

**Skliros et al., 2023. Table S2.** Average relative transcript abundances ( $\pm$ SE) of *Vibrio alginolyticus* strain V1 genes and its respective resistant strains to bacteriophages  $\phi$ St2 (VaphiSt2) and Athena1 (VaAthena1). **A** for QS cassette genes, **B** for genes regulated by QS cascade. Heat maps that appear in Figure 3 of main text correspond to the presented colored values here. *P* value represents t-tests between Wild type and respective resistant strain. All treatments passed normality t-test. If equal variance test failed a Welch's test was applied. Statistical significance ( $P \leq 0.05$ ) is represented by bold *P* value.

**A.**

Relative expression levels of QS cassette genes															
	<i>LuxQ</i>	$\pm$ SE	<i>P</i>	<i>LuxM</i>	$\pm$ SE	<i>P</i>	<i>Hfq</i>	$\pm$ SE	<i>P</i>	<i>LuxU</i>	$\pm$ SE	<i>P</i>	<i>aphA</i>	$\pm$ SE	<i>P</i>
Wild type	0.072	0.014	na	0.120	0.003	na	1.048	0.080	na	0.289	0.011	na	3.633	0.039	na
VaphiSt2	0.059	0.003	0.509	0.057	0.010	<b>0.007</b>	0.746	0.154	0.230	0.024	0.005	<b>0.000</b>	1.618	0.116	<b>0.002</b>
VaAthena1	0.015	0.000	0.077	0.046	0.011	<b>0.006</b>	0.407	0.108	<b>0.018</b>	0.006	0.001	<b>0.000</b>	0.306	0.015	<b>0.000</b>
	<i>LuxP</i>	$\pm$ SE	<i>P</i>	<i>CqsA1</i>	$\pm$ SE	<i>P</i>	<i>LuxO1</i>	$\pm$ SE	<i>P</i>	<i>LuxO2</i>	$\pm$ SE	<i>P</i>	<i>LuxN</i>	$\pm$ SE	<i>P</i>
Wild type	0.438	0.005	na	0.371	0.164	na	0.016	0.001	na	0.067	0.008	na	1.284	0.131	na
VaphiSt2	0.065	0.000	<b>0.034</b>	0.002	0.000	0.208	0.006	0.001	<b>0.011</b>	0.012	0.000	<b>0.032</b>	0.032	0.006	<b>0.016</b>
VaAthena1	0.088	0.001	<b>0.038</b>	0.004	0.000	0.209	0.051	0.007	<b>0.050</b>	0.006	0.001	<b>0.024</b>	0.016	0.003	<b>0.016</b>
	<i>LuxR</i>	$\pm$ SE	<i>P</i>	<i>LuxS</i>	$\pm$ SE	<i>P</i>	<i>CqsA2</i>	$\pm$ SE	<i>P</i>	<i>CqsS</i>	$\pm$ SE	<i>P</i>			
Wild type	1.233	0.135	na	0.753	0.108	na	0.036	0.001	na	0.112	0.006	na			
VaphiSt2	0.045	0.009	<b>0.018</b>	0.269	0.003	<b>0.021</b>	0.031	0.002	0.262	0.117	0.008	0.694			
VaAthena1	0.008	0.004	<b>0.018</b>	0.579	0.057	0.308	0.016	0.002	<b>0.002</b>	0.027	0.005	<b>0.000</b>			

B.

Relative expression levels of QS cascade regulated genes									
	<i>Uhpc</i>	$\pm$ SE	<i>P</i>	<i>trh</i>	$\pm$ SE	<i>P</i>	<i>trpE</i>	$\pm$ SE	<i>P</i>
Wild type	0.117	0.050	na	0.194	0.047	na	0.116	0.010	na
VaphiSt2	0.004	0.000	<b>0.04</b>	0.052	0.006	0.102	0.034	0.015	<b>0.050</b>
VaAthena1	0.002	0.000	<b>0.03</b>	0.031	0.005	0.127	0.059	0.014	<b>0.023</b>
	<i>fur</i>	$\pm$ SE	<i>P</i>	<i>Wza</i>	$\pm$ SE	<i>P</i>	<i>Bcr/Cfla</i>	$\pm$ SE	<i>P</i>
Wild type	0.783	0.030	na	0.023	0.001	na	4.270	1.057	na
VaphiSt2	0.642	0.017	<b>0.040</b>	0.001	0.000	<b>0.006</b>	0.059	0.004	<b>0.031</b>
VaAthena1	0.245	0.042	<b>0.002</b>	0.000	0.000	<b>0.005</b>	0.020	0.009	<b>0.030</b>