Pipeline benchmark report

This report was generated by the 'benchmark_calculations.py' script. A summary table of the raw data is available under the name 'reference_table.tsv' For further information on the data and how percentages were calculated, take a look at the README file The sensitivity and specificity were calculated using the data from the following paper: https://www.sciencedirect.com/science/article/pii/S1198743X15600660?via%3Dihub

Sample information (Gram Negative)

| Total samples | Carbapenem resistant samples (MIC Eucast) | Carbapenem susceptible samples (MIC Eucast) |
|----------------------|--|---|
| 15 | 12 | 3 |

Phenotype (MIC) Sensitivity and Specificity

| Diag Pipelines 2.6.0 | New Pipeline |
|----------------------|-------------------|
| Sensitivity: 92 % | Sensitivity: 92 % |
| Specificity: 33 % | Specificity: 33 % |

Microarray Sensitivity

| Diag Pipelines 2.6.0 | New Pipeline |
|----------------------|-------------------|
| Sensitivity: 91 % | Sensitivity: 94 % |

Sample information (Gram Positive)

| Total samples | Vancomycin or Methicilin resistant samples (PCR confirmed) |
|---------------|--|
| 40 | 20 |

PCR Sensitivity and Specificity for vanA and mecA genes

| Diag Pipelines 2.6.0 | New Pipeline |
|----------------------|-------------------|
| Sensitivity: 100 % | Specficity: 100 % |