Supplementary File

Deciphering the molecular mechanisms underlying anti-pathogenic potential of a polyherbal formulation Enteropan® against multi-drug resistant *Pseudomonas aeruginosa*

Sweety Parmar[1#], Gemini Gajera[1#], Nidhi Thakkar[1#], Hanmanthrao S Palep[2], Vijay Kothari[1*]
[1]Institute of Science, Nirma University, Ahmedabad, 382481, India.
[2]Dr. Palep's Medical Research Foundation, Mumbai, India
[#]Contributed equally
[*]Correspondence: vijay.kothari@nirmauni.ac.in

Table S1. Antibiogram of *P. aeruginosa* generated through Kirby-Bauer Disc Diffusion assay

Antibiotic	Concentration (µg/disc)	Interpretation
Imipenem (IPM)	10	Sensitive
Ciprofloxacin (CIP)	5	Sensitive
Tobramycin (TOB)	10	Sensitive
Moxifloxacin (MO)	5	Sensitive
Ofloxacin (OF)	5	Sensitive
Sparfloxacin (SPX)	5	Sensitive
Levofloxacin (LE)	5	Sensitive
Norfloxacin (NX)	10	Sensitive
Co-Trimoxazole (COT)	25	Resistant
Colistin (CL)	10	Sensitive
Nalidixic acid (NA)	30	Sensitive
Augmentin (AMC)	30	Resistant
Kanamycin (K)	30	Intermediate
Gatifloxacin (GAT)	5	Sensitive
Gentamicin (GEN)	10	Sensitive
Amikacin (AK)	30	Sensitive
Streptomycin (S)	25	Resistant
Ceftriaxone (CTR)	30	Sensitive
Cefpodoxime (CPD)	10	Sensitive
Ticarcillin (TI)	75	Sensitive

Antibiotic susceptibility profile of the organism was generated using the antibiotic discs- Icosa GI Minus (HiMedia, Mumbai) through disc diffusion assay on cation-adjusted Mueller-Hinton agar (HiMedia) as per CLSI guidelines (https://doi.org/10.1177/001857870403900608). The zones of inhibition were measured and the interpretation (S- sensitive, I - intermediate, R - resistant) was drawn as per zone size interpretative chart provided by the manufacturer

Table S2. Quantification of extracted RNA

Sr. No.	Sample Name	ng/µl	260/280	260/230	Quant (ng/µl)	RIN Value	QC Remark
1	Control	3744.4	2.15	2.22	1984	7.6	Pass
2	Experimental	2523.3	1.94	1.75	976	7.3	Pass

Table S3. Library preparation and quality control

Sr. No.	Sample Name	ng/µl	Quant (ng/µl)	Index	QC Remark
1	Control	4.58	271	52	Pass
2	Experimental	0.912	281	53	Pass

Table S4. Temperature profile for the RT-PCR assay

Temperature (ºC)	**Time** (Seconds)
PCR stage (45 Cycles)	
95	15
59	60
Melt curve stage	
95	15
60	60
95	15

Table S5. Enteropan pre-treatment modulated bacterial susceptibility to some antibiotics

Antibiotic	**Symbol**	**Concentration** (µg/disc)	**Zone of inhibition** (mm)		**% Difference**
			Control (Mean ± SD)	**Experimental** (Mean ± SD)	
Imipenem	IMP	10	25.6±2	29.6±1.5	15.58* ± 7.9
Ciprofloxacin	CIP	5	40±2.6	39±3.5	Not significant
Tobramycin	TOB	10	31±3	29±1.5	
Moxifloxacin	MO	5	30±0.5	31±2	
Ofloxacin	OF	5	32±2	30±2.3	
Sparfloxacin	SPX	5	29±0.5	30±0.5	
Levofloxacin	LE	5	37±2.5	37±2.5	
Norfloxacin	NX	10	33±1.5	34±1	
Co-Trimoxazole	COT	25	0	0	
Colistin	CL	10	20±0.5	20±0.5	
Nalidixic acid	NA	30	15±0.5	17±1.7	
Augmentin	AMC	30	10	0	100*** ± 0
Kanamycin	K	30	12±1	13±2	Not significant
Gatifloxacin	GAT	5	31±1	32±1	
Gentamicin	GEN	10	22±2	21±1	
Amikacin	AK	30	24.5±1.5	23±5	
Streptomycin	S	25	0	0	
Ceftriaxone	CTR	30	21±0.5	23±1	
Cefpodoxime	CPD	10	22±3	22±4	
Ticarcillin	TI	15	19	20	

Antibiotic susceptibility profile of the bacterium was generated using the antibiotic discs- Icosa G-I Minus (HiMedia, Mumbai), through disc diffusion assay performed as per CLSI guidelines. The zones of inhibition were measured and the interpretation (S - sensitive, I - intermediate, R - resistant) was drawn as per zone size interpretative chart provided by the manufacturer. *$p<0.05$

Table S6. List of Up-regulated genes in Enteropan exposed *P. aeruginosa* satisfying the dual criteria of log fold change ≥2 and FDR≤0.001

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
1	PA2399	*pvdD*	pyoverdine synthetase D	14.13	3.68311E-15
2	PA1094	*fliD*	B-type flagellar hook-associated protein	13.98	5.10836E-15
3	PA1091	*fgtA*	flagellar glycosyl transferase FgtA	13.75	1.25225E-14
4	PA3160	*Wzz*	O-antigen chain length regulator	13.75	1.25225E-14
5	PA3145	*wbpL*	glycosyltransferase WbpL	13.56	3.78409E-14
6	PA3153	*Wzx*	O-antigen translocase	13.39	9.85022E-14
7	PA3487	*pldA*	phospholipase D	13.32	1.32823E-13
8	PA2732	NA	hypothetical protein	13.26	1.56091E-13
9	PA2398	*fpvA*	ferripyoverdine receptor	13.26	1.56091E-13
10	PA1095	NA	B-type flagellar protein FliS	13.10	4.2517E-13
11	PA3154	*Wzy*	B-band O-antigen polymerase	13.05	5.42286E-13
12	PA3157	NA	Acetyltransferase	12.92	1.05141E-12
13	PA3488	NA	hypothetical protein	12.91	1.09728E-12
14	PA1087	*flgL*	flagellar hook-associated protein FlgL	12.81	1.80849E-12
15	PA3866	NA	pyocin protein	12.78	2.0428E-12
16	PA2735	NA	restriction-modification system protein	12.75	2.39147E-12
17	PA3159	*wbpA*	UDP-N-acetyl-d-glucosamine 6-dehydrogenase	12.74	2.40102E-12
18	PA1428a	NA	hypothetical protein	12.53	8.39067E-12
19	PA2818	*Arr*	aminoglycoside response regulator	12.53	8.39067E-12
20	PA2119	NA	alcohol dehydrogenase	12.42	1.42681E-11
21	PA0561	NA	hypothetical protein	12.36	2.02829E-11
22	PA0985	*pyoS5*	pyocin S5	12.28	3.36661E-11
23	PA0498	NA	hypothetical protein	12.26	3.74703E-11
24	PA0826	NA	hypothetical protein	12.21	4.64138E-11
25	PA0821	NA	hypothetical protein	12.21	4.64138E-11
26	PA1939	NA	hypothetical protein	12.19	5.11036E-11
27	PA1888	NA	hypothetical protein	12.06	1.12609E-10
28	PA3868	NA	hypothetical protein	12.05	1.12609E-10
29	PA3506	NA	hypothetical protein	11.98	1.80412E-10
30	PA0497	NA	hypothetical protein	11.96	1.94271E-10
31	PA3147	*wbpJ*	glycosyl transferase WbpJ	11.91	2.42097E-10
32	PA4797	NA	Transposase	11.91	2.42097E-10
33	PA3993	NA	Transposase	11.88	2.53006E-10
34	PA2319	NA	Transposase	11.85	2.80745E-10
35	PA0716	NA	hypothetical protein	11.80	3.72012E-10
36	PA0978	NA	hypothetical protein	11.78	3.8445E-10
37	PA3500	NA	hypothetical protein	11.78	3.87946E-10
38	PA2219	*opdE*	transcriptional regulator OpdE	11.76	4.22853E-10
39	PA2734	NA	hypothetical protein	11.76	4.22853E-10

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
40	PA3146	*wbpK*	NAD-dependent epimerase/dehydratase	11.76	4.22853E-10
41	PA2690	NA	Transposase	11.71	2.33324E-10
42	PA1370	NA	hypothetical protein	11.70	2.41787E-10
43	PA3504	NA	aldehyde dehydrogenase	11.68	2.44885E-10
44	PA2101	NA	hypothetical protein	11.68	2.44885E-10
45	PA0981	NA	hypothetical protein	11.67	2.44885E-10
46	PA0188	NA	hypothetical protein	11.67	2.47595E-10
47	PA3434	NA	Transposase	11.67	2.50443E-10
48	PA1366	NA	hypothetical protein	11.64	2.75999E-10
49	PA1372	NA	hypothetical protein	11.63	2.92294E-10
50	PA2073	NA	transporter membrane subunit	11.61	3.15239E-10
51	PA0445	NA	Transposase	11.58	3.73749E-10
52	PA2459	NA	hypothetical protein	11.58	3.79803E-10
53	PA1093	NA	hypothetical protein	11.57	3.8445E-10
54	PA1368	NA	hypothetical protein	11.56	3.87946E-10
55	PA3497	NA	hypothetical protein	11.53	4.25297E-10
56	PA3549	*algJ*	alginate o-acetylase AlgJ	11.53	4.25297E-10
57	PA2100	NA	transcriptional regulator	11.52	4.62825E-10
58	PA2099	NA	short-chain dehydrogenase	11.48	5.95777E-10
59	PA2091	NA	hypothetical protein	11.46	6.50932E-10
60	PA2566	NA	hypothetical protein	11.44	7.44011E-10
61	PA2220	NA	transcriptional regulator	11.38	1.00798E-09
62	PA3158	*wbpB*	UDP-N-acetyl-2-amino-2-deoxy-D-glucuronate oxidase	11.38	1.00798E-09
63	PA0715	NA	hypothetical protein	11.32	1.39194E-09
64	PA0982	NA	hypothetical protein	11.31	1.48398E-09
65	PA1938	NA	hypothetical protein	11.26	1.96615E-09
66	PA2221	NA	hypothetical protein	11.25	2.0238E-09
67	PA0820	NA	hypothetical protein	11.24	2.08366E-09
68	PA2228	NA	hypothetical protein	11.22	2.41626E-09
69	PA0187	NA	hypothetical protein	11.13	3.9928E-09
70	PA3867	NA	DNA invertase	11.13	4.12502E-09
71	PA3513	NA	hypothetical protein	11.12	4.2233E-09
72	PA1351	NA	ECF subfamily sigma-70 factor	11.11	4.28719E-09
73	PA1088	NA	hypothetical protein	11.07	5.45271E-09
74	PA3149	*wbpH*	glycosyltransferase WbpH	11.07	5.64638E-09
75	PA1380	NA	transcriptional regulator	11.06	5.79808E-09
76	PA3155	*wbpE*	UDP-2-acetamido-2-deoxy-3-oxo-D-glucuronate aminotransferase	11.06	5.79808E-09
77	PA2730	NA	hypothetical protein	11.02	7.11987E-09
78	PA3151	*hisF2*	imidazole glycerol phosphate synthase subunit HisF	11.00	8.02025E-09
79	PA3150	*wbpG*	LPS biosynthesis protein WbpG	10.97	9.4834E-09

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
80	PA3152	*hisH2*	imidazole glycerol phosphate synthase subunit HisH	10.88	1.61662E-08
81	PA3510	NA	hypothetical protein	10.88	1.61662E-08
82	PA2104	NA	cysteine synthase	10.86	1.81848E-08
83	PA0824	NA	hypothetical protein	10.86	1.81848E-08
84	PA3511	NA	short-chain dehydrogenase	10.83	2.06736E-08
85	PA1379	NA	short-chain dehydrogenase	10.83	2.121E-08
86	PA3514	NA	ABC transporter ATP-binding protein	10.82	2.20676E-08
87	PA0984	NA	colicin immunity protein	10.80	2.42855E-08
88	PA2733	NA	hypothetical protein	10.79	2.5397E-08
89	PA2461	NA	hypothetical protein	10.75	3.192E-08
90	PA2103	NA	molybdopterin biosynthesis protein MoeB	10.74	3.32203E-08
91	PA3142	NA	hypothetical protein	10.73	3.41347E-08
92	PA3143	NA	hypothetical protein	10.72	3.57971E-08
93	PA2223	NA	hypothetical protein	10.71	3.75532E-08
94	PA3148	*wbpI*	UDP-2,3-diacetamido-2,3-dideoxy-D-glucuronate 2-epimeras	10.68	4.62232E-08
95	PA2460	NA	hypothetical protein	10.68	4.62232E-08
96	PA2106	NA	hypothetical protein	10.64	5.6473E-08
97	PA2736	NA	hypothetical protein	10.63	5.94262E-08
98	PA3498	NA	Oxidoreductase	10.61	6.85628E-08
99	PA3381	NA	transcriptional regulator	10.58	8.06539E-08
100	PA3512	NA	ABC transporter permease	10.58	8.06539E-08
101	PA2218	NA	hypothetical protein	10.57	8.42948E-08
102	PA1887	NA	hypothetical protein	10.56	8.7959E-08
103	PA1937	NA	hypothetical protein	10.55	8.7959E-08
104	PA2564	NA	trans-aconitate 2-methyltransferase	10.47	1.45077E-07
105	PA2387	*fpvI*	RNA polymerase sigma factor	10.45	1.52147E-07
106	PA1378	NA	hypothetical protein	10.43	1.70321E-07
107	PA3865a	NA	hypothetical protein	10.42	1.78934E-07
108	PA1151	*imm2*	pyocin-S2 immunity protein	10.38	2.22683E-07
109	PA0522	NA	hypothetical protein	10.38	2.22683E-07
110	PA0979	NA	hypothetical protein	10.34	2.70275E-07
111	PA0825	NA	hypothetical protein	10.31	3.24308E-07
112	PA2105	NA	Acetyltransferase	10.28	3.67943E-07
113	PA2427	NA	hypothetical protein	10.24	4.7244E-07
114	PA1089	NA	hypothetical protein	10.21	5.30195E-07
115	PA3501	NA	hypothetical protein	10.21	5.30195E-07
116	PA4823	NA	hypothetical protein	10.15	7.3674E-07
117	PA0986	NA	hypothetical protein	10.13	8.31928E-07
118	PA0983	NA	hypothetical protein	10.12	8.31928E-07
119	PA1090	NA	hypothetical protein	10.10	9.57461E-07

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
120	PA0823	NA	hypothetical protein	10.10	9.57461E-07
121	PA0209	NA	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	10.08	1.02062E-06
122	PA3156	*wbpD*	UDP-2-acetamido-3-amino-2,3-dideoxy-D-glucuronate N-acetyltransferase	10.07	1.07604E-06
123	PA2516	*xylZ*	toluate 1,2-dioxygenase electron transfer subunit	10.06	1.07604E-06
124	PA3508	NA	transcriptional regulator	10.03	1.33268E-06
125	PA0213	NA	phosphoribosyl-dephospho-CoA transferase	10.01	1.43263E-06
126	PA3869	NA	hypothetical protein	10.00	1.53914E-06
127	PA1981	NA	hypothetical protein	9.99	1.6561E-06
128	PA3507	NA	short-chain dehydrogenase	9.96	1.93577E-06
129	PA3505	NA	L-aspartate dehydrogenase	9.95	2.0662E-06
130	PA3502	NA	hypothetical protein	9.91	2.41059E-06
131	PA5417	*soxD*	sarcosine oxidase subunit delta	9.77	4.98351E-06
132	PA2102	NA	hypothetical protein	9.72	5.77943E-06
133	PA3509	NA	Hydrolase	9.67	7.5136E-06
134	PA2161	NA	hypothetical protein	9.56	1.26957E-05
135	PA3380	NA	hypothetical protein	9.56	1.26957E-05
136	PA1369	NA	hypothetical protein	9.54	1.38061E-05
137	PA1371	NA	hypothetical protein	9.52	1.51726E-05
138	PA2565	NA	hypothetical protein	9.51	1.51726E-05
139	PA2224	NA	hypothetical protein	9.49	1.82008E-05
140	PA1702	NA	hypothetical protein	9.48	1.82008E-05
141	PA0210	*mdcC*	malonate decarboxylase acyl carrier protein	9.42	2.45359E-05
142	PA3499	NA	hypothetical protein	9.42	2.45359E-05
143	PA2225	NA	hypothetical protein	9.40	2.70635E-05
144	PA2098	NA	Esterase	9.37	2.98572E-05
145	PA1635	*kdpC*	potassium-transporting ATPase subunit C	9.36	3.28091E-05
146	PA2227	*vqsM*	HTH-type transcriptional regulator VqsM	9.30	4.51481E-05
147	PA2222	NA	hypothetical protein	8.84	0.0002
148	PA1700	NA	hypothetical protein	8.62	0.0007
149	PA2368	NA	hypothetical protein	8.58	0.0008
150	PA1849	NA	hypothetical protein	8.41	0.0004
151	PA2226	NA	hypothetical protein	8.30	0.0006
152	PA2457	NA	hypothetical protein	7.58	1.3333E-11
153	PA4894	NA	hypothetical protein	7.40	1.25832E-09
154	PA4860	NA	ABC transporter permease	7.39	1.27621E-09
155	PA0695	NA	hypothetical protein	7.19	4.17225E-09
156	PA2400	*pvdJ*	pyoverdine biosynthesis protein PvdJ	6.95	8.39067E-12

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
157	PA0697	NA	hypothetical protein	6.83	2.97214E-08
158	PA3774	NA	acetylpolyamine aminohydrolase	6.72	5.26668E-08
159	PA1352	NA	hypothetical protein	6.68	6.67308E-08
160	PA2472	NA	major facilitator superfamily transporter	6.65	1.74802E-09
161	PA5401	NA	hypothetical protein	6.61	9.7707E-08
162	PA1698	*popN*	type III secretion outer membrane protein PopN	6.40	2.96117E-07
163	PA0021		hypothetical protein	6.27	1.45581E-08
164	PA4525	*pilA*	type 4 fimbrial protein PilA	6.26	3.21053E-10
165	PA4088		Aminotransferase	6.21	2.09682E-08
166	PA1275	*cobD*	cobalamin biosynthesis protein CobD	6.18	9.57461E-07
167	PA3406	*hasD*	transporter HasD	6.14	4.25628E-09
168	PA2397	*pvdE*	pyoverdine biosynthesis protein PvdE	6.10	1.11433E-09
169	PA4097	NA	alcohol dehydrogenase	6.04	1.87569E-06
170	PA0440	NA	Oxidoreductase	6.00	9.82392E-09
171	PA5392	NA	hypothetical protein	5.79	3.14228E-08
172	PA2336	NA	hypothetical protein	5.76	3.41347E-08
173	PA3379	NA	carbon-phosphorus lyase complex subunit	5.73	8.60461E-06
174	PA4152	NA	branched-chain alpha-keto acid dehydrogenase subunit E2	5.72	2.75675E-07
175	PA2724	NA	hypothetical protein	5.69	3.38903E-07
176	PA0683	NA	type II secretion system protein	5.67	3.78438E-07
177	PA2090	NA	hypothetical protein	5.64	1.31979E-05
178	PA3375	NA	ABC transporter ATP-binding protein	5.60	1.59524E-05
179	PA2092	NA	major facilitator superfamily transporter	5.53	1.24899E-07
180	PA1265	NA	hypothetical protein	5.53	1.28024E-07
181	PA0112	NA	hypothetical protein	5.50	1.48874E-07
182	PA0881	NA	hypothetical protein	5.46	1.8238E-07
183	PA0514	*nirL*	heme d1 biosynthesis protein NirL	5.39	4.37275E-05
184	PA0842	NA	glycosyl transferase family protein	5.38	8.72814E-08
185	PA2343	*mtlY*	xylulose kinase	5.38	2.79528E-07
186	PA0480	NA	3-oxoadipate enol-lactonase	5.38	2.79528E-07
187	PA2699	NA	hypothetical protein	5.30	2.121E-08
188	PA4649	NA	hypothetical protein	5.30	4.46792E-07
189	PA4892	*ureF*	urease accessory protein UreF	5.27	2.91953E-06
190	PA0525	NA	denitrification protein NorD	5.27	1.67072E-07
191	PA3543	*algK*	alginate biosynthesis protein AlgK	5.27	6.235E-08
192	PA2257	*pvcD*	paerucumarin biosynthesis protein PvcD	5.26	7.71862E-05
193	PA0513	NA	heme d1 biosynthesis protein NirG	5.26	7.71862E-05
194	PA1486	NA	hypothetical protein	5.24	5.77796E-07
195	PA1021	NA	enoyl-CoA hydratase	5.24	5.93922E-07

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
196	PA2923	*hisJ*	histidine ABC transporter substrate-binding protein HisJ	5.18	7.9005E-07
197	PA2396	*pvdF*	pyoverdine synthetase F	5.18	2.70275E-07
198	PA4884	NA	hypothetical protein	5.16	8.70272E-07
199	PA2515	*xylL*	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	5.16	5.39152E-05
200	PA2833	NA	hypothetical protein	5.16	5.08276E-06
201	PA1891	NA	hypothetical protein	5.12	6.80024E-05
202	PA3395	*nosY*	membrane protein NosY	5.12	1.38018E-07
203	PA3905	NA	hypothetical protein	5.08	7.99753E-05
204	PA3560	*fruA*	PTS system fructose-specific transporter subunit IIBC	5.08	4.59066E-07
205	PA2133	NA	hypothetical protein	5.07	7.69971E-06
206	PA4814	*fadH2*	2,4-dienoyl-CoA reductase	5.07	3.3482E-08
207	PA3132	NA	Hydrolase	5.04	2.10785E-07
208	PA4824	NA	hypothetical protein	5.03	1.69411E-06
209	PA2335	NA	TonB-dependent receptor	5.00	1.10949E-07
210	PA1147	NA	amino acid permease	4.99	1.17992E-07
211	PA1694	*pscQ*	type III secretion system protein	4.98	7.39362E-07
212	PA3405	*hasE*	metalloprotease secretion protein	4.93	9.75718E-07
213	PA1237	NA	multidrug resistance efflux pump	4.92	2.92315E-06
214	PA4149	NA	hypothetical protein	4.92	1.03146E-06
215	PA1412	NA	hypothetical protein	4.91	3.14367E-06
216	PA1143	NA	hypothetical protein	4.90	1.72207E-05
217	PA0279	NA	transcriptional regulator	4.89	1.2229E-06
218	PA0184	NA	ABC transporter ATP-binding protein	4.88	1.2564E-06
219	PA2293	NA	hypothetical protein	4.87	2.02805E-05
220	PA3550	*algF*	alginate o-acetyltransferase AlgF	4.86	5.55856E-07
221	PA5431	NA	transcriptional regulator	4.84	1.89055E-07
222	PA1488	NA	hypothetical protein	4.84	4.72529E-06
223	PA4908	NA	ornithine cyclodeaminase	4.83	6.73583E-07
224	PA2933	NA	major facilitator superfamily transporter	4.80	1.94085E-06
225	PA3873	*narJ*	respiratory nitrate reductase subunit delta	4.80	2.8433E-05
226	PA1924	NA	hypothetical protein	4.79	2.98572E-05
227	PA4096	NA	major facilitator superfamily transporter	4.79	5.19758E-07
228	PA2086	NA	epoxide hydrolase	4.79	2.98572E-05
229	PA4864	*ureD*	urease accessory protein	4.78	1.5195E-06
230	PA1019a	NA	Thioesterase	4.73	0.0003
231	PA2125	NA	aldehyde dehydrogenase	4.72	2.92315E-06
232	PA1148	*toxA*	exotoxin A	4.71	2.11109E-07
233	PA4121	NA	hypothetical protein	4.70	1.24257E-06

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
234	PA2984	NA	hypothetical protein	4.70	1.03398E-07
235	PA1695	*pscP*	translocation protein in type III secretion	4.69	2.38081E-06
236	PA2836	NA	secretion protein	4.69	3.2167E-06
237	PA0682	NA	HxcX atypical pseudopilin	4.68	9.79558E-06
238	PA0724	NA	phage coat protein A	4.68	8.06539E-08
239	PA0686	NA	type II secretion system protein HxcR	4.67	2.65599E-06
240	PA2084	NA	asparagine synthetase	4.67	2.65599E-06
241	PA4818	NA	hypothetical protein	4.66	6.90797E-07
242		*mdcD*	malonate decarboxylase subunit beta	4.65	1.17225E-05
243	PA0241	NA	major facilitator superfamily transporter	4.64	4.5535E-07
244	PA2474	NA	hypothetical protein	4.63	3.36902E-06
245	PA1262	NA	major facilitator superfamily transporter	4.56	2.60851E-06
246	PA5353	*glcF*	glycolate oxidase iron-sulfur subunit	4.55	3.36536E-06
247	PA3911	NA	hypothetical protein	4.54	1.88632E-05
248	PA1356	NA	hypothetical protein	4.54	7.00242E-06
249	PA0219	NA	aldehyde dehydrogenase	4.52	1.0321E-06
250	PA2701	NA	major facilitator superfamily transporter	4.49	2.43041E-06
251	PA0185	NA	ABC transporter permease	4.49	1.26305E-06
252	PA2060	NA	ABC transporter permease	4.48	9.30546E-06
253	PA5385	*cdhB*	carnitine dehydrogenase	4.48	2.63877E-05
254	PA4819	NA	glycosyl transferase family protein	4.46	1.08893E-05
255	PA0110	NA	hypothetical protein	4.45	1.08893E-05
256	PA0222	NA	hypothetical protein	4.45	2.04282E-06
257	PA3448	NA	ABC transporter permease	4.44	5.68918E-06
258	PA2088	NA	hypothetical protein	4.44	3.18396E-05
259	PA1286	NA	major facilitator superfamily transporter	4.44	2.16211E-06
260	PA4599	*mexC*	resistance-nodulation-cell division (RND) multidrug efflux membrane fusion protein MexC	4.43	2.36121E-06
261	PA0273	NA	major facilitator superfamily transporter	4.42	5.37164E-06
262	PA2350	NA	methionine ABC transporter ATP-binding protein	4.40	7.1203E-06
263	PA2325	NA	hypothetical protein	4.39	1.4655E-05
264	PA0699	NA	PpiC-type peptidyl-prolyl cis-trans isomerase	4.39	4.07009E-05
265	PA1216	NA	hypothetical protein	4.39	6.4266E-06
266	PA0056	NA	transcriptional regulator	4.38	2.91604E-06
267	PA0238	NA	hypothetical protein	4.37	8.05538E-06
268	PA3394	*nosF*	copper ABC transporter ATP-binding	4.37	1.65505E-05

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
269	PA3442	NA	aliphatic sulfonates ABC transporter ATP-binding subunit	4.36	4.52001E-05
270	PA1214	NA	hypothetical protein	4.36	1.71322E-05
271	PA2214	NA	major facilitator superfamily transporter	4.35	1.07361E-06
272	PA3780	NA	hypothetical protein	4.35	0.0002
273	PA2120	NA	hypothetical protein	4.34	5.00763E-05
274	PA1231	NA	hypothetical protein	4.34	0.0002
275	PA0118	NA	hypothetical protein	4.32	1.56862E-06
276	PA2729	NA	hypothetical protein	4.32	7.58704E-07
277	PA3589	NA	acetyl-CoA acetyltransferase	4.31	2.1781E-05
278	PA0882	NA	hypothetical protein	4.28	1.28758E-05
279	PA3542	*alg44*	alginate biosynthesis protein Alg44	4.27	2.15204E-06
280	PA2314	NA	major facilitator superfamily transporter	4.26	5.37164E-06
281	PA1855	NA	hypothetical protein	4.26	0.0003
282	PA2213	NA	Porin	4.26	1.20688E-05
283	PA2371	NA	ClpA/B-type protease	4.26	1.74233E-06
284	PA2715	NA	Ferredoxin	4.26	0.0003
285	PA0205	NA	ABC transporter permease	4.22	3.22807E-06
286	PA4099	NA	hypothetical protein	4.22	2.79473E-06
287	PA2473	NA	glutathione S-transferase	4.21	8.7287E-05
288	PA3444	NA	alkanesulfonate monooxygenase	4.21	7.03044E-06
289	PA2863	*lipH*	lipase chaperone	4.20	1.08071E-05
290	PA0136	NA	ABC transporter ATP-binding protein	4.17	4.25493E-06
291	PA1908	NA	major facilitator superfamily transporter	4.16	9.29948E-06
292	PA2462	NA	hypothetical protein	4.14	7.71393E-07
293	PA0194	NA	hypothetical protein	4.13	7.71769E-06
294	PA4859	NA	ABC transporter permease	4.13	5.20607E-06
295	PA3773	NA	hypothetical protein	4.13	1.51405E-05
296	PA3592	NA	hypothetical protein	4.12	1.10306E-05
297	PA2689	NA	hypothetical protein	4.11	5.62043E-05
298	PA1827	NA	short-chain dehydrogenase	4.11	2.47374E-05
299	PA1020	NA	acyl-CoA dehydrogenase	4.10	1.2209E-05
300	PA2922	NA	Hydrolase	4.09	1.77328E-05
301	PA3904	NA	hypothetical protein	4.09	2.82303E-05
302	PA4092	*hpaC*	4-hydroxyphenylacetate 3-monooxygenase small subunit	4.08	6.35353E-05
303	PA5391	NA	hypothetical protein	4.07	6.67419E-05
304	PA0987	NA	hypothetical protein	4.07	3.08219E-05
305	PA1980	*eraR*	response regulator EraR	4.07	0.0001
306	PA3885	*tpbA*	protein tyrosine phosphatase TpbA	4.06	3.5273E-05
307	PA1497	NA	Transporter	4.06	2.04756E-05

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
308	PA2141	NA	hypothetical protein	4.06	0.0007
309	PA4103	NA	hypothetical protein	4.06	5.68918E-06
310	PA3591	NA	enoyl-CoA hydratase	4.06	7.32239E-05
311	PA4188	NA	hypothetical protein	4.05	3.28091E-05
312	PA1780	*nirD*	assimilatory nitrite reductase small subunit	4.05	0.0001
313	PA2373	NA	hypothetical protein	4.04	3.71697E-06
314	PA0802	NA	hypothetical protein	4.03	0.0001
315	PA1725	*pscL*	type III secretion system protein	4.03	7.99753E-05
316	PA4083	*cupB4*	chaperone CupB4	4.03	2.44802E-05
317	PA4038	NA	hypothetical protein	4.02	1.33829E-05
318	PA5419	*soxG*	sarcosine oxidase subunit gamma	4.02	1.33829E-05
319	PA1186	NA	hypothetical protein	4.00	4.14744E-05
320	PA2458	NA	hypothetical protein	4.00	4.28134E-06
321	PA1489	NA	hypothetical protein	3.99	2.98572E-05
322	PA0726	NA	hypothetical protein	3.99	3.14367E-06
323	PA2124	NA	Dehydrogenase	3.97	1.77152E-05
324	PA2036	NA	hypothetical protein	3.97	1.40401E-05
325	PA3436	NA	hypothetical protein	3.94	2.61211E-05
326	PA0752	NA	hypothetical protein	3.94	1.10118E-05
327	PA0521	NA	cytochrome C oxidase subunit	3.93	1.26229E-05
328	PA3535	NA	serine protease	3.93	5.19922E-06
329	PA3871	NA	PpiC-type peptidyl-prolyl cis-trans isomerase	3.92	4.01341E-05
330	PA0725	NA	hypothetical protein	3.92	0.0001
331	PA2924	*hisQ*	histidine ABC transporter permease HisQ	3.91	6.17218E-05
332	PA3037	NA	hypothetical protein	3.90	7.46055E-05
333	PA4107	NA	hypothetical protein	3.89	4.71561E-05
334	PA0221	NA	Aminotransferase	3.89	2.08372E-05
335	PA3396	*nosL*	acessory protein NosL	3.88	0.0003
336	PA0798	*pmtA*	phospholipid methyltransferase	3.87	7.61222E-05
337	PA1917	NA	hypothetical protein	3.86	0.0001
338	PA5144	NA	hypothetical protein	3.86	0.0001
339	PA0144	NA	hypothetical protein	3.86	5.48473E-05
340	PA1274	NA	5,6-dimethylbenzimidazole synthase	3.86	9.16933E-05
341	PA1298	NA	hypothetical protein	3.86	9.16933E-05
342	PA4105	NA	hypothetical protein	3.84	9.92969E-05
343	PA2324	NA	hypothetical protein	3.83	4.52001E-05
344	PA0684	NA	type II secretion system protein	3.83	0.0004
345	PA3376	NA	phosphonate C-P lyase system protein PhnK	3.83	0.0004
346	PA4820	NA	hypothetical protein	3.82	4.66203E-05
347	PA4918	NA	hypothetical protein	3.82	4.88946E-06

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
348	PA5418	*soxA*	sarcosine oxidase subunit alpha	3.82	7.61629E-06
349	PA4985	NA	hypothetical protein	3.81	3.71249E-05
350	PA2892	*atuG*	short-chain dehydrogenase	3.80	5.03768E-05
351	PA4593	NA	ABC transporter permease	3.80	3.91345E-05
352	PA4978	NA	hypothetical protein	3.80	1.67058E-05
353	PA2471	NA	hypothetical protein	3.79	7.21024E-05
354	PA3383	NA	phosphonate ABC transporter substrate-binding protein	3.79	1.68888E-05
355	PA1022	NA	acyl-CoA dehydrogenase	3.79	1.56427E-05
356	PA4179	NA	Porin	3.79	8.9392E-06
357	PA3447	NA	ABC transporter ATP-binding protein	3.79	0.0002
358	PA0237	NA	Oxidoreductase	3.78	5.64353E-05
359	PA4392	NA	hypothetical protein	3.78	5.64353E-05
360	PA5400	NA	electron transfer flavoprotein subunit alpha	3.77	5.97376E-05
361	PA2342	*mtlD*	mannitol dehydrogenase	3.77	4.7284E-05
362	PA0212	*mdcE*	malonate decarboxylase subunit gamma	3.76	0.0002
363	PA2255	*pvcB*	paerucumarin biosynthesis protein PvcB	3.73	0.0001
364	PA1876	NA	ABC transporter ATP-binding protein/permease	3.73	3.18396E-05
365	PA1696	*pscO*	translocation protein in type III secretion	3.71	0.0007
366	PA4622	NA	major facilitator superfamily transporter	3.71	1.32569E-05
367	PA1219	NA	hypothetical protein	3.71	0.0007
368	PA4795	NA	hypothetical protein	3.71	0.0007
369	PA1490	NA	transcriptional regulator	3.71	7.95014E-05
370	PA0466	NA	hypothetical protein	3.70	0.0007
371	PA2131	*cupA4*	fimbrial subunit CupA4	3.69	8.42475E-05
372	PA0526	NA	hypothetical protein	3.69	0.0001
373	PA2295	NA	ABC transporter permease	3.68	8.9497E-05
374	PA2217	NA	aldehyde dehydrogenase	3.68	5.80724E-05
375	PA5341	NA	hypothetical protein	3.67	9.21863E-05
376	PA2078	NA	hypothetical protein	3.66	3.27673E-05
377	PA1023	NA	short-chain dehydrogenase	3.66	7.75714E-05
378	PA2349	NA	hypothetical protein	3.65	0.0001
379	PA5354	NA	glycolate oxidase FAD binding subunit	3.65	0.0001
380	PA2216	NA	hypothetical protein	3.64	8.18882E-05
381	PA5266	NA	hypothetical protein	3.64	1.67058E-05
382	PA4148	NA	short-chain dehydrogenase	3.64	0.0001
383	PA1711	NA	hypothetical protein	3.63	0.0004

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384	PA3433	NA	transcriptional regulator	3.63	3.22656E-05
385	PA4802	NA	hypothetical protein	3.62	2.08372E-05
386	PA3358	NA	hypothetical protein	3.62	7.4063E-05
387	PA2163	NA	4-alpha-glucanotransferase	3.61	9.37843E-05
388	PA0137	NA	ABC transporter permease	3.61	2.98572E-05
389	PA3036	NA	hypothetical protein	3.61	5.55792E-05
390	PA1952	NA	hypothetical protein	3.61	0.0004
391	PA2439	NA	hypothetical protein	3.61	5.32018E-05
392	PA0193	NA	hypothetical protein	3.60	9.92969E-05
393	PA0192	NA	TonB-dependent receptor	3.60	2.0619E-05
394	PA3544	*algE*	alginate production protein AlgE	3.60	2.96629E-05
395	PA3320	NA	hypothetical protein	3.60	5.41779E-05
396	PA2925	*hisM*	histidine ABC transporter permease HisM	3.60	9.92969E-05
397	PA2650	NA	hypothetical protein	3.60	5.52034E-05
398	PA0111	NA	hypothetical protein	3.60	0.0005
399	PA2179	NA	hypothetical protein	3.60	0.0001
400	PA5328	NA	mono-heme cytochrome C	3.58	0.0005
401	PA1743	NA	hypothetical protein	3.58	0.0005
402	PA1893	NA	hypothetical protein	3.57	3.30626E-05
403	PA2589	NA	hypothetical protein	3.56	4.7776E-05
404	PA0523	*norC*	nitric oxide reductase subunit C	3.56	6.00389E-05
405	PA2369	NA	hypothetical protein	3.55	7.32239E-05
406	PA3609	*potC*	polyamine ABC transporter permease PotC	3.55	7.32239E-05
407	PA1346	NA	hypothetical protein	3.55	8.55758E-05
408	PA2370	NA	hypothetical protein	3.54	0.0006
409	PA1983	*exaB*	cytochrome C550	3.54	0.0002
410	PA4181	NA	hypothetical protein	3.53	5.62043E-05
411	PA3908	NA	hypothetical protein	3.53	8.18882E-05
412	PA4650	NA	hypothetical protein	3.52	0.0001
413	PA4862	NA	ABC transporter ATP-binding protein	3.52	0.0002
414	PA3373	NA	hypothetical protein	3.52	0.0007
415	PA2463	NA	hypothetical protein	3.51	4.83297E-05
416	PA3875	*narG*	respiratory nitrate reductase subunit alpha	3.51	2.0619E-05
417	PA3519	NA	hypothetical protein	3.51	3.30626E-05
418	PA1213	NA	hypothetical protein	3.51	0.0002
419	PA3561	*fruK*	1-phosphofructokinase	3.51	0.0002
420	PA1954	NA	hypothetical protein	3.51	3.3813E-05
421	PA5282	NA	major facilitator superfamily transporter	3.51	5.02286E-05
422	PA0718	NA	hypothetical protein	3.51	6.14091E-05

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
423	PA0324	NA	ABC transporter permease	3.50	4.73741E-05
424	PA1212	NA	major facilitator superfamily transporter	3.50	6.84991E-05
425	PA1786	NA	hypothetical protein	3.50	6.24084E-05
426	PA0474	NA	Esterase	3.50	0.0004
427	PA4798	NA	hypothetical protein	3.48	3.37782E-05
428	PA4982	NA	two-component sensor	3.48	5.79529E-05
429	PA1279	*cobU*	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	3.47	0.0003
430	PA2835	NA	major facilitator superfamily transporter	3.46	6.14091E-05
431	PA0242	NA	hypothetical protein	3.46	5.93033E-05
432	PA5386	*cdhA*	3-hydroxybutyryl-CoA dehydrogenase	3.45	0.0001
433	PA5326	NA	hypothetical protein	3.45	9.92969E-05
434	PA4592	NA	hypothetical protein	3.44	7.21024E-05
435	PA2085	NA	ring-hydroxylating dioxygenase small subunit	3.44	0.0009
436	PA5399	*dgcB*	dimethylglycine catabolism protein DgcB	3.43	6.46809E-05
437	PA5159	NA	multidrug resistance protein	3.43	9.37843E-05
438	PA5470	NA	peptide chain release factor-like protein	3.43	9.55376E-05
439	PA0173	NA	chemotaxis response regulator protein-glutamate methylesterase	3.42	0.0002
440	PA2362	NA	hypothetical protein	3.41	0.0006
441	PA1848	NA	major facilitator superfamily transporter	3.41	0.0001
442	PA0117	NA	short-chain dehydrogenase	3.41	0.0001
443	PA2890	*atuE*	isohexenylglutaconyl-CoA hydratase	3.41	0.0004
444	PA2837	NA	hypothetical protein	3.39	0.0001
445	PA3772	NA	hypothetical protein	3.39	7.77875E-05
446	PA3547	*algL*	alginate lyase	3.39	8.47958E-05
447	PA0883	NA	acyl-CoA lyase subunit beta	3.38	0.0003
448	PA4920	NA*dE*	NAD synthetase	3.37	5.13913E-05
449	PA1236	NA	major facilitator superfamily transporter	3.35	0.0001
450	PA0244	NA	shikimate 5-dehydrogenase	3.34	0.0003
451	PA1634	*kdpB*	potassium-transporting ATPase subunit B	3.34	0.0001
452	PA5115	NA	hypothetical protein	3.33	0.0003
453	PA2348	NA	hypothetical protein	3.33	0.0004
454	PA0786	NA	Transporter	3.33	0.0008
455	PA2347	NA	hypothetical protein	3.33	0.0008
456	PA3546	*algX*	alginate biosynthesis protein AlgX	3.33	0.0001

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
457	PA3518	NA	hypothetical protein	3.33	0.0001
458	PA2356	*msuD*	methanesulfonate monooxygenase	3.32	0.0004
459	PA4861	NA	ABC transporter ATP-binding protein	3.32	0.0001
460	PA2155	NA	cardiolipin synthase 2	3.32	0.0002
461	PA2061	NA	ABC transporter ATP-binding protein	3.32	0.0002
462	PA1218	NA	hypothetical protein	3.32	0.0002
463	PA4299	*tadD*	type II secretion system protein TadD	3.32	0.0009
464	PA3870	*moaA1*	molybdenum cofactor biosynthesis protein A	3.32	0.0002
465	PA5395	NA	hypothetical protein	3.31	0.0003
466	PA1929	NA	hypothetical protein	3.31	0.0009
467	PA2284	NA	hypothetical protein	3.30	0.0002
468	PA2346	NA	hypothetical protein	3.30	0.0002
469	PA0058	NA	hypothetical protein	3.29	0.0004
470	PA2039	NA	hypothetical protein	3.28	9.41752E-05
471	PA0175	NA	chemotaxis protein methyltransferase	3.28	0.0001
472	PA2803	NA	hypothetical protein	3.28	0.0003
473	PA1435	NA	resistance-nodulation-cell division (RND) efflux membrane fusion protein	3.28	0.0002
474	PA0029	NA	sulfate transporter	3.27	0.0001
475	PA0150	NA	transmembrane sensor	3.27	0.0001
476	PA2596	NA	hypothetical protein	3.27	0.0002
477	PA3360	NA	secretion protein	3.27	0.0003
478	PA4098	NA	short-chain dehydrogenase	3.27	0.0003
479	PA3291	NA	hypothetical protein	3.26	0.0003
480	PA2676	NA	type II secretion system protein	3.26	0.0001
481	PA4586	NA	hypothetical protein	3.25	0.0005
482	PA3416	NA	pyruvate dehydrogenase E1 component subunit beta	3.25	0.0003
483	PA3608	*potB*	polyamine ABC transporter permease PotB	3.25	0.0002
484	PA4189	NA	aldehyde dehydrogenase	3.25	0.0002
485	PA3907	NA	hypothetical protein	3.25	0.0008
486	PA0103	NA	sulfate transporter	3.24	0.0001
487	PA3133	NA	transcriptional regulator	3.24	0.0002
488	PA1270	NA	hypothetical protein	3.24	0.0001
489	PA3912	NA	hypothetical protein	3.24	0.0006
490	PA2421	NA	hypothetical protein	3.23	0.0001
491	PA4883	NA	hypothetical protein	3.22	0.0006
492	PA0511	*nirJ*	heme d1 biosynthesis protein NirJ	3.22	0.0002
493	PA4137	NA	Porin	3.21	0.0001
494	PA0236	NA	transcriptional regulator	3.21	0.0002
495	PA1251	NA	chemotaxis transducer	3.21	0.0001

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
496	PA4830	NA	hypothetical protein	3.21	0.0003
497	PA2132	*cupA5*	chaperone CupA5	3.20	0.0009
498	PA2289	NA	hypothetical protein	3.20	0.0001
499	PA0214	NA	acyl transferase	3.19	0.0006
500	PA1313	NA	major facilitator superfamily transporter	3.18	0.0002
501	PA1782	NA	serine/threonine-protein kinase	3.18	0.0002
502	PA2181	NA	glutamate--cysteine ligase	3.18	0.0003
503	PA2229	NA	hypothetical protein	3.18	0.0003
504	PA5420	*purU2*	formyltetrahydrofolate deformylase	3.17	0.0002
505	PA0197	*tonB2*	transporter TonB	3.17	0.0008
506	PA0702	NA	hypothetical protein	3.17	0.0005
507	PA0166	NA	Transporter	3.17	0.0002
508	PA4095	NA	hypothetical protein	3.17	0.0006
509	PA4167	NA	2,5-diketo-D-gluconate reductase B	3.16	0.0001
510	PA3119	NA	hypothetical protein	3.16	0.0003
511	PA0052	NA	hypothetical protein	3.15	0.0004
512	PA3607	*potA*	polyamine transporter ATP-binding protein PotA	3.15	0.0002
513	PA0252	NA	hypothetical protein	3.15	0.0003
514	PA2056	NA	transcriptional regulator	3.15	0.0007
515	PA4087	NA	hypothetical protein	3.15	0.0003
516	PA4652	NA	hypothetical protein	3.14	0.0001
517	PA2057	NA	hypothetical protein	3.14	0.0001
518	PA5352	NA	hypothetical protein	3.13	0.0007
519	PA2243	*pslM*	FAD-binding dehydrogenase	3.13	0.0003
520	PA2431	NA	hypothetical protein	3.13	0.0002
521	PA3443	NA	ABC transporter permease	3.13	0.0005
522	PA0326	NA	ABC transporter ATP-binding protein	3.12	0.0002
523	PA3415	NA	branched-chain alpha-keto acid dehydrogenase subunit E2	3.12	0.0002
524	PA4027a	NA	hypothetical protein	3.12	0.0002
525	PA0875	NA	hypothetical protein	3.11	0.0001
526	PA4343	NA	major facilitator superfamily transporter	3.11	0.0002
527	PA1215	NA	hypothetical protein	3.10	0.0004
528	PA3884	NA	hypothetical protein	3.10	0.0007
529	PA2783	NA	hypothetical protein	3.09	0.0002
530	PA4120	NA	transcriptional regulator	3.08	0.0005
531	PA3384	*phnC*	phosphonate ABC transporter ATP-binding protein	3.08	0.0005
532	PA0693	*exbB2*	transporter ExbB	3.08	0.0004
533	PA2076	NA	transcriptional regulator	3.07	0.0009
534	PA3323	NA	hypothetical protein	3.06	0.0005

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
535	PA3936	NA	taurine ABC transporter permease	3.06	0.0007
536	PA1092	*fliC*	B-type flagellin	3.06	0.0001
537	PA0477	NA	transcriptional regulator	3.05	0.0002
538	PA4191	NA	iron/ascorbate oxidoreductase	3.04	0.0005
539	PA1975	NA	hypothetical protein	3.04	0.0006
540	PA5132	NA	hypothetical protein	3.03	0.0003
541	PA3521	NA	hypothetical protein	3.02	0.0004
542	PA1633	*kdpA*	potassium-transporting ATPase subunit A	3.02	0.0004
543	PA0311	NA	hypothetical protein	3.02	0.0005
544	PA5539	NA	GTP cyclohydrolase	3.02	0.0005
545	PA4903	NA	major facilitator superfamily transporter	3.02	0.0006
546	PA4073	NA	aldehyde dehydrogenase	3.02	0.0004
547	PA2670	NA	hypothetical protein	3.02	0.0003
548	PA5387	*cdhC*	carnitine dehydrogenase	3.01	0.0006
549	PA3749	NA	major facilitator superfamily transporter	3.01	0.0002
550	PA2520	*czcA*	resistance-nodulation-cell division (RND) divalent metal cation efflux transporter CzcA	3.01	0.0003
551	PA3750	NA	hypothetical protein	3.01	0.0009
552	PA1281	*cobV*	adenosylcobinamide-GDP ribazoletransferase	3.00	0.0004
553	PA2097	NA	flavin-binding monooxygenase	3.00	0.0006
554	PA2598	NA	hypothetical protein	3.00	0.0006
555	PA3937	NA	taurine ABC transporter ATP-binding protein	3.00	0.0009
556	PA0189	NA	Porin	2.99	0.0005
557	PA1017	*pauA*	pimeloyl-CoA synthetase	2.99	0.0003
558	PA1172	NA*pC*	cytochrome C protein NapC	2.98	0.0007
559	PA0685	NA	type II secretion system protein	2.97	0.0003
560	PA3393	*nosD*	copper-binding periplasmic protein	2.95	0.0006
561	PA1232	NA	hypothetical protein	2.95	0.0004
562	PA3296	*phoA*	alkaline phosphatase	2.95	0.0003
563	PA1417	NA	hypothetical protein	2.95	0.0006
564	PA0057	NA	hypothetical protein	2.95	0.0006
565	PA0153	*pcaH*	protocatechuate 3,4-dioxygenase subunit beta	2.94	0.0005
566	PA1783	NA*sA*	nitrate transporter	2.94	0.0007
567	PA1781	*nirB*	assimilatory nitrite reductase large subunit	2.94	0.0004
568	PA4911	NA	branched-chain amino acid ABC transporter permease	2.93	0.0005
569	PA3391	*nosR*	regulatory protein NosR	2.93	0.0003

Sr. No.	Gene ID	Symbol	Product name	Log FC	FDR
570	PA0433	NA	hypothetical protein	2.93	0.0009
571	PA5158	NA	hypothetical protein	2.93	0.0005
572	PA1138	NA	transcriptional regulator	2.92	0.0007
573	PA3409	NA	transmembrane sensor	2.91	0.0006
574	PA4037	NA	ABC transporter ATP-binding protein	2.91	0.0006
575	PA0051	*phzH*	phenazine-modifying protein	2.90	0.0005
576	PA2283	NA	hypothetical protein	2.90	0.0005
577	PA3954	NA	hypothetical protein	2.90	0.0005
578	PA4166	NA	Acetyltransferase	2.90	0.0009
579	PA2691	NA	hypothetical protein	2.89	0.0007
580	PA4898	*opdK*	vanillate porin OpdK	2.89	0.0007
581	PA4190	*pqsL*	Monooxygenase	2.89	0.0008
582	PA5544	NA	hypothetical protein	2.88	0.0004
583	PA1923	NA	cobaltochelatase subunit CobN	2.88	0.0006
584	PA1922	NA	TonB-dependent receptor	2.88	0.0006
585	PA0528	NA	transcriptional regulator	2.87	0.0004
586	PA1027	NA	aldehyde dehydrogenase	2.87	0.0006
587	PA3176	*gltS*	glutamate/sodium ion symporter GltS	2.87	0.0007
588	PA4342	NA	Amidase	2.87	0.0007
589	PA1360	NA	hypothetical protein	2.86	0.0008
590	PA0516	*nirF*	heme d1 biosynthesis protein NirF	2.86	0.0007
591	PA4136	NA	major facilitator superfamily transporter	2.86	0.0005
592	PA1373	*fabF2*	3-oxoacyl-ACP synthase	2.86	0.0006
593	PA4100	NA	Dehydrogenase	2.86	0.0008
594	PA5294	NA	multidrug efflux protein NorA	2.85	0.0007
595	PA1400	NA	pyruvate carboxylase	2.85	0.0005
596	PA3392	*nosZ*	nitrous-oxide reductase	2.85	0.0005
597	PA3619	NA	hypothetical protein	2.84	0.0005
598	PA0435	NA	hypothetical protein	2.84	0.0008
599	PA3532	NA	hypothetical protein	2.82	0.0005
600		*pfeA*	ferric enterobactin receptor	2.82	0.0005
601	PA0143	*nuh*	nonspecific ribonucleoside hydrolase	2.82	0.0007
602	PA1019	*mucK*	cis,cis-muconate transporter MucK	2.81	0.0008
603	PA0781	NA	hypothetical protein	2.81	0.0006
604	PA3638	NA	tRNA (Ile)-lysidine synthase	2.80	0.0006
605	PA4540	NA	hypothetical protein	2.80	0.0007
606	PA4779	NA	hypothetical protein	2.80	0.0009
607	PA3562	*fruI*	PTS system fructose-specific transporter subunit FruI	2.79	0.0007
608	PA1450	NA	hypothetical protein	2.79	0.0007
609	PA4648	NA	hypothetical protein	2.79	0.0008
610	PA5393	NA	hypothetical protein	2.77	0.0009

Sr. No.	**Gene ID**	**Symbol**	**Product name**	**Log FC**	**FDR**
611	PA5160	NA	drug efflux transporter	2.74	0.0007
612	PA3760	NA	N-acetyl-D-glucosamine phosphotransferase system transporter	2.73	0.0008
613	PA0183	*atsA*	Arylsulfatase	2.73	0.0008
614	PA0524	*norB*	nitric oxide reductase subunit B	2.73	0.0009
615	PA5430	NA	hypothetical protein	2.71	0.0009
616	PA5471	NA	hypothetical protein	2.68	0.0009

Genes are arranged in decreasing order of Fold Change; Databases consulted for gene functions were: NCBI gene database (https://www.ncbi.nlm.nih.gov/nuccore/NC_002516); KEGG (Kyoto Encyclopedia of Genes and Genomes: https://www.genome.jp/kegg/); Uniprot (https://www.uniprot.org/). NA: Not Applicable; FDR: False Discovery Rate

Table S7. Node degree score of the top up-regulated genes

No.	Gene ID/Symbol	Identifier	Node degree
1	*wbpI*	208964.PA3148	27
2	PA0192	208964.PA0192	26
3	PA2730	208964.PA2730	26
4	PA3501	208964.PA3501	25
5	*wbpJ*	208964.PA3147	25
6	PA2090	208964.PA2090	24
7	*wbpB*	208964.PA3158	24
8	*wbpD*	208964.PA3156	24
9	*wbpG*	208964.PA3150	24
10	*wbpH*	208964.PA3149	24
11	*wbpK*	208964.PA3146	24
12	PA1786	208964.PA1786	23
13	PA3498	208964.PA3498	23
14	*hisF2*	208964.PA3151	23
15	*hisH2*	208964.PA3152	23
16	*norB*	208964.PA0524	23
17	*nosZ*	208964.PA3392	23
18	*wbpE*	208964.PA3155	23
19	PA0184	208964.PA0184	22
20	PA0185	208964.PA0185	22
21	PA0521	208964.PA0521	22
22	PA1372	208964.PA1372	22
23	PA3513	208964.PA3513	22
24	PA3514	208964.PA3514	22
25	*nirF*	208964.PA0516	22
26	*nosD*	208964.PA3393	22
27	*nosR*	208964.PA3391	22
28	*wbpA*	208964.PA3159	22
29	*wbpL*	208964.PA3145	22
30	PA1400	208964.PA1400	21
31	PA3504	208964.PA3504	21
32	PA3506	208964.PA3506	21
33	*nirG*	208964.PA0513	21
34	*nosL*	208964.PA3396	21
35	*wzx*	208964.PA3153	21
36	PA2324	208964.PA2324	20
37	PA2325	208964.PA2325	20
38	PA2596	208964.PA2596	20
39	PA3512	208964.PA3512	20
40	PA3912	208964.PA3912	20
41	NA*rG*	208964.PA3875	20
42	*nirJ*	208964.PA0511	20
43	*pvdJ*	208964.PA2400	20
44	PA2347	208964.PA2347	19
45	PA3157	208964.PA3157	19
46	PA3535	208964.PA3535	19
47	PA3760	208964.PA3760	19
48	*nirL*	208964.PA0514	19
49	*norC*	208964.PA0523	19
50	*pscQ*	208964.PA1694	19
51	*wzz*	208964.PA3160	19
52	*xylZ*	208964.PA2516	19

Rest 558 genes with node degree score ‘≤18’ are not listed.

Table S8. Top six cytoHubba ranked up-regulated genes from among the top-52 in Table S7

No.	**Gene ID**	**Number of methods ranking this protein among top 10**	**Names of 12 ranking methods of CytoHubba and rank score provided by them**											
			Degree	**MNC**	**DMNC**	**MCC**	**Bottleneck**	**EcCentricity**	**Closeness**	**Radiality**	**Betweenness**	**Stress**	**CC**	**EPC**
1	PA3156	8	17	17	1.01	1.87E+11	3	-	23.76	3.68	-	-	-	25.32
2	PA3158	7	18	18	-	1.87E+11	-	-	24.26	3.70	-	1390	-	25.48
3	PA3150	7	18	18	-	1.87E+11	-	-	24.26	3.70	-	1390	-	25.44
4	PA3149	7	17	17	1.01	1.87E+11	-	-	23.76	3.68	-	-	-	25.33
5	PA3147	6	18	18	-	1.87E+11	-	-	24.26	3.70	-	1390	-	-
6	PA3151	6	16	16	1.01	1.87E+11	-	-	-	-	-	-	0.97	25.35

"-": This method did not rank the shown protein among top 10.

MNC: Maximum Neighborhood Component; DMNC: Density of Maximum Neighborhood Component; MCC: Maximal Clique Centrality; CC: Clustering Co-efficient; EPC: Edge Percolated Component

Table S9. List of down regulated genes in Enteropan-exposed *P. aeruginosa* satisfying the dual criteria of log fold-change ≥2 and FDR≤0.001

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
1	PA3266	*capB*	major cold shock protein CspA	6.63	7.761E-13
2	PA0905	*rsmA*	carbon storage regulator	6.48	1.8058E-12
3	PA3126	*ibpA*	heat-shock protein IbpA	6.32	4.361E-12
4	PA2853	*oprI*	outer membrane lipoprotein OprI	6.26	5.52E-12
5	PA4747	*secG*	preprotein translocase subunit SecG	6.11	1.3333E-11
6	PA1159	NA	cold-shock protein	6.08	1.788E-11
7	PA4432	*rpsI*	30S ribosomal protein S9	5.93	3.7893E-11
8	PA4945	*miaA*	tRNA delta (2)-isopentenylpyrophosphate transferase	5.83	6.3081E-11
9	PA0456	NA	cold-shock protein	5.76	9.1501E-11
10	PA4463	NA	hypothetical protein	5.75	1.0075E-10
11	PA3530	NA	hypothetical protein	5.73	1.3508E-10
12	PA5526	NA	hypothetical protein	5.64	2.4488E-10
13	PA2619	*infA*	translation initiation factor IF-1	5.63	2.421E-10
14	PA2604	NA	hypothetical protein	5.57	2.4488E-10
15	PA3031	NA	hypothetical protein	5.54	2.6678E-10
16	PA2966	*acpP*	acyl carrier protein	5.46	3.8445E-10
17	PA3496	NA	hypothetical protein	5.40	6.7265E-10
18	PA1802	*clpX*	ATP-dependent protease ATP-binding subunit ClpX	5.34	7.0703E-10
19	PA0665	NA	iron-sulfur cluster insertion protein ErpA	5.32	9.4678E-10
20	PA4669	*Ipk*	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	5.31	9.033E-10
21	PA3601	NA	50S ribosomal protein L31 type B	5.30	1.1507E-09
22	PA2738	*himA*	integration host factor subunit alpha	5.26	1.2062E-09
23	PA1804	*hupB*	DNA-binding protein HU	5.25	1.1942E-09
24	PA3229	NA	hypothetical protein	5.23	1.893E-09
25	PA3822	NA	preprotein translocase subunit YajC	5.21	1.748E-09
26	PA5049	*rpmE*	50S ribosomal protein L31	5.17	1.893E-09
27	PA1343	NA	hypothetical protein	5.17	1.9576E-09
28	PA0621	NA	hypothetical protein	5.14	2.6641E-09
29	PA1178	*oprH*	PhoP/Q and low Mg2+ inducible outer membrane protein H1	5.11	2.4212E-09
30	PA5053	*hslV*	ATP-dependent protease peptidase subunit	5.03	4.2563E-09

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
31	PA0623	NA	bacteriophage protein	5.00	5.2599E-09
32	PA0622	NA	bacteriophage protein	4.95	6.4156E-09
33	PA4876	*osmE*	OsmE family transcriptional regulator	4.94	7.5021E-09
34	PA3623	NA	hypothetical protein	4.90	8.839E-09
35	PA4386	*groES*	co-chaperonin GroES	4.82	1.4969E-08
36	PA2621	NA	ATP-dependent Clp protease adapter protein Clp	4.80	1.8185E-08
37	PA4741	*rpsO*	30S ribosomal protein S15	4.78	1.8185E-08
38	PA4387	NA	phage exclusion suppressor FxsA	4.77	2.0181E-08
39	PA4406	*lpxC*	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	4.76	2.0531E-08
40	PA2830	*htpX*	protease HtpX	4.75	2.121E-08
41	PA2637	*nuoA*	NADH-quinone oxidoreductase subunit A	4.70	3.0696E-08
42	PA4264	*rpsJ*	30S ribosomal protein S10	4.69	2.7571E-08
43	PA4268	*rpsL*	30S ribosomal protein S12	4.67	3.3193E-08
44	PA4550	*fimU*	type 4 fimbrial biogenesis protein FimU	4.67	3.3482E-08
45	PA4241	*rpsM*	30S ribosomal protein S13	4.58	6.235E-08
46	PA0805	NA	hypothetical protein	4.58	5.2105E-08
47	PA5288	*glnK*	nitrogen regulatory protein P-II 2	4.58	5.4587E-08
48	PA1985	*pqqA*	coenzyme PQQ synthesis protein A	4.57	8.1886E-08
49	PA2883	NA	hypothetical protein	4.54	6.7776E-08
50	PA0635	NA	hypothetical protein	4.44	1.3231E-07
51	PA1596	*htpG*	chaperone protein HtpG	4.42	1.2852E-07
52	PA1847	NA	Fe/S biogenesis protein NfuA	4.40	1.4521E-07
53	PA0634	NA	hypothetical protein	4.40	1.7148E-07
54	PA2826	NA	glutathione peroxidase	4.39	1.8238E-07
55	PA3745	*rpsP*	30S ribosomal protein S16	4.38	1.7728E-07
56	PA4563	*rpsT*	30S ribosomal protein S20	4.38	1.699E-07
57	PA0633	NA	hypothetical protein	4.33	2.068E-07
58	PA1777	*oprF*	outer membrane porin F	4.32	2.1424E-07
59	PA3235	NA	hypothetical protein	4.29	3.8138E-07
60	PA1198	NA	hypothetical protein	4.25	3.3656E-07
61	PA4249	*rpsH*	30S ribosomal protein S8	4.21	4.3194E-07
62	PA3245	*minE*	cell division topological specificity factor MinE	4.21	5.8917E-07
63	PA1592	NA	hypothetical protein	4.18	4.5957E-07
64	PA0624	NA	hypothetical protein	4.18	5.1763E-07
65	PA3815	*iscR*	HTH-type transcriptional regulator	4.17	5.2217E-07

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
66	PA2741	*rplT*	50S ribosomal protein L20	4.17	5.2629E-07
67	PA2207	NA	bacteriophage protein	4.16	5.3019E-07
68	PA0038	NA	hypothetical protein	4.15	5.7104E-07
69	PA4752	*ftsJ*	cell division protein FtsJ	4.13	6.6714E-07
70	PA4567	*rpmA*	50S ribosomal protein L27	4.12	6.7979E-07
71	PA4251	*rplE*	50S ribosomal protein L5	4.11	7.7139E-07
72	PA4761	*d*NA*K*	molecular chaperone DnaK	4.10	7.2619E-07
73	PA1831	NA	hypothetical protein	4.09	8.2392E-07
74	PA3812	*iscA*	iron-binding protein IscA	4.08	1.0485E-06
75	PA0258	NA	hypothetical protein	4.08	1.0765E-06
76	PA4568	*rplU*	50S ribosomal protein L21	4.05	9.5746E-07
77	PA4237	*rplQ*	50S ribosomal protein L17	4.05	1.0021E-06
78	PA1584	*sdhB*	succinate dehydrogenase iron-sulfur subunit	4.04	1.0485E-06
79	PA0736a	NA	hypothetical protein	4.03	1.0987E-06
80	PA1179	*phoP*	two-component response regulator PhoP	4.02	1.2631E-06
81	PA0645	NA	hypothetical protein	4.01	1.5332E-06
82	PA2970	*rpmF*	50S ribosomal protein L32	4.00	1.4326E-06
83	PA1053	NA	hypothetical protein	3.97	1.4326E-06
84	PA5332	*Crc*	catabolite repression control protein	3.96	1.6483E-06
85	PA1610	*fabA*	3-hydroxydecanoyl-ACP dehydratase	3.92	2.0256E-06
86	PA3049	*Rmf*	ribosome modulation factor	3.91	1.9734E-06
87	PA4944	*Hfq*	RNA-binding protein Hfq	3.90	2.047E-06
88	PA5570	*rpmH*	50S ribosomal protein L34	3.89	2.2916E-06
89	PA3928	NA	hypothetical protein	3.88	3.0977E-06
90	PA4451	NA	hypothetical protein	3.87	2.6749E-06
91	PA3808	NA	hypothetical protein	3.86	2.9232E-06
92	PA0996	*pqsA*	anthranilate--CoA ligase	3.82	3.1437E-06
93	PA0779	NA	ATP-dependent protease	3.82	3.1073E-06
94	PA2638	*nuoB*	NADH-quinone oxidoreductase subunit B	3.82	3.395E-06
95	PA1581	*sdhC*	succinate dehydrogenase subunit C	3.79	3.7159E-06
96		NA	hypothetical protein	3.79	3.9236E-06
97	PA3299	*fadD1*	long-chain-fatty-acid--CoA ligase	3.78	3.9538E-06
98	PA0039	NA	hypothetical protein	3.77	4.1824E-06
99	PA1970	NA	hypothetical protein	3.77	6.2279E-06
100	PA2501	NA	hypothetical protein	3.75	8.0269E-06
101	PA2860	NA	hypothetical protein	3.73	5.529E-06

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
102	PA1800	*Tig*	trigger factor	3.73	5.085E-06
103	PA1755	NA	hypothetical protein	3.73	6.0821E-06
104	PA3009	NA	hypothetical protein	3.73	5.5826E-06
105	PA4542	*clpB*	chaperone protein ClpB	3.73	5.1376E-06
106	PA4475	NA	hypothetical protein	3.72	5.5826E-06
107	PA4456	NA	ABC transporter ATP-binding protein	3.72	5.5826E-06
108	PA4395	NA	nucleotide-binding protein	3.71	6.0559E-06
109	PA4751	*ftsH*	cell division protein FtsH	3.71	5.5826E-06
110	PA4575	NA	hypothetical protein	3.71	5.9754E-06
111	PA4762	*grpE*	heat shock protein GrpE	3.69	6.1602E-06
112	PA0320	NA	hypothetical protein	3.68	7.7555E-06
113	PA2586	*gacA*	response regulator GacA	3.67	7.0246E-06
114	PA0995	*ogt*	methylated-DNA--protein-cysteine methyltransferase	3.67	7.7555E-06
115	PA5240	*trxA*	Thioredoxin	3.66	7.0875E-06
116	PA4306	*flp*	type IVb pilin Flp	3.66	8.6046E-06
117	PA5424	NA	hypothetical protein	3.66	7.6997E-06
118	PA1776	*sigX*	RNA polymerase sigma factor SigX	3.65	7.8723E-06
119	PA4739	NA	hypothetical protein	3.64	1.0396E-05
120	PA3533	NA	hypothetical protein	3.63	8.2688E-06
121	PA3385	*amrZ*	alginate and motility regulator Z	3.62	8.6046E-06
122	PA4971	*aspP*	adenosine diphosphate sugar pyrophosphatase	3.62	9.6659E-06
123	PA2960	*pilZ*	type 4 fimbrial biogenesis protein PilZ	3.60	1.2687E-05
124	PA2851	*efp*	elongation factor P	3.60	1.0377E-05
125	PA0490	NA	hypothetical protein	3.58	1.2505E-05
126	PA4245	*rpmD*	50S ribosomal protein L30	3.58	1.7314E-05
127	PA0628	NA	hypothetical protein	3.58	1.1723E-05
128	PA1769	NA	phosphoenolpyruvate synthase regulatory protein	3.58	1.1783E-05
129	PA3201	NA	intracellular septation protein A	3.57	1.2666E-05
130	PA4935	*rpsF*	30S ribosomal protein S6	3.55	1.2832E-05
131	PA4385	*groEL*	molecular chaperone GroEL	3.54	1.2823E-05
132	PA4714	NA	hypothetical protein	3.54	1.3806E-05
133	PA3162	*rpsA*	30S ribosomal protein S1	3.53	1.3389E-05
134	PA0619	NA	bacteriophage protein	3.52	1.6798E-05
135	PA4276	*secE*	preprotein translocase subunit SecE	3.51	1.6245E-05
136	PA5561	*atpI*	ATP synthase subunit I	3.50	1.9018E-05

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
137	PA4090	NA	hypothetical protein	3.49	1.8936E-05
138	PA4499	NA	transcriptional regulator	3.48	1.7788E-05
139	PA3809	*fdx2*	(2Fe-2S) ferredoxin	3.47	2.1541E-05
140	PA0646	NA	hypothetical protein	3.47	1.9778E-05
141	PA3647	NA	hypothetical protein	3.47	2.2257E-05
142	PA1035	NA	hypothetical protein	3.45	2.5059E-05
143	PA4061	NA	Thioredoxin	3.44	2.3019E-05
144	PA0643	NA	hypothetical protein	3.43	2.4912E-05
145	PA3351	*flgM*	protein FlgM	3.42	2.3889E-05
146	PA0640	NA	bacteriophage protein	3.42	2.6587E-05
147	PA1830	NA	hypothetical protein	3.41	2.6521E-05
148	PA0644	NA	hypothetical protein	3.40	3.8331E-05
149	PA2957	NA	transcriptional regulator	3.39	3.0822E-05
150	PA0618	NA	bacteriophage protein	3.39	3.0334E-05
151	PA4661	*pagL*	lipid A 3-O-deacylase	3.39	2.9857E-05
152	PA1544	*Anr*	transcriptional regulator Anr	3.38	2.9857E-05
153	PA0625	NA	hypothetical protein	3.37	3.0878E-05
154	PA1882	NA	Transporter	3.36	3.8331E-05
155	PA0762	*algU*	RNA polymerase sigma factor AlgU	3.35	3.3711E-05
156	PA0408	*pilG*	pilus biosynthesis/twitching motility protein PilG	3.35	3.5749E-05
157	PA2623	*Icd*	isocitrate dehydrogenase	3.34	3.4664E-05
158	PA0329	NA	hypothetical protein	3.34	3.5624E-05
159	PA2196	NA	transcriptional regulator	3.32	4.8798E-05
160	PA1414	NA	hypothetical protein	3.32	3.8315E-05
161	PA0139	*ahpC*	alkyl hydroperoxide reductase	3.31	3.9996E-05
162	PA0506	NA	acyl-CoA dehydrogenase	3.30	4.2353E-05
163	PA5528	NA	hypothetical protein	3.30	4.2743E-05
164	PA0615	NA	hypothetical protein	3.29	5.3202E-05
165	PA0636	NA	hypothetical protein	3.29	4.7284E-05
166	PA4248	*rplF*	50S ribosomal protein L6	3.28	5.0377E-05
167	PA0286	*desA*	delta-9 fatty acid desaturase DesA	3.27	5.0229E-05
168	PA4261	*rplW*	50S ribosomal protein L23	3.27	6.0809E-05
169	PA1963	NA	hypothetical protein	3.26	6.3188E-05
170	PA0639	NA	hypothetical protein	3.26	5.9738E-05
171	PA1100	*fliE*	flagellar hook-basal body complex protein FliE	3.25	6.0542E-05
172	PA5276	*lppL*	lipopeptide LppL	3.24	6.323E-05
173	PA1801	*clpP*	ATP-dependent Clp protease proteolytic subunit	3.24	5.9579E-05

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
174	PA3600	NA	50S ribosomal protein L36	3.24	0.0001
175	PA0577	*dna*G	DNA primase	3.24	5.9075E-05
176	PA1775	*cmpX*	hypothetical protein	3.23	6.0807E-05
177	PA2485	NA	hypothetical protein	3.23	7.0464E-05
178	PA4765	*omlA*	outer membrane lipoprotein OmlA	3.23	6.321E-05
179	PA4453	NA	hypothetical protein	3.22	6.8002E-05
180	PA0003	*recF*	DNA replication and repair protein RecF	3.22	6.5082E-05
181	PA4870	NA	hypothetical protein	3.22	6.903E-05
182	PA0626	NA	hypothetical protein	3.21	6.9739E-05
183	PA5559	*atpE*	ATP synthase subunit C	3.20	8.2487E-05
184	PA2797	NA	hypothetical protein	3.19	8.3721E-05
185	PA2667	NA	hypothetical protein	3.19	7.5932E-05
186	PA1749	NA	hypothetical protein	3.18	7.9156E-05
187	PA4724.1	NA	hypothetical protein	3.17	0.0001
188	PA1430	*lasR*	transcriptional regulator LasR	3.17	8.3473E-05
189	PA4421	NA	cell division protein MraZ	3.16	8.4673E-05
190	PA2755	*eco*	Ecotin	3.15	9.1806E-05
191	PA1548	NA	hypothetical protein	3.15	0.0001
192	PA0865	*hpd*	4-hydroxyphenylpyruvate dioxygenase	3.15	8.8442E-05
193	PA0576	*rpoD*	RNA polymerase sigma factor RpoD	3.15	8.5466E-05
194	PA1840	NA	hypothetical protein	3.15	0.0001
195	PA4462	*rpoN*	RNA polymerase factor sigma-54	3.14	9.2754E-05
196	PA3814	*iscS*	cysteine desulfurase	3.14	9.2754E-05
197	PA0648	NA	hypothetical protein	3.13	0.0001
198	PA3006	*psrA*	transcriptional regulator PsrA	3.13	9.6962E-05
199	PA4611	NA	hypothetical protein	3.11	0.0001
200	PA5239	*rho*	transcription termination factor Rho	3.10	0.0001
201	PA3014	*faoA*	fatty acid oxidation complex subunit alpha	3.10	0.0001
202	PA3645	*fabZ*	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	3.10	0.0001
203	PA1112b	NA	hypothetical protein	3.09	0.0001
204	PA1580	*gltA*	citrate synthase	3.09	0.0001
205	PA4500	NA	ABC transporter	3.08	0.0001
206	PA4454	NA	hypothetical protein	3.08	0.0001
207	PA3811	*hscB*	co-chaperone HscB	3.08	0.0001
208	PA4238	*rpoA*	DNA-directed RNA polymerase subunit alpha	3.07	0.0001

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
209	PA0638	NA	bacteriophage protein	3.07	0.0001
210	PA0627	NA	hypothetical protein	3.07	0.0001
211	PA2952	*etfB*	electron transfer flavoprotein subunit beta	3.07	0.0001
212	PA3622	*rpoS*	RNA polymerase sigma factor RpoS	3.07	0.0001
213	PA1869	NA	acyl carrier protein	3.07	0.0001
214	PA3224	NA	hypothetical protein	3.06	0.0001
215	PA1793	*ppiB*	peptidyl-prolyl cis-trans isomerase B	3.06	0.0001
216	PA5068	*tatA*	twin-arginine translocation protein TatA	3.05	0.0001
217	PA0968	NA	hypothetical protein	3.04	0.0001
218	PA5560	*atpB*	ATP synthase subunit A	3.04	0.0001
219	PA0579	*rpsU*	30S ribosomal protein S21	3.04	0.0001
220	PA1742	NA	Amidotransferase	3.03	0.0001
221	PA2023	*galU*	UTP-glucose-1-phosphate uridylyltransferase	3.03	0.0001
222	PA2798	NA	two-component response regulator	3.02	0.0001
223	PA4275	*nusG*	transcription antitermination protein NusG	3.02	0.0001
224	PA2743	*infC*	translation initiation factor IF-3	3.01	0.0001
225	PA4693	*pssA*	phosphatidylserine synthase	3.01	0.0001
226	PA0336	*ygdP*	RNA pyrophosphohydrolase	3.01	0.0001
227	PA4253	*rplN*	50S ribosomal protein L14	3.00	0.0001
228	PA0532	NA	hypothetical protein	3.00	0.0001
229	PA4753	NA	hypothetical protein	2.99	0.0001
230	PA2971	NA	hypothetical protein	2.99	0.0001
231	PA0872	*phhA*	phenylalanine 4-monooxygenase	2.98	0.0002
232	PA0392	NA	hypothetical protein	2.98	0.0002
233	PA4465	NA	hypothetical protein	2.98	0.0002
234	PA1623	NA	hypothetical protein	2.97	0.0002
235	PA5253	*algP*	alginate regulatory protein AlgP	2.97	0.0002
236	PA2407	NA	adhesion protein	2.96	0.0002
237	PA2985	NA	hypothetical protein	2.96	0.0002
238	PA3295	NA	HIT family protein	2.96	0.0002
239	PA5054	*hslU*	ATP-dependent protease ATP-binding subunit HslU	2.96	0.0002
240	PA4433	*rplM*	50S ribosomal protein L13	2.95	0.0002
241	PA2780	NA	hypothetical protein	2.95	0.0002
242	PA1814	NA	hypothetical protein	2.95	0.0002

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
243	PA2951	*etfA*	electron transfer flavoprotein subunit alpha	2.94	0.0002
244	PA0997	*pqsB*	hypothetical protein	2.93	0.0002
245	PA5489	*dsbA*	thiol:disulfide interchange protein DsbA	2.92	0.0002
246	PA5011	*waaC*	heptosyltransferase I	2.92	0.0002
247	PA3244	*minD*	cell division inhibitor MinD	2.92	0.0002
248	PA0637	NA	hypothetical protein	2.92	0.0003
249	PA4963	NA	hypothetical protein	2.92	0.0002
250	PA0297	*spuA*	glutamine amidotransferase	2.92	0.0002
251	PA1852	NA	hypothetical protein	2.91	0.0002
252	PA2756	NA	hypothetical protein	2.91	0.0002
253	PA1463	NA	hypothetical protein	2.91	0.0002
254	PA0284	NA	hypothetical protein	2.91	0.0002
255	PA3552	*arnB*	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	2.90	0.0003
256	PA4471	NA	hypothetical protein	2.90	0.0003
257	PA1509	NA	hypothetical protein	2.90	0.0003
258	PA4263	*rplC*	50S ribosomal protein L3	2.90	0.0002
259	PA1002	*phnB*	anthranilate synthase component II	2.90	0.0003
260	PA2805	NA	hypothetical protein	2.89	0.0002
261	PA0970	*tolR*	translocation protein TolR	2.89	0.0003
262	PA4324	NA	hypothetical protein	2.88	0.0003
263	PA4243	*secY*	preprotein translocase subunit SecY	2.88	0.0003
264	PA1456	*cheY*	chemotaxis protein CheY	2.88	0.0003
265	PA4574	NA	hypothetical protein	2.88	0.0003
266	PA0036	*trpB*	tryptophan synthase subunit beta	2.88	0.0003
267	PA2747a	NA	hypothetical protein	2.87	0.0003
268	PA1583	*sdhA*	succinate dehydrogenase flavoprotein subunit	2.87	0.0003
269	PA3017	NA	hypothetical protein	2.86	0.0003
270	PA2146	NA	hypothetical protein	2.86	0.0003
271	PA3257	*prc*	tail-specific protease	2.86	0.0003
272	PA5301	NA	transcriptional regulator	2.85	0.0003
273	PA0363	*coaD*	phosphopantetheine adenylyltransferase	2.85	0.0003
274	PA1076	NA	hypothetical protein	2.84	0.0003
275	PA1797a	NA	hypothetical protein	2.84	0.0003
276	PA4551	*pilV*	type 4 fimbrial biogenesis protein PilV	2.84	0.0003

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
277	PA1942	NA	hypothetical protein	2.84	0.0004
278	PA1307	NA	hypothetical protein	2.82	0.0004
279	PA4842	NA	hypothetical protein	2.82	0.0004
280	PA2790	NA	hypothetical protein	2.82	0.0004
281	PA2614	*lolA*	outer-membrane lipoprotein carrier protein	2.80	0.0004
282	PA0943	NA	hypothetical protein	2.80	0.0004
283	PA0567	NA	hypothetical protein	2.80	0.0005
284	PA4419	*ftsL*	cell division protein FtsL	2.80	0.0006
285	PA1494	NA	hypothetical protein	2.80	0.0004
286	PA4259	*rpsS*	30S ribosomal protein S19	2.80	0.0004
287	PA0563	NA	hypothetical protein	2.79	0.0004
288	PA4239	*rpsD*	30S ribosomal protein S4	2.79	0.0004
289	PA2742	*rpmI*	50S ribosomal protein L35	2.79	0.0004
290	PA4748	*tpiA*	triosephosphate isomerase	2.79	0.0004
291	PA4114	NA	spermidine acetyltransferase	2.78	0.0004
292	PA4674	NA	hypothetical protein	2.78	0.0004
293	PA2491	NA	Oxidoreductase	2.78	0.0004
294	PA0422	NA	hypothetical protein	2.78	0.0005
295	PA0667	NA	hypothetical protein	2.78	0.0004
296	PA5369	*pstS*	phosphate ABC transporter substrate-binding protein	2.77	0.0005
297	PA3940	NA	DNA binding protein	2.76	0.0005
298	PA4738	NA	hypothetical protein	2.76	0.0006
299	PA5482	NA	hypothetical protein	2.75	0.0007
300	PA0951a	NA	hypothetical protein	2.75	0.0007
301	PA1013	*purC*	phosphoribosylaminoimidazole-succinocarboxamide synthase	2.75	0.0005
302	PA0394	NA	hypothetical protein	2.74	0.0005
303	PA5128	*secB*	preprotein translocase subunit SecB	2.74	0.0005
304	PA1308	NA	hypothetical protein	2.74	0.0006
305	PA2312a	NA	hypothetical protein	2.73	0.0007
306	PA2737	NA	hypothetical protein	2.72	0.0006
307	PA4498	NA	Metallopeptidase	2.72	0.0006
308	PA1821	NA	enoyl-CoA hydratase	2.71	0.0007
309	PA4271	*rplL*	50S ribosomal protein L7/L12	2.71	0.0006
310	PA0250	NA	hypothetical protein	2.70	0.0007
311	PA4141	NA	hypothetical protein	2.69	0.0007
312	PA3835	NA	hypothetical protein	2.69	0.0007
313	PA3472	NA	hypothetical protein	2.68	0.0007

Sr. No	Gene ID	Symbol	Product name	Log FC	FDR
314	PA2446	*gcvH2*	glycine cleavage system protein H	2.67	0.0008
315	PA3578	NA	hypothetical protein	2.67	0.0007
316	PA4257	*rpsC*	30S ribosomal protein S3	2.67	0.0007
317	PA3085	NA	hypothetical protein	2.67	0.0008
318	PA3656	*rpsB*	30S ribosomal protein S2	2.67	0.0007
319	PA3686	*adk*	adenylate kinase	2.67	0.0008
320	PA2746a	NA	hypothetical protein	2.67	0.0008
321	PA2779	NA	hypothetical protein	2.66	0.0009
322	PA3813	*iscU*	scaffold protein	2.66	0.0008
323	PA1443	*fliM*	flagellar motor switch protein FliM	2.66	0.0008
324	PA4570	NA	hypothetical protein	2.65	0.0008
325	PA0973	*oprL*	peptidoglycan associated lipoprotein OprL	2.65	0.0008
326	PA1034	NA	hypothetical protein	2.64	0.0009
327	PA2321	NA	Gluconokinase	2.64	0.0009
328	PA1527	NA	hypothetical protein	2.64	0.0008
329	PA1571	NA	hypothetical protein	2.64	0.0009
330	PA5227	NA	hypothetical protein	2.63	0.0009
331	PA1455	*fliA*	flagellar biosynthesis sigma factor FliA	2.63	0.0009
332	PA4134	NA	hypothetical protein	2.63	0.001
333	PA2854	NA	hypothetical protein	2.63	0.0009
334	PA5200	*amgR*	osmolarity response regulator	2.62	0.0009
335	PA5264	NA	hypothetical protein	2.62	0.0009
336	PA4671	NA	50S ribosomal protein L25/general stress protein Ctc	2.62	0.0009

Genes are arranged in decreasing order of Fold Change; Databases consulted for gene functions were: NCBI gene database (https://www.ncbi.nlm.nih.gov/nuccore/NC_002516); KEGG (Kyoto Encyclopedia of Genes and Genomes: https://www.genome.jp/kegg/); Uniprot (https://www.uniprot.org/). NA: Not Applicable; FDR: False Discovery Rate

Table S10. Node degree score of the top down-regulated genes

No.	Gene ID/Symbol	Identifier	Node degree
1	*rpsB*	208964.PA3656	79
2	*rplM*	208964.PA4433	76
3	*rpsL*	208964.PA4268	76
4	*rpoA*	208964.PA4238	75
5	*rplU*	208964.PA4568	74
6	*ftsH*	208964.PA4751	72
7	*rplT*	208964.PA2741	72
8	*rpmF*	208964.PA2970	72
9	*rplC*	208964.PA4263	70
10	*rpsD*	208964.PA4239	70
11	*rpsJ*	208964.PA4264	70
12	*tig*	208964.PA1800	70
13	*rplN*	208964.PA4253	69
14	*rpsO*	208964.PA4741	69
15	*rpmA*	208964.PA4567	67
16	*rpsF*	208964.PA4935	67
17	*rpsM*	208964.PA4241	67
18	*rpsA*	208964.PA3162	66
19	*secY*	208964.PA4243	66
20	*rplF*	208964.PA4248	65
21	*rplL*	208964.PA4271	65
22	*rpsT*	208964.PA4563	65
23	*efp*	208964.PA2851	64
24	*infC*	208964.PA2743	64
25	*rplQ*	208964.PA4237	64
26	*rpoD*	208964.PA0576	64
27	*dnaK*	208964.PA4761	63
28	*groEL*	208964.PA4385	63
29	*rpmI*	208964.PA2742	63
30	*rpsP*	208964.PA3745	63
31	*rplE*	208964.PA4251	62
32	*rpmD*	208964.PA4245	62
33	*acpP*	208964.PA2966	61
34	*infA*	208964.PA2619	60
35	*rplY*	208964.PA4671	60
36	*rpsH*	208964.PA4249	60
37	*secE*	208964.PA4276	60
38	*nusG*	208964.PA4275	59
39	*rpoS*	208964.PA3622	59
40	*rpsC*	208964.PA4257	59
41	*rpsI*	208964.PA4432	59
42	*rplW*	208964.PA4261	58
43	*rpsS*	208964.PA4259	58
44	*groES*	208964.PA4386	57
45	*atpE*	208964.PA5559	56
46	*rpsU*	208964.PA0579	55
47	PA4463	208964.PA4463	54
48	*hfq*	208964.PA4944	53
49	*rpmE*	208964.PA5049	53
50	*rpmJ2*	208964.PA3600	53

Rest 277 genes with node degree score ‘≤52’ are not listed

Table S11. Top ten cytoHubba ranked down-regulated genes from among the top-50 in Table S10

No.	Gene ID	Gene Name	Number of methods ranking this protein among top 10	Names of 12 ranking methods of CytoHubba and rank score provided by them											
				Degree	MNC	DMNC	MCC	Bottleneck	EcCentricity	Closeness	Radiality	Betweenness	Stress	CC	EPC
1	PA3656	*rpsB*	10	49	49	-	1.06E+45	1	1	49	2.06	14.07	336	-	26.06
2	PA4239	*rpsD*	10	49	49	-	1.06E+45	2	1	49	2.06	14.07	336	-	25.76
3	PA4268	*rpsL*	9	49	49	-	1.06E+45	-	1	49	2.06	14.07	336	-	25.55
4	PA4251	*rplE*	8	47	47	-	1.06E+45	-	-	48	2.02	10.08	250	-	26.3
5	PA4238	*rpoA*	7	48	48	-	-	-	-	48.5	2.04	12.73	304	-	25.65
6	PA2741	*rplT*	7	47	47	-	-	-	-	48	2.02	9.83	246	-	25.65
7	PA4264	*rpsJ*	7	47	47	-	1.06E+45	-	-	48	2.02	-	234	-	25.73
8	PA4253	*rplN*	7	47	47	-	1.06E+45	-	-	48	2.02	9.21	238	-	-
9	PA4271	*rplL*	7	47	47	-	-	-	-	48	2.02	11.89	278	-	25.32
10	PA4248	*rplF*	6	47	47	-	-	-	-	48	2.02	9.88	248	-	-

"-": This method did not rank the shown protein among top 10

MNC: Maximum Neighborhood Component; DMNC: Density of Maximum Neighborhood Component; MCC: Maximal Clique Centrality; CC: Clustering Co-efficient;EPC: Edge Percolated Component

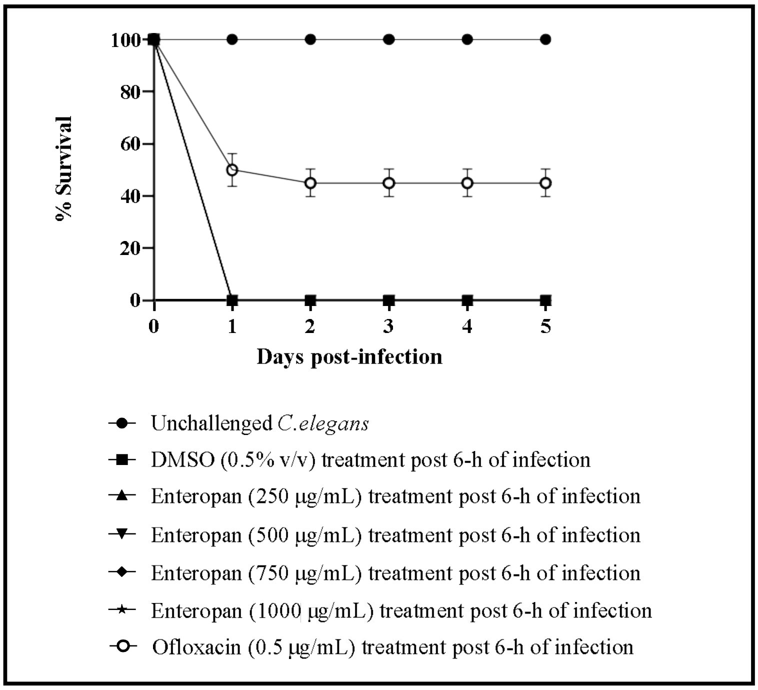

Figure S1. Enteropan could not rescue the host worm post 6-h of *P. aeruginosa* infection. Ofloxacin (0.5 µg/mL) employed as positive control post 6-h infection conferred 45% ± 5.47 ($p<0.001$) survival benefit on host worm. Neither DMSO nor Enteropan showed any toxicity towards the worm population at tested concentrations.

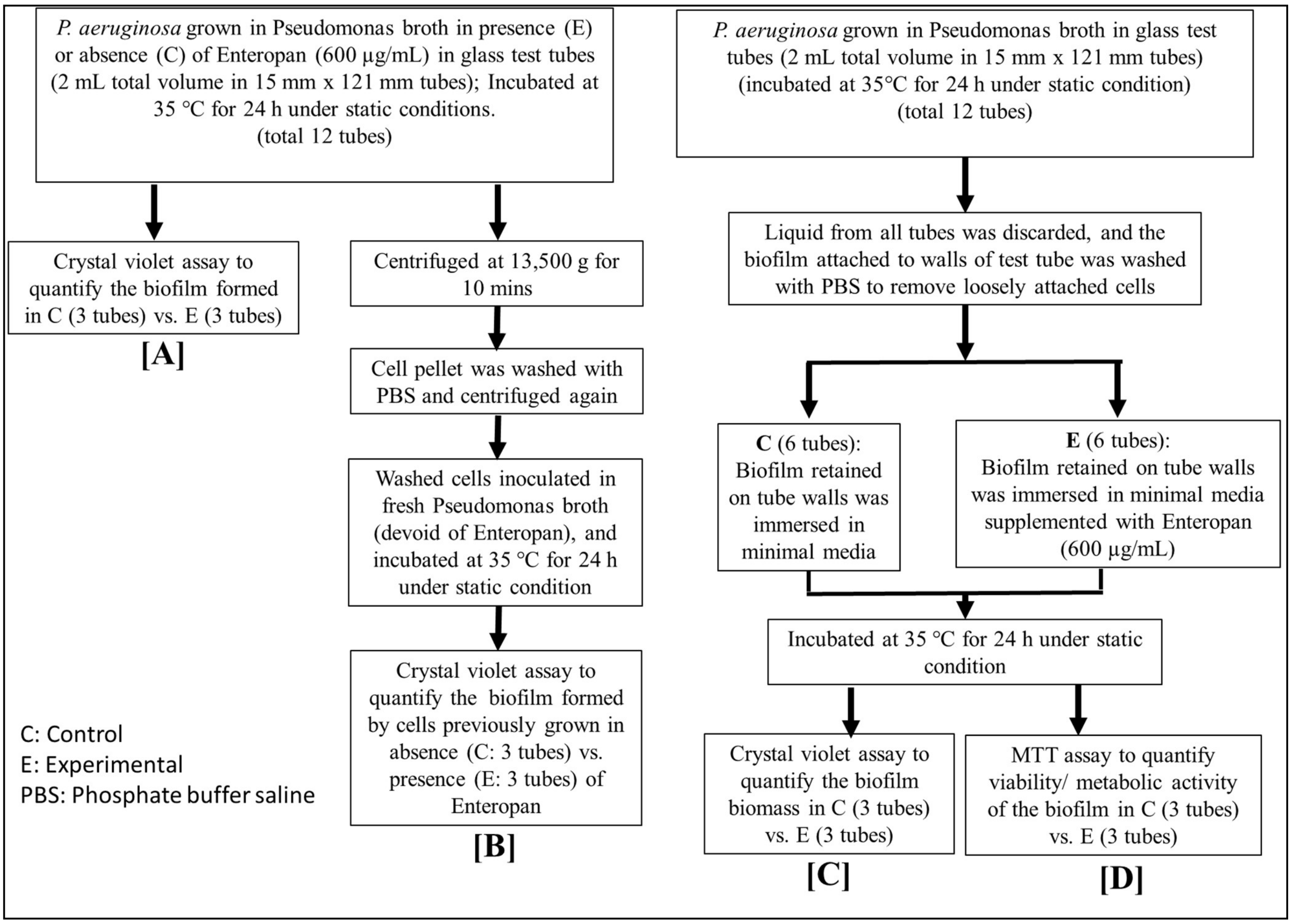

Figure S2: Flowchart depicting schematic of all biofilm assays

(A) Quantification of biofilm formation in presence or absence of Enteropan; **(B)** Quantification of biofilm formation by Enteropan-pre-treated vs. non-pre-treated *P. aeruginosa* cells; **(C)** Quantification of biofilm eradication after adding Enteropan onto pre-formed biofilm; **(D)** Quantification of Enteropan's effect on metabolic activity of pre-formed biofilm

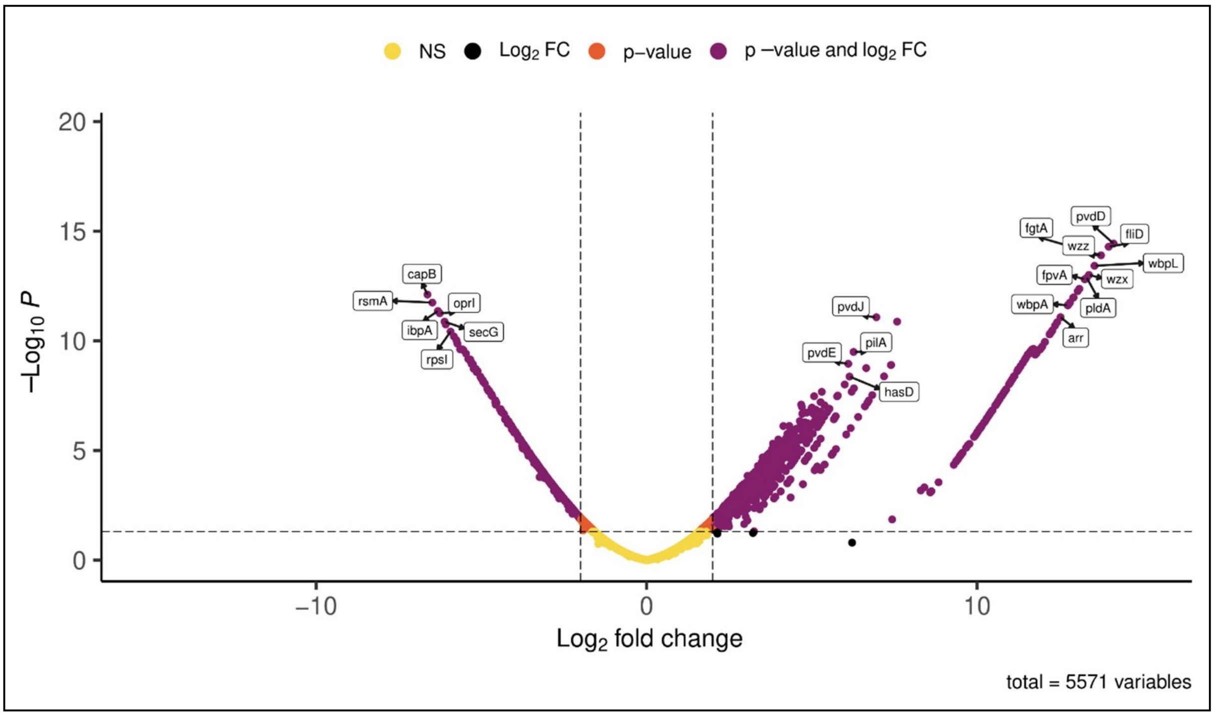

Figure S3. Volcano plot of experimental versus control samples. Volcano plot of expressed genes of experimental culture compared to control culture. The y- axis illustrates −log 10 p values, and the x-axis corresponds to a log 2-fold change of gene expression between both cultures. The purple points represent differently expressed genes satisfying the dual criteria of FDR< 0.05 and log fold change ≥2.