

**Table S3:** Respiratory activity (absorbance at 492 nm) of different *Pseudomonas aeruginosa* strains after 24, 48, 72, 96, 120, 144 and 168 h of culture in continuous flow, on the surface of endotracheal tubes, in the presence and absence of bacteriophage cocktail.

Incubation time	Strain	Group				p*	
		Control		Bacteriophages cocktail			
		Mean ± Standard Deviation (Median)	95% Confidence interval (Minimum – Maximum)	Mean ± Standard Deviation (Median)	95% Confidence interval (Minimum – Maximum)		
24 h	<i>P. aeruginosa</i> 27853	0.02 ± 0.02 (0.02)	0.00; 0.04 (0.00 – 0.05)	0.04 ± 0.01 (0.05)	< 0.001 <sup>†</sup>	0.050	
	<i>P. aeruginosa</i> 2110	0.01 ± 0.01 (0.01)	0.00; 0.02 (0.00 – 0.02)	0.00 ± 0.01 (0.00)		1.000	
	<i>P. aeruginosa</i> 2112	0.05 ± 0.02 (0.05)	< 0.001 <sup>†</sup>	0.03; 0.06 (0.03 – 0.07)	< 0.001 <sup>†</sup>	0.096	
48 h	<i>P. aeruginosa</i> 27853	0.09 ± 0.03 (0.08)	0.06; 0.12 (0.07 – 0.15)	0.09 ± 0.03 (0.10)	0.05; 0.12 (0.03 – 0.12)	1.000	
	<i>P. aeruginosa</i> 2110	0.09 ± 0.04 (0.08)	0.04; 0.13 (0.04 – 0.16)	0.04 ± 0.03 (0.03)	0.01; 0.08 (0.02 – 0.11)	0.394	
	<i>P. aeruginosa</i> 2112	0.15 ± 0.04 (0.16)	0.023 <sup>†</sup>	0.11; 0.19 (0.10 – 0.20)	0.17 ± 0.02 (0.17)	< 0.001 <sup>†</sup>	1.000
72 h	<i>P. aeruginosa</i> 27853	0.14 ± 0.01 (0.14)	0.13; 0.15 (0.13 – 0.15)	0.20 ± 0.04 (0.21)	< 0.001 <sup>†</sup>	0.049	
	<i>P. aeruginosa</i> 2110	0.19 ± 0.03 (0.18)	0.16; 0.22 (0.16 – 0.23)	0.11 ± 0.05 (0.09)	0.06; 0.16 (0.05 – 0.18)	0.004	
	<i>P. aeruginosa</i> 2112	0.21 ± 0.05 (0.19)	0.007 <sup>†</sup>	0.16; 0.27 (0.17 – 0.31)	0.21 ± 0.02 (0.21)	< 0.001 <sup>†</sup>	1.000
96 h	<i>P. aeruginosa</i> 27853	0.24 ± 0.06 (0.25)	0.18; 0.30 (0.13 – 0.30)	0.27 ± 0.10 (0.30)	0.001 <sup>†</sup>	1.000	
	<i>P. aeruginosa</i> 2110	0.21 ± 0.04 (0.20)	0.16; 0.25 (0.16 – 0.27)	0.12 ± 0.05 (0.10)	0.07; 0.17 (0.08 – 0.20)	0.308	
	<i>P. aeruginosa</i> 2112	0.33 ± 0.08 (0.34)	0.008 <sup>†</sup>	0.25; 0.42 (0.20 – 0.43)	0.27 ± 0.04 (0.27)	0.001 <sup>†</sup>	1.000
120 h	<i>P. aeruginosa</i> 27853	0.27 ± 0.04 (0.26)	0.23; 0.31 (0.23 – 0.32)	0.21 ± 0.06 (0.22)		0.664	
	<i>P. aeruginosa</i> 2110	0.28 ± 0.04 (0.27)	0.24; 0.31 (0.24 – 0.33)	0.19 ± 0.06 (0.18)	0.035 <sup>†</sup>	0.059	
	<i>P. aeruginosa</i> 2112	0.31 ± 0.07 (0.31)	0.24; 0.38 (0.23 – 0.41)	0.30 ± 0.05 (0.31)	0.004 <sup>†</sup>	0.25; 0.35 (0.24 – 0.36)	1.000
144 h	<i>P. aeruginosa</i> 27853	0.23 ± 0.07 (0.25)	0.16; 0.30 (0.15 – 0.30)	0.20 ± 0.09 (0.18)		1.000	
	<i>P. aeruginosa</i> 2110	0.25 ± 0.07 (0.24)	0.18; 0.31 (0.16 – 0.32)	0.23 ± 0.02 (0.24)		1.000	
	<i>P. aeruginosa</i> 2112	0.29 ± 0.04 (0.28)	0.24; 0.33 (0.25 – 0.35)	0.24 ± 0.08 (0.26)		0.16; 0.32 (0.13 – 0.33)	1.000
168 h	<i>P. aeruginosa</i> 27853	0.33 ± 0.03 (0.33)	0.30; 0.37 (0.29 – 0.38)	0.19 ± 0.05 (0.20)		0.004	
	<i>P. aeruginosa</i> 2110	0.27 ± 0.03 (0.27)	0.23; 0.31 (0.22 – 0.32)	0.29 ± 0.03 (0.30)	0.037 <sup>†</sup>	0.26; 0.32 (0.23 – 0.32)	1.000
	<i>P. aeruginosa</i> 2112	0.33 ± 0.12 (0.31)	0.20; 0.45 (0.19 – 0.50)	0.31 ± 0.09 (0.30)		0.22; 0.40 (0.22 – 0.44)	1.000

Metabolic activity was analyzed by multiple comparisons considering strains and bacteriophages in a Generalized Linear Model with Bonferroni correction. \* It indicates p value for comparisons between control and bacteriophages cocktail. <sup>†</sup> It indicates p value for comparisons between strains.