

SUMMARY

[0004] In one exemplary embodiment, a method for quantitation of biological material in a biological sample is provided. The method includes receiving amplification data from amplification of a first and a second reference sample and receiving amplification data from amplification of a biological sample. The method further includes determining an efficiency from the received amplification data from amplification of the first and second reference sample. The method includes determining a relative PCR efficiency for the biological sample. Next, the method includes determining a quantity of biological material in the biological sample using the relative PCR efficiency.

[0005] In one aspect, there is provided a computer-readable storage medium encoded with processor-executable instructions for quantitation of biological material in a biological sample, the instructions comprising instructions for: receiving amplification data from amplification of a first and a second reference sample; receiving amplification data from amplification of a biological sample; determining an efficiency from the received amplification data from amplification of the first and second reference sample; determining a relative PCR efficiency for the biological sample; and determining a quantity of biological material in the biological sample using the relative PCR efficiency. In another aspect, there is provided a system for quantitation of biological material in a biological sample, the system comprising: a processor; and a memory configured to store processor-executable instructions for: receiving amplification data from amplification of a first and a second reference sample; receiving amplification data from amplification of a first and a second reference sample; receiving amplification data from amplification of a biological sample; determining an efficiency from the received amplification data from amplification of the first and second reference sample; determining a relative PCR efficiency for the biological sample; and determining a quantity of biological material in the biological sample using the relative PCR efficiency. In some embodiments, the relative PCR efficiency is determined with the following equation:

$$\varepsilon_{S2A2} = \varepsilon_{S1A1}^{\frac{CT_{100\%S1A1}}{CT_{100\%S2A2}}}$$

BRIEF DESCRIPTION OF THE DRAWINGS

[0006] FIG. 1 illustrates a workflow comparing current quantitation methods and quantitation methods according to various embodiments described herein;

[0007] FIG. 2 illustrates a method of quantitation according to various embodiments described herein;

[0008] FIG. 3 illustrates a method of quantitation according to various embodiments described herein;

[0009] FIG. 4 illustrates an exemplary plate layout method of quantitation according to various embodiments described herein;

[0010] FIG. 5 illustrates an exemplary scattered plot of calculated %C using a traditional standard curve Vs. Input %C;

[0011] FIG. 6 illustrates an exemplary scattered plot of calculated %C not using standard curve Vs. Input %C according to various embodiments described herein;