

Experiment:

Gene name:

Data:

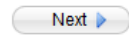
```

mock 1dpi 1 25.14 1000
mock 1dpi 1 25.26 1000
mock 1dpi 1 28.77 100
mock 1dpi 1 29.23 100
mock 1dpi 2 24.82 1000
mock 1dpi 2 24.45 1000
mock 1dpi 2 27.66 100
mock 1dpi 2 27.76 100
mock 1dpi 3 24.40 1000
mock 1dpi 3 24.27 1000
mock 1dpi 3 27.94 100
mock 1dpi 3 28.06 100
mock 1dpi 4 25.52 1000
mock 1dpi 4 25.24 1000
mock 1dpi 4 29.06 100
mock 1dpi 4 29.05 100
mock 3dpi 1 25.56 1000
mock 3dpi 1 25.54 1000
mock 3dpi 1 29.27 100
mock 3dpi 1 29.05 100
mock 3dpi 2 24.71 1000
mock 3dpi 2 24.78 1000
mock 3dpi 2 28.49 100
    
```

Standard curve:

```

20.11 10000
20.05 10000
24.31 1000
24.31 1000
27.52 100
27.35 100
30.67 10
30.83 10
    
```

Next 

Additional file 3: qPCR data import screenshot. Data for the samples are imported in the following format: sample name [tab] C_q [tab] relative quantity. Standard curve data are imported in the following format: C_q [tab] quantity (relative for the relative quantification and absolute in the case of absolute quantification). Each line represents one qPCR reaction. In the example, each sample has two dilutions, with two technical replicates each, while there are four serial dilutions with two replicates for the standard curve.