



Supplementary Table 1. Genotypes of evolved ecotypes from the Early (315 generations) and Late (1,050 generations) populations. Variants were discovered by Illumina sequencing, and were covered by two forward and two reverse reads, with Phred scores greater than 30. Mutations are specific to single clones, which were sequenced to 103-229x coverage and subsequently verified by Sanger sequencing.

Generation	Ecotype	Locus	Mutation	Annotation
Early	Studded	YP_837213	E481D	Monooxygenase
Early	Studded	YP_835154	R204S	2-oxoglutarate
				dehydrogenase
Early	Studded	YP_834472	Del 38, del 39,	Transcriptional
			L40V	regulator 5' to lysR
Early	Studded	n/a	Del, 95 genes	yciR, and 94 genes
				downstream (incl.
				monooxygenase)
Early	Studded	YP_834525	Stop @ 263	manC
Early	Ruffled	YP_837186	A106P	yciR
Early	Wrinkly	YP_837416	I196N	wspA
Early	Wrinkly	YP_833988	A1318V	rpoC
Late	Shared*	YP_837213	E481D	Monooxygenase
Late	Shared*	YP_835154	R204S	2-oxoglutarate
				dehydrogenase
Late	Shared*	YP_834472	Del 38, del 39,	Transcriptional
			L40V	regulator 5' to lysR

Late	Shared*	n/a	Del, 95 genes	yciR, and 94 genes
				downstream (incl.
				monooxygenase)
Late	Shared*	YP_834525	Stop @ 263	manC
Late	Shared*	YP_835839	-10 promoter	5' of bacterioferritin
			$region,G\to A$	
Late	Studded	n/a	Del, 49 genes	Deletion incl.
				oxalate
				decarboxylase
				(Bcen2424_4588)
Late	Studded	YP_837566	Synonymous	Succinate
				dehydrogenase
Late	Ruffled	YP_834838	A209P	DUF88
Late	Ruffled	YP_834185	-10 promoter	5' of mltA
			region, $G \rightarrow A$	
Late	Ruffled	Bcen2424_1770	$G\toC$	146 bp 5' of <i>rhlB</i>
Late	Ruffled	YP_837420	L35P	wspD
Late	Wrinkly	YP_837416	A407V	wspA

<sup>\*</sup>Shared mutations were identified in the Studded, Ruffled, and Wrinkly clones from the Late population.