

METHODS AND SYSTEMS FOR QUANTIFICATION WITHOUT STANDARD CURVES

BACKGROUND

[0001] Quantitative nucleic acid analysis is extensively used in biological research and clinical analysis. Some of the applications which make use of this technology include: measurement of gene expression, monitoring of biological responses to stimuli, genomic-level gene quantitation, and pathogen detection. Typically, these methodologies utilize Polymerase Chain Reaction (PCR) as a means for selectively amplifying nucleic acid sequences in a manner that allows for their detection.

[0002] While it is generally desirable to automate the quantitation process, conventional methodologies often require a degree of user input in the form of subjective interpretation and/or approximation. For example, many reference samples may need to be run to determine a standard curve. The standard curve is then used to determine quantities of unknown samples. In some other applications, reference assays and reference samples are used to provide a reference point or as training sets for relative quantitation, such as in CNV and genotyping. As a result, these techniques may suffer from reduced accuracy and significant user-induced variability. As most optimized assays are specific with high PCR efficiencies, some assays are limited by the template sequence or the primer design. The difference in PCR efficiencies and Ct0 (Ct value at one unit of template concentration) between reference and test assays reduces quantitation accuracy with conventional methods. Furthermore, in high-throughput applications where many samples are to be processed simultaneously, it is desirable to provide increased automation capabilities to improve the speed with which the analysis may be conducted.

[0003] The aforementioned limitations of conventional techniques illustrate the need for an improved method for analyzing data generated by PCR-based quantitation techniques that may increase the potential for automation while improving the quantitative accuracy, simplicity, and reproducibility of the analysis.

SUMMARY

[0004] In one aspect, a computer-implemented 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 using PCR (Polymerase Chain Reaction) and receiving amplification data from amplification of a biological sample using PCR. The method further includes determining a specific PCR 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, wherein the relative PCR efficiency is determined with the following equation:

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

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, $CT_{100\%S1A1}$ represents a cycle threshold of the first assay, $CT_{100\%S2A2}$ represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay.

[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 using PCR (Polymerase Chain Reaction); 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, wherein the relative PCR efficiency is determined with the following equation:

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

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, CT100%S1A1 represents a cycle threshold of the first assay, CT100%S2A2 represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay. 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 using PCR (Polymerase Chain Reaction); 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, wherein the relative PCR efficiency is determined with the following equation:

$$\epsilon_{S2A2} = \epsilon_{S1A1} \frac{CT_{100\%S1A1}}{CT_{100\%S2A2}},$$

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, CT100%S1A1 represents a cycle threshold of the first assay, CT100%S2A2 represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay.

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;

- [0012] FIG. 7 illustrates another exemplary scattered plot of calculated %C using a traditional standard curve Vs. Input %C with Dual Primer Set with 8 assays;
- [0013] FIG. 8 illustrates another exemplary scattered plot of calculated %C not using a standard curve Vs. Input %C with Dual Primer Set with 8 assays, according to various embodiments of the present teachings.
- [0014] FIG. 9 illustrates measured methylation levels using the quantitation method vs. input methylation levels according to various embodiments described herein;
- [0015] FIG. 10 illustrates an exemplary block diagram of a computing system for implementing the quantitation method according to various embodiments described herein;
- [0016] FIG. 11 illustrates a table of a plurality of experiments used with the quantitation method according to various embodiments described herein;
- [0017] FIG. 12 illustrates an exemplary thermal profile used in experiments to generate data according to the quantitation method according to various embodiments described herein;
- [0018] FIG. 13 illustrates an overview of the quantitation method according to various embodiments described herein;
- [0019] FIG. 14A illustrates a plot of quantitation results with (a) bisulfite converted gDNA and (b) synthetic templates according to various embodiments described herein;
- [0020] FIG. 14B illustrates a plot of quantitation results with (a) bisulfite converted gDNA and (b) synthetic templates according to various embodiments described herein;
- [0021] FIG. 15 illustrates mean deviation by different methods with BIS gDNA and synthetic templates according to various embodiments described herein;
- [0022] FIG. 16 illustrates various applications that may use the quantitation method according to various embodiments described herein;

[0023] FIG. 17 illustrates a table of various assay types and reference samples for different application that may use the quantitation method according to various embodiments described herein;

[0024] FIG. 18 illustrates a chart of copy number determination using a traditional method vs. the quantitation method according to various embodiments described herein; and

[0025] FIG. 19 illustrates the impact of using relative Eff(S2A2) on accuracy of quantitation. The table shows the values of Eff determined by different methods (measure Vs relative).

DETAILED DESCRIPTION

[0026] To provide a more thorough understanding of the present invention, the following description sets forth numerous specific details, such as specific configurations, parameters, examples, and the like. It should be recognized, however, that such description is not intended as a limitation on the scope of the present invention, but is intended to provide a better description of the exemplary embodiments.

[0027] As mentioned above, traditionally, standard curves are established for a sample type so that quantities of unknown samples may be determined. By determining an assay specific relative efficiency and a cycle threshold (Ct) for a sample, quantities of samples may be determined without generating a standard curve. The use of relative PCR efficiency improves the accuracy of relative quantitation and allows the use of assays with different efficiencies in relative quantitation. Using the relative PCR efficiency, according to various embodiments described herein, eliminates the need of using assays of matching performances (similar efficiencies and Ct). Thus, virtually any assay may be used using the quantitation method according to various embodiments of the present teachings.

[0028] According to various embodiments, the quantitation method may be used in a plurality of applications such as, but not limited to, determining methylation levels, genotyping (SNP ratios), determining allelic ratios, determining copy number variance (CNV), and determining species ratios. Various applications that may use the quantitation according to various embodiments described herein are illustrated in FIG. 16.

Methylation Level Determination Example

[0029] For example, DNA methylation has strong association with regulation of gene expressions, chromosomal stability and cell development. The change in DNA methylation level of specific loci can be used as biomarkers for early diagnosis, progression and prognosis of cancer and aging. However, measuring the 10-20% change in methylation level with conventional qPCR methods cannot be achieved without generating one or two sets of standard curves.

[0030] According to various embodiments, a more simple method is provided to detect the small change in DNA methylation level with SYBR without the complications of generating a standard curve. The quantitation method can provide a simple and accurate method to determine the relative abundance of two states with two assays of equal or different PCR efficiencies with either SYBR or Taqman assays, for example.

[0031] Instead of running a standard curve, the actual reaction efficiency is calculated from two reference points according to various embodiments. For example, for a DNA Methylation assay, 10% and 100% methylated control samples may be used as reference points. The percentage of methylation of any sample can be calculated from the equation $e^{-(C_{tc} - C_{ts})}$ where c = reference with 100% methylation and s = sample with $n\%$ methylation. This quantitation method has been tested with 12 assays with both synthetic templates and bisulfite converted gDNA of various level of methylation. In the exemplary results, the level of methylation can be accurately measured at all levels tested with a standard error of prediction <4%.

[0032] General Overview

[0033] As mentioned above, according to various embodiments, the quantitation method can also be applied to calculate the relative ratio of two components in other applications, such as genotyping (SNP ratios), determining allelic ratios, determining copy number variance (CNV), determining species ratios, and determining methylation levels as in the example described above.

[0034] The quantitation method utilizes the specific PCR efficiency of the assay of interest and Ct values to calculate the relative percentage of one of the two states of a specific location or the relative abundance of the two targets in a sample.

[0035] With reference to FIG. 1, workflow 100 shows a current quantitation method using a standard curve. Workflow 102 shows the quantitation method according to various embodiments described herein. In workflow 100, reference samples 104 are run to determine a standard curve shown in plot 106. The unknown samples are then amplified to generate amplification curves shown in plot 110. A Ct value may be determined from plot 110 for the unknown samples. Δ Ct for the samples are determined and the standard curve is used to determine a x/y ratio result 112.

[0036] In comparison, workflow 102 illustrates the quantitation method according to various embodiments described herein. As in workflow 100, reference samples 114 are amplified. However, since a standard curve does not need to be generated, fewer reference samples 114 need to be run to determine a assay specific relative PCR efficiency, ϵ 116. Unknown samples 108 are amplified similarly to workflow 100 and a Ct for the sample is determined. Using the assay specific relative PCR efficiency, ϵ 116 and the Ct value, the x/y ratio result 112 is determined. As illustrated, workflow 102 is more simple and does not require as many reference samples to be run.

[0037] Using this quantitation method, according to various embodiment, in a methylation level measurement example, the two states are “C” for methylated strand after bisulfite conversion or “U” for unmethylated strand after bisulfite conversion. For Genotyping, the two states are SNP1 and SNP2. For CNV (Copy Number Variance), the two targets are the reference gene and the target gene. Assay can be designed with a single set of primer, specific to either state of strand; or dual set of primers, specific to both states of the strands or the targets in the sample.

[0038] For Methylation level measurement and Genotyping, the specific PCR efficiency of the assay(s) are determined by using two reference points. The reference samples may be, for example, 10% C/90%U and 100%C for a single primer assay. In another example, three reference points are used. The reference samples are 100% S1 control, 10% S1/90% S2 and 100% S2 control samples for a dual primer assay design, where S1 and S2 are the control samples with specific states. For Methylation level measurement, S1 can be 100% methylated control sample and S2 can be 100% unmethylated control sample. For Genotyping, S1 can be homozygous SNP1 and S2 can be homozygous SNP2. For CNV assay, the PCR efficiencies of

the assays are determined by the reference samples of known ratio of Reference to Target gene copies.

[0039] Examples of other assay types and reference samples for various applications where the method according to various embodiments described herein can be found in table 1700 of FIG. 17.

[0040] For methylation level measurement, the specific PCR efficiency of one of the assays, S1A1, is determined by the equation

$$\varepsilon = 10^{\left(\frac{1}{\Delta CT}\right)} \text{ where } \Delta CT = CT_{10\%A1} - CT_{100\%A1}.$$

[0041] For the second assay S2A2, the relative PCR efficiency is calculated as

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

[0042] The use of relative PCR efficiency for S2A2 improves the accuracy of relative quantitation and allows the use of assays with different efficiencies in relative quantitation. Using the relative PCR efficiency, according to various embodiments described herein, eliminates the need of using assays of matching performances (similar efficiencies and Ct). Thus, virtually any assay may be used using the quantitation method according to various embodiments of the present teachings. FIG. 19 illustrates the impact of using relative Eff(S2A2) on accuracy of quantitation. The table shows the values of Eff determined by different methods (measure Vs relative).

[0043] For CNV and Genotyping, PCR efficiency of S1A1 (CNV: A1=Reference assay, S1=Reference gene ; Genotyping: A1=SNP1 assay, S1=SNP1) is assumed to be 2.0 as most of the Reference Assays are optimized. For CNV, the PCR efficiency of S2A2 (A2=Target assay, S2=Target gene) is calculated from the Reference samples with known copy numbers for both Reference gene (X) and Target gene (Y). For Genotyping, the PCR efficiency of S2A2 (A2=SNP2 assay, S2=SNP2) can be calculated from the Reference samples with Homozygous SNP1, Homozygous SNP2 and heterozygous SNP1/SNP2.

The Principal

[0044] With reference to FIG. 2, according to various embodiments, a method for single Primer assay design (Sample = S1 and S2, Primer designed for Assay 1) is illustrated.

[0045] For a sample with two states (S1 and S2 at x:y ratio) at the location of assay, two reactions, S1-A1 and S2-A2, occur simultaneously. With the same amount of input template(s), at the same threshold, the product generated from the 100% S1 reference (REF1) is equivalent to the product generated from the sample.

[0046] At the same threshold,

$$P_{R1} = P_1 + P_2$$

[0047] Where R1 = 100% S1 reference, x = % of S1 in sample and y = % of S2 in sample where x + y = 1.

[0048] By definition, the amount of product can be expressed as ϵ^{CT} .

[0049] Substituting terms

$$x\epsilon_{S1A1}^{CT_1} + y\epsilon_{S2A1}^{CT_1} = \epsilon_{S1A1}^{CT_{R1}}$$

$$x\epsilon_{S1A1}^{CT_1} + (1 - x)\epsilon_{S2A1}^{CT_1} = \epsilon_{S1A1}^{CT_{R1}}$$

$$x\% = \left(\frac{\epsilon_{S1A1}^{CT_{R1}} - \epsilon_{S2A1}^{CT_1}}{\epsilon_{S1A1}^{CT_1} - \epsilon_{S2A1}^{CT_1}} \right) \times 100\%$$

[0050] For assays with good specificity, $\epsilon_{S2A1} \ll \epsilon_{S1A1}$ and $\epsilon_{S2A1}^{CT_1}$ can be ignored. The equation can be simplified as

$$x\% \approx \epsilon_{S1A1}^{(CT_{R1}-CT_1)} \times 100\%$$

Dual Primer Assay Design (Sample = S1 and S2, Assay = A1 and A2)

[0051] A method of a duel primer assay design according to various embodiments, is illustrated in FIG. 3, for example. With dual primer assay design, 4 reactions occur simultaneously. Applying the same principal, at the same threshold, products generated in different reaction wells are equal.

[0052] At the same threshold,

$$P = P_1 + P_2 \text{ with both assays}$$

[0053] Amount of products can be expressed as $P = m\varepsilon^{CT}$ where P = product, m = amount of starting strands and ε = PCR efficiency

[0054] Therefore, for Assay 1

$$P1 = x\varepsilon_{S1A1}^{CT_1}, P2 = y\varepsilon_{S2A1}^{CT_1}$$

[0055] And for Assay 2,

$$P1 = x\varepsilon_{S1A2}^{CT_2}, P2 = y\varepsilon_{S2A2}^{CT_2}$$

[0056] Substituting terms

$$x\varepsilon_{S1A1}^{CT_1} + y\varepsilon_{S2A1}^{CT_1} = x\varepsilon_{S1A2}^{CT_2} + y\varepsilon_{S2A2}^{CT_2}$$

$$\frac{x}{y} = \frac{\varepsilon_{S2A2}^{CT_2} - \varepsilon_{S2A1}^{CT_1}}{\varepsilon_{S1A1}^{CT_1} - \varepsilon_{S1A2}^{CT_2}}$$

[0057] If the specificity of the assay is very good, efficiencies for mismatched reactions are significantly lower than the matched reactions, $\varepsilon_{S1A2} \ll \varepsilon_{S1A1}$ and $\varepsilon_{S2A1} \ll \varepsilon_{S2A2}$. Terms $\varepsilon_{S2A1}^{CT_1}$ and $\varepsilon_{S1A2}^{CT_2}$ can be ignored. The equations can then be simplified as

$$\frac{x}{y} \approx \frac{\varepsilon_{S2A2}^{CT_2}}{\varepsilon_{S1A1}^{CT_1}}$$

[0058] For Methylation level measurement, the sum of % methylated strand (x) and % unmethylated strand (y) = 100%. To calculate % methylation (x) in the sample, rewrite the equation as

$$R = \frac{x}{y} = \frac{x}{1 - x}$$

$$x = \frac{R}{1 + R}$$

[0059] For CNV, the PCR efficiency of S2A2 is determined from the Reference Samples with known copy numbers of both Reference. For each sample, X = Known Copy number of Reference gene and Y = Unknown Copy number of Target gene in the sample. The ratio between Reference gene to Target gene = x/y. Applying the equation:

$$\frac{x}{y} = R = \frac{\epsilon_{S2A2}^{CT_2}}{\epsilon_{S1A1}^{CT_1}} \text{ where } R = \text{ratio of Reference gene to Target gene.}$$

[0060] Rearranging the equation,

$$R (\epsilon_{S1A1}^{CT_1}) = \epsilon_{S2A2}^{CT_2}$$

$$\log[R (\epsilon_{S1A1}^{CT_1})] = CT_2 (\log \epsilon_{S2A2})$$

[0061] ϵ_{S2A2} can be expressed as

$$\epsilon_{S2A2} = 10^{\frac{\log [R (\epsilon_{S1A1}^{CT_1})]}{CT_2}}$$

[0062] As the copy numbers of Reference gene (X) and Target gene (Y) in the Reference samples are known, R is known. With ϵ_{S1A1} assumed to be 2.0, ϵ_{S2A2} can be calculated for each Reference Sample. If multiple Reference Samples with different x/y ratio is used, the average ϵ_{S2A2} is used.

[0063] In the sample where $T = \text{sum of copy number of Reference gene and copy number of Target gene}$, $x = X/T$ and $y = Y/T$.

$$T = x + y \text{ and}$$

$$x = \frac{R}{1 + R}$$

[0064] As X is a known value, T can be calculated as

$$T = x / \text{Known Copy Number of Reference Gene}$$

[0065] Therefore,

$$Y = T - X$$

[0066] For Genotyping, $x = \% \text{SNP1}$ and $y = \% \text{SNP2}$. ε_{S2A2} can be calculated as

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

[0067] with two Reference Samples of homozygous SNP1 and homozygous SNP2 with ε_{S1A1} assumed to be 2.0. If a Reference Sample is heterozygous SNP1/SNP2, ε_{S2A2} can be calculated as

$$\varepsilon_{S2A2} = 10^{\frac{\log[R(\varepsilon_{S1A1}^{CT_1})]}{CT_2}}$$

[0068] where $R = 1$ and ε_{S1A1} assumed to be 2.0.

[0069] The genotype of the sample can be determined from the ratio ($R = x/y$) with the equations

$$\frac{x}{y} \approx \frac{\varepsilon_{S2A2}^{CT_2}}{\varepsilon_{S1A1}^{CT_1}} \text{ and } x = \frac{R}{1 + R}.$$

Example 1

[0070] In this section, examples of experiments using the quantitation method according to various embodiments are described.

[0071] In this example, the Assay and Primer = targeted 4 cancer promoter regions, each with different primer sequences as follows:

Assay	Forward	Reverse	Template	Assay
A02_F0_R0	F0	R0	<u>AGAATTGAGGGTGGTATAGAAGC</u> GGGTAAAGGGCGATCGGATTCGAGTTTAGGGAGGCGTATATAGGGGCGTCGAGGTTGAGAAGG	A02F0R0
A02_F0_R2	F0	R2	<u>AGAATTGAGGGTGGTATAGAAGC</u> GGGTAAAGGGCGATCGGATTCGAGTTTAGGGAGGCGTATATAGGGGCGTCGAGGTTGAGAAGG	A02F0R2
A44_F3_R0	F3	R0	<u>GCGAGGGAGAAATCGGTC</u> GTTTTTTTCGAAAGGTCGAAGTCGAGAGAAATAATTGATTCGATAGGTTTGTTTCGTTTAGTTTTGATAGTGAGGGG	A44F3R0
A44_F3_R2	F3	R2	<u>GCGAGGGAGAAATCGGTC</u> GTTTTTTTCGAAAGGTCGAAGTCGAGAGAAATAATTGATTCGATAGGTTTGTTTCGTTTAGTTTTGATAGTGAGGGG	A44F3R2
A51_F1_R1	F1	R1	<u>CGGT</u> TAGGGATGTTTTGCGTTTTTCGGGCGGTTTCGGGTTTAGTTATTTGTTTCGTCGGGAAGGTAGGTTTC	A51F1R1
A51_F1_R4	F1	R4	<u>CGGT</u> TAGGGATGTTTTGCGTTTTTCGGGCGGTTTCGGGTTTAGTTATTTGTTTCGTCGGGAAGGTAGGTTTC	A51F1R4
A54_F0_R2	F0	R2	<u>GGTAGATTGAGGCGGTC</u> GGGGAGTGAGGAGTCGCGGGAGAGAGTCGCGGCGTTTTTCGGGATAATGCGGCGGCGGTTGTTGTTAGGTGGGGCGCGTGC	A54F0R2
A54_F2_R5	F2	R5	<u>GGTAGATTGAGGCGGTC</u> GGGGAGTGAGGAGTCGCGGGAGAGAGTCGCGGCGTTTTTCGGGATAATGCGGCGGCGGTTGTTGTTAGGTGGGGCGCGTGC	A54F2R5

[0072] Master Mix = SYBR®Select Master Mix

[0073] Sample = Synthetic Templates

[0074] Assay 1 = Primer G, Assay 2 = Primer A

Template ID	Synthetic Template Sequence
A51_AIIC	<u>CGGGTAGGGATGTTTTGCGTTTTTCGGGCGGTTTCGGGTTTAGTTATTTGTTTCGTCGGGAAGGTAGGTTTC</u>
A51_AIU	UGGGTAGGGATGTTTTTUGGTTTTUGGGUGGTTTUGGGTTTAGTTATTTGTTTUGTUGGGGAAGGTAGGTTTC
A54_AIIC	<u>GGTAGATTGAGGCGGTC</u> GGGGAGTGAGGAGTCGCGGGGAGAGAGTCGCGGCGTTTTTCGGGATAATGCGGCGGCGGTTTGTAGGTGGGGCGCGTGCGGTTATTT
A54_AIU	GGTAGATTGAGGUGGTTUGGGAGTGAGGAGTUGUGGGGAGAGAGTUGUGGUGTTTTTUGGGATAATGUGGUGGUGGTTTGTAGGTGGGGUGUGTGUGGTTATTT
A02_AIIC	<u>AGAATTGAGGGTGGTATAGAAGC</u> GGGTAAAGGGCGATCGGATTCGAGTTTAGGGAGGCGTATATAGGGGCGTCGAGGTTGAGAAGG
A02_AIU	AGAATTGAGGGTGGTATAGAAGUGGGTAAAGGGGUGATUGGATTUGAGTTTAGGGAGGUGTATATAGGGGUGTUGAGGTTUGAGAAGG
A44_AIIC	<u>GCGAGGGAGAAATCGGTC</u> GTTTTTTTCGAAAGGTCGAAGTCGAGAGAAATAATTGATTCGATAGGTTTGTTTCGTTTAGTTTTGATAGTGAGGGG
A44_AIU	GUGAGGGAGAAATUGGTUGTTTTTTTUGAAAGGTUGAAGTUGAGAGAAATAATTGATTUGATAGGTTTGTTTUGTTTAGTTTTGATAGTGAGGGG

[0075] To generate samples of various methylation levels, the AIIC and AIU templates were mixed at specific ratios. 12 levels of methylation states were generated : 100%, 99%, 90%, 75%, 60%, 50%, 35%, 20%, 10%, 5%, 1% and 0%.

[0076] An exemplary plate layout is illustrated in FIG. 4.

[0077] Replicates = 2 technical replicates. 10uL reaction mix per well.

[0078] **Run condition** = Assay plate was run on Vii7 using standard PCR method for 40 cycles. PCR condition = s: 95°C(2minutes) followed by 40 cycles of 95°C(15seconds)-60°C(1minute) on ViiA7.

[0079] **Threshold** was set to 0.15 for all wells in this run.

[0080] Average CT of the 2 replicates was used in calculation.

Calculations

[0081] In this set of experimental values, the accuracy of the quantification method with Single and Dual primer assay designs according to various embodiments were compared with conventional method with standard curves.

Single Primer Assay Design

Calculation Using Standard Curve

[0082] For comparison purpose, the 12 samples at different methylation levels were divided to 2 groups: Standards and Unknowns. A standard curve of CT Vs Log(%C) was generated with 6 data points (1%, 10%, 35%, 60% and 99%) of methylated samples. Slope and intercept of the standard curve were calculated from the data set and used to calculate the %C of the Unknowns were calculated using the slope and intercept from the standard curve. FIG. 5 illustrates scattered plot 500 of calculated %C using a standard curve Vs Input %C.

Calculation Without Using a Standard Curve

[0083] Data points 10% and 100% methylated samples were used as Reference to calculated PCR efficiency of the specific assay using the equation $\varepsilon = 10^{\left(\frac{1}{\Delta CT}\right)}$ where $\Delta CT = CT_{10\%C} - CT_{100\%C}$.

[0084] %C of the other 10 samples were calculated with the equation

$$x\% \approx \varepsilon_{S1A1}^{(CT_{R1}-CT_1)} \times 100\%$$

[0085] where %x = %C in this example, $CT_{RI} = CT_{100\%C}$ and $CT_I = CT$ of unknown sample. FIG. 6 illustrates scattered plot 600 of calculated %C without standard curve Vs Input %C.

Dual Primer Assay Design

Calculation Using a Standard Curve -

[0086] For comparison purpose, the 12 samples at different methylation levels were divided to 2 groups: Standards and Unknowns. A standard curve of dCT Vs Log(%C/%U) was generated with 6 data points (1%, 10%, 35%, 60% and 99%) of methylated samples, where dCT = CT with Primer G - Ct with Primer A of each standard sample. Slope and intercept of the standard curve were calculated from the data set and used to calculate the %C of the Unknowns were calculated using the slope and intercept from the standard curve. FIG. 7 illustrates a scattered plot 700 of calculated %C with standard curve Vs Input %C with Dual Primer Set with 8 assays using a standard curve, according to various embodiments of the present teachings.

Calculation Without Using a Standard Curve

[0087] Data for 10% and 100% methylated samples were used as Reference to calculate PCR efficiency of the specific (C-G) assay using the equation $\varepsilon = 10^{\left(\frac{1}{\Delta CT}\right)}$ where $\Delta CT = CT_{10\%C} - CT_{100\%C}$ with Primer Set G (Assay 1).

[0088] The %C/%U ratio of the other 10 samples were calculated with the equation

$$\frac{x}{y} \approx \frac{\varepsilon_{S2A2}^{CT_2}}{\varepsilon_{S1A1}^{CT_1}}$$

[0089] Where, ε_{S1A1} = calculated PCR efficiency of C-G reaction

[0090] ε_{S2A2} = relative PCR efficiency of U-A reactions with reference to C-G reaction

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

[0091] where $CT_{100\%S1A1}$ = CT of 100%C Standard with Primer G, and

[0092] $CT_{100\%S2A2} = CT \text{ of } 0\%C (100\% U) \text{ Standard with Primer A}$

[0093] %C of the Unknown samples was calculated from the x/y ratio (R) with the equation

$$\%C = \frac{R}{1+R}$$

[0094] FIG. 8 illustrates scattered plot of calculated %C without standard curve Vs Input %C with Dual Primer Set with 8 assays, according to various embodiments of the present teachings.

Example 2: Measuring %C in Bisulfite converted gDNA templates with Single Primer Set

Experiment Design

[0095] 6 Assays at 5 cancer promoter regions

[0096] Template DNA = 0% and 100% Bisulfite converted gDNA from Qiagen. A series of samples at different %C level (0%, 5%, 10%, 15%, 40%, 70%, 90%, 100%) was generated by mixing the 0% and 100% gDNA. Samples with 10% and 100%C were used as Reference to calculate PCR efficiency.

[0097] Assay 1= G primer set

[0098] PCR condition = 95C(2m) – [95C(15s)-60C(1m)]₄₀ on ViiA7

[0099] %C of samples were calculated using Single Primer Assay design without Standard Curve

[00100] The results, according to various embodiments described herein are shown in FIG. 9. Scattered plot 900 shows measured %C Vs. Input %C.

Computer-Implemented System

[00101] Those skilled in the art will recognize that the operations of the various embodiments described herein may be implemented using hardware, software, firmware, or combinations thereof, as appropriate. For example, some processes can be carried out using processors or other digital circuitry under the control of software, firmware, or hard-wired logic. (The term

“logic” herein refers to fixed hardware, programmable logic and/or an appropriate combination thereof, as would be recognized by one skilled in the art to carry out the recited functions.)

Software and firmware can be stored on non-transitory computer-readable media. Some other processes can be implemented using analog circuitry, as is well known to one of ordinary skill in the art. Additionally, memory or other storage, as well as communication components, may be employed in embodiments of the invention.

[00102] FIG. 10 is a block diagram that illustrates a computer system 1000 that may be employed to carry out processing functionality, according to various embodiments. Instruments to perform experiments may be connected to the exemplary computing system 1000. Computing system 1000 can include one or more processors, such as a processor 1004. Processor 1004 can be implemented using a general or special purpose processing engine such as, for example, a microprocessor, controller or other control logic. In this example, processor 1004 is connected to a bus 1002 or other communication medium.

[00103] Further, it should be appreciated that a computing system 1000 of FIG. 10 may be embodied in any of a number of forms, such as a rack-mounted computer, mainframe, supercomputer, server, client, a desktop computer, a laptop computer, a tablet computer, hand-held computing device (e.g., PDA, cell phone, smart phone, palmtop, etc.), cluster grid, netbook, embedded systems, or any other type of special or general purpose computing device as may be desirable or appropriate for a given application or environment. Additionally, a computing system 1000 can include a conventional network system including a client/server environment and one or more database servers, or integration with LIS/LIMS infrastructure. A number of conventional network systems, including a local area network (LAN) or a wide area network (WAN), and including wireless and/or wired components, are known in the art. Additionally, client/server environments, database servers, and networks are well documented in the art. According to various embodiments described herein, computing system 1000 may be configured to connect to one or more servers in a distributed network. Computing system 1000 may receive information or updates from the distributed network. Computing system 1000 may also transmit information to be stored within the distributed network that may be accessed by other clients connected to the distributed network.

[00104] Computing system 1000 may include bus 1002 or other communication mechanism for communicating information, and processor 1004 coupled with bus 1002 for processing information.

[00105] Computing system 1000 also includes a memory 1006, which can be a random access memory (RAM) or other dynamic memory, coupled to bus 1002 for storing instructions to be executed by processor 1004. Memory 1006 also may be used for storing temporary variables or other intermediate information during execution of instructions to be executed by processor 1004. Computing system 1000 further includes a read only memory (ROM) 1008 or other static storage device coupled to bus 1002 for storing static information and instructions for processor 1004.

[00106] Computing system 1000 may also include a storage device 1010, such as a magnetic disk, optical disk, or solid state drive (SSD) is provided and coupled to bus 1002 for storing information and instructions. Storage device 1010 may include a media drive and a removable storage interface. A media drive may include a drive or other mechanism to support fixed or removable storage media, such as a hard disk drive, a floppy disk drive, a magnetic tape drive, an optical disk drive, a CD or DVD drive (R or RW), flash drive, or other removable or fixed media drive. As these examples illustrate, the storage media may include a computer-readable storage medium having stored therein particular computer software, instructions, or data.

[00107] In alternative embodiments, storage device 1010 may include other similar instrumentalities for allowing computer programs or other instructions or data to be loaded into computing system 1000. Such instrumentalities may include, for example, a removable storage unit and an interface, such as a program cartridge and cartridge interface, a removable memory (for example, a flash memory or other removable memory module) and memory slot, and other removable storage units and interfaces that allow software and data to be transferred from the storage device 1010 to computing system 1000.

[00108] Computing system 1000 can also include a communications interface 1018. Communications interface 1018 can be used to allow software and data to be transferred between computing system 1000 and external devices. Examples of communications interface 1018 can include a modem, a network interface (such as an Ethernet or other NIC card), a communications

port (such as for example, a USB port, a RS-232C serial port), a PCMCIA slot and card, Bluetooth, etc. Software and data transferred via communications interface 1018 are in the form of signals which can be electronic, electromagnetic, optical or other signals capable of being received by communications interface 1018. These signals may be transmitted and received by communications interface 1018 via a channel such as a wireless medium, wire or cable, fiber optics, or other communications medium. Some examples of a channel include a phone line, a cellular phone link, an RF link, a network interface, a local or wide area network, and other communications channels.

[00109] Computing system 1000 may be coupled via bus 1002 to a display 1012, such as a cathode ray tube (CRT) or liquid crystal display (LCD), for displaying information to a computer user. An input device 1014, including alphanumeric and other keys, is coupled to bus 1002 for communicating information and command selections to processor 1004, for example. An input device may also be a display, such as an LCD display, configured with touchscreen input capabilities. Another type of user input device is cursor control 1016, such as a mouse, a trackball or cursor direction keys for communicating direction information and command selections to processor 1004 and for controlling cursor movement on display 1012. This input device typically has two degrees of freedom in two axes, a first axis (e.g., x) and a second axis (e.g., y), that allows the device to specify positions in a plane. A computing system 1000 provides data processing and provides a level of confidence for such data. Consistent with certain implementations of embodiments of the present teachings, data processing and confidence values are provided by computing system 1000 in response to processor 1004 executing one or more sequences of one or more instructions contained in memory 1006. Such instructions may be read into memory 1006 from another computer-readable medium, such as storage device 1010. Execution of the sequences of instructions contained in memory 1006 causes processor 1004 to perform the process states described herein. Alternatively hard-wired circuitry may be used in place of or in combination with software instructions to implement embodiments of the present teachings. Thus implementations of embodiments of the present teachings are not limited to any specific combination of hardware circuitry and software.

[00110] The term "computer-readable medium" and "computer program product" as used herein generally refers to any media that is involved in providing one or more sequences or one

or more instructions to processor 1004 for execution. Such instructions, generally referred to as “computer program code” (which may be grouped in the form of computer programs or other groupings), when executed, enable the computing system 1000 to perform features or functions of embodiments of the present invention. These and other forms of non-transitory computer-readable media may take many forms, including but not limited to, non-volatile media, volatile media, and transmission media. Non-volatile media includes, for example, solid state, optical or magnetic disks, such as storage device 1010. Volatile media includes dynamic memory, such as memory 1006. Transmission media includes coaxial cables, copper wire, and fiber optics, including the wires that comprise bus 1002.

[00111] Common forms of computer-readable media include, for example, a floppy disk, a flexible disk, hard disk, magnetic tape, or any other magnetic medium, a CD-ROM, any other optical medium, punch cards, paper tape, any other physical medium with patterns of holes, a RAM, PROM, and EPROM, a FLASH-EPROM, any other memory chip or cartridge, a carrier wave as described hereinafter, or any other medium from which a computer can read.

[00112] Various forms of computer readable media may be involved in carrying one or more sequences of one or more instructions to processor 1004 for execution. For example, the instructions may initially be carried on magnetic disk of a remote computer. The remote computer can load the instructions into its dynamic memory and send the instructions over a telephone line using a modem. A modem local to computing system 1000 can receive the data on the telephone line and use an infra-red transmitter to convert the data to an infra-red signal. An infra-red detector coupled to bus 1002 can receive the data carried in the infra-red signal and place the data on bus 1002. Bus 1002 carries the data to memory 1006, from which processor 1004 retrieves and executes the instructions. The instructions received by memory 1006 may optionally be stored on storage device 1010 either before or after execution by processor 1004.

[00113] It will be appreciated that, for clarity purposes, the above description has described embodiments of the invention with reference to different functional units and processors. However, it will be apparent that any suitable distribution of functionality between different functional units, processors or domains may be used without detracting from the invention. For example, functionality illustrated to be performed by separate processors or controllers may be

performed by the same processor or controller. Hence, references to specific functional units are only to be seen as references to suitable means for providing the described functionality, rather than indicative of a strict logical or physical structure or organization.

Example 3: Copy Number determination: Copy Number of C4A, C4B, C4S and C4L

[00114] 4 Target Assays (FAM) and 1 Reference Assay (VIC)

C4A Hs07226349_cn
C4B Hs07226350_cn
C4S Hs07226351_cn
C4L Hs07226352_cn

[00115] Sample = gDNA with 33 Unknowns, 3 Calibrators (Reference) and 3 NTC. 10ng gDNA per well. 4 Replicate runs per sample.

[00116] Master Mix = GT MMx

[00117] Thermocycling profile:

Thermocycling			
Stage	Temp	Time	Cycles
Hot Start	95C	10min	Hold
Denature	95C	15sec	40 cycles
Anneal/Extend	60C	1min	

[00118] For comparison purpose, analysis was done with CopyCaller software v2.0. Copy number predicted with the software was generated for the samples.

Determining Copy Number for Target gene in sample

[00119] PCR Efficiency of Reference Assay (S1A1) is assumed to be 2.0.

[00120] PCR efficiency of the Target Assay (S2A2) was determined with

$$\varepsilon_{S2A2} = 10^{\frac{\log[R(\varepsilon_{S1A1}^{CT_1})]}{CT_2}}$$

[00121] where R = Copy number of Ref gene / Copy of Target Gene in each reference sample.
 CT_1 = CT of Reference sample at VIC channel. CT_2 = CT of Reference sample at FAM channel.

The average ε_{S2A2} calculated from all three Reference samples was used for determination of copy numbers of Target genes in samples.

[00122] For the samples, Ratio ($R = x/y$) was determined with equation

$$\frac{x}{y} \approx \frac{\varepsilon_{S2A2}^{CT_2}}{\varepsilon_{S1A1}^{CT_1}}$$

[00123] and x was calculated with equation

$$x = \frac{R}{1 + R}$$

[00124] where CT_1 = CT of Sample at VIC channel and CT_2 = CT of Sample at FAM channel. The copy number of the Reference gene (X) = 2 and copy number of the Target gene in each sample is calculated as $Y = X/x \dots X$. The calculated copy number of Target gene in samples were compared with the Copy Number predicted by the CopyCaller.

Example 4: Determining Genotype in Sample

[00125] Assays = Standard Genotyping assays for SNP1 (FAM) and SNP2 (VIC)

[00126] Reference samples = Homozygous SNP1/SNP1 and Homozygous SNP2/SNP2 and/or Heterozygous SNP1/SNP2

[00127] Sample = gDNA samples with unknown genotype at target locus

[00128] Run plate on qPCR instrument with standard run protocol for 40 cycles. Collect real time data on instrument.

[00129] The PCR efficiency of SNP1 assay (S1A1) is assumed to be 2.0. Calculate the PCR efficiency of SNP2 assay, ε_{S2A2} with the two homozygous reference samples, SNP1/SNP1 and SNP2/SNP2 with equation

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

[00130] where $CT_{100\%S1A1}$ = CT of SNP1/SNP1 at FAM channel and $CT_{100\%S2A2}$ = CT of SNP2/SNP2 at VIC channel. Calculate the PCR efficiency for ϵ_{S2A2} with

$$\epsilon_{S2A2} = 10^{\frac{\log [R (\epsilon_{S1A1}^{CT_1})]}{CT_2}}$$

[00131] where CT_1 = CT of Heterozygous SNP1/SNP2 sample at FAM channel and CT_2 = CT of Heterozygous SNP1/SNP2 sample at VIC channel. Calculate the average ϵ_{S2A2} .

[00132] Calculate the SNP1/SNP2 ratio for each sample using equation

$$\frac{x}{y} \approx \frac{\epsilon_{S2A2}^{CT_2}}{\epsilon_{S1A1}^{CT_1}}$$

[00133] where CT_1 = CT of sample at FAM channel and CT_2 = CT of sample at VIC channel.

[00134] Determine x with

$$x = \frac{R}{1 + R}$$

[00135] where $R = x/y$. If x of the sample is approximately 1, the sample has genotype of SNP1/SNP1. If x the sample is approximately 0.5, the sample has genotype of SNP1/SNP2. If x of the sample is approximately 0, the sample has genotype of SNP2/SNP2.

Example 5

[00136] Understanding the changes in DNA methylation level provides important insight into gene regulation and cancer. Here we present a simple, accurate and cost effective quantitative method using SYBR® assay. By combining the high performance of SYBR® Select Master Mix and a new quantitation method, accurate methylation level was determined in a simple workflow with high flexibility without the need of standard curves. Consistent amplification and high specificity were found with 93% (128 of 138) assays designed with wide %GC (16-100%) range. The mean deviation of methylation level determined for bisulfate converted gDNA and synthetic templates was $\approx 4\%$. This work validated SYBR® Select Master Mix as an efficient and cost effective reagent for methylation assays. Although various embodiments have been described

with respect to certain exemplary embodiments, examples, and applications, it will be apparent to those skilled in the art that various modifications and changes may be made without departing from the present teachings.

[00137] DNA methylation has strong association with regulation of gene expression, chromosomal stability and cell development. Change in methylation state can be used as biomarkers for early diagnosis, progression and prognosis of cancer as well as aging rate comparison and other applications. Numerous quantitative methods have been developed with various platforms to measure level of DNA methylation¹, including qPCR with TaqMan® assays or SYBR® assays with standard curves.

[00138] Life Technologies' SYBR® Select Master Mix is a high performance master mix with high specificity and consistent amplification across a wide dynamic range. In this study, its potential as a cost effective option for methylation study was evaluated.

[00139] A new quantitation method has been developed to provide accurate quantitative measurement of change in methylation level without the generation of standard curve with SYBR® assays. The workflow and performance of this new method is compared with the conventional quantitation method with standard curves.

Experimental Design

[00140] Targets and Assay Design: 138 assays for 100%MeC strand were designed for 10 randomly selected cancer promoter regions without specific screening. The only criterion used in the assay design was to keep T_m around 60°C. As a result, assays with a wide range of GC contents (16-100%) and length (10-32bp) were generated. The targets and assay properties are summarized in Table 1100 shown in FIG. 11. For quantitative measurements, a second assay was designed for 0%MeC strand.

[00141] Samples / Targets: EpiTect Control DNA, methylated (Qiagen) was used as 100%MeC gDNA and EpiTect Control DNA, unmethylated (Qiagen) was used as 0%MeC gDNA. Synthetic templates for 4 of the assays were ordered as Ultramers from IDT and pooled at 1:1 ratio. For quantitative measurements, 100%MeC and 0%MeC target sequences were mixed at various ratio to create samples with different methylation levels between 0%-100%.

Primers: All primers used were synthesized in-house. Master Mix: A special version of SYBR® Select Master Mix without UDG was prepared for this study to avoid the digestion of dU in the bisulfite converted gDNA. PCR runs: All reactions were run in 384 well plates with 2 technical replicates for each reaction using the same thermal cycling conditions (FIG. 11) on ViiA™ 7 Real-Time PCR System (Applied Biosystems®). Each reaction started with 5 ng of gDNA or 0.04 fmol of synthetic template pools with 500 nM of each primer in 10µL reaction volume per well.

[00142] FIG. 12 illustrates the thermal profile used for all runs in this example.

[00143] Data Analysis: ViiA™ 7 software (Applied Biosystems®) was used for data analysis. Same threshold was used for the entire plate. Average CT of the technical replicates is used for all calculations.

[00144] FIG. 13 illustrates an overview schematic of the quantitation method used in this example, according to various embodiments of the present teachings.

Evaluation of Quantitation Method

[00145] %MeC of a set of samples was determined with the method(s) described and compared with the result determined with standard curves and the input level. Assay for 100%MeC is defined as Assay1 and assay for 0%MeC is defined as Assay2. Representative result with gDNA and synthetic template is presented in Figure 3a and 3b. Results demonstrated that it is essential to use relative PCR efficiency in the calculation. All methods based on relative PCR efficiency demonstrated excellent correlation with input %MeC and calculated %MeC with standard curves. Comparable results were obtained with the 3 options in the calculations (2-Assay(4 terms), 2-Assay(2 terms) and 1-Assay), with least bias found with 2-Assay(4 terms) method (Figure 4). Mean deviation was defined as $\sqrt{[(\sum(x-x_i)^2)/n]}$. Among the 4 gDNA assays, A51 was a poor performing assay with low PCR efficiency (measured $\epsilon_{S1A1}=1.55$ and measured $\epsilon_{S2A2}=4.4$). The mean deviation with A51 was <15% with 2 of the 3 options. With all other assays, the mean deviation with the 3 options was 3.7% with 2-Assay(4 terms), 4.4% with 2-Assay(2 terms) and 4.9% with 1-Assay method.

[00146] FIGs. 14A and 14B shows a representative quantitation result with (a) bisulfite converted gDNA and (b) synthetic templates. This data illustrates the impacting of using relative efficiency (plot 1400) versus calibrated efficiency (plot 1402).

[00147] FIG. 15 illustrates plot 200 showing the mean deviation by different methods with BIS gDNA and synthetic templates.

Conclusion

[00148] We have demonstrated here a simple, cost effective and accurate method for methylation level measurement, according to various embodiments. SYBR® Select Master Mix performs well with bisulfite converted gDNA and assays with a wide range of GC content. Consistent and robust amplification with high specificity and excellent discrimination makes it a reliable cost effective option for methylation studies. We have also described a simple quantitative method for accurate measurement of methylation level, with mean bias $\approx 4\%$. Without the need of creating standard curves, the workflow and plate design is simplified. Using the Single-Assay method, only two reference runs are needed for the determination of PCR efficiency of Assay1 (or 100%MeC), offering maximum flexibility and simplicity. With the 2-Assay method, the accuracy is higher making it preferable for applications where the relative abundance of two sequences is to be determined.

[00149] According to the present teachings, the quantitation method produces similar results than the quantitation methods currently used. For example, FIG. 18 illustrates a chart of copy number determination using a traditional method vs. the quantitation method according to various embodiments described herein.

[00150] Although various embodiments have been described with respect to certain exemplary embodiments, examples, and applications, it will be apparent to those skilled in the art that various modifications and changes may be made without departing from the present teachings.

CLAIMS

1. A computer-implemented method for quantitation of biological material in a biological sample, the method comprising:

receiving amplification data from amplification of a first and a second reference sample using PCR (Polymerase Chain Reaction);
receiving amplification data from amplification of a biological sample using PCR;
determining a specific PCR 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, wherein the relative PCR efficiency is determined with the following equation:

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

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, $CT_{100\%S1A1}$ represents a cycle threshold of the first assay, $CT_{100\%S2A2}$ represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay.

2. The method of claim 1, comprising the step of amplification of a first and a second reference sample, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first and second reference sample is performed with a single primer assay specific for either of the two states.

3. The method of claim 1, wherein the quantity of biological material relates to a methylation level of the biological sample.

4. The method of claim 3, wherein the methylation level of the biological sample is determined by the following equation:

$$x\% \approx \varepsilon_{S1A1}^{(CT_{R1}-CT_1)} \times 100\%,$$

wherein $x\%$ is the methylation level of the biological sample, CT_{R1} is a reference cycle threshold of a reference sample having a methylation level of 100%, and CT_1 is a cycle threshold of the biological sample.

5. The method of claim 1, wherein the quantity of biological material relates to determining a genotyping result.

6. The method of claim 1, wherein the quantity of biological material relates to determining a copy number variation result.

7. The method of claim 1, further comprising:

receiving amplification data from amplification of a third reference sample; and
determining the efficiency from amplification of the first, second, and third reference sample.

8. The method of claim 7, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first, second, and third reference sample is performed with a dual primer assay specific for both states.

9. 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 using PCR (Polymerase Chain Reaction);

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, wherein the relative PCR efficiency is determined with the following equation:

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

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, $CT_{100\%S1A1}$ represents a cycle threshold of the first assay, $CT_{100\%S2A2}$ represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay.

10. The computer-readable storage medium of claim 9, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first and second reference sample is performed with a single primer assay specific for either of the two states.

11. The computer-readable storage medium of claim 9, wherein the quantity of biological material relates to a methylation level of the biological sample.

12. The computer-readable storage medium of claim 11, wherein the methylation level of the biological sample is determined by the following equation:

$$x\% \approx \epsilon_{S1A1}^{(CT_{R1}-CT_1)} \times 100\%,$$

wherein $x\%$ is the methylation level of the biological sample, CT_{R1} is a reference cycle threshold of a reference sample having a methylation level of 100%, and CT_1 is a cycle threshold of the biological sample.

13. The computer-readable storage medium of claim 9, wherein the quantity of biological material relates to determining a genotyping result.

14. The computer-readable storage medium of claim 9, wherein the quantity of biological material relates to determining a copy number variation result.

15. The computer-readable storage medium of claim 9, wherein the instructions further comprise instructions for:

receiving amplification data from amplification of a third reference sample; and

determining the efficiency from amplification of the first, second, and third reference sample.

16. The computer-readable storage medium of claim 15, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first, second, and third reference sample is performed with a dual primer assay specific for both states.

17. 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 using PCR (Polymerase Chain Reaction);

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, wherein the relative PCR efficiency is determined with the following equation:

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

wherein S1A1 represents a first assay for a reference gene, S2A2 represents a second assay for a target gene, $CT_{100\%S1A1}$ represents a cycle threshold of the first assay, $CT_{100\%S2A2}$ represents a cycle threshold in the second assay, ϵ_{S1A1} is the specific PCR efficiency of the first assay, and ϵ_{S2A2} is the relative PCR efficiency of the second assay.

18. The system of claim 17, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first and

second reference sample is performed with a single primer assay specific for either of the two states.

19. The system of claim 17, wherein the quantity of biological material relates to a methylation level of the biological sample.

20. The system of claim 19, wherein the methylation level of the biological sample is determined by the following equation:

$$x\% \approx \varepsilon_{51A1}^{(CT_{R1}-CT_1)} \times 100\%,$$

wherein $x\%$ is the methylation level of the biological sample, CT_{R1} is a reference cycle threshold of a reference sample having a methylation level of 100%, and CT_1 is a cycle threshold of the biological sample.

21. The system of claim 17, wherein the quantity of biological material relates to determining a genotyping result.

22. The system of claim 17, wherein the quantity of biological material relates to determining a copy number variation result.

23. The system of claim 17, wherein the instructions further comprise instructions for:

receiving amplification data from amplification of a third reference sample; and
determining the efficiency from amplification of the first, second, and third reference sample.

24. The system of claim 23, wherein a first and a second state are defined for the respective first and second reference sample, and wherein the amplification of the first, second, and third reference sample is performed with a dual primer assay specific for both states.