

Figure S1

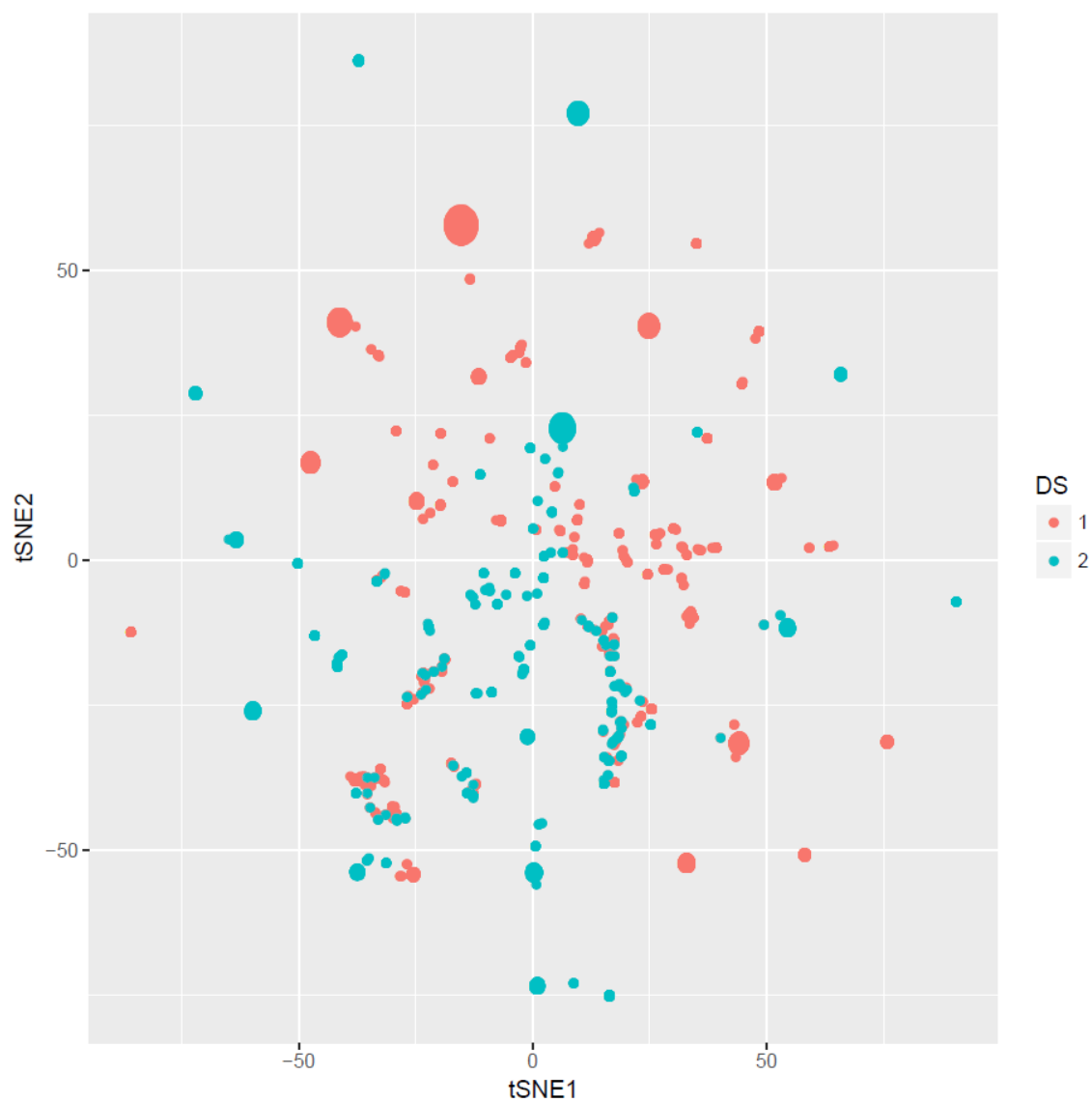


Figure S1. A comparison of the Dataset (DS1, red) 1 and Dataset 2 (DS2, green) samples using t-SNE. Individual amino acid positions that were used to define PBP type were used as the starting dimensions.

Figure S2

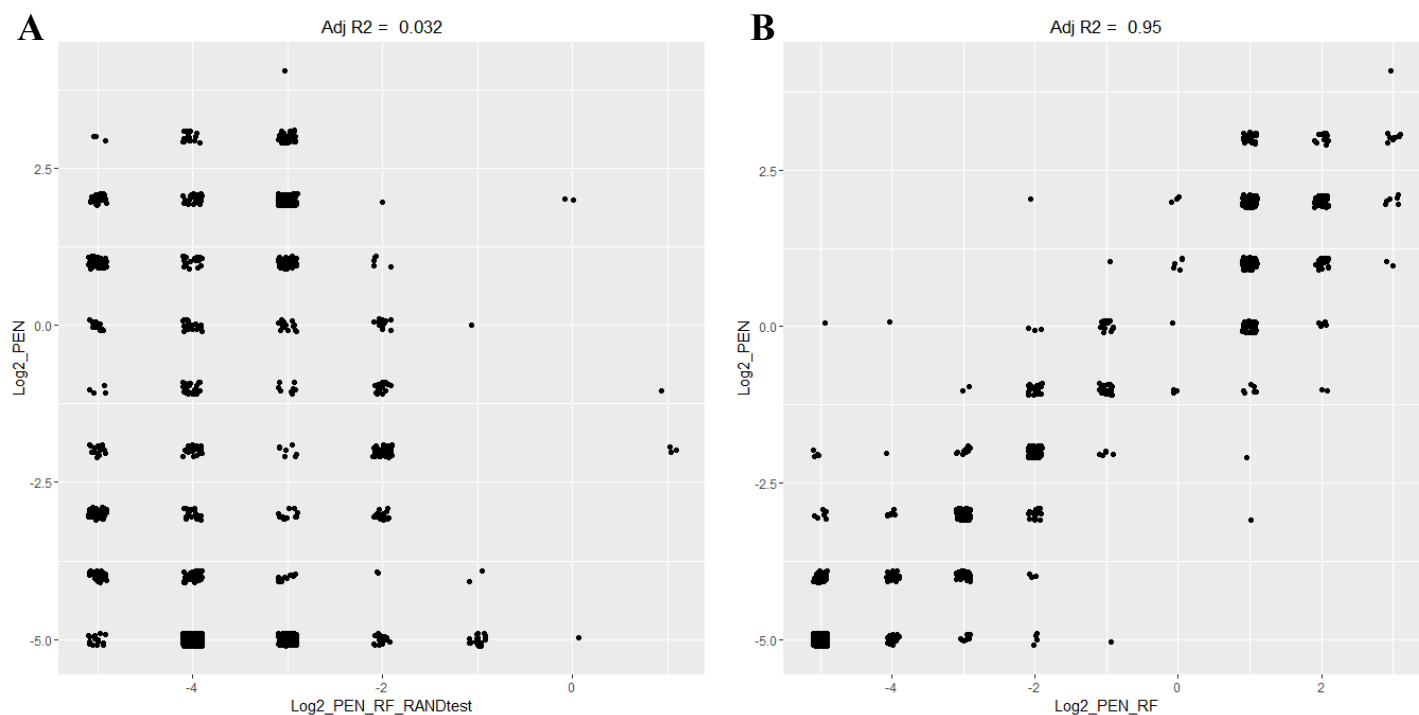


Figure S2. A randomization test of the “leave-one-type out” cross-validation. (A) The MIC labels were randomized over the input PBP sequences before the “leave-one-type out” cross-validation using the RF method. MIC values were log2 transformed and rounded to the nearest integer. Correlation between the true penicillin MIC (Log2_PEN) and predicted MIC (Log2_PEN_RANDtest) is shown. A small amount of random variation to the location of each point was added to aid visualization. Adjusted R^2 from a linear regression are shown on top. (B) Results from the “leave-one-type out” cross-validation in which the true MIC labels were used.

Figure S3

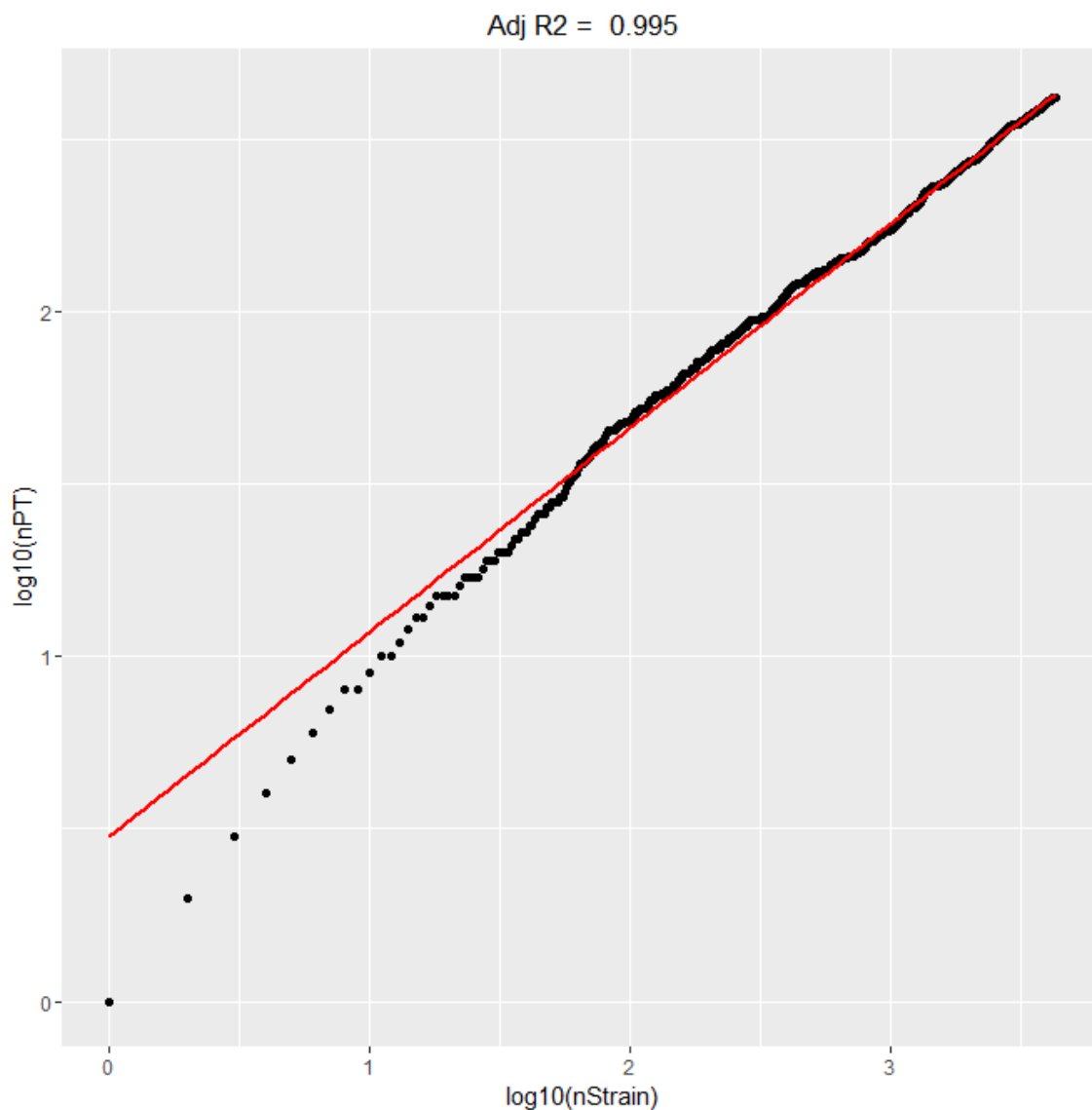


Figure S3. Log-log plot of the number of strains (nStrain) and the number of PBP types (nPT) for the 4309 strains and 417 PBP types observed in Datasets 1 and 2. Redline indicates the fitted line of a linear regression. R^2 estimation of the linear regression are shown on top.

Figure S4

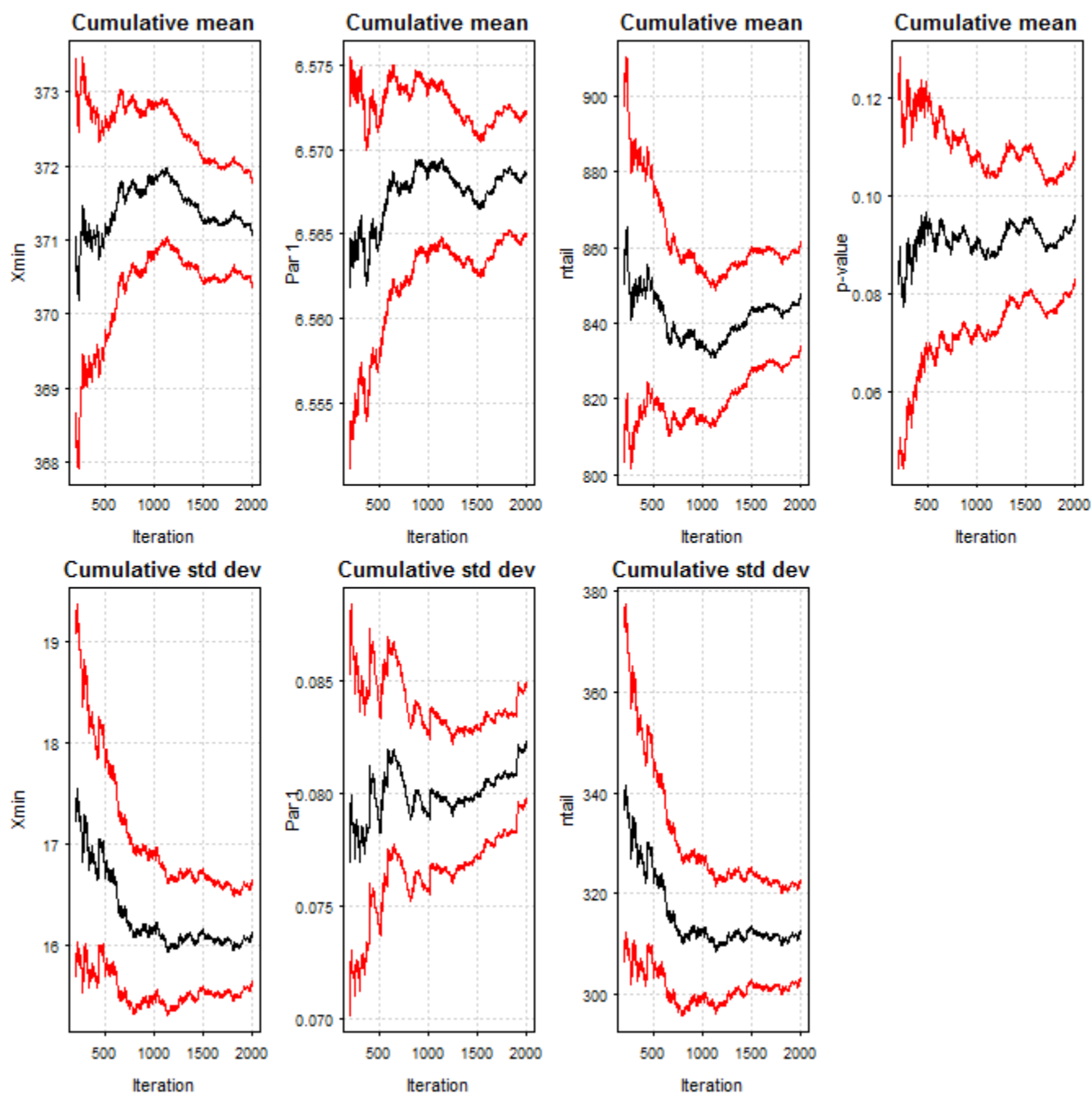


Figure S4. Results from the bootstrap procedure for the power law model. The dashed-lines give approximate 95% confidence intervals.