

Table S1. Differentially expressed genes (DEGs) associated with adhesion as determined by transcriptome analysis [1].

Gene name	Product name	Log ₂ FC ¹	FDR ²	p-value
<i>cgrC</i>	cupA gene regulator C, CgrC	-2.48	1.57 x 10 ⁻²	5.00 x 10 ⁻⁴
<i>cheY</i>	two-component response regulator CheY	-2.16	4.13 x 10 ⁻²	1.80 x 10 ⁻³
<i>cheZ</i>	chemotaxis protein CheZ	-2.46	2.26 x 10 ⁻²	7.00 x 10 ⁻⁴
<i>fimU</i>	type 4 fimbrial biogenesis protein FimU	-2.39	2.57 x 10 ⁻²	9.00 x 10 ⁻⁴
<i>pilV</i>	type 4 fimbrial biogenesis protein PilV	-2.27	3.55 x 10 ⁻²	1.40 x 10 ⁻³

¹Log₂ FC, Log₂ relative fold changes of the gene expression levels in response to hydroquinine, compared to the untreated control. ²FDR, false discovery rate showed statistical significances.

Reference

1. Rattanachak, N.; Weawsiangsang, S.; Daowtak, K.; Thongsri, Y.; Ross, S.; Ross, G.; Nilsri, N.; Baldock, R.A.; Pongcharoen, S.; Jongjitvimol, T.; et al. High-throughput transcriptomic profiling reveals the inhibitory effect of hydroquinine on virulence factors in *Pseudomonas aeruginosa*. *Antibiotics*. **2022**, *11*, 1436, doi:10.3390/antibiotics11101436.