Edinburgh Genome Foundry

## Sabotage report

This report highlights the parts which significantly impair the success of assemblies they belong to.

## Significant parts

| $\begin{aligned} & 1.00 \\ & \text { F1 } \\ & \text { SCORE } \end{aligned}$ |  |  |  |
| :---: | :---: | :---: | :---: |
|  |  |  |  |
| Part | $p$-value | Effect | Twins |
| 124 | 0.000 | +95\% |  |

These parts have been selected because they tend to appear in assemblies that fail more, and be absent of assemblies that succeed.

The p-value (from an ANOVA test) indicates how statistically significant this pattern is for each selected part. Smaller p-values mean greater significance.

The "Effect" indicates how impactful the part is, i.e. how much the part belonging to a assembly increases this assembly's chances of failure, in average.

Twins indicate other parts which appear exactly in the same assemblies as the significant part. As a consequence, we cannot know if it is this part causing the failures, or one of its twins (or maybe several of them ?).

The F1 score, between 0 and 1 (1 being best) indicates how accurately one could predict the success or failure of a assembly, simply knowing which of these parts are in the assembly. A low score (below 0.5 ) indicates that this report hasn't found any significant effect of a assembly's parts on its success rate.

## Were these parts appear

The next table shows the different assemblies, from the less to the most successful in average, and which failureassociated parts each assembly contains.

The "Mystery" column, when featuring two stars or more, indicates assemblies with a success rate that is not well explained by the presence of these parts. This means either that the assembly was particularly successful while containing failure-associated parts, or on the contrary that the assembly was unsuccessful despite containing no such part. In both cases, this indicates that the assembly's success was mainly driven by external factors.

| Assembly | Failure Rate (\%) | 124 | Mystery |
| :---: | :---: | :---: | :---: |
| construct_1 | 100 | $\checkmark$ |  |
| construct_2 | 0 |  |  |
| construct_3 | 0 |  |  |

