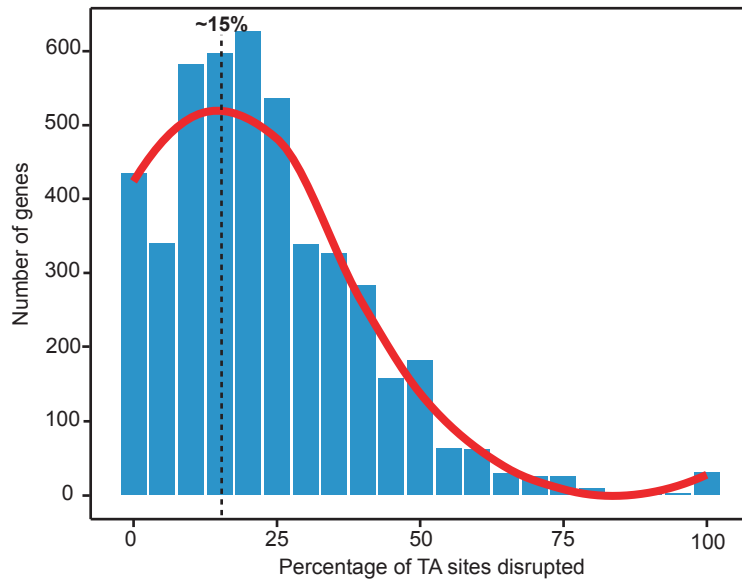
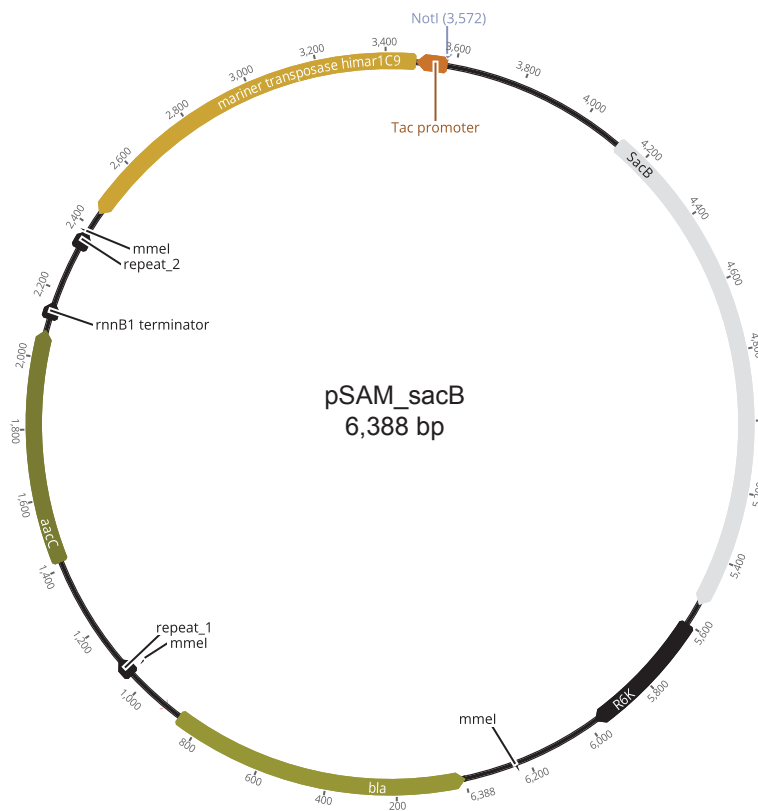


Supplementary Information

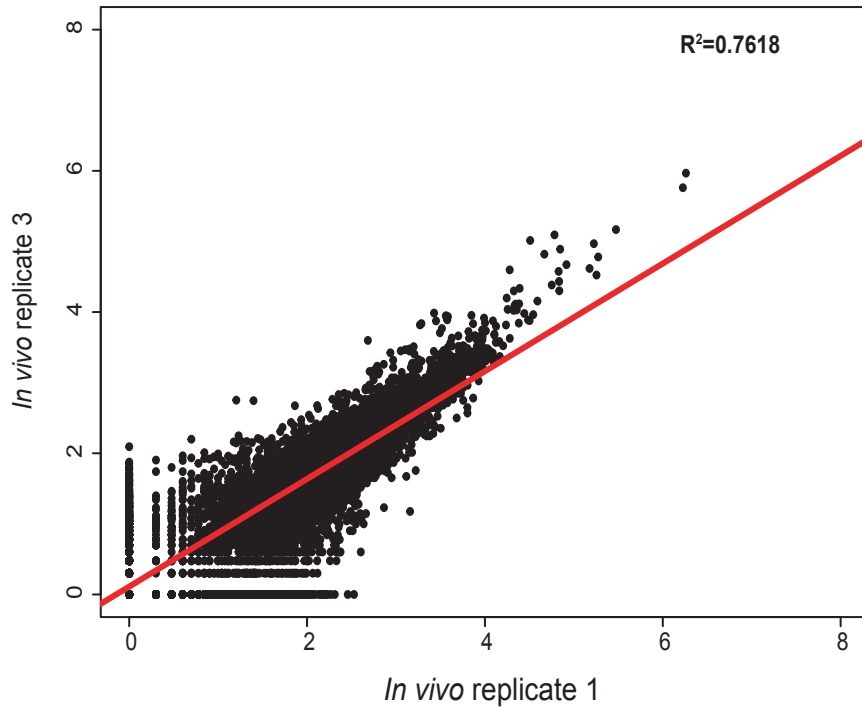
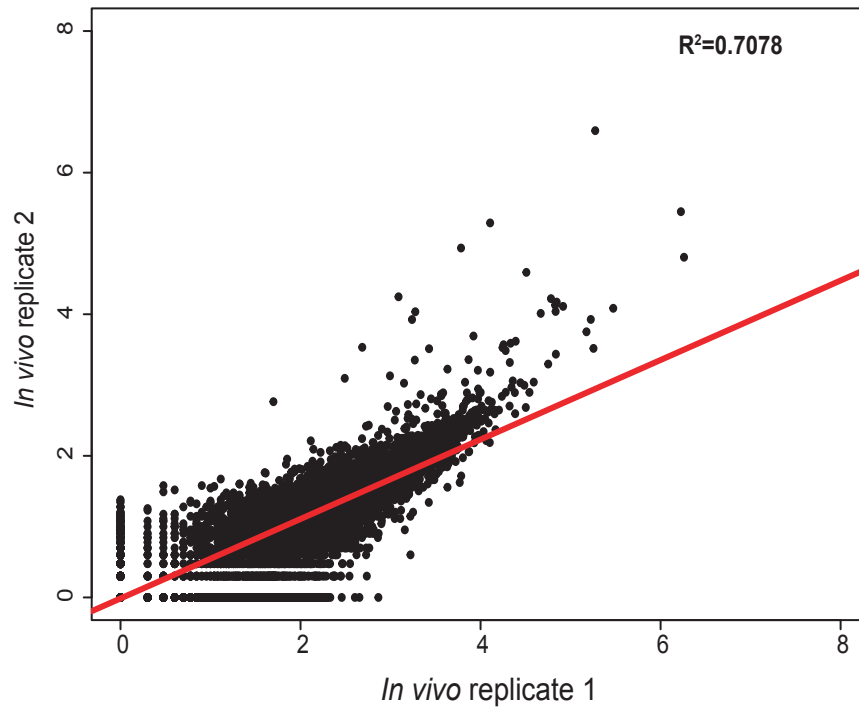
a



b

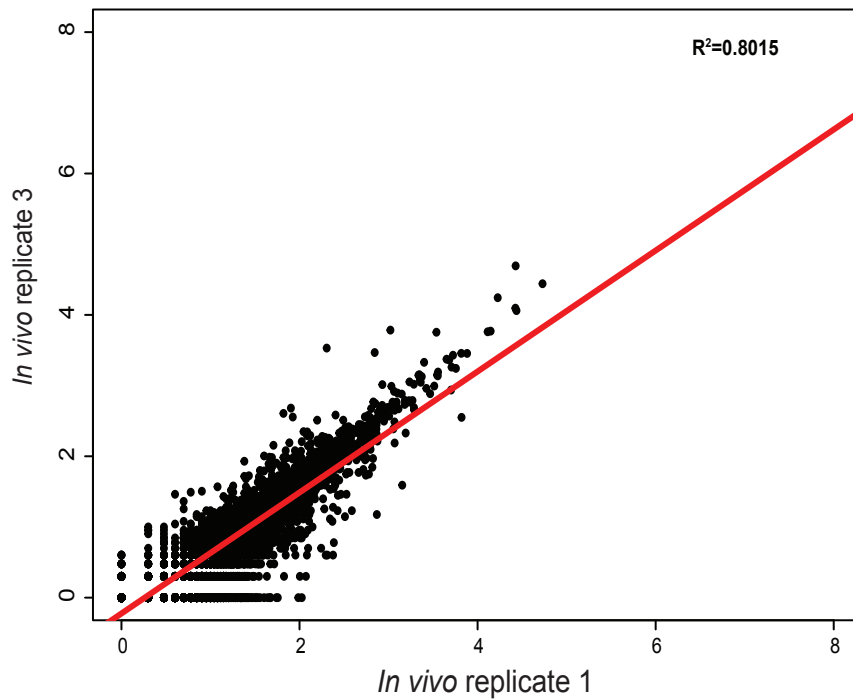
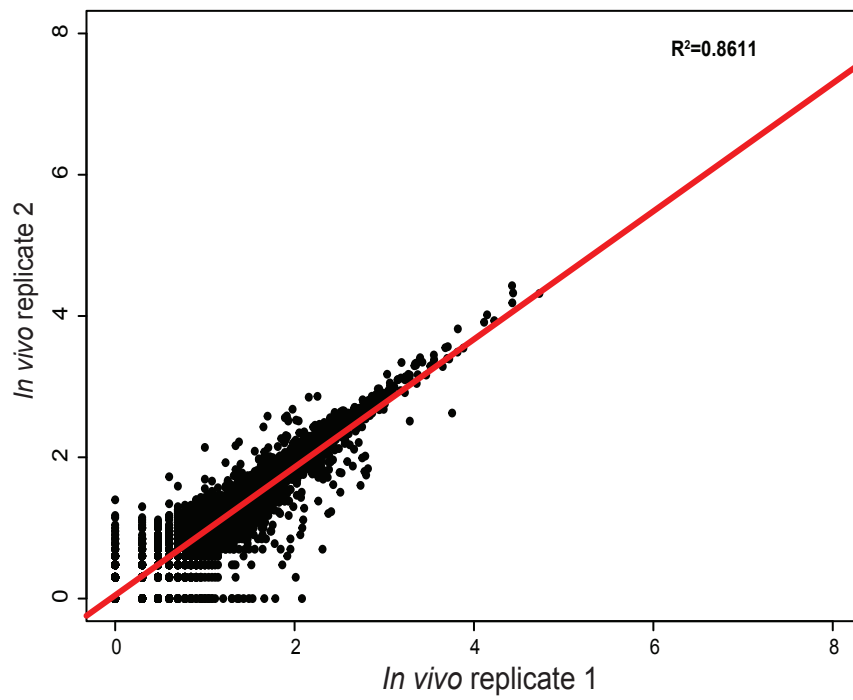


Supplementary Figure 1. Modifying the transposon mutagenesis system to increase AIEC library saturation. **a.** Histogram showing the percentage of “TA” sites disrupted per gene in AIEC strain NRG857c using the original transposon system. Shown is $n = 1$ of 3 technical replicates of the AIEC transposon mutant library that showed similar distribution. **b.** Map illustration of plasmid pSAM_SacB.



Supplementary Figure 2. Correlation plots between different *in vivo* mutant libraries.

Each point represents the \log_{10} value of the number of mapped reads of one mutant in each of two libraries. The correlation coefficient (R^2) on log-transformed abundance values is shown.



Supplementary Figure 3. Correlation plots between different *in vivo* transcriptomes. Each point represents the \log_{10} value of the number of mapped reads per gene in each of the two libraries. The correlation coefficient (R^2) on log-transformed abundance values is shown.