

Table S2: Comparison of growth rates for selected knockouts with those for WT or rho^* cells in the MG1655 background. For each gene considered, the median RNA \log_2 ratio (rho^* / rho^{WT}) is shown for sense and antisense probes before and after the slash, respectively; the selection Z-score for all probes centered inside the target gene is also shown. Note that the RNA is isolated from WT and rho^* cells, not the knockouts under consideration. Growth rate ratios Γ are defined as described in the text. Confidence intervals (95%) for the growth rate ratios are calculated based on 10,000 samples from the posterior distribution of model parameters. All significant quantities (defined as described in the text) are bolded. †: Growth rates calculated using spline-guided fitting.

Strain	Compound	RNA \log_2 ratio	WT selection Z-score	rho^* selection Z-score	WT Γ (95% CI)	rho^* Γ (95% CI)
$\Delta yagM$	STP (2.0 $\mu\text{g}/\text{mL}$)	-0.501 / -0.707	-7.423	-0.589	0.532† (0.476-0.592)	0.953† (0.880 - 1.031)
$\Delta ykgL$		-0.232 / -0.669	10.646	-1.408	0.890† (0.827-0.958)	1.001† (0.934 - 1.071)
$\Delta envZ$	CML (1.875 $\mu\text{g}/\text{mL}$)	0.316 / 0.111	-5.010	-5.758	1.554 (1.471 - 1.618)	1.537 (1.454 - 1.597)
$\Delta yadM$		-0.558 / -0.101	1.509	12.886	1.010 (0.947 - 1.052)	1.020 (0.957 - 1.058)
$\Delta sthA$	M9t/AKG	0.283 / 0.079	-0.857	-7.118	0.977 (0.945 - 1.005)	0.946 (0.913 - 0.973)
$\Delta aroM$		0.032 / -0.082	1.295	9.086	0.982† (0.948-1.017)	0.907† (0.880-0.936)
$\Delta ppdD$	M9t/NADM	0.455 / 0.213	0.100	6.846	1.122 (1.056-1.191)	0.870 (0.802-0.945)
$\Delta yadN$		-0.111 / -0.600	2.409	-11.071	0.959 (0.901-1.021)	0.863 (0.796-0.937)