

Skliros et al., 2020. Table S1. Average relative transcript abundances (\pm SE) of *Vibrio alginolyticus* strain V1 genes and its respective resistant strains to bacteriophages Aphrodite1 (VaAphrodite1), ϕ St2 (VaphiSt2) and Ares1 (VaAres1). **A** for receptors genes, **B** for genes involved in sugar transportation, **C** for genes involved in amino acid transporations, **D** for genes involved in major biochemical processes. Heat maps that appear in Figure 5 of main text correspond to the presented colored values here. *P* value represents t-tests between Control (wild type) and each resistant strain. Statistical significant is represented by bold *P* value. Mean primers' efficiency is also presented in table **E**.

A.

Relative expression levels of phage receptors												
	<i>tolC</i>	\pm SE	<i>P</i>	<i>ompF</i>	\pm SE	<i>P</i>	<i>btuB</i>	\pm SE	<i>P</i>	<i>lamB</i>	\pm SE	<i>P</i>
Control	0.2925	0.0139	na	0.0400	0.0039	na	0.1906	0.0142	na	5.7379	1.2186	na
VaAphrodite1	0.6417	0.0189	0.0002	0.0066	0.0002	0.0023	0.1164	0.0096	0.0243	3.6332	0.2073	0.237
VaphiSt2	0.5827	0.0215	0.0007	0.0061	0.0008	0.0023	0.1214	0.0156	0.0557	0.1063	0.0051	0.0195
VaAres1	0.6088	0.0581	0.0124	0.0414	0.0067	0.893	0.1775	0.0395	0.810	0.8058	0.0373	0.0298

B.

Relative transcript levels of genes involved in sugars transportation												
	<i>ptsG 1</i>	\pm SE	<i>P</i>	<i>ptsG 2</i>	\pm SE	<i>P</i>	<i>crr</i>	\pm SE	<i>P</i>	<i>celB</i>	\pm SE	<i>P</i>
Control	0.3775	0.0856	na	1.4519	0.1877	na	1.6949	0.4925	na	0.9120	0.0521	na
VaAphrodite1	1.3587	0.0258	0.0036	0.3239	0.0395	0.0002	0.2358	0.0428	0.046	0.1731	0.0516	0.0004
Va ϕ St2	0.2810	0.0994	0.428	0.6870	0.1674	0.0040	0.4834	0.1204	0.047	0.2966	0.0845	0.0027
VaAres1	0.2200	0.0184	0.216	0.6007	0.0645	0.889	0.5378	0.1469	0.0584	0.8508	0.1208	0.686
	<i>rbsA</i>	\pm SE	<i>P</i>	<i>treB</i>	\pm SE	<i>P</i>	<i>mtlA</i>	\pm SE	<i>P</i>	<i>fruA</i>	\pm SE	<i>P</i>
Control	1.5333	0.0949	na	1.0427	0.1180	na	0.7908	0.1704	na	0.3136	0.0331	na
VaAphrodite1	0.2333	0.0427	0.002	0.1652	0.1069	0.0038	0.6234	0.0468	0.482	0.1980	0.0143	0.0230
Va ϕ St2	0.5638	0.1894	0.055	0.8708	0.0177	0.253	0.0755	0.0490	0.0301	0.1924	0.0353	0.0764
VaAres1	0.5664	0.1793	0.048	0.6453	0.0358	0.0580	0.7221	0.0476	0.767	0.3474	0.0409	0.585

	<i>ptsN</i>	\pm SE	<i>P</i>	<i>ptsH</i>	\pm SE	<i>P</i>
Control	1.0454	0.0709	na	0.7503	0.0700	na
VaAphrodite1	0.1212	0.0257	0.0002	1.0928	0.1022	0.0604
Va ϕ St2	0.2781	0.1157	0.0040	0.2722	0.0915	0.0160
VaAres1	1.0167	0.1654	0.889	0.5863	0.0292	0.162

C.

Relative transcript levels of genes involved in amino acids transportation															
	<i>lysE</i>	± SE	<i>P</i>	<i>tyrP</i>	± SE	<i>P</i>	<i>metI</i>	± SE	<i>P</i>	<i>metN</i>	± SE	<i>P</i>	<i>metQ</i>	± SE	<i>P</i>
Control	0.6267	0.1318	na	0.3810	0.1075	na	1.1441	0.1223	na	1.2661	0.0236	na	0.9026	0.1715	na
VaAphrodite1	0.0081	0.0031	0.0186	0.3319	0.0034	0.561	0.3791	0.0692	0.0017	0.1174	0.0375	0.0000	0.1265	0.0566	0.00680
Va ϕ St2	0.6481	0.0164	0.901	0.2690	0.0964	0.728	0.6151	0.0431	0.0094	0.4308	0.1407	0.0085	0.5843	0.1493	0.239
VaAres1	0.5162	0.0533	0.560	0.3636	0.0566	0.913	1.0528	0.1392	0.668	1.2330	0.0666	0.713	0.9403	0.0840	0.839
	<i>rhtB 1</i>	± SE	<i>P</i>	<i>rhtB 2</i>	± SE	<i>P</i>	<i>tcyP</i>	± SE	<i>P</i>	<i>hisP</i>	± SE	<i>P</i>	<i>azlC 1</i>	± SE	<i>P</i>
Control	0.6020	0.0980	na	0.3086	0.0481	na	0.4799	0.0541	na	0.7633	0.0824	na	0.0363	0.0025	na
VaAphrodite1	0.2410	0.0582	0.0570	0.3459	0.0564	0.702	0.0723	0.0272	0.0043	0.3324	0.0329	0.0145	0.0512	0.0027	0.0298
Va ϕ St2	0.1928	0.0422	0.0334	0.3796	0.1071	0.647	0.0931	0.0022	0.0053	0.2552	0.1285	0.0325	0.0168	0.0006	0.0035
VaAres1	0.4428	0.0289	0.298	0.2417	0.0559	0.500	0.2172	0.0146	0.0187	0.5578	0.0522	0.160	0.0344	0.0039	0.747

	<i>artP</i>	± SE	<i>P</i>	<i>artL</i>	± SE	<i>P</i>	<i>livB</i>	± SE	<i>P</i>
Control	0.0152	0.0006	na	0.2992	0.0152	na	0.0021	0.0003	na
VaAphrodite1	0.0037	0.0016	0.0022	0.0695	0.0207	0.0006	0.0009	0.0001	0.0346
Va ϕ St2	0.0119	0.0019	0.236	0.4801	0.1178	0.279	0.0001	0.0000	0.0044
VaAres1	0.0117	0.0040	0.510	0.1239	0.0239	0.0052	0.0007	0.0001	0.0155
	<i>azlC 2</i>	± SE	<i>P</i>	<i>livH</i>	± SE	<i>P</i>			
Control	0.0121	0.0010	na	0.0107	0.0015	na			
VaAphrodite1	0.0178	0.0024	0.152	0.0041	0.0010	0.0382			
Va ϕ St2	0.0164	0.0022	0.221	0.0017	0.0006	0.0091			
VaAres1	0.0064	0.0005	0.0118	0.0041	0.0002	0.0211			

D.

Relative transcript levels of genes involved in major biochemical processes of the cell															
	<i>ald</i>	± SE	<i>P</i>	<i>agxT</i>	± SE	<i>P</i>	<i>panD</i>	± SE	<i>P</i>	<i>lysA 2</i>	± SE	<i>P</i>	<i>pykA</i>	± SE	<i>P</i>
Control	0.5209	0.2187	na	0.0365	0.0138	na	0.0005	0.0002	na	0.1652	0.0323	na	0.4902	0.1586	na
VaAphrodite1	1.3178	0.0204	0.0415	0.0275	0.0085	0.676	0.0001	0.0000	0.377	0.4523	0.0637	0.0304	0.6395	0.2170	0.674
VaøSt2	3.6661	0.5307	0.0110	0.0143	0.0026	0.266	0.0001	0.0000	0.330	0.5538	0.0256	0.001	0.0535	0.0051	0.127
VaAres1	0.2191	0.0509	0.334	0.0420	0.0054	0.776	0.0003	0.0001	0.286	1.1338	0.1234	0.003	1.4136	0.3587	0.087
	<i>lysA 1</i>	± SE	<i>P</i>	<i>gltA</i>	± SE	<i>P</i>	<i>murE</i>	± SE	<i>P</i>	<i>ppc</i>	± SE	<i>P</i>	<i>mdh 1</i>	± SE	<i>P</i>
Control	0.0367	0.0034	na	5.0889	0.6599	na	0.2192	0.0288	na	0.3602	0.0903	na	5.4497	0.0115	na
VaAphrodite1	0.0183	0.0015	0.502	6.1671	0.7864	0.439	0.1487	0.0122	0.140	0.1440	0.0282	0.1620	1.6533	0.1745	0.000
VaøSt2	0.0177	0.0030	0.986	0.7964	0.2812	0.0081	0.1143	0.0058	0.0434	0.1606	0.0317	0.1000	0.4048	0.0654	0.000
VaAres1	0.0488	0.0126	0.388	4.5747	0.6796	0.681	0.1890	0.0157	0.494	0.2558	0.0164	0.4060	5.5623	0.5020	0.864

	<i>frd</i>	± SE	<i>P</i>	<i>pykF</i>	± SE	<i>P</i>	<i>pckA</i>	± SE	<i>P</i>
Control	2.8835	0.1460	na	1.0785	0.1462	na	7.2277	0.7000	na
VaAphrodite1	14.1752	1.5394	0.0039	1.3193	0.1288	0.370	13.2575	0.6990	0.0076
VaϕSt2	0.1669	0.0165	0.0001	1.4789	0.1546	0.199	0.4540	0.1260	0.0014
VaAres1	1.7651	0.0954	0.0063	0.9863	0.0656	0.663	5.5833	0.5228	0.199
	<i>mdh 2</i>	± SE	<i>P</i>	<i>mdh 3</i>	± SE	<i>P</i>			
Control	0.4060	0.1487	na	0.9289	0.2133	na			
VaAphrodite1	0.5390	0.1245	0.605	1.0160	0.1629	0.804			
VaϕSt2	0.6721	0.0793	0.267	0.8036	0.0051	0.657			
VaAres1	0.6324	0.2170	0.521	0.6264	0.0339	0.317			



E.

Gene studied	Mean of primer's efficiency	Gene studied	Mean of primer's efficiency	Gene studied	Mean of primer's efficiency
<i>tolC</i>	1.969	<i>tcyP</i>	1.981	<i>pykF</i>	1.988
<i>ompF</i>	1.988	<i>hisP</i>	1.960	<i>pckA</i>	1.993
<i>btuB</i>	1.988	<i>azlC 1</i>	1.984		
<i>lamB</i>	1.973	<i>azlC 2</i>	1.981		
<i>ptsG 1</i>	1.913	<i>artP</i>	1.994		
<i>ptsG 2</i>	1.989	<i>artL</i>	1.985		
<i>crr</i>	1.967	<i>livB</i>	1.832		
<i>celB</i>	1.981	<i>livH</i>	1.990		
<i>rbsA</i>	1.977	<i>ald</i>	1.980		
<i>treB</i>	1.994	<i>agxT</i>	1.985		
<i>mtlA</i>	1.991	<i>panD</i>	1.989		
<i>fruA</i>	1.980	<i>lysA 1</i>	1.991		
<i>ptsN</i>	1.990	<i>lysA 2</i>	1.982		
<i>ptsH</i>	1.970	<i>pykA</i>	1.988		
<i>lysE</i>	1.952	<i>gltA</i>	1.994		
<i>tyrP</i>	1.993	<i>murE</i>	1.990		
<i>metL</i>	1.989	<i>ppc</i>	1.946		
<i>metN</i>	1.969	<i>mdh 1</i>	1.992		
<i>metQ</i>	1.981	<i>mdh 2</i>	1.976		
<i>rhtB 1</i>	1.956	<i>mdh 3</i>	1.992		
<i>rhtB 2</i>	1.971	<i>frd</i>	1.991		