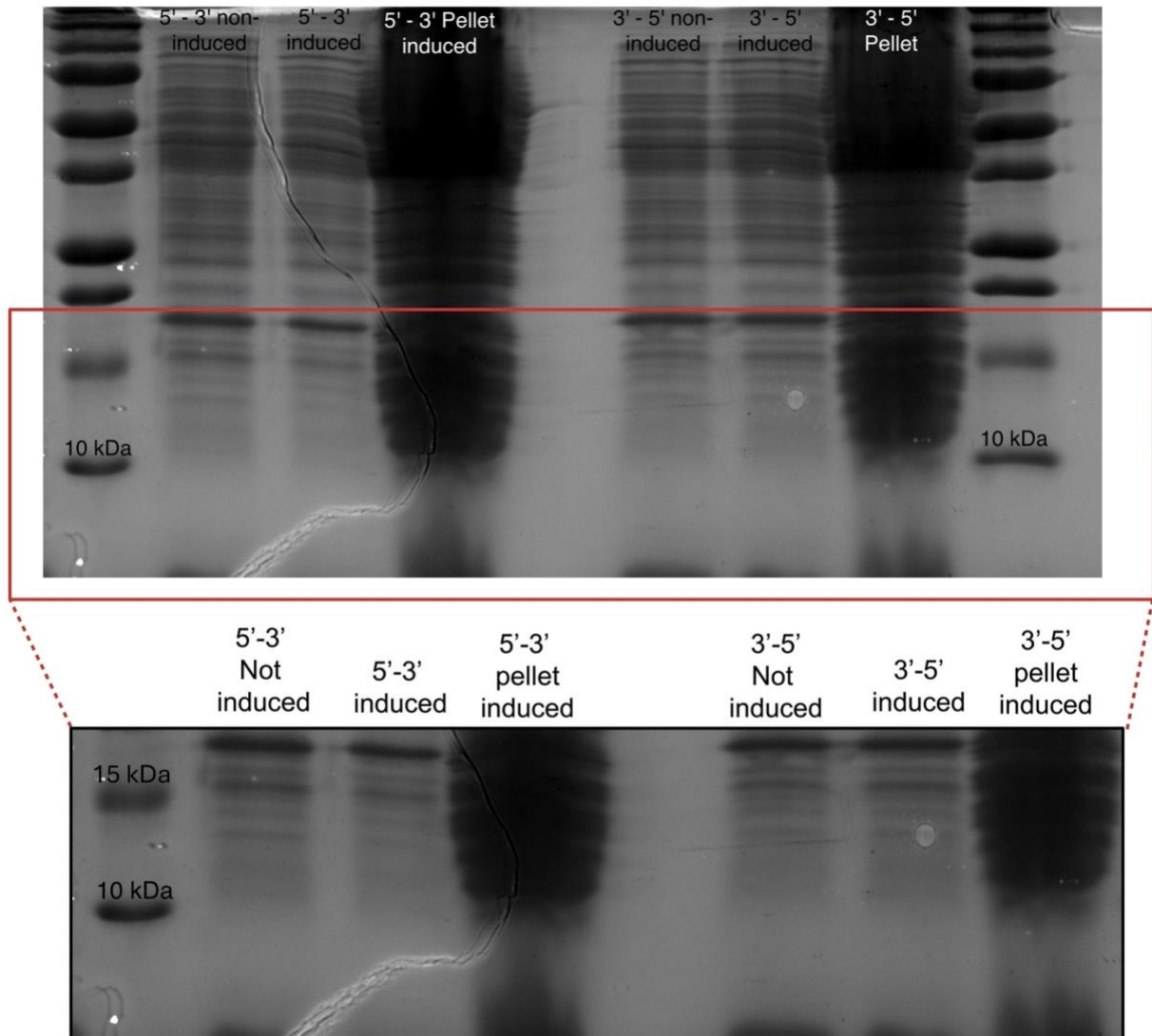


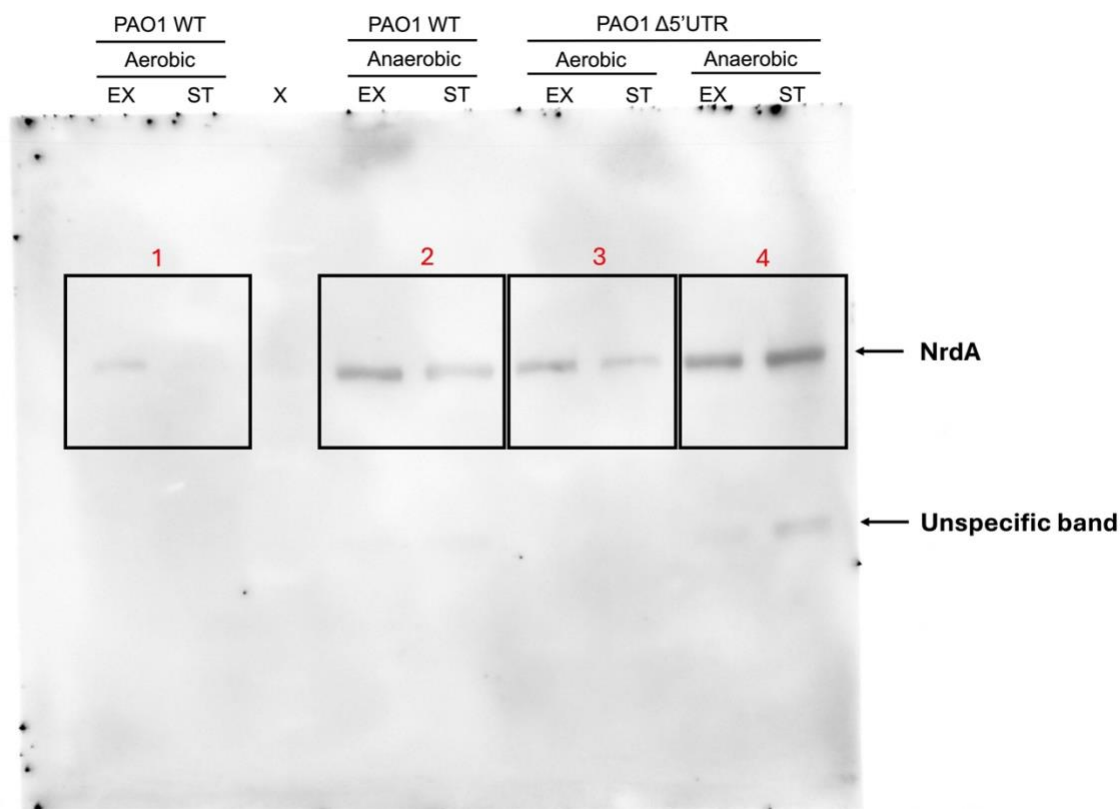
Figure S4. Original and cropped gels/blots from Figure 1c, Figure 3b, Figure 6c, Figure S3c



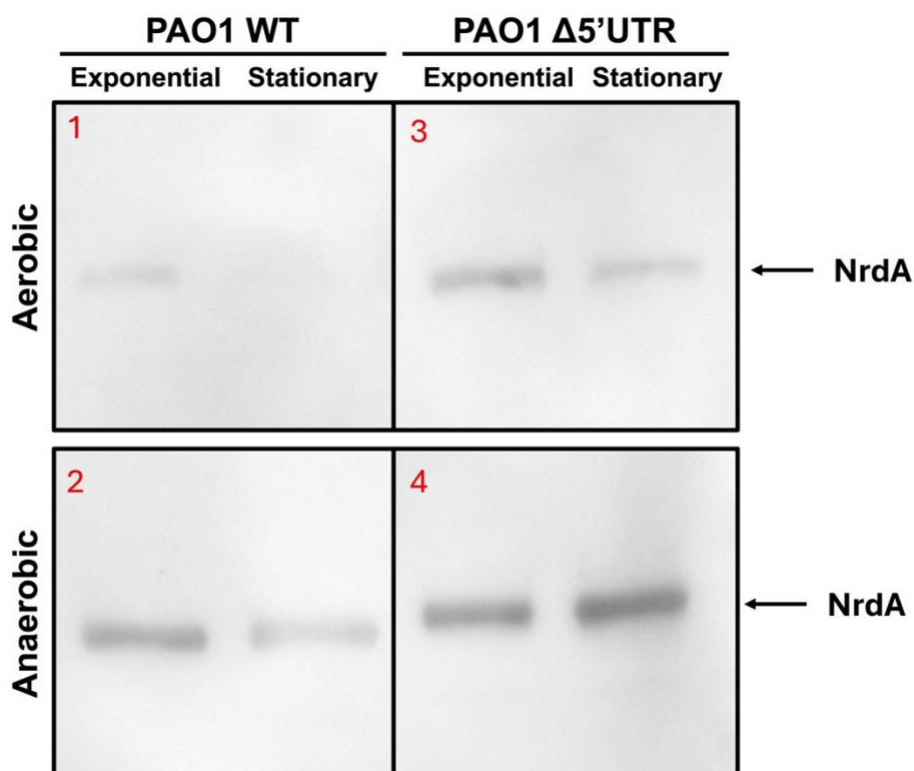
ORIGINAL



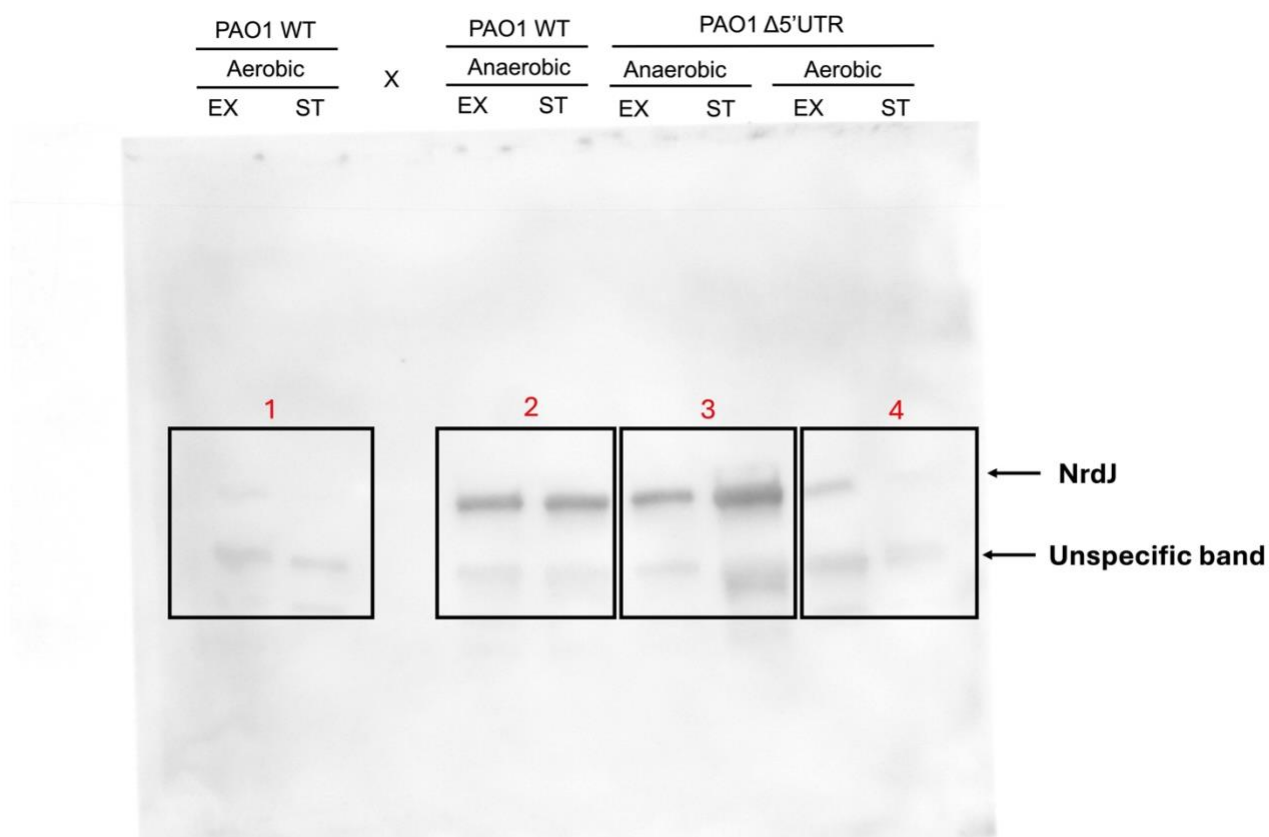
CROPPED (Figure 3b)



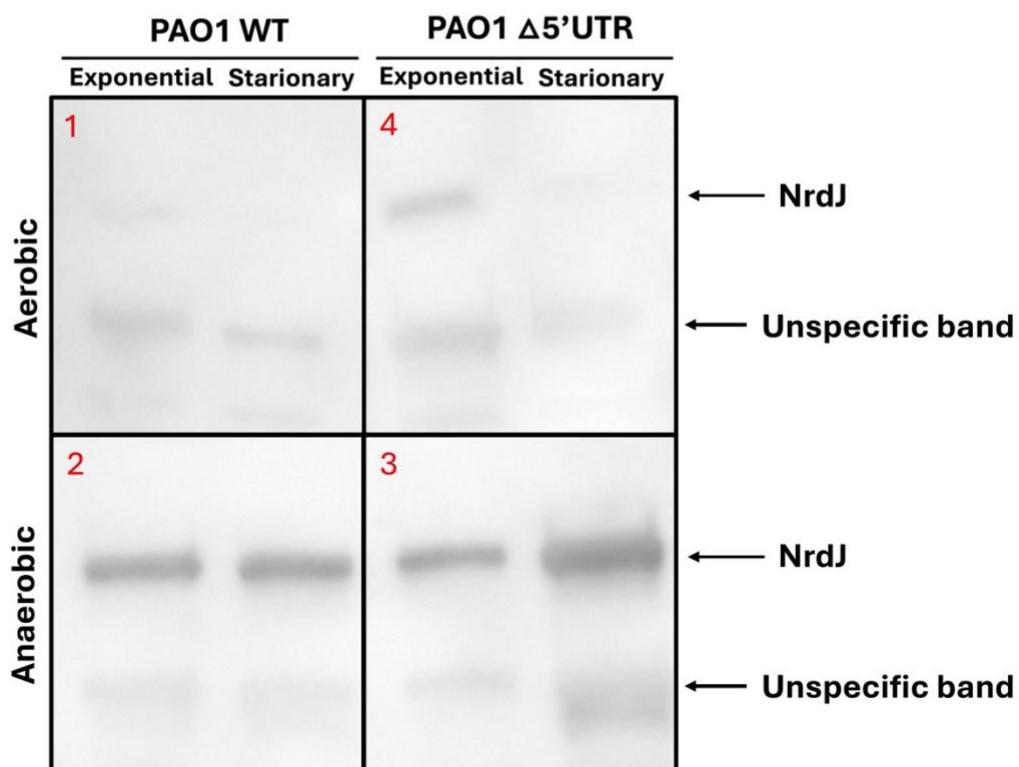
ORIGINAL



CROPPED (Figure 6c)



ORIGINAL



CROPPED (Figure S3c)

1. Sjöberg, B. M. & Torrents, E. Shift in ribonucleotide reductase gene expression in *Pseudomonas aeruginosa* during infection. *Infect Immun* **79**, 2663–2669 (2011).
2. Crespo, A., Pedraz, L., Van Der Hofstadt, M., Gomila, G. & Torrents, E. Regulation of ribonucleotide synthesis by the *Pseudomonas aeruginosa* two-component system AlgR in response to oxidative stress. *Sci Rep* **7**, 1–15 (2017).
3. Newman, J. R. & Fuqua, C. Broad-host-range expression vectors that carry the L-arabinose-inducible *Escherichia coli* *araBAD* promoter and the *araC* regulator. *Gene* **227**, 197–203 (1999).
4. Pankratz, D. *et al.* An Expanded CRISPR–Cas9-Assisted Recombineering Toolkit for Engineering Genetically Intractable *Pseudomonas aeruginosa* Isolates. *Nature Protocols* vol. 18 (Springer US, 2023).
5. Jacobs, M. A. *et al.* Comprehensive transposon mutant library of *Pseudomonas aeruginosa*. *Proc Natl Acad Sci U S A* **100**, 14339–14344 (2003).
6. Singh, P., Bandyopadhyay, P., Bhattacharya, S., Krishnamachari, A. & Sengupta, S. Riboswitch detection using Profile Hidden Markov Models. *BMC Bioinformatics* **10**, 1–13 (2009).
7. Mukherjee, S. & Sengupta, S. Riboswitch Scanner: an efficient pHMM-based web-server to detect riboswitches in genomic sequences. *Bioinformatics* **32**, 776–778 (2016).