SUPPLEMENTAL MATERIALS

	Percent identity	**Query coverage**	**E-value**	**Query**	**Subject (*P. aeruginosa* PAO1 complete genome)**
T7 reverse primer	99.31%	91%	0	nt83 to nt951	nt2530389 to nt2531258
Internal forward primer	99.76%	88%	0	nt15 to nt831	nt2531233 to nt2530418
T7 forward primer	99.40%	83%	0	nt163 to nt991	nt2531840 to nt2531012
Internal reverse primer	100%	76%	0	nt23 to nt697	nt2531166 to nt2531840

Table S1. Alignment of pM3CRYY reads to *P. aeruginosa* PAO1 complete genome demonstrates high sequence identity. pM3CRYY was isolated from pM3CRYY(+) *E. coli* BL21 stock prepared by Rocha *et al.* (7) and submitted for Sanger Sequencing with two universal primers and two custom internal primers. NCBI BLAST was used to align the sequencing reads against the *P. aeruginosa* PAO1 complete genome (NC_002516.2). Reads from the T7 reverse primer and internal forward primer provided coverage of *chiC* from nucleotide 2530389 to 2531258, while reads from the T7 forward primer and internal reverse primer covered *chiC* from nucleotide 2531012 to 2531840.

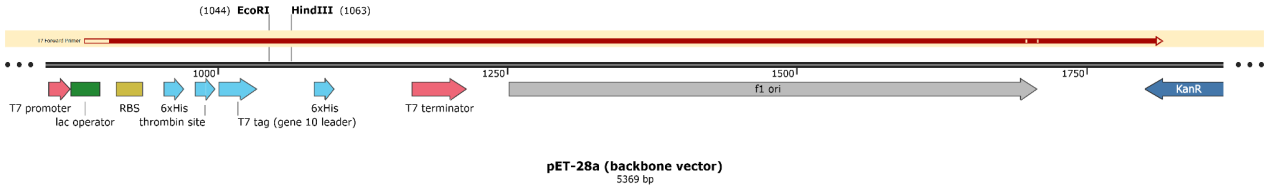

Figure S1. Sanger Sequencing of pET-28a negative control confirms the absence of *chiC*. To verify our negative control for use in downstream experiments, we isolated the backbone vector, pET-28a, from pET-28a(+) DH5α *E. coli* and submitted it for Sanger Sequencing with a universal primer. Alignment of this sequencing read to a reference pET-28a (https://www.addgene.org/browse/sequence_vdb/2565/) sequence demonstrated high sequence identity and confirmed the absence of *chiC*.