

Quorum sensing in *Pseudomonas aeruginosa* mediated by RhIR is regulated by a small RNA PhrD

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Table S1 List of putative targets of PhrD in RNA Predator program

Rank	Energy (kJ/mole)	Z score	Targets
1	-21.53	-4.67	major facilitator transporter
2	-21.22	-4.56	TolR protein
3	-20.54	-4.32	putative transporter
4	-19.76	-4.04	hypothetical protein PA2935
5	-19.52	-3.95	hypothetical protein PA4536
6	-19.47	-3.93	Transposase
7	-19.39	-3.9	hypothetical protein PA2777
8	-19.38	-3.9	Hcp1
9	-19.24	-3.85	hypothetical protein PA2126
10	-19.12	-3.8	DNA polymerase III subunit alpha
11	-18.98	-3.75	4 hydroxy 3 methylbut 2 enyl diphosphate reductase
12	-18.87	-3.71	hypothetical protein PA4712
13	-18.44	-3.56	hypothetical protein PA0819
14	-18.37	-3.53	hypothetical protein PA5132
15	-18.28	-3.5	hypothetical protein PA4685
16	-17.99	-3.4	putative serine/threonine protein kinase
17	-17.99	-3.4	putative glycosyl transferase
18	-17.88	-3.36	hypothetical protein PA2462
19	-17.87	-3.35	putative glutathione peroxidase
20	-17.74	-3.31	chemotaxis specific methyltransferase
21	-17.72	-3.3	hemin importer ATP binding subunit
22	-17.69	-3.29	apolipoprotein N acyltransferase
23	-17.68	-3.29	NADH dehydrogenase subunit N
24	-17.66	-3.28	putative aminopeptidase
25	-17.62	-3.26	type III secretion system protein
26	-17.59	-3.25	hypothetical protein PA2222
27	-17.54	-3.23	pyrroloquinoline quinone biosynthesis protein F
28	-17.53	-3.23	NosY protein
29	-17.48	-3.21	multidrug efflux protein NorA
30	-17.46	-3.21	GbdR
31	-17.32	-3.16	ClpB protein
32	-17.28	-3.14	arginyl tRNA synthetase
33	-17.10	-3.08	branched chain amino acid ABC transporter permease
34	-17.08	-3.07	hypothetical protein PA1111
35	-17.02	-3.05	putative iron sulfur cluster binding protein; Rieske family
36	-16.92	-3.01	PvdJ
37	-16.89	-3	transcriptional regulator RhlR
38	-16.81	-2.97	'two component response regulator; CopR '
39	-16.81	-2.97	4 amino 4 deoxy L arabinose transferase
40	-16.76	-2.95	hypothetical protein PA2502
41	-16.69	-2.93	hypothetical protein PA4612
42	-16.60	-2.9	ABC transporter permease
43	-16.56	-2.88	hypothetical protein PA3127
44	-16.55	-2.88	putative oxidoreductase
45	-16.51	-2.86	major facilitator transporter
46	-16.45	-2.84	BifA

47	-16.44	-2.84	putative transcriptional regulator
48	-16.38	-2.82	transcriptional regulator
49	-16.26	-2.77	manganese transport protein MntH
50	-16.22	-2.76	hypothetical protein PA2984

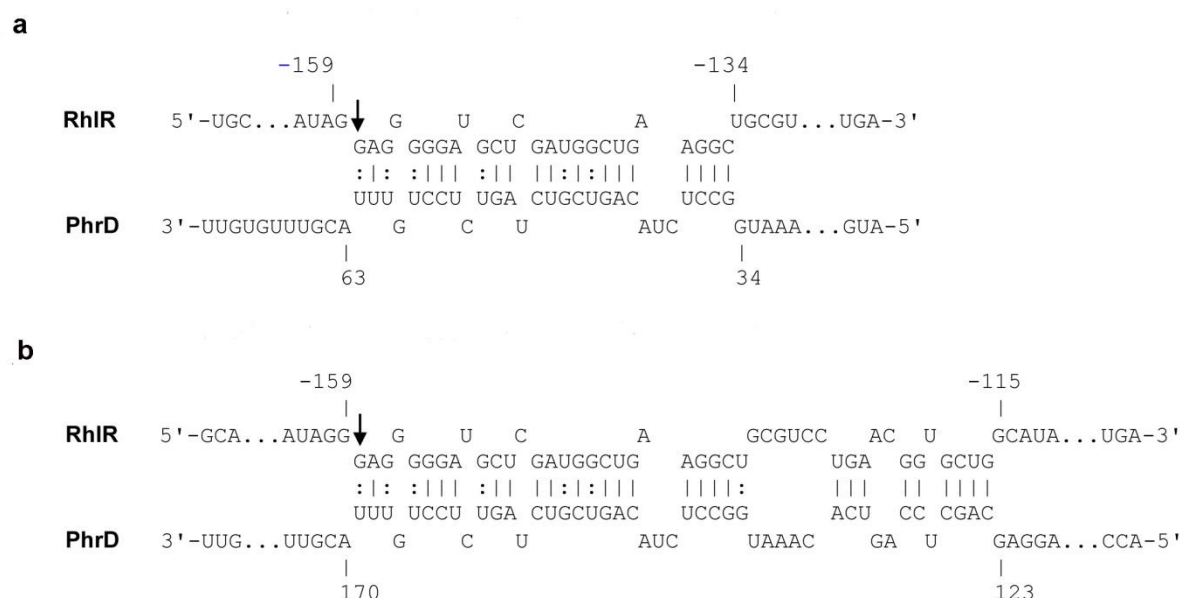


Figure S1 Comparison of RNA-RNA interaction of *rhlR* with *PhrD* expressed from the chromosome (a) and plasmid (b). The former interaction is completely seen in the later as indicated by IntaRNA program. The numbers on *PhrD* indicate nucleotide from the transcription start site.

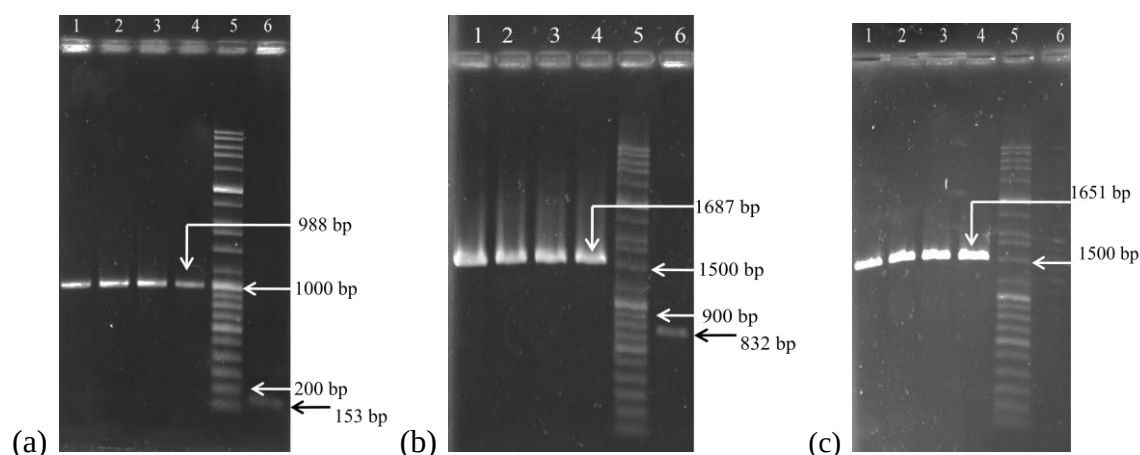


Figure S2 Confirmation of *phrD* disruption by PCR. **(a)** *PhrD* ncRNA F/R primers; Lane 1-4: Double cross over *phrD* mutants, Lane 5: High range marker (100-10,000 bp), Lane 6: PAO1 WT (amplicon of 153bp from WT *PhrD*) **(b)** *PhrD* ncRNA F/ *PhrD* Dn R primers; Lane 1-4: Double cross over *phrD* mutants, Lane 5: High range marker (100-10,000 bp), Lane 6: PAO1 WT **(c)** Gm F/ *PhrD* Dn R primers; Lane 1-4: Double cross over mutants, Lane 5: High range marker (100-10,000 bp), Lane 6: PAO1 WT (no amplification due to absence of gentamicin cassette).

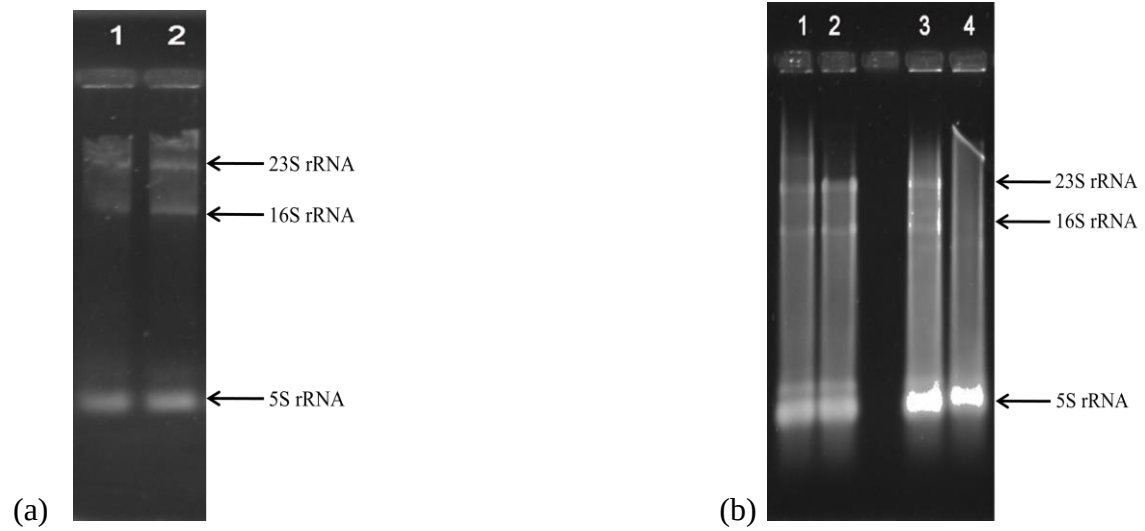


Figure S3 RNA for northern blot of *phrD* expression under different nutrient conditions. **(a)** Lane 1 and 2: RNA extracted from cells grown in PPGAS medium. **(b)** Lane 1 and 2: RNA extracted from cells grown in Luria broth, Lane 3 and 4: RNA extracted from cells grown in MMP medium.