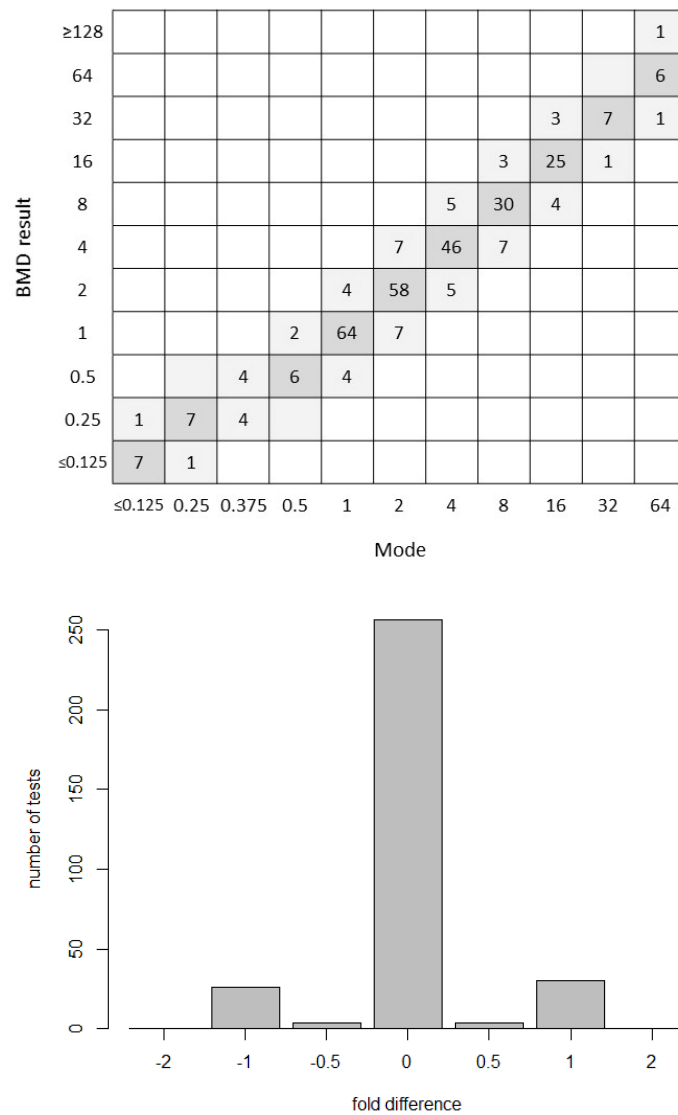


**Supplementary Figure 1: A** distribution of the daptomycin MICs by BMD of all isolates in the testing method correction dataset, by *Enterococcus* species, vancomycin resistance. **B** distribution of isolates selected for repeatability testing, selected as representative of all included *faecium* and *faecalis* isolates.



**Supplementary Figure 2:** Total days of therapy (DOT) per month in the hospital for IV vancomycin.

Dotted lines show the fit results from the interrupted time series analysis.

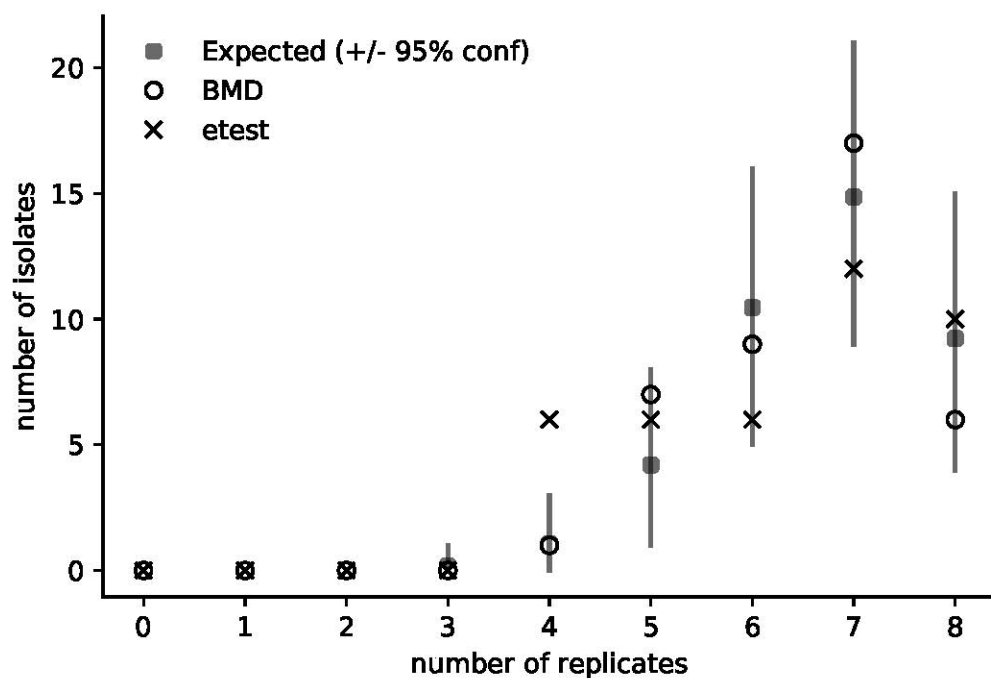


**Supplementary Figure 3:** Repeatability of the reference BMD scores. **A** Comparison of mode of all eight repeat BMD values for each sample to individual BMD results by MIC. **B** Summary of the fold difference between the sample mode and individual test values (n=320).

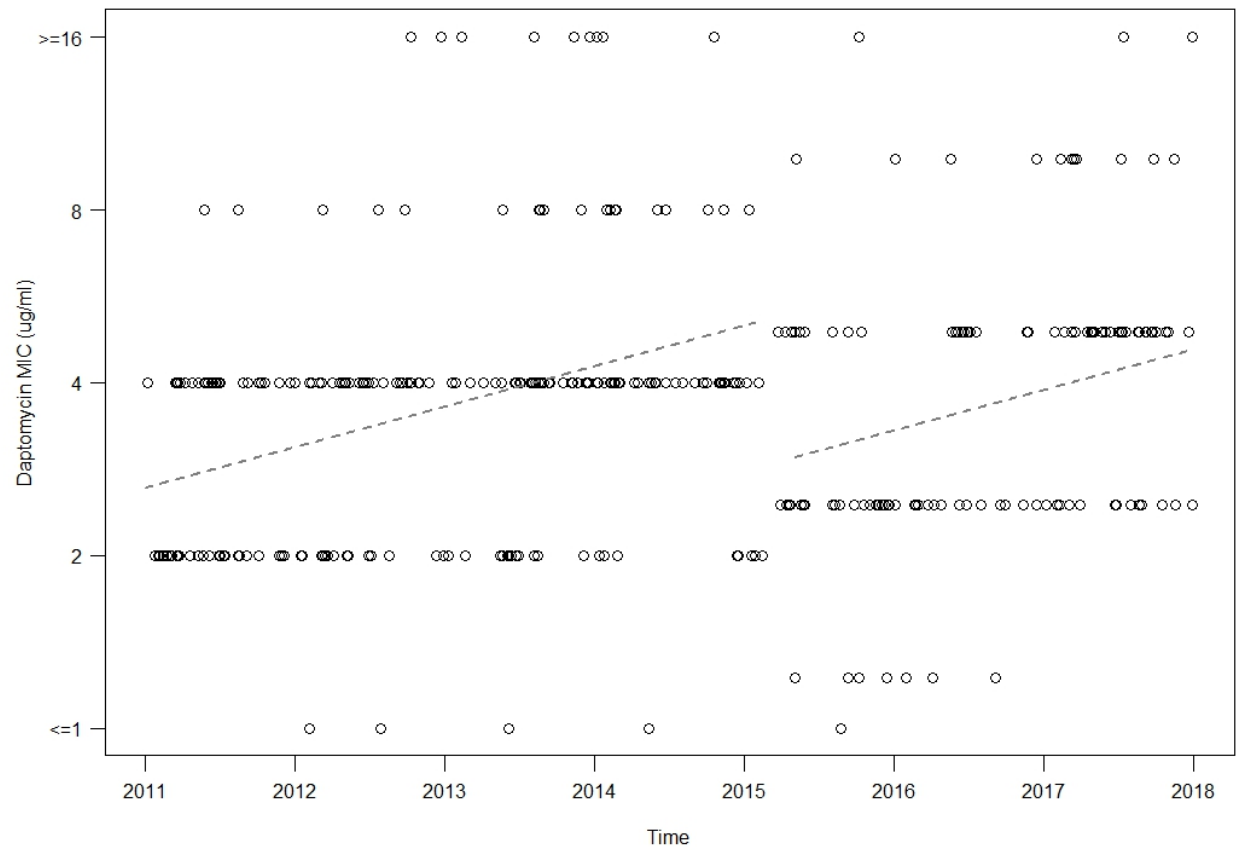
## Analysis of repeated measurement

For this analysis, we assume that for any given bacterial isolated and antibiotic resistance assay there is a probability that the result of the assay is the 'true' result, and refer to this as  $p_t$ . For each of the 40 isolates with repeated measurement of the MIC we calculated  $p_t$  as follows. If  $p_i$  is the proportion of replicates in which the MIC was measured to be  $i$ , the probability of getting the same MIC in two measurements is  $\sum_i p_i^2$ . This sum was measured for each isolate, with the average across 40 isolates being 0.721 for BMD and 0.723 for Etest. This probability combines the chance of getting the same results because the true MIC was measured twice, and because the false MIC was measured twice. If we further assume there is only 1 false MIC value, as was the case in 36 of the 40 isolates,  $p_t^2 + (1 - p_t)^2 = 0.721$ . Thus,  $p_t = 0.832$  for BMD and  $p_t = 0.834$  for Etest.

We next looked for evidence that some isolates are more or less repeatable than others. To do this we asked whether the frequency distribution of the most commonly found MIC match the expected frequency distribution if all 40 isolates with repeated testing had the same level of repeatability. For BMD, the repeatability matched the expectation if all isolates had similar repeatability. However, for Etest there was an overabundance of 4/8 splits (6/40) compared to the expectation, which found only 66 out of a million of all isolates had equal splits. Even when correcting for the 18 comparisons, the probability of this observation occurring by chance is  $p = 0.0012$ , suggesting there may be mild differences in repeatability between some isolates when using the Etest.



**Supplementary Figure 4:** The frequency distribution of the most commonly observed MIC out of 8 trials for 40 independent isolates (black circles and black x), compared to the expected frequency distribution if every measurement has the same probability of giving the true value  $p_t = 0.832$  (grey circles).



**Supplementary Figure 5:** Corrected initial VRE *faecium* daptomycin MICs over time. Dotted lines are interrupted time series analysis fits for pre- and post- intervention.

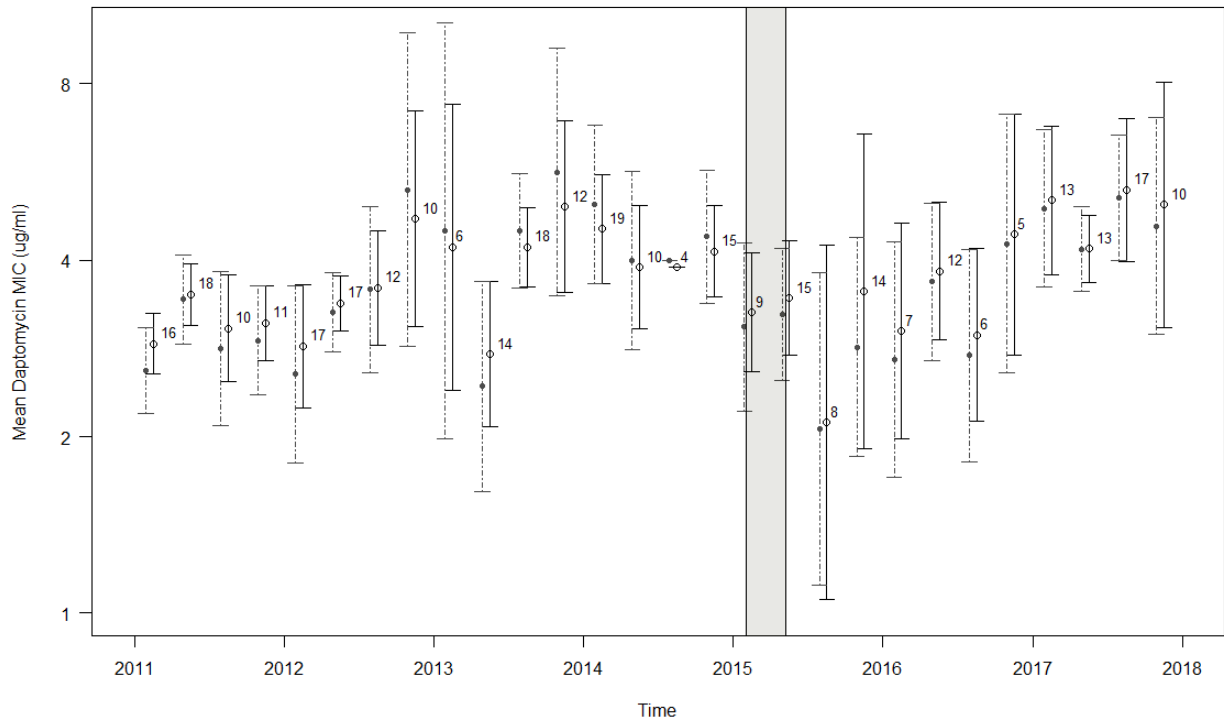
## Correction by Etest

### Adjusting for testing method

The relationship between the initial Trek and retest Etest MICs fit a quadratic model (Eq2). The relationship between initial Etest and retest Etest MICs was linear (Eq 3).

$$\log_2(Etest_{retest}) = 0.050 \log_2(MIC_{Trek})^3 - 0.158 \log_2(MIC_{Trek})^2 + 0.930 \log_2(MIC_{Trek}) + 0.623 \quad (2)$$

$$\log_2(Etest_{retest}) = 0.690 \log_2(MIC_{Etest}) + 0.578 \quad (3)$$



**Supplementary Figure 6:** Mean daptomycin MIC for VRE *faecium* initial isolates by quarter. Open circles are calculated from the Etest corrected values, and closed circles are calculated from the Trek corrected values. Error bars represent 95% CI of the mean and the numbers are the number of infections in each quarter.