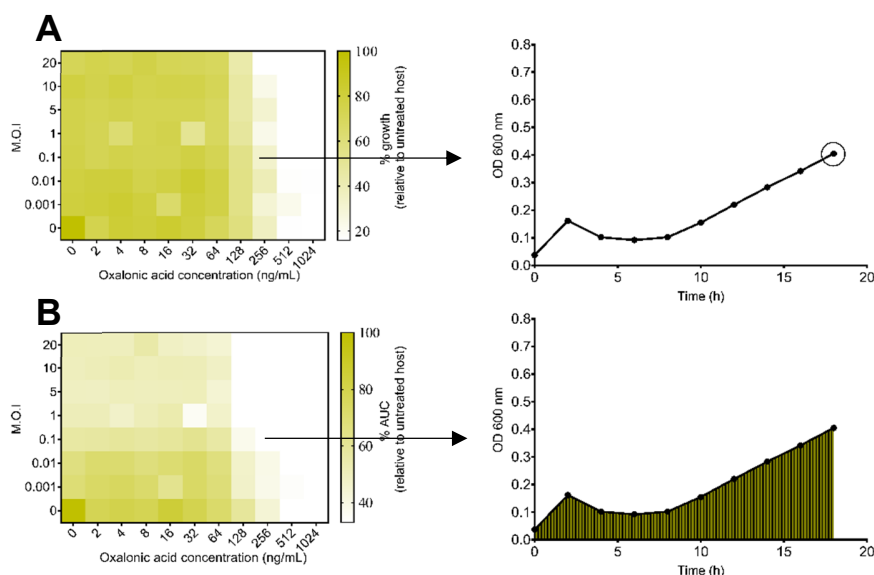
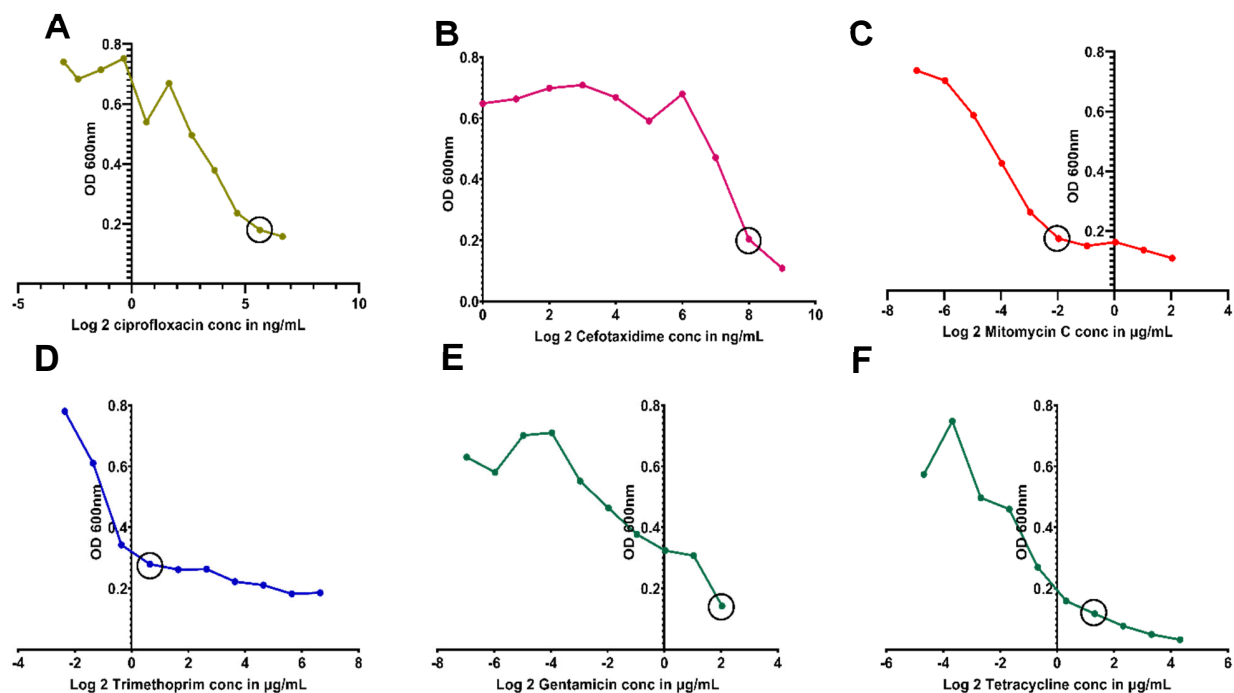


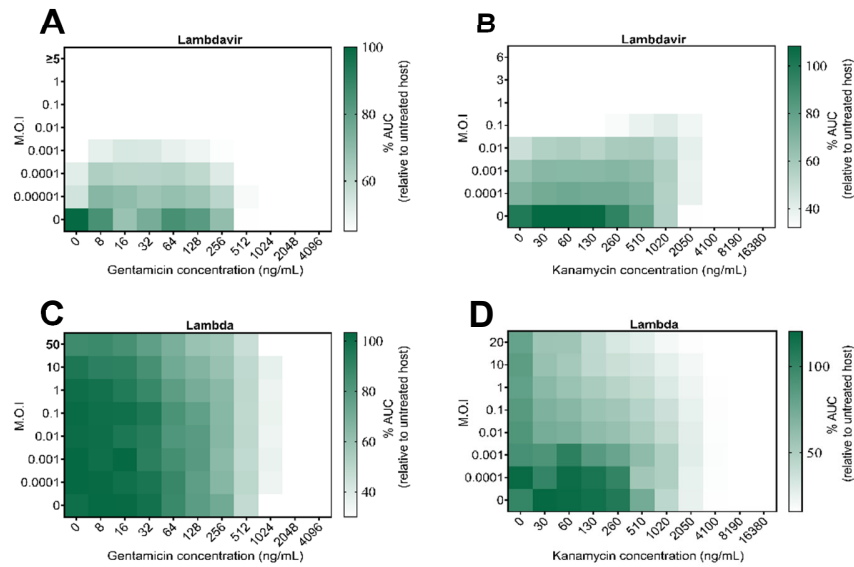
SFig 1. Endpoint readings after 18 hours of wild-type *E. coli* K-12 tracked in the absence and presence of serial concentrations of **(A)** Nalidixic acid, **(B)** Oxolinic acid, **(C)** Levofloxacin, **(D)** Ciprofloxacin, **(E)** Mitomycin C, **(F)** Trimethoprim, **(G)** Cefotaxidime, **(H)** Ampicillin, **(I)** Cefotaxime, **(J)** Cefixime, **(K)** Gentamicin, **(L)** Kanamycin, **(M)** Tetracycline and **(N)** Azithromycin averaged among 3 biological replicates. MIC is labelled in black circle.



SFig 2. Illustration of the difference between **(A)** heat map based on end point reading and growth curve at MOI of 1 and oxolinic acid concentration of 256 ng/mL **(B)** heat map based on time point readings (AUC) and growth curve at the same point illustrating AUC. Both for oxolinic acid challenged with HK97.



SFig 3. Endpoint readings after 18 hours of *recA* mutant tracked in the absence and presence of serial concentrations of **(A)** Cefotaxidime, **(B)** Mitomycin C, **(c)** Trimethoprim, **(D)** Gentamicin and **(E)** Tetracycline averaged among 3 biological replicates. MIC is labelled in black circle.



S Fig 4. Checkerboard assay of lambdavirus and: **(A)** gentamicin and **(B)** kanamycin. Area under the curve relative to untreated bacterial control, averaged among 3 biological replicates, plotted as a heatmap. Checkerboard assay of lambda and: **(C)** gentamicin and **(D)** kanamycin. Area under the curve relative to untreated bacterial control, averaged among 3 biological replicates, plotted as a heatmap.