

NUCLEIC ACID RATIO DETERMINATION

Incorporation by Cross-Reference

This application claims priority from Australian provisional patent application
5 number 2017905138 filed on 21 December 2017, the entire contents of which are incorporated herein by cross-reference.

Technical Field

The present invention relates generally to the field of molecular biology. More specifically, the present invention provides methods for quantitative data normalisation,
10 and/or ascertaining levels of transcription in cells, organisms, viruses, and the like. The methods can be used in numerous applications including, but not limited to, determining transcriptional upregulation and downregulation, identifying transcriptional perturbation, determining viability/death, and assessing responses to treatment with agents (e.g. resistance or sensitivity to drugs).

15 *Background*

Advancements in molecular biology have greatly improved the ability to characterize cells and interrogate their genomes and transcriptomes for evidence of changes associated with disease and/or external stimuli. For example, specific variations in sequence are found in association with acquired or inherited diseases, such as cancer or
20 cystic fibrosis. Changes in expression of the gene are associated with both disease states and response to stimuli. Further, the presence of a foreign sequence can indicate the presence of infectious agents such as bacteria or viruses. Nucleic Acid Amplification Technology (NAAT) testing has broad application in all these fields for basic research, clinical research and clinical diagnostics.

25 Methods of *in vitro* nucleic acid amplification have wide-spread applications in NAAT testing. Such methods include polymerase chain reaction (PCR), strand displacement amplification (SDA), helicase-dependent amplification (HDA), Recombinase Polymerase Amplification (RPA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated amplification
30 (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA). Various types of PCR have been described including quantitative real time PCR, reverse transcription polymerase chain reaction (RT-PCR) and digital PCR. Each of these target amplification strategies requires the use of

oligonucleotide primers. The process of amplification results in the exponential amplification of target sequences which incorporate the oligonucleotide primers at their 5' termini and which contain newly synthesized copies of the sequences located between the primers. Signal amplification techniques such as EzyAmp, Branched Chain Reaction or DoC can also be used for NAAT testing.

Normalization of gene expression (RNA levels) is a contentious topic, with various pros and cons existing for each of the strategies available. These include, normalization to sample size, to total RNA or ribosomal RNA, to mRNA of housekeeping genes and to genomic DNA. Normalization to mRNA of housekeeping genes requires judicious selection of targets as their stability and expression levels can be affected by experimental or environmental conditions. Further, in bacteria, expression levels can vary during the bacterial developmental cycle. Levels of ribosomal RNA (rRNA) although abundant and displaying longer half-lives, can also alter expression in response experimental or environmental conditions; and similarly levels in bacteria can change during the development cycle. Furthermore, with rRNA making up 80% of the total RNA fraction, there is a significant imbalance between rRNA and mRNA, the later comprising only 2-5%. Genomic DNA is thought to be a good candidate for gene expression normalization as it is always present, stable and it is generally invariable. Genomic DNA has been shown to generated more accurate and reproducible results.

There are, however, several limitations of using genomic DNA as a target for normalization of RNA levels. Most protocols do not simultaneously extract both RNA and DNA from a sample and hence these are extracted separately, quantified and subsequently amplified separately in parallel reactions which typically contain, or lack, reverse transcriptase respectively. As such there is a great deal of scope for error in comparing these two very different protocols and using the results from (i) a first protocol (DNA extraction and amplification by, for example, PCR) to normalize the results from (ii) a second protocol (RNA extraction and amplification by, for example, RT-PCR). Further, such parallel protocols are expensive, laborious and time consuming.

NAATs provide a gold standard for analysis of bacterial infections, due to their high sensitivity and specificity, fast turnaround time, ability to be performed on a variety of sample types, and their capacity to target any bacterial species. However, for some specific applications, current methods have disadvantages. In particular, they are not well suited to distinguishing between viable and dead pathogens. For example, bacterial DNA is not a good marker of cell viability because this DNA can survive for weeks after cell death has occurred. This fact sheds light on the limits of available assays, with

uninformative use of quantification methods and inefficient monitoring of infection status or effectiveness of treatment. Potential overestimation of positivity may also occur.

The demand for more informative and accurate detection methods is imperative, especially when applied to sexually transmitted infections (STIs). New tools are urgently
5 needed, particularly for cases where pathogens are present, but the patients are asymptomatic, and/or where pathogens have high rates of antimicrobial resistance (AMR). For such infections a test of cure (TOC) is required to confirm successful clearance. This confirmation of cure will reduce the potential for further complications, correlated with the initial infection, and will limit the prevalence and spread of pathogens
10 and drug resistant strains. TOC methods are currently limited to NAAT assays, performed at a single time-point post treatment, and the optimal time can change depending on the species causing the STI. A positive result may infer treatment failure but could also reflect detection of non-viable DNA and/or RNA fragments.

Several techniques exist to tackle this issue. Methods for determining viability
15 include metabolic monitoring through new culture methods, evaporation-induced stimulation of bacterial osmoregulation, antibiotic susceptibility testing (AST) such as Smarticles technology, bacteriophage-based detection and ratiometric pre-rRNA analysis. Although these have shown some success in differentiating viable and dead bacteria, all of the above still rely on culture procedures to attain a result. Alternate viability
20 techniques steer away from culture methods. For example, some focus on intercalating dyes, applied prior to the DNA extraction process, for example ethidium monoazide (EMA) and propidium monoazide (PMA). The dyes bind to double stranded DNA, existing outside cells or following infiltration of dye through the broken walls of cells. This makes the DNA of dead bacteria resistant to subsequent PCR amplification. This
25 approach has been widely applied on clinical samples, environmental and foodborne pathogen detection, however, the limitations are also evident and have been reviewed The dyes are not suitable for all types of samples or bacteria, with variability in both the incubation conditions and concentrations needed. It has been extensively shown that signal inhibition can arise from dye penetrating live cells and false-positive detection can
30 occur as a consequence of a high non-viable bacterial load.

Detection of RNA is another method with potential for assessing cell viability since it is less stable than DNA and thus a truer reflection of viability. These methods, however, require further improvements since RNA transcripts have also been shown to persist for extended lengths of time, following treatment or cell death. This makes it vital
35 to have judicious selection of appropriate transcripts & amplicon parameters along with the ability to fully eliminate contaminating DNA from RNA preparations. Thus, there is

the need for more investigation into accurate RNA-based strategies to quantify viable bacteria.

A further area of need is for methods which allow screening for drug resistance or sensitivity. In particular, rapid antimicrobial susceptibility tests are urgently required for informing individual patient's therapy to prevent the spread of resistant pathogens. Further, such method could be used as screening methods for drug discovery programs. The invention described herein can generate more informative results, differentiating between the presence and absence of infectious agents, and in turn between uncleared and cleared infections. It involves an alternative approach of simultaneously analysing both RNA and DNA present in a single total nucleic acid (TNA) sample.

The invention described in this document has application in these areas and others. It provides a method for normalising the level of active transcription in a single reaction. Previous studies which have attempted to normalize RNA levels to DNA have shortcomings. In such studies researchers have extracted RNA and DNA from a specimen, amplified these in separate, parallel RT-PCR and PCR reactions and then normalized gene expression levels (RNA) to levels generated from DNA. There are many problems with this approach. Firstly, although the RNA & DNA may have originated from the same sample, they are processed differently to extract the two different species of nucleic acid (DNA versus RNA) and hence the efficiency of extraction is unlikely to be equal. Similarly, there can be sampling bias of these two extracted samples when aliquots are placed in separate tubes for analysis. Further, since they are amplified in different PCR reaction mixes, which differ in composition (e.g. at least by the presence or absence of reverse transcriptase) and often in thermocycling profiles, it is difficult to make meaningful comparisons. The following invention overcomes these limitations.

It is well known in the art that it is possible to simultaneously co-extract both DNA and RNA, which together are referred to as "total nucleic acid" (TNA). However, one aspect of an RT-PCR, which is not generally discussed in the literature, is that protocols which amplify a specific RNA transcript (RNA-X) in a TNA sample will also co-amplify the DNA (DNA-X) of the gene from which the specific target RNA-X was transcribed. The converse is also true in that, in a reverse transcriptase reaction, it is not possible to only amplify a specific DNA sequence (DNA-X), if that DNA is a gene or sequence which is actively transcribed, because the transcribed RNA (RNA-X) will also co-amplify. In other words, the amplification products of an RT-PCR from a TNA sample are always the sum of the amplicons derived from both RNA-X and DNA-X (RNA-X plus DNA-X), if DNA-X is transcribed to generate RNA-X. As such, it is not possible to

normalize a specific unrelated RNA-Y with a genomic DNA-X sequence if that sequence is transcribed.

The present invention seeks to overcome one or more of the difficulties existing in the prior art by preparing nucleic acid samples comprising both DNA and RNA (e.g. TNA), and co-amplifying (i) one gene (DNA-X) and its associated RNA transcription products (RNA-X), along with an unrelated region of DNA (DNA-N) which is not transcribed. The DNA-N can then be used to normalize levels of the DNA-X plus RNA-X. Further, it is possible to use multiple primer sets targeting multiple transcribed genes or regions and their associated transcripts, for example DNA-X plus RNA-X and DNA-Y plus RNA-Y can be normalized to a non-transcribed DNA-N. Optionally, for convenience, the ratio obtained by dividing the data from analysis of multiple transcribed DNA/RNA targets by that from a single non-transcribed DNA-N can be again be divided by the number of primer sets targeting the sets of transcribed DNA/RNA species. The invention will be further clarified by way of the following examples.

Summary

The present disclosure may involve co-amplification of three nucleic acid species (e.g. simultaneously) in a sample comprising both DNA and RNA (e.g. of a sample of total nucleic acid (TNA)). These species are (i) gene(s), (ii) transcripts expressed from those gene(s), and (iii) non-expressed (i.e. non-transcribed) DNA sequences. Together the combined measurement of a gene and its corresponding transcripts is often referred to herein as GAT (Gene And Transcript) and the measurement of non-transcribed DNA is often referred to herein as NED (Non-Expressed DNA). The methods of the present disclosure involve co-amplifying these species together or separately, and using the ratio of the estimates of GAT and the NED as an indicator of transcriptional capacity, which can in turn be used to assess characteristics such as cell viability, cell death, functional perturbation of cells resulting from an external stimulus or a disease state, and the like. In one aspect, the present disclosure refers to a method for normalising quantitative data obtained by amplification of nucleic acids from a cell, organism, or virus, the method comprising:

- (i) obtaining quantitative data
 - from amplification of genomic DNA from a first gene and RNA transcribed from the first gene, and
 - from amplification of a sequence of non-transcribed DNA in the cell, organism, or virus; and

(ii) using the quantitative data to derive a normalised value (nV) representative of the relative amounts of:

- said genomic DNA and RNA transcripts of the first gene, to
- said genomic DNA that is not transcribed,

5 present within the nucleic acid sample prior to said amplification;

wherein said genomic DNA from the first gene and RNA transcribed from the first gene, and said sequence of non-transcribed DNA, are co-amplified in the same reaction.

The present disclosure relates, at least in part, to examples 1-48 listed below:

Example 1. A method for normalising quantitative data obtained by amplification of
10 nucleic acids from a cell, organism, or virus, the method comprising:

(i) obtaining quantitative data

- from amplification of genomic DNA from a first gene and RNA transcribed from the first gene, and

- from amplification of a sequence of non-transcribed DNA in the cell,
15 organism, or virus; and

(ii) using the quantitative data to derive a normalised value (nV) representative of the relative amounts of:

- said genomic DNA and RNA transcripts of the first gene, to
 - said genomic DNA that is not transcribed,
- present within the nucleic acid sample prior said amplification.

Example 2. The method of example 1, wherein the quantitative data is amplicon copy number, and the method comprises:

- obtaining a value A (vA) representing total amplicon number generated from the amplification of said genomic DNA and RNA transcripts of the first gene, and a value B (vB) representing total amplicon number generated from the sequence of non-transcribed DNA;

- calculating a normalised value (nV) using the equation:

$$vA/vB = nV$$

or an equivalent form thereof.

Example 3. The method of example 1, wherein the quantitative data is amplicon copy number, and the method comprises:

- obtaining a value X (vX) representing total amplicon number generated from: the amplification of genomic DNA and RNA transcripts from the first gene, and amplification of genomic DNA and RNA transcripts from at least one additional gene;

- obtaining a value B (vB) representing total amplicon number generated from the sequence of non-transcribed DNA,

- calculating a normalised value (nV) using the equation:

$$vX / (vB \times (X+1)) = nV$$

or an equivalent form thereof,

wherein X is the number of said additional gene(s).

Example 4. The method of example 2 or example 3, wherein the amplification is digital polymerase chain reaction (dPCR).

Example 5. The method of example 1, wherein the quantitative data is threshold value (Ct), and the method comprises:

- obtaining a cycle threshold value CtA from the amplification of said genomic DNA and RNA transcripts of the first gene,

- obtaining a cycle threshold value CtB from the amplification of the sequence of non-transcribed DNA; and

- calculating a normalised value (nV) using the equation:

$$2^{CtB - CtA} = nV$$

or an equivalent form thereof.

Example 6. The method of example 1, wherein the quantitative data is threshold value (Ct), and the method comprises:

- obtaining a cycle threshold value CtX from: the amplification of said genomic DNA and RNA transcripts of the first gene, and from amplification of genomic DNA and RNA transcripts from at least one additional gene;

- obtaining a cycle threshold value CtB from the amplification of the sequence of non-transcribed DNA; and

- calculating a normalised value (nV) using the equation:

$$2^{CtB - CtX} / (X + 1) = nV$$

or an equivalent form thereof,

wherein X is the number of said additional gene(s).

Example 7. The method of example 5 or example 6, wherein the amplification is quantitative polymerase chain reaction (qPCR).

Example 8. The method of any one of examples 1 to 7, wherein the sequence of non-transcribed DNA is genomic DNA.

Example 9. The method of any one of examples 1 to 8, further comprising conducting said amplification of the nucleic acids from the cell, organism, or virus.

Example 10. The method of any one of examples 1 to 9, wherein the nucleic acids from the cell, organism, or virus are an extract of total nucleic acids.

Example 11. The method of any one of examples 1 to 10, wherein any said amplification is conducted using: polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), strand displacement amplification (SDA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), recombinase polymerase amplification (RPA), helicase dependant amplification (HDA), strand invasion based amplification (SIBA), transcript-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), or any combination thereof.

Example 12. The method of any one of examples 1 to 11, further comprising using the normalised value (nV) to assess the level of transcriptional activity in the cell, organism, or virus.

Example 13. The method of any one of examples 1 to 12, further comprising:

- obtaining a transcription-negative normalised value (nV-) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the transcription-negative normalised value (nV-), to thereby assess the level of transcriptional activity in the cell, organism, or virus.

5 Example 14. The method of example 13, wherein the transcription-negative normalised value (nV-) is a mean value generated from said series of said normalised values (nV).

Example 15. The method of example 13 or example 14, wherein:

 - the transcription-negative normalised value (nV-) is used as a base value for
10 assessing a presence or an absence of transcriptional activity in the cell, organism or virus; and

 - an absence of transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or below the transcription-negative normalised value (nV-); or

15 - transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is above the transcription-negative normalised value (nV-).

Example 16. The method of any one of examples 13 to 15, wherein said transcription-negative normalised value (nV-):

20 - incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known not to have transcriptional activity; and/or

 - is provided with a confidence interval that said transcription-negative normalised value (nV-) is predictive of a presence or an absence of transcriptional activity
25 in the cell, organism or virus.

Example 17. The method of example 16, wherein the confidence interval is more than 90%, or more than 95%.

Example 18. The method of any one of examples 13 to 17, further comprising:

 - obtaining a transcription-positive normalised value (nV+) generated using a
30 series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity; and

 - comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the transcription-positive normalised value (nV+), to thereby assess the level of transcriptional activity in the cell, organism, or
35 virus.

Example 19. The method of example 18, wherein the transcription-positive normalised value (nV+) is a mean value generated from said series of said normalised values (nV).

Example 20. The method of example 18 or example 19, wherein:

- 5 - the transcription-positive normalised value (nV+) is used as a base value for transcriptional activity in the cell, organism or virus; and
- a lack or absence of transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is below the transcription-positive normalised value (nV+); or
- 10 - transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or above the transcription-positive normalised value (nV+).

Example 21. The method of any one of examples 18 to 20, wherein said transcription-positive normalised value (nV+):

- 15 - incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to have transcriptional activity; and/or
- is provided with a confidence interval that said transcription-positive normalised value (nV+) is predictive of a presence or an absence of transcriptional
- 20 activity in the cell, organism or virus.

Example 22. The method of example 21, wherein the confidence interval is more than 90%, or more than 95%.

Example 23. The method of example 13, further comprising:

- 25 - obtaining a transcription-negative normalised value (nV-) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity;
- obtaining a transcription-positive normalised value (nV+) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity; and
- 30 - comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to:
 - (i) the transcription-negative normalised value (nV-) and to the transcription-positive normalised value (nV+), or
 - (ii) to a combined transcription normalised value (nV[±]) intermediate
 - 35 to the transcription-negative normalised value (nV-) and the transcription-positive normalised value (nV+),

to thereby assess the level of transcriptional activity in the cell, organism, or virus.

Example 24. The method of example 23, wherein the combined transcription normalised value ($nV^{\pm}$) is calculated using the equation:

$$(nV+) + (nV-) / 2 = (nV^{\pm})$$

5 or an equivalent form thereof.

Example 25. The method of example 24, wherein said combined transcription normalised value ($nV^{\pm}$):

- incorporates statistical variation in said series of transcription-negative normalised value ($nV-$) and/or said transcription-positive normalised value ($nV+$); and/or
- 10 - is provided with a confidence interval that said combined transcription normalised value ($nV^{\pm}$) is predictive of a presence or an absence of transcriptional activity in the cell, organism or virus.

Example 26. The method of example 25, wherein the confidence interval is more than 90%, or more than 95%.

15 Example 27. The method of any one of examples 12 to 26, wherein the level of transcriptional activity in the cell, organism, or virus is assessed for the purpose of determining any one or more of:

- viability of the test cell or the test organism;
- whether the test cell, organism or virus is alive or dead;
- 20 - transcriptional perturbation within the test cell, organism, or virus.

Example 28. The method of any one of examples 1 to 11, further comprising using the normalised value (nV) to assess the level of drug resistance or drug sensitivity in the cell, organism, or virus, wherein:

- said cell, organism, or virus has been treated with a drug prior to said
- 25 amplification of nucleic acids, and
- said normalised value (nV) is compared to a control normalised value (cnV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to be:

- (i) resistant to the drug; or
- 30 (ii) sensitive to the drug,

to thereby assess the level of drug resistance or drug sensitivity in the cell, organism, or virus.

Example 29. The method of any one of examples 1 to 11 or 28, further comprising:

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- obtaining a drug-sensitive normalised value (dsV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to be sensitive to the drug; and

5 - comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the drug-sensitive normalised value (dsV), to thereby assess the level of drug resistance or drug sensitivity or in the cell, organism, or virus, wherein the cell, organism, or virus has been treated with a drug prior to said amplification of nucleic acids.

Example 30. The method of example 29, wherein the drug-sensitive normalised value (dsV) is a mean value generated from said series of said normalised values (nV).
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Example 31. The method of example 29 or example 30, wherein:

- the drug-sensitive normalised value (dsV) is used as a base value for assessing a presence or an absence of resistance or sensitivity to the drug in the cell, organism or virus; and

15 - resistance to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is above the drug-sensitive normalised value (dsV); or

20 - sensitivity to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or below the drug-sensitive normalised value (dsV).

Example 32. The method of any one of examples 29 to 31, wherein said drug-sensitive normalised value (dsV):

25 - incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to be sensitive to the drug; and/or

- is provided with a confidence interval that said drug-sensitive normalised value (dsV) is predictive of a presence or an absence of:

(i) resistance to the drug in the cell, organism or virus; or

(ii) sensitivity to the drug in the cell, organism or virus.

30 Example 33. The method of example 32, wherein the confidence interval is more than 90%, or more than 95%.

Example 34. The method of any one of examples 1 to 11 or 28, further comprising:

- obtaining a drug-resistant normalised value (drV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to resistant to the drug; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the drug-resistant normalised value (drV), to thereby assess the level of drug resistance or drug sensitivity or in the cell, organism, or virus, wherein the cell, organism, or virus has been treated with a drug prior to said amplification of nucleic acids.

Example 35. The method of example 34, wherein the drug-resistant normalised value (drV) is a mean value generated from said series of said normalised values (nV).

Example 36. The method of example 34 or example 35, wherein:

- the drug-resistant normalised value (drV) is used as a base value for assessing a presence or an absence of resistance or sensitivity to the drug in the cell, organism or virus; and

- resistance to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or above the drug-resistant normalised value (drV); or

- sensitivity to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is below the drug-resistant normalised value (drV).

Example 37. The method of any one of examples 34 to 36, wherein said drug-resistant normalised value (drV):

- incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to be resistant to the drug; and/or

- is provided with a confidence interval that said drug-resistant normalised value (drV) is predictive of a presence or an absence of:

(i) resistance to the drug in the cell, organism or virus; or

(ii) sensitivity to the drug in the cell, organism or virus.

Example 38. The method of example 37, wherein the confidence interval is more than 90%, or more than 95%.

Example 39. The method of one of examples 1 to 11, further comprising using the normalised value (nV) to assess the level of drug resistance or drug sensitivity in the cell, organism, or virus, wherein:

- a first population of said cell, organism, or virus which has been treated with a drug prior to said amplification of nucleic acids, is used to generate a first said normalized value (nV),
- a second population of said cell, organism, or virus which has not been treated
5 with a drug prior to said amplification of nucleic acids, is used to generate a second said normalized value (nV),
- said first normalized value (nV) and said second normalized value (nV) are compared to assess the level of transcriptional activity in the cell, organism, or virus with or without drug treatment, and thereby assess the level of drug resistance or drug
10 sensitivity in the cell, organism, or virus.

Example 40. The method of example 39, wherein said drug sensitivity is indicated when said first normalized value (nV) is lower than said second normalized value (nV).

Example 41. The method of any one of examples 27 to 40, wherein the drug is
15 an antimicrobial.

Example 42. The method of any one of examples 27 to 41, wherein the drug is an antimicrobial of a class selected from: Aminoglycosides, ansamycins, carbacephem, carbapenems, cephalosporins, glycopeptides, macrolidespenicillins, monobactams, polypeptides, quinolones, sulphonamides, tetracyclines.

Example 43. The method of any one of examples 27 to 42, wherein the drug is
20 Ciprofloxacin, Azithromycin, Rifampicin, or Doxycycline.

Example 44. The method of any one of examples 27 to 43, wherein the first gene is a gene from a Chlamydia species (e.g. Chlamydia trachomatis), a Gonorrhea species, or a mycoplasma species (e.g. Mycoplasma genitalium).

Example 45. The method of any one of examples 1 to 44, wherein said genomic
25 DNA from the first gene and RNA transcribed from the first gene, and said sequence of non-transcribed DNA are co-amplified in the same reaction.

Example 46. The method of example 45, wherein said reaction comprises using reverse transcriptase.

Example 47. The method of any one of examples 1 to 46, wherein the cell is a
30 mammalian cell, a human cell, an animal cell, a plant cell, a bacterial cell, a host cell infected by viruses, or a host cell of infected by bacteria.

Example 48. The method of any one of examples 1 to 47, wherein the organism
35 is a mammal, a human, a plant, a bacterium, a virus, a fungus, an alga, an archaeon or a protozoan.

The present disclosure also relates, at least in part, to examples 1-23 listed below:

Example 1. A method for assessing the transcriptional activity of a cell or an organism, the method comprising:

- performing a nucleic acid amplification reaction on total nucleic acid from the cell or organism, wherein the nucleic acid amplification comprises:

- contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a first gene and RNA transcribed from the first gene,

- contacting the total nucleic acid sample with one or multiple primers capable of amplifying a region of non-coding genomic DNA that is not transcribed in the cell or organism;

- analysing kinetics of the nucleic acid amplification reaction to derive a ratio of:

- (i) said genomic DNA and RNA transcripts of the first gene, to
 - (ii) said region of non-coding DNA,

wherein the ratio is representative of the relative amount of (i) and (ii) present within the total nucleic acid sample prior to performing the nucleic acid amplification reaction; and

- analysing the ratio to assess the transcriptional activity of the cell or organism, wherein:

- a ratio of 1 indicates an absence of transcriptional activity in the cell or organism, and

- a ratio of more than 1 indicates that transcriptional activity exists or may exist in the cell or organism.

Example 2. The method of example 1, wherein a ratio of more than: 1.5, 1.7, 1.9, 2, 2.2, 2.4, 2.5, 2.7, 2.9 or 3, indicates transcriptional activity in the cell or organism.

Example 3. The method of example 1, wherein a ratio of less than: 1.5, 1.4, 1.3, 1.2 or 1.1 indicates an absence of transcriptional activity in the cell or organism.

Example 4. A method for assessing the viability of a cell or an organism, the method comprising:

- performing a nucleic acid amplification reaction on total nucleic acid the cell or organism, wherein the nucleic acid amplification comprises:

- contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a first gene and RNA transcribed from the first gene,

- contacting the total nucleic acid sample with one or multiple primers capable of amplifying a region of non-coding genomic DNA that is not transcribed in the cell or organism;

- analysing kinetics of the nucleic acid amplification reaction to derive a ratio of:
 - (i) said genomic DNA and RNA transcripts of the first gene, to
 - (ii) said region of non-coding DNA,
 wherein the ratio is representative of the relative amount of (i) and (ii) present within the

5 total nucleic acid sample prior to performing the nucleic acid amplification reaction; and
 - analysing the ratio to assess the transcriptional activity of the cell or organism,
 wherein:
 - a ratio of 1 indicates the cell or organism is not viable, and
 - a ratio of more than 1 indicates that the cell or organism is or may be viable.
- 10 Example 5. The method of example 4, wherein a ratio of more than: 1.5, 1.7, 1.9, 2, 2.2, 2.4, 2.5, 2.7, 2.9 or 3, indicates that the cell or organism is viable.
- Example 6. The method of example 4, wherein a ratio of less than: 1.5, 1.4, 1.3, 1.2 or 1.1 indicates that the cell or organism is not viable.
- Example 7. A method for determining whether a cell or an organism is dead, the

15 method comprising:

 - performing a nucleic acid amplification reaction on total nucleic acid from the cell or organism, wherein the nucleic acid amplification comprises:
 - contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a first gene and RNA transcribed from the first gene,
 - 20 contacting the total nucleic acid sample with one or multiple primers capable of amplifying a region of non-coding genomic DNA that is not transcribed in the cell or organism;
 - analysing kinetics of the nucleic acid amplification reaction to derive a ratio of:
 - (i) said genomic DNA and RNA transcripts of the first gene, to
 - 25 (ii) said region of non-coding DNA,
 wherein the ratio is representative of the relative amount of (i) and (ii) present within the total nucleic acid sample prior to performing the nucleic acid amplification reaction; and
 - analysing the ratio to assess the transcriptional activity of the cell or organism,
 wherein:
 - 30 a ratio of 1 indicates that the cell or organism is dead, and
 - a ratio of more than 1 indicates that the cell or organism is alive or may be alive.

Example 8. The method of example 7, wherein a ratio of more than: 1.5, 1.7, 1.9, 2, 2.2, 2.4, 2.5, 2.7, 2.9 or 3, indicates that the cell or organism is alive.

Example 9. The method of example 7, wherein a ratio of less than: 1.5, 1.4, 1.3, 1.2

35 or 1.1 indicates that the cell or organism is not alive.

Example 10. A method for detecting transcriptional perturbation within a cell, the method comprising:

- performing a nucleic acid amplification reaction on total nucleic acid from the cell or organism, wherein the nucleic acid amplification comprises:

5 contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a first gene and RNA transcribed from the first gene,

 contacting the total nucleic acid sample with one or multiple primers capable of amplifying a region of non-coding genomic DNA that is not transcribed in the cell or organism;

10 - analysing kinetics of the nucleic acid amplification reaction to derive a ratio of:

 (i) said genomic DNA and RNA transcripts of the first gene, to

 (ii) said region of non-coding DNA,

 wherein the ratio is representative of the relative amount of (i) and (ii) present within the total nucleic acid sample prior to performing the nucleic acid amplification reaction; and

15 - analysing the ratio to assess the transcriptional activity of the cell or organism, wherein:

 a ratio of 1 indicates complete transcriptional perturbation in the cell or organism, and

20 a ratio of more than 1 indicates a lack of transcriptional perturbation in the cell or organism.

Example 11. The method of example 10, wherein a ratio of more than: 1.5, 1.7, 1.9, 2, 2.2, 2.4, 2.5, 2.7, 2.9 or 3, indicates a lack of transcriptional perturbation in the cell or organism.

Example 12. The method of example 10, wherein a ratio of less than: 1.5, 1.4, 25 1.3, 1.2 or 1.1 indicates partial or complete transcriptional perturbation in the cell or organism.

Example 13. The method of any one of examples 1 to 12, comprising generating and a cycle threshold (Ct) value for:

 (i) said region of non-coding DNA, and

30 (ii) said genomic DNA and RNA transcripts of the first gene;

 during said nucleic acid amplification reaction and deriving the ratio by comparing said values.

Example 14. The method of any one of examples 1 to 13, wherein the method comprises:

35

- generating a cycle threshold value ctA for said genomic DNA and RNA transcripts of the first gene, and, generating a cycle threshold value CtB for said region of non-coding DNA, following commencement of the nucleic acid amplification reaction;

- calculating a fold change between the CtB and ctA values using the equation:

5
$$2^{CtB - CtA} = 2^{\Delta Ct}; \text{ and}$$

- generating the ratio using the equation:

$$2^{\Delta Ct}/TR$$

wherein TR is a ratio of copies of the genomic DNA of the first gene to copies of the region of non-coding genomic DNA in the total nucleic acid sample of the cell.

10 Example 15. The method of any one of examples 1 to 14, wherein:

- performing the nucleic acid amplification reaction further comprises contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a second gene and RNA transcribed from the second gene, and

15 - the kinetics of the nucleic acid amplification reaction are analysed to derive a ratio representative of the relative amount of:

(i) said region of non-coding DNA, to

(ii) said genomic DNA and RNA transcripts of the first and second genes present within the total nucleic acid sample prior to performing the nucleic acid amplification reaction.

20 Example 16. The method of example 15, wherein the method comprises:

- generating a cycle threshold value ctA for said genomic DNA and RNA transcripts of the first and second genes, and, generating a cycle threshold value CtB for said region of non-coding DNA, following commencement of the nucleic acid amplification reaction;

25 - calculating a fold change between the CtB and ctA values using the equation:

$$2^{CtB - CtA} = 2^{\Delta Ct}$$

- generating the ratio using the equation

$$2^{\Delta Ct}/TR$$

wherein TR is a ratio of copies of the genomic DNA of the first and second genes to copies of the region of non-coding genomic DNA in the total nucleic acid sample of the cell.

30 Example 17. The method of any one of examples 1 to 16, wherein said analysing the ratio comprises comparing the ratio to a threshold ratio derived from performing the method on a series of negative or positive control cells or organisms and deriving a mean threshold ratio value indicative of a phenotype.

Example 18. A method for detecting drug resistance or drug sensitivity in a cell or organism, the method comprising:

- performing a first nucleic acid amplification reaction on total nucleic acids obtained from a first sample of the cell or organism that has not been treated with the drug; and
- 5 - performing a second nucleic acid amplification reaction on total nucleic acids obtained from a second sample of the cell or organism that has been treated with the drug; wherein each said nucleic acid amplification reaction is performed separately and comprises:

contacting the total nucleic acid sample with one or multiple primers capable of amplifying genomic DNA from a first gene and RNA transcribed from the first gene,

contacting the total nucleic acid sample with one or multiple primers capable of amplifying a region of non-coding genomic DNA that is not transcribed in the cell or organism;

- analysing kinetics of each said nucleic acid amplification reaction to derive first and second ratios of:

- (i) said genomic DNA and RNA transcripts of the first gene, to
- (ii) said region of non-coding DNA,

wherein the ratio is representative of the relative amount of (i) and (ii) present in the total nucleic acid sample prior to performing the nucleic acid amplification reaction; and

- 20 - comparing the ratios to assess whether the cell or organism has resistance to the drug, wherein:

complete drug resistance in the cell or organism is indicated when the first and second ratios are equal, and

sensitivity of the cell or organism to the drug is indicated when the second ratio is lower than the first ratio.

Example 19. The method of example 18, wherein the cell or organism is deemed to have resistance to the drug when the value of second ratio is no more than: 1%, 2%, 5%, 7.5%, 10%, 12%, 15% or 20%; lower than the value of first ratio.

Example 20. The method of example 18, wherein the cell or organism is deemed to be sensitive to the drug when the value of second ratio is at least: 10%, 20%, 30%, 40% or 50%; than the first ratio.

Example 21. The method of any one of examples 1 to 20, wherein the amplification method is selected from the group consisting of: polymerase chain reaction (PCR), strand displacement amplification (SDA), helicase dependent amplification (HDA), Recombinase Polymerase Amplification (RPA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated

amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), reverse transcription polymerase chain reaction (RT-PCR), and any combination thereof.

Example 22. The method of any one of examples 1 to 21, wherein the cell is a mammalian cell, a human cell, a plant cell, a bacterial cell, a host cell infected by viruses, or a host cell of infected by bacteria.

Example 23. The method of any one of examples 1 to 21, wherein the organism is a bacterium, a virus, a fungi, an algae, an archaeon or a protozoan.

The present disclosure is generally compatible with current procedures used in research or diagnostic laboratories and can use the same sample types, extraction methods and amplification methods. The nucleic acids (e.g. TNA) to be analysed may be a derived from any suitable source such as, for example, prokaryotic or eukaryotic cells, or from a virus. The present disclosure can determine the presence or absence of active transcription, an increase or decrease in RNA expression levels or unchanged RNA expression levels.

Brief Description of the Drawings

Embodiments of the present invention will now be described, by way of non-limiting example only, with reference to the accompanying Figures 1-12 as set out below.

Figure 1: Schematic showing steps in VITA PCR. A Reverse Transcriptase PCR (RT-PCR) is performed using total nucleic acid as template. This VITA PCR assay has at least one set of primers which is capable of co-amplifying the DNA of a specific gene (DNA-X) together with the RNA transcribed from this gene (RNA-X). It also contains a set of primers targeting a region of DNA which is not transcribed into RNA (DNA-N). During the reverse transcriptase step the RNA-X is copied into cDNA-X and then during PCR thermocycling DNA-X, cDNA-X and DNA-N are all amplified. The signal from the GAT (Gene And Transcript), which measures the sum of amplicons originating from DNA-X plus RNA-X can be read through a single Fluorophore Channel A, whilst the signal from the NED (Non-Expressed DNA), which is a measure of amplicons from DNA-N, can be read through a second Fluorophore Channel B. The difference in Cycle threshold (Ct) values between GAT and NED in a specimen allows an estimate of the fold change (FC) in a specimen observed for these targets, wherein $FC = 2^{Ct_{NED} - Ct_{GAT}} = 2^{\Delta Ct}$. The VITA Index can be calculated by dividing the fold change observed in the sample by the theoretical ratio (TR) anticipated in the absence of active transcription, assuming the gene and NED locus are present in equal copy numbers. If one transcript & gene are used to measure the GAT and one DNA sequence is used to measure NED, then the TR = (1 x

DNA-X) divided by $(1 \times \text{DNA-Y}) = 1$. If two transcripts & genes (X and Z) are used to measure the GAT and one DNA sequence (X) is used to measure NED, then the TR = $(1 \times \text{DNA-X} + 1 \times \text{DNA-Z})$ divided by $(1 \times \text{DNA-Y}) = 2$. The ability to measure GAT using more than one gene(s) and its transcripts allows tests to be built which capture a range of transcripts which may be expressed at various times within the cell cycle. The VITA Index provides a normalized measure of transcriptional activity which can be compared between samples regardless of the amount of sample analysed. Cells which are dead and have no residual RNA detected would be anticipated to have a VITA Index close to 1; and as the level of active transcription increases, the VITA Index will increase correspondingly.

Figure 2: Schematics of assays according to embodiments of the present invention.

Figure 2A: The methods described herein can be used to determine if cells or pathogens are dead or alive. Evidence of the presence of dead or alive pathogens could in turn provide a method for Test of Cure (TOC). The protocol involves performing VITA PCR amplifying GAT and NED from TNA and then using the resultant Ct values to calculate the VITA Index of the sample. Hypothetical amplification plots are depicted. A sample with no active transcription (dead cells) would be anticipated to have a VITA Index at or near 1. A threshold value can be set using empirical data for specific VITA PCR assays, amplifying specific GAT(s) and NED combinations, present within specific cell types and/or specific pathogens. Cells which are alive and are undergoing active transcription will have a VITA Index above the threshold. **Figure 2B:** The methods described herein can be used to determine drug sensitivity or drug resistance. A sample can be split and incubated in the presence or absence of one or more drugs. TNA extracted after incubation can be analysed by VITA PCR to obtain VITA Indices for the treated and untreated sample and the ratio between the VITA Indices gives an indication of drug sensitivity or resistance. Hypothetical amplification plots are depicted. If the sample were sensitive to the drug, the VITA Indices of the sample in the presence of drug would be expected to be lower than in the absence of drug. In contrast, if the sample were resistant to the drug, the VITA Index of the sample in the presence of drug would not be expected to be lower than in the absence of drug and may be similar.

Figure 3: Immunofluorescent staining of cells and analysis by PCR. *Chlamydia trachomatis* (serovar D) samples, grown in HEp-2 cells were treated with different concentrations of Azithromycin as described in Example 1, Treatment Protocol A (1.2.1). Specifically, cells were treated with i) No antibiotic, or ii) below the MIC ($< \text{MIC}$, 0.008 $\mu\text{g/mL}$), iii) at the MIC (0.064 $\mu\text{g/mL}$) or iv) above the MIC ($> \text{MIC}$ 0.512 $\mu\text{g/mL}$). **Panel i** shows representative images for the determination of viability of untreated cells

and cells treated at each antibiotic dose. These images were obtained through immunofluorescence staining of infected HEp-2 cells and analysed at 100X magnification with a fluorescent microscope IN Cell Analyser 2200 (GE Healthcare Life Sciences).

Panel ii shows the quantified viability post-infection (PI) measured as the Inclusion Forming Units per mL (IFU/mL) for each antibiotic dose treatment, at concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC), and for untreated cells (No Antibiotic), calculated from the images obtained in panel i. Results were normalised against the value obtained for the sample treated at an antibiotic concentration above the MIC. **Panel iii** shows analysis of TNA from these cells, which were infected with chlamydia, and amplified by one set of primer capable of amplifying both Major outer membrane porin (omp1) DNA and omp1 RNA. The TNA was amplified by RT-PCR (to amplify omp1 DNA and RNA) and by PCR (to only amplify omp1 DNA). **Panel iii** depicts the fold change, being the difference (ΔC_t) between the C_t of omp1 DNA in PCR and the C_t of omp1 RNA plus omp1 DNA in the RT-PCR, calculated as $2^{\Delta C_t}$, for each antibiotic treatment dose, at concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC), and untreated cells (No Antibiotic).

Figure 4: Analysis of assays according to embodiments of the present invention. Analysis of candidate GAT and NED targets by amplification of RNA or TNA samples, and comparison between results for PCR (to amplify DNA only) and RT-PCR (to amplify DNA and RNA). **Panels i and ii** show amplification plots generated using potential GAT primers (omp1), where the template was RNA only (**panel i**) or TNA (**panel ii**). The difference (ΔC_t) between C_t of omp1 DNA detection only by PCR (dotted lines), and omp1 DNA plus omp1 RNA detection by RT-PCR, (solid lines) is indicated. **Panels iii and iv** shows amplification plots using potential NED primers (InfAIGR), where the template was RNA only (**panel iii**) or TNA (**panel iv**). The differences (ΔC_t) between C_t of InfAIGR DNA detection only by PCR (dotted lines), and InfAIGR DNA plus InfAIGR 1 RNA (if present) detection by RT-PCR, (solid lines) is indicated.

Figure 5: Analysis of assays according to embodiments of the present invention. Analysis of chlamydia by VITA PCR. **Panel i** shows the VITA indices for untreated cells (No Antibiotic) and for each antibiotic treatment dose as described in Example 1 and depicted in Figure 3 panels i and ii. This VITA PCR amplified from TNA and used one gene and its transcripts to measure GAT and one non-transcribed DNA region to measure NED in the single RT-PCR reaction. **Panel i** shows the RT-PCR data from the samples imaged, quantified in and depicted in Figure 3 panels i and ii respectively. **Panel ii** shows analysis of chlamydia by VITA PCR. The VITA indices for untreated cells (No Antibiotic) and for each antibiotic treatment dose. This VITA PCR

amplified two amplicons of a gene and its transcripts (2 GAT) and one non-transcribed NED in the same RT-PCR and hence has a TR is 2 (2 GAT divided by 1 NED).

Figure 6: Assay and analysis according to an embodiment of the present invention. Analysis of chlamydia VITA PCR from a patient urine sample. **Panel i** schematically depicts the process of sample preparation. **Panel ii** shows analysis of chlamydia expression from patient urine sample in comparison to positive (viable) and negative (non-viable) chlamydia reference samples obtained through culture methods.

Figure 7: Assays and analysis according to embodiments of the present invention. Analysis of chlamydia expression by VITA PCR in response to short incubations with antibiotics. **Panel i** schematically depicts the process of sample preparation, wherein a test sample is either untreated (No drug) or treated with various antibiotics (Plus drug) and then incubated for various time intervals at either room temperature, or at 37°C with 5% CO₂. TNA is then extracted from all samples and time points and amplified by VITA PCR. **Panel ii** shows the VITA Indices obtained by analysis of TNA for each treatment group either with (dark grey) and without (light grey) azithromycin. The ratios of the VITA Indices (Δ VITA) plus and minus azithromycin are indicated above the bars. The VITA Indices were significantly lower following incubation with the drug at 37°C for either 1 hour or 6 hours indicating the samples were sensitive to azithromycin and this resulted in decreased transcription levels. The magnitude of the Δ VITA Ratio may reflect the extent of killing following incubation for specific times and under specific conditions. **Panel iii** shows the VITA Indices obtained by analysis of TNA for each treatment group with the ratio of the VITA Indices (Δ VITA) indicated above the bars. The decrease in the VITA Index following treatment with 0.128 μ g/mL of azithromycin at 37°C for 30 minutes and 1 hour indicated the samples were sensitive to this antibiotic and this was reflected as decreased transcription levels. **Panel iv** shows the VITA Indices obtained by analysis of TNA for each treatment group of susceptible and resistant strain, when treated with 0.256 μ g/mL of rifampicin. The decrease in the VITA Index following antibiotic treatment for the susceptible strain after 5 minutes of incubation at 37°C supply indicated the samples were sensitive to the antibiotic. Alongside this, the VITA Index for the resistant strain under the same conditions did not change significantly in the presence rifampicin at either time point indicated the samples were indeed resistant to the antibiotic **Panel v** shows the VITA Indices obtained by analysis of TNA for each treatment group for strain known to be susceptible and resistant, when treated with 0.256 μ g/mL of rifampicin for 15 minutes at room temperature. The VITA Indices of the susceptible strain showed a significant decrease in VITA Index in the presence of drug, consistent with sensitivity to Rifampicin; whilst the VITA Index for the

resistant strain, under the same conditions, displayed a significant increase in VITA Index, reflecting resistance to rifampicin.

Figure 8: Assays and analysis according to embodiments of the present invention. Analysis of chlamydia by VITA PCR in response to increasing doses of antibiotic. **Panel i** schematically depicts the process of sample preparation, treatment without and with various concentrations of the same antibiotic (azithromycin), incubation for 1 hour at 37°C with 5% CO₂ supply, extraction of TNA from untreated samples and samples treated with the various antibiotic concentrations. **Panel ii** displays the VITA Indices obtained by analysis of TNA for each dose of antibiotic and extracted using phenol:chloroform:isoamyl. Statistical differences between treated and untreated samples are represented above the compared to groups. The decrease in the VITA Index following antibiotic treatment indicated samples were sensitive to the antibiotic used. The VITA Indices displayed a decrease with increasing concentration of azithromycin (0.128 µg/mL, 0.192 µg/mL and 0.256 µg/mL respectively), with this correlation producing an $R^2 = 0.98$. **Panel iii** exhibits the VITA Indices obtained by analysis of TNA for each dose of antibiotic and extracted using a column-based extraction kit. Statistical differences between treated and untreated samples are indicated above the treatment groups. The decrease in the VITA Index following antibiotic treatment demonstrated samples were sensitive to azithromycin and VITA Indices correlated to the doses of antibiotic used 0.128 µg/mL, 0.192 µg/mL, 0.256 µg/mL and 0.512 µg/mL respectively, producing an $R^2 = 0.83$.

Figure 9: Analysis of assays according to embodiments of the present invention. Analysis of chlamydia by VITA PCR in response to a short incubation with various antibiotics, using TNA extracted from a series of strains previously characterized as either susceptible and resistant to specific antibiotics. **Panel i** depicts the VITA Indices obtained for each strain tested (strains 1-3 and 5) following analysis of TNA by VITA PCR for each treatment group. The decrease in VITA Index following treatment with azithromycin (0.256 µg/mL) indicated all strains were susceptible to the antibiotic with disruption caused to transcription. Statistical differences between treated and untreated samples are displayed above the compared samples. **Panel ii** illustrates the VITA Indices obtained for each strain tested (strains 1-3 and 5) following analysis of TNA for each treatment group. The decrease in VITA Index following treatment with doxycycline (0.256 µg/mL) indicated all strains were susceptible to the antibiotic with transcription activity disrupted. Statistical differences between treated and untreated samples are displayed above the compared samples. **Panel iii** shows the VITA Indices obtained for each strain tested (strain 1- 5) following analysis of TNA for each treatment group, using

the antibiotic rifampicin (0.256 µg/mL). The decrease in VITA Index following treatment indicated strains 1-4 are susceptible to the antibiotic with transcription activity disrupted. Statistical differences between the treated and untreated samples is displayed above the compared groups. The VITA Indices obtained with strain 5, in both untreated and treated sample, were not significantly different and reflected the resistance of this particular strain to Rifampicin.. **Panel iv** demonstrates the Δ VITA ratio calculated from each replicate tested for each strain which was treated with Rifampicin depicted in Panel iii. Cells were grouped according to their susceptibility profile, with susceptible cells generating a greater Δ VITA ratio compared to resistant cells.

Figure 10: Schematic of assays according to embodiments of the present invention. Hypothetical example demonstrating the process of Antibiotic Susceptibility Testing directly from a clinical specimen, with incubation with either no drug, or in the presence of azithromycin, ceftriaxone and doxycycline and further testing for *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (GC) and *Mycoplasma genitalium* (MG)GC-dual relates to the dual antibiotic therapy.

Figure 11: Analysis of assays according to embodiments of the present invention. VITA PCR Analysis of chlamydia TNA samples containing different viable loads of the organism. **Panel i** illustrates the VITA Index obtained from each sample containing a determined percentage of viable chlamydia in the background of non-viable chlamydia. Displaying statistical differences between non-viable sample and viable samples. **Panel ii** depicts the average Ct value for GAT1/2 and NED in each of the samples tested.

Figure 12: Analysis of assays according to embodiments of the present invention. Analysis of chlamydia in TNA samples by an alternative VITA PCR system which targets longer regions for GAT1 and GAT 2. It displays the VITA Indices for untreated cells (No Treatment) and for each antibiotic treatment dose as per Example 1 and Figure 3 panel i and ii. This VITA PCR amplified two long amplicons of a gene and its transcripts (2 GAT) and one non-transcribed NED in the same reaction and hence has a TR of 2.

Definitions

As used in this application, the singular form “a”, “an” and “the” include plural references unless the context clearly dictates otherwise. For example, the phrase “polynucleotide” also includes a plurality of polynucleotides.

As used herein, the term “comprising” means “including”. Variations of the word “comprising”, such as “comprise” and “comprises,” have correspondingly varied meanings. Thus, for example, a polynucleotide “comprising” a sequence of nucleotides may consist exclusively of that sequence of nucleotides or may include one or more additional nucleotides.

As used herein, the terms “cycle threshold”, “cycle threshold value”, “threshold cycle”, “threshold cycle value”, “Ct” and “Ct value” are used interchangeably and have the same meaning, being the number of amplification cycles required to generate a detectable amount of amplicon during a nucleic acid amplification reaction.

As used herein, the term “amplification” when used in the context of nucleic acids will be understood to encompass any reaction capable of generating copies of one more more nucleic acid template sequence(s), unless clearly indicated otherwise. Non-limiting examples of suitable reactions include polymerase chain reaction (PCR), strand displacement amplification (SDA), helicase-dependent amplification (HDA), Recombinase Polymerase Amplification (RPA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), and nucleic acid sequence based amplification (NASBA).

As used herein, the term “quantitative value” is intended to encompass any measurement of a given factor by quantity including, for example, quantitative measurements of amplification reaction products (e.g. by Ct value, by amplicon copy number, and the like).

As used herein the term “plurality” means more than one. In certain specific aspects or embodiments, a plurality may mean 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, or more, and any integer derivable therein, and any range derivable therein.

As used herein, the term “subject” includes any animal of economic, social or research importance including bovine, equine, ovine, primate, avian and rodent species. Hence, a “subject” may be a mammal such as, for example, a human or a non-human mammal. Also encompassed are microorganism subjects including, but not limited to, bacteria, viruses, fungi/yeasts, protists and nematodes. A “subject” in accordance with the present invention also includes infectious agents such as prions.

As used herein, the terms “polynucleotide” and “nucleic acid” may be used interchangeably and refer to a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases, or analogues, derivatives, variants, fragments or combinations

thereof, including but not limited to DNA, methylated DNA, alkylated DNA, RNA, methylated RNA, microRNA, siRNA, shRNA, mRNA, tRNA, snoRNA, stRNA, smRNA, pre- and pri-microRNA, other non-coding RNAs, ribosomal RNA, derivatives thereof, amplicons thereof or any combination thereof. By way of non-limiting example, the source of a nucleic acid may be selected from the group comprising synthetic, mammalian, human, animal, plant, fungal, bacterial, viral, archael or any combination thereof. The terms “polynucleotide” and “nucleic acid” “oligonucleotide” include reference to any specified sequence as well as to the sequence complementary thereto, unless otherwise indicated.

As used herein, the term “total nucleic acid” refers to samples containing both RNA and DNA.

As used herein, the term “GAT” is an acronym for “Gene And Transcript” and refers to the combined measurement of DNA from one gene and RNA transcribed from that gene, or from a group of genes and the RNAs transcribed from those genes. As used herein, the term “NED” is an acronym for “Non-expressed DNA” and refers to the measurement of DNA originating from a region which is not transcribed to RNA.

As used herein, the term “oligonucleotide” refers to a segment of DNA or a DNA-containing nucleic acid molecule, or RNA or RNA-containing molecule, or a combination thereof. Examples of oligonucleotides include nucleic acid targets; substrates, for example, those which can be modified by an MNase; primers such as those used for *in vitro* target amplification by methods such as PCR; and components of MNases. The term “oligonucleotide” includes reference to any specified sequence as well as to the sequence complementary thereto, unless otherwise indicated. Oligonucleotides may comprise at least one addition or substitution, including but not limited to the group comprising 4-acetylcytidine, 5-(carboxyhydroxymethyl)uridine, 2'-O-methylcytidine, 5-carboxymethylaminomethyl thiouridine, dihydrouridine, 2'-O-methylpseudouridine, beta D-galactosylqueosine, 2'-O-methylguanosine, inosine, N6-isopentenyladenosine, 1-methyladenosine, 1-methylpseudouridine, 1-methylguanosine, 1-methylinosine, 2,2-dimethylguanosine, 2-methyladenosine, 2-methylguanosine, 3-methylcytidine, 5-methylcytidine, N6-methyladenosine, 7-methylguanosine, 5-methylaminomethyluridine, 5-methoxyaminomethyl-2-thiouridine, beta D-mannosylmethyluridine, 5-methoxycarbonylmethyluridine, 5-methoxyuridine, 2-methylthio-N6-isopentenyladenosine, N-((9-beta-ribofuranosyl-2-methylthiopurine-6-yl)carbamoyl)threonine, N-((9-beta-ribofuranosylpurine-6-yl)N-methylcarbamoyl)threonine, uridine-5-oxyacetic acid methylester, uridine-5-oxyacetic acid (v), wybutoxosine, pseudouridine, queosine, 2-thiocytidine, 5-methyl-2-thiouridine, 2-

thiouridine, 4-thiouridine, 5-methyluridine, N-((9-beta-D-ribofuranosylpurine-6-yl)carbamoyl)threonine, 2'-O-methyl-5-methyluridine, 2'-O-methyluridine, wybutosine, 3-(3-amino-3-carboxypropyl)uridine, beta D-arabinosyl uridine, beta D-arabinosyl thymidine.

5 As used herein, the terms “complementary”, and “complementarity” refer to the capacity of nucleotides (e.g. deoxyribonucleotides, ribonucleotides or combinations thereof) to hybridise to each other via either Watson-Crick base-pairing or wobble base pairing. Bonds can be formed via Watson-Crick base-pairing between adenine (A) bases and uracil (U) bases, between adenine (A) bases and thymine (T) bases, between cytosine
10 (C) bases and guanine (G) bases. A wobble base pair is a non-Watson-Crick base pairing between two nucleotides in a polynucleotide duplex (e.g. guanine-uracil, inosine-uracil, inosine-adenine, and inosine-cytosine). Nucleotides referred to as “complementary” or that are the “complement” of each other are nucleotides which have the capacity to hybridise together by either Watson-Crick base pairing or by wobble base pairing
15 between their respective bases.

As used herein, an “enzyme” refers to any molecule which can catalyze a chemical reaction (e.g. amplification of a polynucleotide, cleavage of a polynucleotide etc.)

As used herein, “target amplification” refers to any method that amplified a target nucleic acid including but not limited to the polymerase chain reaction (PCR), strand
20 displacement amplification (SDA), helicase dependent amplification (HDA), Recombinase Polymerase Amplification (RPA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), or reverse transcription polymerase chain reaction (RT-PCR).

25 As used herein, an “amplicon” refers to nucleic acid (e.g. DNA or RNA, or a combination thereof) that is a product of natural or artificial nucleic acid amplification or replication events including, but not limited to, PCR, RT-PCR, SDA, HDA, RPA, LAMP, RCA, TMA, 3SR or NASBA.

As used herein, the terms “nucleic acid enzyme”, “catalytic nucleic acid”, “nucleic
30 acid with catalytic activity”, and “catalytic nucleic acid enzyme” are used herein interchangeably and shall mean a DNA or DNA-containing molecule or complex, or an RNA or RNA-containing molecule or complex, or a combination thereof (i.e. DNA-RNA hybrid molecule or complex), which may recognize at least one substrate and catalyse a modification (such as ligation or cleavage) of the at least one substrate. The nucleotide
35 residues in the catalytic nucleic acids may include the bases A, C, G, T, and U, as well as derivatives and analogues thereof. The terms above include uni-molecular nucleic acid

enzymes which may comprise a single DNA or DNA-containing molecule (also known in the art as a “DNA enzyme”, “deoxyribozyme” or “DNAzyme”) or an RNA or RNA-containing molecule (also known in the art as a “ribozyme”) or a combination thereof, being a DNA-RNA hybrid molecule which may recognize at least one substrate and catalyse a modification (such as ligation or cleavage) of the at least one substrate. The terms above include nucleic acid enzymes which comprise a DNA or DNA-containing complex or an RNA or RNA-containing complex or a combination thereof, being a DNA-RNA hybrid complex which may recognize at least one substrate and catalyse a modification (such as ligation or cleavage) of the at least one substrate. The terms “nucleic acid enzyme”, “catalytic nucleic acid”, “nucleic acid with catalytic activity”, and “catalytic nucleic acid enzyme” include within their meaning MNAzymes.

As used herein, the terms “MNzyme” and “multi-component nucleic acid enzyme” as used herein have the same meaning and refer to two or more oligonucleotide sequences (e.g. partzymes) which, only in the presence of an MNzyme assembly facilitator (for example, a target), form an active nucleic acid enzyme that is capable of catalytically modifying a substrate. MNAzymes can catalyse a range of reactions including cleavage of a substrate, ligation of substrates and other enzymatic modifications of a substrate or substrates. MNAzymes are also known in the art as “PlexZymes”. The MNzyme only forms when the sensor arms of partzymes A and B hybridize adjacent to each other on the assembly facilitator. The substrate arms of the MNzyme engage the substrate, the modification (e.g. cleavage) of which is catalyzed by the catalytic core of the MNzyme, formed by the interaction of the catalytic domains of partzymes A and B. Cleavage of a DNA/RNA chimeric reporter substrate. The MNzyme may cleave the substrate between a fluorophore and a quencher dye pair, thus generating signal. The terms “multi-component nucleic acid enzyme” and “MNzyme” comprise bipartite structures, composed of two molecules, or tripartite structures, composed of three nucleic acid molecules, or other multipartite structures, for example those formed by four or more nucleic acid molecules.

It will be understood that the terms “MNzyme” and “multi-component nucleic acid enzyme” as used herein encompass all known MNAzymes and modified MNAzymes including those disclosed in any one or more of PCT patent publication numbers WO/2007/041774, WO/2008/040095, WO2008/122084, and related US patent publication numbers 2007-0231810, 2010-0136536, and 2011-0143338 (the contents of each of these documents are incorporated herein by reference in their entirety). Non-limiting examples of MNAzymes and modified MNAzymes encompassed by the terms “MNzyme” and “multi-component nucleic acid enzyme” include MNAzymes with

cleavage catalytic activity (as exemplified herein), disassembled or partially assembled MNAzymes comprising one or more assembly inhibitors, MNAzymes comprising one or more aptamers (“apta-MNAzymes”), MNAzymes comprising one or more truncated sensor arms and optionally one or more stabilizing oligonucleotides, MNAzymes
5 comprising one or more activity inhibitors, multi-component nucleic acid inactive proenzymes (MNAi), and MNAzymes with ligase catalytic activity (“MNAzyme ligases”), each of which is described in detail in one or more of WO/2007/041774, WO/2008/040095, WO2008/122084, US 2007-0231810, US 2010-0136536, and/or US 2011-0143338.

10 As used herein, the terms “partzyme”, “component partzyme” and “partzyme component” refer to a DNA-containing or RNA-containing or DNA-RNA-containing oligonucleotide, two or more of which, only in the presence of an MNAzyme assembly facilitator as herein defined, can together form an “MNAzyme.” In certain preferred embodiments, one or more component partzymes, and preferably at least two, may
15 comprise three regions or domains: a “catalytic” domain, which forms part of the catalytic core that catalyzes a modification; a “sensor arm” domain, which may associate with and/or bind to an assembly facilitator; and a “substrate arm” domain, which may associate with and/or bind to a substrate. Partzymes may comprise at least one additional component including but not limited to an aptamer, referred to herein as an “apta-
20 partzyme.” A partzyme may comprise multiple components, including but not limited to, a partzyme component with a truncated sensor arm and a stabilizing arm component which stabilises the MNAzyme structure by interacting with either an assembly facilitator or a substrate.

The terms “assembly facilitator” and “MNAzyme assembly facilitator” as used
25 herein refer to entities that can facilitate the self-assembly of component partzymes to form a catalytically active MNAzyme by interaction with the sensor arms of the MNAzyme. As used herein, assembly facilitators may facilitate the assembly of MNAzymes which have cleavage, ligase or other enzymatic activities. In preferred embodiments an assembly facilitator is required for the self-assembly of an MNAzyme.
30 An assembly facilitator may be comprised of one molecule, or may be comprised of two or more “assembly facilitator components” that may pair with, or bind to, the sensor arms of one or more oligonucleotide “partzymes”. The assembly facilitator may comprise one or more nucleotide component/s which do not share sequence complementarity with sensor arm/s of the MNAzyme. The assembly facilitator may be a target. The target may
35 be a nucleic acid selected from the group consisting of DNA, methylated DNA, alkylated DNA, RNA, methylated RNA, microRNA, siRNA, shRNA, tRNA, mRNA, snoRNA,

stRNA, smRNA, pre- and pri-microRNA, other non-coding RNAs, ribosomal RNA, derivatives thereof, amplicons, or any combination thereof. The nucleic acid may be an “amplicon” and the amplification may comprise one or more of: PCR, RT-PCR, SDA, HDA, RPA, LAMP, RCA, TMA, 3SR, NASBA or the ligase chain reaction.

5 The term “detectable effect” as used herein is an effect that can be detected or quantified as an indication that modification of substrate/s has occurred. The magnitude of the effect may be indicative of the quantity of an input such as an assembly facilitator (e.g. a target). The detectable effect may be detected by a variety of methods, including fluorescence spectroscopy, surface plasmon resonance, mass spectroscopy, NMR,
10 electron spin resonance, polarization fluorescence spectroscopy, circular dichroism, immunoassay, chromatography, radiometry, photometry, scintigraphy, electronic methods, electrochemical methods, UV, visible light or infra-red spectroscopy, enzymatic methods or any combination thereof.

 The term “substrate” as used herein include any single- or double-stranded polymer
15 of deoxyribonucleotide or ribonucleotide bases, or analogues, derivatives, variants, fragments or combinations thereof, including but not limited to DNA, methylated DNA, alkylated DNA, RNA, methylated RNA, microRNA, siRNA, shRNA, mRNA, tRNA, snoRNA, stRNA, smRNA, pre- and pri-microRNA, other non-coding RNAs, ribosomal RNA, derivatives thereof, amplicons thereof or any combination thereof (including mixed
20 polymers of deoxyribonucleotide and ribonucleotide bases), which is capable of being recognized, acted upon or modified by an enzyme including a catalytic nucleic acid enzyme. A “substrate” may be modified by various enzymatic activities including but not limited to cleavage or ligation. Modification of a “polynucleotide substrate” or “substrate” may provide a “detectable effect” for monitoring the catalytic activity of an
25 enzyme.

 A “reporter substrate” as used herein is a substrate that is particularly adapted to facilitate measurement of either the disappearance of a substrate or the appearance of a product in connection with a catalyzed reaction. Reporter substrates can be free in solution or bound (or “tethered”), for example, to a surface, or to another molecule. A
30 reporter substrate can be labelled by any of a large variety of means including, for example, fluorophores (with or without one or more additional components, such as quenchers), radioactive labels, biotin (e.g. biotinylation) or chemiluminescent labels.

 The terms “probe” as used herein refers to an oligonucleotide that is used for detection of a target nucleic acid. Non-limiting examples of probes include TaqMan
35 probes; Molecular Beacon probes; and nucleic acid enzyme substrates capable of catalytic modification by a nucleic acid enzyme.

As used herein, the term “base” will be understood to have the same meaning as the term “nucleotide”.

Any description of prior art documents herein, or statements herein derived from or based on those documents, is not an admission that the documents or derived statements
5 are part of the common general knowledge of the relevant art.

For the purposes of description all documents referred to herein are hereby incorporated by reference in their entirety unless otherwise stated.

Abbreviations

The following abbreviations are used herein and throughout the specification:

10

GAT: Gene And Transcript

NED: Non-Expressed DNA

FC: Fold Change

TR: Theoretical ratio

15

Ct: Threshold Cycle/Cycle threshold

DMEM: Dulbecco's Modified Eagle medium

LLE: Liquid-Liquid extraction

MOI: Multiplicity of Infection

PI: Post-infection

20

PT: Post-treatment

TNA: Total Nucleic Acid

IF: immunofluorescence

IFU: Inclusion Forming Units

MIC: Minimum Inhibitory Concentration

25

TOC: Test of Cure

NAAT: Nucleic Acid Amplification Technology

STI: Sexually Transmitted Infection

AMR: antimicrobial resistance

EMA: ethidium monoazide

30

PMA: propidium monoazide

MNAzyme: multi-component nucleic acid enzyme, or multipartite nucleic acid enzyme;

Partzyme: Partial enzyme containing oligonucleotide;

ave; average

PCR: polymerase chain reaction;

35

gDNA: genomic DNA

- dsDNA*: double stranded DNA
- rc*: reverse complement
- NTC*: No template control
- qPCR*: Real-time quantitative PCR
- 5 R^2 ; Correlation coefficient
- nM*; Nanomolar
- mM*; Millimolar
- μL ; Microlitre
- dNTP*; Deoxyribonucleotide triphosphate
- 10 *NF-H₂O*: nuclease-free water;
- F*: fluorophore;
- Q*: quencher;
- N* = A, C, T, G, or any analogue thereof;
- N'* = any nucleotide complementary to *N*, or able to base pair with *N*;
- 15 *W*: A or T;
- R*: A, G, or AA;
- rN*: any ribonucleotide base;
- rR*: A or G;
- rY*: C or U;
- 20 *M*: A or C;
- H*: A, C, or T;
- D*: G, A, or T;
- JOE* or *6-JOE*: 6-carboxy-4',5'-dichloro-2',7'-dimethoxyfluorescein;
- FAM* or *6-FAM*: 6-Carboxyfluorescein.
- 25 *BHQ1*: Black Hole Quencher 1
- BHQ2*: Black Hole Quencher 2
- RT-PCR*: reverse transcription polymerase chain reaction
- SDA*: strand displacement amplification
- HDA*: helicase dependent amplification
- 30 *RPA*: Recombinase Polymerase Amplification
- LAMP*: loop-mediated isothermal amplification
- RCA*: rolling circle amplification
- TMA*: transcription-mediated amplification
- 3SR*: self-sustained sequence replication
- 35 *NASBA*: nucleic acid sequence based amplification
- IB*: Iowa Black® FQ

IBR: Iowa Black® RQ

mRNA: messenger RNA

tRNA: transfer RNA

rRNA: ribosomal RNA

5 *Detailed Description*

The following detailed description conveys exemplary embodiments of the present invention in sufficient detail to enable those of ordinary skill in the art to practice the present invention. Features or limitations of the various embodiments described do not necessarily limit other embodiments of the present invention or the present invention as a whole. Hence, the following detailed description does not limit the scope of the present invention, which is defined only by the claims.

The present invention provides methods capable of detecting the presence, absence and/or perturbation of transcription in cells, organisms, viruses and the like. The methods may be used, for example, to detect the presence or absence of active transcription; to detect perturbation or alteration of transcription levels in response to agents or in disease states; to detect the absence of active transcription in samples containing dead cells and associated cell debris; and/or to differentiate between live and dead cells. By way of non-limiting example, when a subject is infected with bacteria, antibiotics can be administered with the aim of clearing the infection. For such infections a test of cure (TOC) is desirable to confirm successful clearance of bacteria. Previously reported methods for measuring viability of bacteria include protocols for measuring bacterial RNA or bacterial DNA. The problem with these approaches is that residual RNA and or DNA associated with dead cells or cell debris may persist for considerable time following cell death and cure. Further, methods that attempt to normalise levels of RNA using DNA, for example AST, require accurate quantification of extracted nucleic acids.

The present invention provides, among other things, improved methods for differentiating between specimens containing viable cells or pathogens undergoing active transcription and those containing dead cells or nucleic acid debris. Further, the invention provides improved methods for normalising of data relating to measurements of expressed RNA and which allow inter-sample comparison without the need to quantify the concentration of total TNA present in each of the sample. Since the method allows inter-sample comparison and elucidation of upregulation or downregulation the data generated using this invention can be represented in the format of heat maps.

Vita Index

The strategy involves amplification of specific genes and their RNA transcripts which are then normalised to a specific DNA sequence which is known to not be transcribed. During RT-PCR, primers which target a specific transcript will also amplify
 5 the gene from which it was transcribed. A measure of a gene and its associated transcripts is termed herein as GAT (Gene And Transcript). Further, during RT-PCR, if primers are present for a region of DNA which is not transcribed into RNA then this DNA only can also be amplified. This is referred to as NED (Non-Expressed DNA). Target amplification protocols for the simultaneous estimation of GAT and NED are termed
 10 VITA (Viable Transcript Analysⁱs) tests, and hence when amplification is by PCR the method is termed VITA PCR.

Analysis of VITA PCR allows measurement of the levels of active transcription which can be calculated in various manners. By way of example, the data can be used to obtain a VITA Index which equals the Fold Change (FC) for the Specimen calculated as
 15 $2^{\Delta Ct}$ divided by Theoretical Ratio (TR) anticipated in the absence of active transcription (residual DNA only). For, example the difference in Ct values between GAT and NED in a specimen allows an estimate of the FC observed for GAT (DNA plus RNA) versus DNA only (NED), wherein the $FC = 2^{\Delta Ct} = 2^{(Ct_{NED} - Ct_{GAT})}$. The TR anticipated in the absence of active transcription from GAT equals the number of genes amplified when
 20 calculating the GAT divided by the number of sequences amplified to calculate the NED. Assuming the NED is measured for a single DNA sequence, then if GAT measures amplification a single gene, the $TR = \text{number of primer sets for GAT} / \text{number of primer sets for NED} = 1/1 = 1$; if GAT measures amplification of two genes (or regions) the $TR = 2/1 = 2$, and if GAT measures amplification of three genes the TR
 25 would be $3/1 = 3$ and so on. For example, the VITA Index for a specimen with a Ct (GAT) of 10 and a Ct (NED) of 13 would have a FC value $= 2^{\Delta Ct} = 2^3 = 8$ which would result in a VITA Index of 8 (if $TR = 1$) or a VITA Index of 4 (if $TR = 2$).

The VITA Index provides a measure of transcriptional activity with the cell population which is valid regardless of whether the cells are (i) viable, (ii) dead (with or
 30 without total clearance of residual, but detected, low levels of nucleic acids) or (iii) under some level of metabolic stress due to the presence of an external stimuli, for example the presence of a compound or drug.

The approach overcomes the problems encountered by previous investigators who have tried to use either RNA or DNA as a marker of the presence of live cells. These
 35 studies have shown that in some cases RNA and/or DNA can persist for weeks following cell death. The VITA Index provides a measure of levels of active transcription per gene

copy as a method to establish the presence of live organisms. By way of example, this protocol could be used for assessing test of cure (TOC) in patients who have been given antibiotics to treat a bacterial infection.

Further, the method can measure more subtle perturbations of transcriptional activity. For example if cells are incubated in the presence of a compound which has deleterious effects on cell viability and/or vitality, the impact of this compound can be quantified using the VITA Index. An example of an application whereby this measure would be useful would be when specimens containing infectious bacteria are incubated in the presence of antibiotics and analysed using VITA PCR. If the bacteria are sensitive to the antibiotic then the VITA Index will decrease. Conversely if bacteria are resistant to the antibiotic then the Index would not change significantly.

Amplification Reactions

The methods of the present invention can be applied to quantitative measurements of products arising from nucleic acid amplification reactions. Any nucleic acid amplification reaction capable of generating amplicons from target DNA and/or target RNA (e.g. mRNA) sequences can be used. For example, polymerase chain reaction (PCR) amplifications such as reverse-transcriptase PCR (RT-PCR), quantitative PCR (qPCR), and/or digital PCR (dPCR) may be used. Other non-limiting examples of suitable amplification reactions include strand displacement amplification (SDA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), recombinase polymerase amplification (RPA), helicase dependant amplification (HDA), strand invasion based amplification (SIBA), transcript-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), and combinations thereof.

Quantitative measurements of products arising from the amplification reactions can be made using any suitable methods known in the art. The methods may be based, for example, on amplicon copy number, cycle threshold (Ct) and the like, and involve, for example, measuring fluorescence.

30

Test Subjects

The methods of the present invention can be applied to any suitable subject in which the degree of transcription is of interest (for example, as a measure of any one or more of transcription level, perturbation of transcription, viability, death, response to agents such as drugs and other compounds, and so on).

35

In some embodiments, the subject is a cell, or a population of cells. The cells may be unicellular organisms (e.g. bacteria, archae, protozoa, unicellular algae, unicellular fungi, unicellular amoeba). In other embodiments, the subject is a virus.

Cells and viruses analysed in accordance with the methods of the present invention may be components of a biological sample. Non-limiting examples of biological samples include whole blood or a component thereof (e.g. blood cells, plasma, serum), urine, saliva, lymph, bile fluid, sputum, tears, cerebrospinal fluid, bronchioalveolar lavage fluid, synovial fluid, semen, ascitic tumour fluid, breast milk and pus.

10 ***Exemplary Embodiments***

In some embodiments the present invention provides methods for determining a combined transcription normalised value ($nV_{\pm}$), which is predictive of a presence or an absence of transcriptional activity in a cell, organism or virus (and the like). Similar methods can be applied for determining the differences in transcriptional activity between two populations of samples, such as population of the cells, organisms, or viruses known to be (i) resistant to the drug and (ii) sensitive to the drug.

By way of non-limiting example only:

$nV_{\pm}$ may be calculated as a midpoint between the critical point in the lower-tailed test of nV_{+} and the critical point in the upper-tailed test nV_{-} , both with 95% confidence level.

$$nV_{\pm} = ((nV_{+} - 1.645 * \delta_{+}) + (nV_{-} + 1.645 * \delta_{-})) / 2$$

25 where:

nV_{+} is the mean of nV values obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity.

nV_{-} is the mean of nV values obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity.

30 δ_{+} is the standard deviation of nV values obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity and the critical point.

δ_{-} is the standard deviation nV values obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity.

35

Examples

The present invention will now be described with reference to the following specific examples, which should not be construed as in any way limiting.

Example 1: *In vitro* generation of chlamydia samples in presence or absence of antibiotics, analysis of viability using immunofluorescence and methods for extraction of TNA from samples.

5

1.1 Culture

Chlamydia trachomatis (serovar D, lab strain UW-3/Cx) samples were grown in HEp-2 cells and either not treated (not incubated with the antibiotic Azithromycin) to reproduce a Positive Control for “Alive bacteria”, or incubated with different
10 concentrations of Azithromycin, to create samples which simulate dead bacteria. (Azithromycin is the first line treatment of chlamydial genital infections). The conditions were as follows.

The human epithelial cell line (HEp-2) (ATCC® CCL-23™) were grown in Dulbecco’s Modified Eagle medium (DMEM) (Sigma-Aldrich) supplemented with 10%
15 heat-inactivated Fetal Bovine Serum (FBS) (Sigma-Aldrich), 100 mg/mL Streptomycin (Invitrogen Corporation), 50 mg/mL Gentamicin (Life Technologies) and 20 mM Glutamine (Sigma Aldrich), incubated at 37°C with 5% CO₂. *Chlamydia trachomatis* (serovar D) was inoculated on a HEp-2 monolayer, present on a flat bottomed 6-well plate (Thermo Fisher) at a Multiplicity of Infection (MOI) of 1. The infection was completed
20 by centrifugation-assisted inoculation at 500 g for 30 minutes at a temperature of 28°C and subsequently incubated, under conditions specified above.

1.1.1 Treatment Protocol A

At 4 hours post-infection (PI), DMEM was replaced with addition of variable doses
25 of the antibiotic Azithromycin (Sigma Aldrich) and again incubated at 37°C with 5% CO₂ until harvested. The different antibiotic concentrations used were i) No antibiotic (0 µg/mL), ii) < MIC (0.008 µg/mL), iii) MIC (0.064 µg/mL) and iv) > MIC (0.512 µg/mL). The “MIC dose” chosen for these experiments is slightly higher than that observed in the laboratory using this current strain; however, it was specifically chosen to ensure
30 reproducible killing of the bacteria. The dose used is also consistent with documented MIC analysis in the literature. At 44 hours PI, cells were harvested using sucrose-phosphate-glutamate (SPG) buffer (250 mM sucrose, 10 mM sodium phosphate and 5 mM L-glutamate). Half the volume was stored for viability counts through immunofluorescent

staining (See 1.2 Viability/Immunofluorescence staining); the other half was kept for extraction of TNA and/or RNA. Samples were stored at -80°C until further processing. Each condition was cultured in triplicate.

5 1.1.2 ***Treatment Protocol B***

At 4 hours PI, DMEM was replaced, with addition of cycloheximide and incubation was continued. Once in an exponential growth phase, 24 hours PI, treatment was applied. This was achieved by replacing the DMEM for each infection, with addition of either i) no antibiotic, or ii) antibiotic at a level higher than the MIC for azithromycin
10 (0.128 µg/mL). Samples were then harvested for either 30 minutes, 1 hour or 6 hours Post Treatment (PT) using SPG buffer and stored at -80°C until further processing.

1.1.3 ***Treatment Protocol C***

After infection, there was no change of media at the 4 hour time point, essentially
15 creating an unsynchronised population, which would be more similar to *in vivo* conditions. Once at an exponential growth phase, 20 hours PI, treatment was applied. This was achieved by replacing the DMEM for each well, with addition of either i) no antibiotic, or ii) antibiotic (0.256 µg/mL of Rifampicin). Samples were then either incubated at 37°C with 5% CO₂ and harvested after 5 minutes PT; or incubated at room
20 temperature and harvested after 15 minutes PT. SPG buffer was used for harvest and TNA was extracted immediately after. Strains used for this treatment protocol were Strain 1) serovar D lab strain (UW-3/Cx), susceptible to rifampicin, and Strain 5) serovar L2 lab created mutant strain, resistant to Rifampicin.

25 1.1.4 ***Treatment Protocol D***

After infection, there was no change of media at the 4h time point. Once in an exponential growth phase, either 20 or 24 hours PI, cells were treated with varying doses of azithromycin achieved by replacing the DMEM in each well with addition of desired amount of antibiotic. Doses of antibiotic treatment added to the infection were i) no
30 antibiotic, ii) 0.128 µg/mL, iii) 0.192 µg/mL, iv) 0.256 µg/mL and v) 0.512 µg/mL. Samples were then incubated at 37°C with 5% CO₂ and harvested at 1 hour PT, using SPG buffer and stored at -80°C until further processing or extracted immediately after harvest.

1.1.5 *Treatment Protocol E*

After infection, there was no change of media at the 4h time point. Once in an exponential growth phase, 20 hours PI, cells were treated with a single dose of different antibiotics. Antibiotics used were i) Azithromycin, ii) Doxycycline and iii) Rifampicin, each at a dose of 0.256 $\mu\text{g/mL}$. Strains used for this treatment protocol were Strain 1) serovar D lab strain (UW-3/Cx), Strain 2) serovar L2 wild type lab strain (434/Bu), Strain 3) serovar L2 lab created mutant strain, resistant to trimethoprim, Strain 4) serovar L2 lab created mutant strain, resistant to Spectinomycin and Strain 5) serovar L2 lab created mutant strain, resistant to Rifampicin. MIC for all serovars and each antibiotic was predetermined, using standard procedures documented in literature, and listed in the table below. According to the MIC analysis (Table 1), all strains used were susceptible to Azithromycin and Doxycycline antibiotics. Strains 1, 2, 3 and 4 are also susceptible to rifampicin, whilst strain 5 is resistant to that same antibiotic. Samples were then incubated at 37°C with 5% CO₂ and harvested at 1 hour PT, using SPG buffer and extracted immediately. Two biological replicates were obtained for each condition.

Table 1: Minimum inhibitory concentration (MIC) of antibiotics used for antibiotic susceptibility testing

	Antibiotic dose ($\mu\text{g/mL}$)				
	Strain 1	Strain 2	Strain 3	Strain 4	Strain 5
Azithromycin	0.032	0.032	0.016	0.016	0.032
Doxycycline	0.128	0.064	0.032	0.064	0.064
Rifampicin	0.008	0.004	0.004	0.004	8.192

1.1.6 *Treatment Protocol F*

At 4 hours PI, DMEM was replaced with addition of cycloheximide (1 $\mu\text{g/mL}$) to synchronise the infection and halt the production of proteins by the host-cell. At this time point, addition of antibiotic was also carried out, with half the number of wells left untreated and the other half treated with a high dose of the antibiotic Azithromycin. Cells were again incubated at 37°C with 5% CO₂ until harvested. The different conditions used were i) No antibiotic representing “Alive CT” or ii) Plus antibiotic (0.512 $\mu\text{g/mL}$) – representing “Dead CT”. At 44 hours PI the cells were harvested using SPG buffer and mixed at different ratios to create samples with varying percentages of viable and non-viable cells, as per the table below. Half the volume was stored for viability counts through immunofluorescent staining (See 1.2 Viability/Immunofluorescence staining;

data not included); the other half was kept for extraction of TNA. These were then stored at -80°C until further processing.

Viable load	“Alive” sample volume (uL)	“Dead” sample volume (uL)	Total volume (uL)	Total volume used in extraction (uL)
0%	0	500	500	300
0.1%	0.5	499.5	500	300
0.2%	1	499	500	300
0.5%	2.5	497.5	500	300
1%	5	495	500	300
10%	50	450	500	300
20%	100	400	500	300
50%	250	250	500	300
100%	500	0	500	300

5 1.2 Viability/Immunofluorescence staining

Samples harvested for viability count were serially diluted and cultured on a fresh HEp-2 monolayer, present on a flat bottomed 96 well plate (Nunc™, Thermo Fisher). The infection was completed by centrifugation-assisted inoculation at 500 g for 30 minutes at a temperature of 28°C and subsequently incubated at 37°C with 5% CO₂. Each sample was cultured in triplicates. At 38 hours PI the cultures were fixed with methanol and stained for microscopy.

Direct immunofluorescence (IF) staining was performed using antibodies against CtHtrA, MOMP (Biodesign), and secondary antibodies conjugated to Alexa fluor dyes (Invitrogen). DAPI (4', 6-Diamidino-2-Phenylindole, Dilactate) (Invitrogen) was also added for host cell staining. The specimens were examined at a 100x magnification with the fluorescent microscope IN Cell Analyser 2200 (GE Healthcare Life Sciences). HEp-2 cells displayed a blue colour, whilst chlamydia inclusions were presented in green. Inclusion forming units (IFU mL⁻¹) was determined by counting inclusions from 10 representative fields of view, for each well and each serial dilution. Extrapolation of the field of view size to the size of wells was done to calculate the total number of inclusion in a given well. Dilutions and volumes added were also accounted for.

Immunofluorescent imaging of cells treated as described in Treatment Protocol A (1.1.1) are shown in Figure 3 panel i and the results obtained by counting IFU/ml from these images are shown in Figure 3 panel ii; with results normalised to the value obtained for cells treated above the MIC (>MIC). Cells which were untreated, and treated with various doses of antibiotic, each had different numbers of infective units of chlamydia.

1.3 Total Nucleic Acid (TNA) extraction

1.3.1 Extraction Protocol A

Samples harvested for TNA extraction were thawed on ice and cell debris was pelleted at 800 g for 10 minutes at 4°C, followed by centrifugation of the supernatant at 14000 rpm for 20 minutes at 4°C. The pellet was re-suspended in a proteinase K digestion mix (10mg/mL Proteinase K (Ambion), 1mM Tris pH7.5, 0.5M EDTA, 5M NaCl, 10% SDS and nuclease free water (Ambion) and incubated at 56°C for 60 minutes. Following digestion, Phenol:Chloroform:Isoamyl (25:24:1, pH 6.5-6.9, Sigma Aldrich) was added to the mix, vortexed vigorously and centrifuged for 5 minutes at maximum speed. The upper phase was kept with addition of sodium acetate (3M, pH5.2, Sigma Aldrich) and 100% ethanol (Sigma Aldrich). This was again vortexed and incubated for 20 minutes (10 minutes at room temperature and 10 minutes at -20°C). TNA was then pelleted at high speed (14000 rpm) for 10 minutes, following two washing steps using 70% ethanol. The pellet was then air dried for 15 minutes before elution in 50 µL of water. The eluate was quantified and stored at -80°C.

1.3.2 Extraction Protocol B

Samples harvested were thawed on ice, followed by pelleting of cells at 14000rpm for 20min at 4°C. Following this step, the manufacturer's instructions for simultaneous extraction of DNA and RNA were followed, using the PuriSpin FireMonkey extraction kit (RevoluGen).

1.3.3 Extraction Protocol C

Samples harvested were thawed on ice, followed by pelleting of cells at 14000rpm for 20min at 4°C. Following this step, the manufacturer's instructions for Purification of Total RNA from Animal Cells, with additional on-column DNase digestion were followed. The extraction was done using the RNeasy Mini Kit (Qiagen).

Example 2: Analysis of a gene and its transcripts in untreated and treated cells in a two well assay

The following example estimates levels of DNA and GAT in TNA samples extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells which were not incubated with antibiotic (untreated, viable cells), and from cells incubated with antibiotic at a concentration eight times below the MIC (<MIC), at the MIC (MIC) or at 8 times greater than the MIC (> MIC), as described in example 1 (1.1.1 Treatment Protocol A). Chlamydia DNA and RNA was amplified using primers

targeting the omp1 gene and its transcripts. The levels of GAT were estimated by RT-PCR wherein both the omp1 gene and its transcripts (DNA plus RNA) were amplified. The levels of the omp1 gene only (DNA only) were measured in a separate PCR which lacked reverse transcriptase.

5

2.1 Partzyme Oligonucleotides

Partzymes were designed to assemble into active MNazymes when they bound to amplicons generated by amplification of both the omp1 gene or omp1 transcripts. Once assembled, the MNzyme could cleave the reporter substrate Sub2-FB. The sequences of Partzyme A and Partzyme B are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNzyme and bases in italic refer to sequence which hybridizes to the substrate.

10

SEQ ID NO: 1 Partzyme A omp1_A4/2-P

TGGTCTCGAGCATTGAACGAACAACGAGAGGAAACCTT/3Phos/

15

SEQ ID NO: 2 Partzyme B omp1_B5/2-P

TGCCCAGGGAGGCTAGCT**CATGTTCTCGATTAAGGCTG**/3Phos/

2.2 Reporter Substrate

In the current example, the substrate was end-labelled with a 6-FAM moiety at the 5' end (indicated by a "F" in the name of the substrate below) and an IABkFQ quencher moiety at the 3' end (indicated by an "IB" in the name of the substrate below). Cleavage of the substrate was monitored at 516 nm (FAM emission wavelength) with excitation at 492 nm (FAM excitation wavelength). The reporter substrate for this example is shown below with the sequence, 5' to 3'. The lower case bases represent RNA and the upper case bases represent DNA.

25

SEQ ID NO: 3 Sub2-FB

AAGGTTTCCTCguCCCTGGGCA

2.3 PCR primers for amplification of the omp1 gene and transcripts

In vitro amplification of TNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse primers were used to amplified DNA within the omp1 gene by PCR, and both DNA and RNA within the omp1 gene and transcripts by RT-PCR. All sequences are written 5' to 3'.

35

SEQ ID NO: 4 Forward primer 5omp1:

CTTCTTCCTGGGACGAACG

SEQ ID NO: 5 Reverse primer 3omp1:

TGGCCTGAGGAATGTCTTGC

2.4 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells as per example 1 (1.1 Culture and 1.1.1 Treatment Protocol A). Extraction was performed as a liquid-liquid extraction (LLE) technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A).

2.5 PCR and RT-PCR mixes

Both PCR and RT-PCR mixes contained 40 nM of 5' primer, 200 nM of 3' primer, 200 nM of partzyme A, 200 nM of partzyme B, 200 nM of Sub2-FB, 1x SensiFAST Probe No-ROX Mix (Bioline), 8 mM MgCl₂ (Bioline), and nuclease free water (Ambion) in a total volume of 20 µL. In addition RT-PCR mixes contained 0.2 U/µL RiboSafe RNase Inhibitor (Bioline) and 0.2 µL of Reverse Transcriptase (Bioline). Reactions were performed in triplicate on a BioRad® CFX96 thermocycler using the same cycling parameters: 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (minus 0.5°C per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. RT-PCR and PCR mixes contained either 5 µL of TNA template (1/100 dilution) or no template (dH₂O).

2.6 Results

Chlamydia DNA and RNA (GAT), or DNA only, was amplified by RT-PCR and PCR respectively using TNA extracted from viable untreated cells and from cells incubated with antibiotic at concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC). Table 2 shows the threshold cycle (Ct) values measured for each reaction type and sample. The ΔCt was calculated as the differences between the Ct values for the PCR (DNA only) and RT-PCR (GAT) obtained from amplification plots. In turn, the fold change (ratio of the numbers of copies of RNA plus DNA (GAT) versus DNA only, which would theoretically lead to those ΔCt values, was estimated as $2^{\Delta Ct}$ and plotted in Figure 3 panel iii. The results were then compared to the viability in each cell population (Figure 3 panel ii).

Table 2: Results of PCR and RT-PCR analysis of TNA from treated and untreated samples

Sample	Threshold (Ct)		ΔCt (CtA – CtB)	Fold Change $2^{\Delta Ct}$
	A: PCR amplifying OmpI DNA only	B: RT-PCR amplifying OmpI DNA and omp1 RNA		
No Antibiotic	11.42	10.33	1.10	2.14
< MIC	13.96	12.76	1.19	2.29
MIC	21.88	21.42	0.47	1.38
> MIC	21.84	21.47	0.37	1.29
No TNA	No Ct	No Ct		

Theoretically, if cells were no longer infected with chlamydia, no transcripts or only very low residual levels of transcripts or their fragments would be detectable. Similarly, only low residual levels of genomic DNA, or fragments of this, would be detectable, however, the amount of DNA detected could be anticipated to be greater than the amount of RNA since DNA is inherently more stable than RNA.

Analysis of results shows that when TNA samples, extracted from untreated samples, or from samples treated at below the MIC, were amplified then the Ct value for RT-PCR observed was lower than that observed for the PCR (Table 2), consistent with active transcription in these samples. For reactions using TNA from culture treated at the MIC level or above, the ΔCt values were lower (Table 2), consistent with little or no transcription.

Previous studies have shown that detection of either DNA or RNA *per se* is not a reliable measure of clearance of *Chlamydia trachomatis*. The data from this example demonstrates that the ratios of the fold changes between DNA (measured by PCR) and GAT, (DNA plus RNA, measured by RT-PCR) has a similar trend as the measure of viability (PI) for untreated and treated cells as evidenced by comparison of graph in Figures 3 panels ii and iii. Whilst this example demonstrates the utility of examining RNA and DNA ratios, this experiment does not exemplify the invention as the DNA only target is still expressed in both reactions. As such determination of the DNA/RNA versus DNA only required two parallel reactions performed with and without reverse transcriptase. This makes direct comparison of results more difficult. As such a more preferred approach would use a method as per the invention wherein different nucleic

acid subpopulations (DNA only versus DNA plus RNA) could be co-amplified in a single VITA RT-PCR.

Example 3: Screening of GAT and NED targets

The following example demonstrates the methods of screening for appropriate targets for GAT and NED assays. Nucleic acids were extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA and RNA were extracted from viable cells harvested at 24h PI. Nucleic acids were then amplified using primer pairs targeting the selected gene and its transcripts (GAT), or a non-transcribed gene only (NED). The appropriateness of each a target was determined by comparison of the (i) detection of RNA by RT-PCR in total RNA, wherein both the gene and its transcripts would be detected and (ii) detection of DNA by PCR wherein only the gene DNA would be detected. In theses experiment it would be predicted atht the Ct of GAT to display a difference between both reactions, whereas the Ct of NED should display no difference.

3.1 Partzyme Oligonucleotides

Partzymes were designed to assemble into active MNAzymes when they bound to amplicons generated by amplification of either the omp1 gene or omp1 transcripts. Once assembled, the MNzyme could cleave the reporter substrate Sub102(20)-FB. A second pair of partzymes was designed to assemble into an active MNAzymes when bound to amplicons generated by amplification of a non-transcribed DNA region denoted infA_IGR thus providing a measure of NED. Once assembled, this MNzyme could cleave the reporter substrate Sub72-A1B. The sequences of Partzyme A and Partzyme B for each MNzyme are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNzyme and bases in italic refer to sequence which hybridizes to the substrate.

SEQ ID NO: 6 Partzyme A for GAT omp1_A4/102-P

TGGTCTCGAGCATTGAACGAACAACGAGGGACGTCTGA/3Phos/

SEQ ID NO: 7 Partzyme B for GAT omp1_B5/102(20)-P

CGGTAGAGGAGGCTAGCTCATGTTCTCGATTAAGGCTG/3Phos/

SEQ ID NO:8 Partzyme A for NED CTinfAIGR_A4/72-P

TCGACTAAACAGAAAATGTCAAAAACAACGAGAGGCGTGAT/3Phos/

SEQ ID NO:9 Partzyme B for NED CTinfAIGR_B5/72-P

CTGGGAGGAGAGGCTAGCTCAACTTGTCAAAAAACAGAAGG/3Phos/

3.2 Reporter Substrate

In the current example, two different reporter substrates were used, each labelled with distinct fluorophores. Sub102(20)-FB was end-labelled at the 5' end with 6-FAM and with IABkFQ at the 3' end, and its cleavage was monitored at 516 nm with excitation at 492 nm. Sub72-A1B was labelled with ATTO™ Rho101 at the 5' end and with IAbRQSp at the 3' end, and its cleavage was monitored at 609 nm with excitation at 592 nm. The reporter substrates for this example are shown below with the sequence, 5' to 3'. The lower case bases represent RNA and the upper case bases represent DNA.

SEQ ID NO: 10 for GAT Sub102(20)-FB

TCGACGTCCCguCCTCTACCG

SEQ ID NO: 11 for NED Sub72-A1B

ATCACGCCTCguCTCCTCCCAG

3.3 PCR primers for amplification GAT and NED

In vitro amplification of TNA and RNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse primers were used to amplify a region of the omp1 gene and transcripts (GAT) and infA_IGR DNA (NED) by PCR and RT-PCR. All sequences are written 5' to 3'.

SEQ ID NO: 4 Forward primer for GAT 5omp1:

CTTCTTCCTGGGACGAACG

SEQ ID NO: 5 Reverse primer for GAT 3omp1:

TGGCCTGAGGAATGTCTTGC

SEQ ID NO: 12 Forward primer for NED 5CTinfAIGR_2

GAGAGAGTGATTATATCGACTAA

SEQ ID NO: 13 Reverse primer for NED 3CTinfAIGR_1

CAAGAGAGAATGTCAAAAGATAC

3.4 Preparation of TNA and RNA

Nucleic acids were extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture). At 4 hours PI, DMEM was replaced with cycloheximide, to synchronise the infection and stop protein synthesis by the host. Cells were again incubated at 37°C with 5% CO₂ until harvested at 24h post-infection, at an exponential growth phase of the bacteria.

Extraction of TNA was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA))

extraction, 1.3.1 Extraction Protocol A). with the following modification; cell debris pelleting step was not performed during extraction of the samples in this example.

Extraction of RNA was performed using the RNeasy Mini Kit (Qiagen), as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.3 Extraction Protocol C) and following manufacturer's instructions for Purification of Total RNA from Animal Cells with additional on-column DNase digestion.

3.5 PCR and RT-PCR mixes

Both PCR and RT-PCR mixes contained 40 nM of 5' primer, 200 nM of 3' primer, 200 nM of partzyme A, 200 nM of partzyme B, 200 nM of Sub2-FB for GAT and 200 nM of Sub72-A1B for NED, 1x SensiFAST Probe No-ROX Mix (Bioline), 8 mM MgCl₂ (Bioline) and nuclease free water (Ambion) in a total volume of 20 µL. In addition RT-PCR mixes contained 0.2 U/µL RiboSafe RNase Inhibitor (Bioline) and 0.2 µL of Reverse Transcriptase (Bioline). Reactions were performed on a BioRad® CFX96 thermocycler using the same cycling parameters: 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (minus 0.5°C per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. RT-PCR and PCR mixes contained either 5 µL of TNA or RNA template (1/100 dilution) or no template (dH₂O).

3.6 Results

Chlamydia DNA and RNA, or DNA only, was amplified by RT-PCR and PCR respectively in RNA and TNA samples, harvested from viable untreated cells at 24 hours PI. Table 3A denotes the amplicon types and origin from reactions performed. Table 3B shows the threshold cycle (Ct) values measured for each reaction type and sample. The ΔCt was calculated as the differences between the Ct values for the PCR (DNA only) and RT-PCR (DNA and RNA) obtained from amplification plots (Figure 4).

Table 3A: Potential Amplicon Types and Origin

	Sample	Nucleic Acid Species with potential to generate amplicons	
		PCR	RT-PCR
Omp 1 GAT	RNA	Contaminating DNA (omp1 gene)	RNA - omp1 transcripts Contaminating DNA (Omp1 gene)
	TNA	Genomic DNA - omp1 gene	Genomic DNA and RNA - omp1 gene and omp1 transcript
InfAIG	RNA	Contaminating DNA	Contaminating DNA

NED		(infAIGR DNA)	(infAIGR DNA)
	TNA	Genomic DNA infAIG DNA	Genomic DNA infAIG DNA

Table 3B: Threshold Values from PCR and RT-PCR analysis of TNA and RNA samples

		Threshold (Ct)		Δ Ct PCR – RT-PCR
	Sample	DNA only (PCR)	DNA and RNA (RT-PCR)	
Omp 1 GAT	RNA	19.85	7.09	12.76
	No RNA	No Ct	No Ct	
	TNA	17.36	12.44	4.92
	No TNA	No Ct	No Ct	
InfAIG NED	RNA	20.12	19.29	0.83
	No RNA	No Ct	No Ct	
	TNA	18.31	18.36	-0.05
	No TNA	No Ct	No Ct	

5 The results using candidate GAT primers and TNA (Table 3 B) suggest that the omp1 primers are capable of amplification of both omp1 DNA and omp1 RNA (Figure 4 panel i and ii) and thus fit the criteria for suitability as GAT primers. Further, since the Ct for the RT-PCR is 4.92 cycles ahead of the Ct of the PCR this suggests there are many copies of RNA per omp1 DNA gene copy, in the TNA sample. This is also supported by
10 the results using omp1 primers on RNA (Figure 4 panel i), where there was a large Ct difference of 11.51 observed between the RT-PCR and PCR results, reflecting strong amplification of omp1 RNA in purified RNA samples and only a very late Ct detected for the PCR which is most likely due to small amounts of contaminating DNA in the RNA preparation.

15 The results using candidate NED primers and TNA (Table 3 B) suggest that the InfAIGR primers are capable of amplification of the infA intergenic DNA sequence (Figure 4 panel iv). Further, since the Ct for the RT-PCR the PCR are very similar (Δ Ct - 0.05) this demonstrates that these NED primers do not amplify additional RNA sequence in the TNA consistent with a lack of RNA transcription associated with this sequence. As
20 such, these primers fit the criteria for suitability as NED primers. This is also supported by the results using InfAIGR primers on RNA (Figure 4 panel iii), where only late Ct

values are generated, which are similar for PCR and RT-PCR, and as before, likely to merely represent amplicons generated from contaminating DNA in the RNA preparation.

This example provides a method which is suitable for screening candidate sequences for use as GAT primers or for use as NED primers. Further, the example shows evidence of contaminating DNA in a purified RNA preparation, despite performing additional DNase digestion procedure during extraction. The observation highlights the need for improved methods, such as VITA PCR, as it is most likely contaminating DNA is the source of at least some false positives observed when amplification of RNA is used as a measure of cell viability in specimens, including clinical specimens. Previous studies have shown that detection of either RNA (or DNA) *per sec* is not a reliable measure of clearance of *Chlamydia trachomatis*

Example 4 - Analysis of GAT and NED in untreated and treated cells by VITA PCR.

The following example estimates levels of NED and GAT in TNA samples extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells which were not incubated with antibiotic (untreated, viable cells), and from cells incubated with antibiotic at a concentration eight times below the MIC (<MIC), at the MIC (MIC) or at 8 times greater than the MIC (> MIC), as described in example 1, Treatment Protocol A (1.1.1). Chlamydia DNA and RNA (GAT) was amplified by RT-PCR using primers targeting the *omp1* gene and its transcripts. Chlamydia DNA only (NED) was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA, designated *infAIGR*, which is not transcribed. The Ct values for GAT and NED were determined.

4.1 Partzyme Oligonucleotides

Partzymes were designed to assemble into an active MNazymes when they bound to amplicons generated by amplification of both the *omp1* gene and *omp1* transcripts. Once assembled, this MNazyme could cleave the reporter substrate Sub2-FB. A second pair of partzymes was designed to assemble into an active MNazymes when bound to amplicons generated by amplification of a non-transcribed region denoted *infA_IGR*. Once assembled, this MNazyme could cleave the reporter substrate Sub72-A1B. The sequences of Partzyme A and Partzyme B are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNazyme and bases in italic refer to sequence which hybridizes to the substrate.

SEQ ID NO: 1 Partzyme A for GAT *omp1_A4/2-P*

TGGTCTCGAGCATTGAACGAACAACGAGAGGAAACCTT/3Phos/

SEQ ID NO: 2 Partzyme B for GAT omp1_B5/2-P

TGCCCAGGGAGGCTAGCTCATGTTCTCGATTAAGGCTG/3Phos/

SEQ ID NO: 8 Partzyme A for NED CTinfAIGR_A4/72-P

5 **TCGACTAAACAGAAAATGTCAAAAACAACGAGAGGCGTGAT/3Phos/**

SEQ ID NO: 9 Partzyme B for NED CTinfAIGR_B5/72-P

CTGGGAGGAGAGGCTAGCTCAACTTGTCAAAAAACAGAAGG/3Phos/

4.2 Reporter Substrates

10 In the current example, two different reporter substrates were used, each labelled with distinct fluorophores. Sub2-FB was end-labelled at the 5' end with 6-FAM and IABkFQ at the 3' end, and its cleavage was monitored at 516 nm with excitation at 492 nm. Sub72-A1B was labelled with ATTO™ Rho101 at the 5' end and with IAbRQSp at the 3' end, and its cleavage A1B was monitored at 609 nm with excitation at 592 nm. The
15 reporter substrate for this example is shown below with the sequence, 5' to 3'. The lower case bases represent RNA and the upper case bases represent DNA.

SEQ ID NO: 3 Sub2-FB for GAT

AAGGTTTCCTCguCCCTGGGCA

SEQ ID NO: 11 Sub72-A1B for NED

20 ATCACGCCTCguCTCCTCCCAG

4.3 PCR primers for amplification of the omp1 gene and transcripts

In vitro amplification of TNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse
25 primers were used to amplified omp1 RNA and DNA (GAT) and inf_AGR DNA (NED) by RT-PCR. All sequences are written 5' to 3'.

SEQ ID NO: 4 Forward primer for GAT 5omp1:

CTTCTTCCTGGGACGAACG

SEQ ID NO: 5 Reverse primer for GAT 3omp1:

30 TGGCCTGAGGAATGTCTTGC

SEQ ID NO: 12 Forward primer for NED 5CTinfAIGR_2

GAGAGAGTGATTATATCGACTAA

SEQ ID NO: 13 Reverse primer for NED 3CTinfAIGR_1

CAAGAGAGAATGTCAAAAGATAC

35

4.4 Preparation of TNA

RNA and DNA (TNA) were co- extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells as per example 1 (1.1 Culture, 1.1.1 Treatment Protocol A). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A).

4.5 Reaction components

All reactions contained 40 nM of each Forward primer, 200 nM of each Reverse primer, 200 nM of each partzyme A, 200 nM of each partzyme B, 200 nM of each substrate, 1x SensiFAST Probe No-ROX Mix (Bioline), 2 mM MgCl₂ (Bioline), 0.2 U/μL RiboSafe RNase Inhibitor (Bioline), 0.2 μL of Reverse Transcriptase enzyme (Bioline) and nuclease free water (Ambion) in a total volume of 20 μL. All reactions were performed in triplicate on a BioRad® CFX96 thermocycler. The cycling parameters were 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (with a 0.5°C decrease in temperature per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. The reactions contained either 5 μL of TNA template (1/100 dilution) or no target (dH₂O).

4.6 Results

Chlamydia DNA and RNA (GAT), or DNA only (NED), were co-amplified in single RT-PCR from TNA extracted from viable untreated cells and from cells incubated with antibiotic at concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC) (Figure 5 panel i). Table 4 shows the threshold cycle (Ct) values measured for the GAT or NED in each sample. The ΔCt was calculated as the differences between the Ct values of the NED and GAT signals. In turn, the fold change (ratio of GAT to NED) which would theoretically lead to those ΔCt values was estimated as 2^{ΔCt} (Table 4) and VITA indices were plotted in Figure 5 panel i. The results were then compared to the viability in each cell population (Figure 3 panels i and ii).

Table 4: Results of VITA PCR (duplex RT-PCR) analysis of TNA from treated and untreated samples

Sample	Threshold (Ct)		ΔC_t NED - GAT	FC $= 2^{\Delta C_t}$	VITA Index
	GAT	NED			
No Antibiotic	10.68	12.08	1.40	2.63	2.63
< MIC	12.86	14.33	1.47	2.77	2.77
MIC	21.81	22.38	0.58	1.49	1.49
> MIC	21.87	22.47	0.60	1.51	1.51
No TNA	No Ct	No Ct			

Theoretically, if cells were no longer infected with chlamydia only very low residual levels of transcripts or their fragments would be detectable. Similarly, only low residual levels of genomic DNA, or fragments of this, would be detectable. The amount of DNA detected could be anticipated to be greater than the amount of RNA since DNA is inherently more stable than RNA. Analysis of results shows that when TNA samples, extracted from samples that were untreated or treated below the MIC, were amplified the Ct value for GAT was lower than the NED (Table 4) consistent with active transcription. For GAT and NED from TNA treated with at the MIC level or above, the differences in Ct value were small (Table 4), indicating little or no transcription. The fold change and VITA Indices were calculated for the four sample types. Since only a single gene and its transcripts were used to calculate the GAT, and only a single non-transcribed region was used to calculate NED, then the fold change and VITA Indices are equal (Table 4).

Previous studies have shown that detection of either DNA or RNA *per sec* is not a reliable measure of clearance of *Chlamydia trachomatis*. The data from this example demonstrates that the VITA Indices correlate with the measure of viability (PI) for untreated and treated cells as evidenced by comparison of graph in Figures 5 panel i and Figure 3 panels i and ii. This example demonstrates that GAT and NED can be measured in a single reaction and the results can be used to calculate VITA Indices which correlate with the observed viability of cells and response to the presence of antibiotics. The example provides a rapid method useful for detection of viability, in this case viability of chlamydia. Further it could provide the basis for a Test of Cure (TOC) in patient specimens by determining whether or not an infection has been cleared.

Example 5 – Use of two regions within a gene and corresponding transcripts to measure GAT by VITA PCR using TNA from untreated and treated cells.

The following example estimates levels of NED and GAT in TNA samples extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells which were not incubated with antibiotic (untreated, viable cells), and from cells incubated with antibiotic at a concentration eight times below the MIC (<MIC), at the MIC (MIC) or at 8 times greater than the MIC (> MIC), as described in example 1, Treatment Protocol A (1.2.1). Chlamydia DNA and RNA (GAT) was amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts (GAT1/2). Chlamydia DNA only (NED) was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA, designated infAIGR (infA intergenic region), which is not transcribed. The Ct values for GAT1/2 and NED were obtained.

5.1 Partzyme oligonucleotides

Partzymes were designed to assemble into two active MNazymes when they bound to amplicons generated by amplification of either the omp1 gene or omp1 transcripts. These two MNazymes were capable of binding to two different amplicons derived by amplification of two separate regions of omp1 (a GAT1 and a GAT2 region). Once assembled, both MNazymes could cleave the same reporter substrate Sub2-FB. A third pair of partzymes was designed to assemble into an active MNazymes when bound to amplicons generated by amplification of a non-transcribed DNA region denoted infA_IGR thus providing a measure of NED. Once assembled, this MNazyme could cleave the reporter substrate Sub72-A1B. The sequences of partzyme A and Partzyme B for each MNazyme are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNazyme and bases in italic refer to sequence which hybridizes to the substrate.

SEQ ID NO: 1 Partzyme A for GAT1 omp1_A4/2-P

TGGTCTCGAGCATTGAACGAACAACGAGAGGAAACCTT/3Phos/

SEQ ID NO: 2 Partzyme B for GAT1 omp1_B5/2-P

TGCCCAGGGAGGCTAGCTCATGTTCTCGATTAAGGCTG/3Phos/

SEQ ID NO: 14 PartzymeA for GAT2 CTomp1_A4/2-P

TTGCACCACTTGGTGTGACGACAACGAGAGGAAACCTT/3phos/

SEQ ID NO: 15 Partzyme B for GAT2 CTomp1_B5/2-P

TGCCCAGGGAGGCTAGCTCTATCAGCATGCGTGTGGGTT/3phos/

SEQ ID NO: 8 Partzyme A for NED CTinfAIGR_A4/72-P

TCGACTAAACAGAAAATGTCAAAACAACGAGAGGCGTGAT/3Phos/
 SEQ ID NO: 9 Partzyme B for NED CTinfAIGR_B5/72-P
 CTGGGAGGAGAGGCTAGCTCAACTTGTCAAAAAACAGAAGG/3Phos/

5.2 Reporter substrates

In the current example, two different reporter substrates were used, each labelled with distinct fluorophores, as per example 4 (4.2 Reporter substrates).

5.3 PCR primers for amplification of GAT1, GAT2 and NED

In vitro amplification of TNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse primers were used to amplify two regions of the omp1 gene and transcripts (GAT1 and GAT2) and infA_IGR DNA (NED) by RT-PCR. All sequences are written 5' to 3'.

SEQ ID NO: 4 Forward primer for GAT1 5omp1
 CTTCTTCCTGGGACGAACG
 SEQ ID NO: 5 Reverse primer for GAT1 3omp1
 TGGCCTGAGGAATGTCTTGC
 SEQ ID NO: 16 Forward primer for GAT2 5CTomp1_1
 TTTCGGCGGAGATCCTTGCGATCC
 SEQ ID NO: 17 Reverse primer for GAT2 3CTomp1_2
 CGAAAACAAAGTCACCGTAGTAACC
 SEQ ID NO: 12 Forward primer for NED 5CTinfAIGR_2
 GAGAGAGTGATTATATCGACTAA
 SEQ ID NO: 13 Reverse primer for NED 3CTinfAIGR_1
 CAAGAGAGAATGTCAAAAGATAC

5.4 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been obtained through in-vitro methods, cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.1 Treatment Protocol A). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A).

5.5 Reaction components

All reactions contained 40 nM of each Forward primer, 200 nM of each Reverse primer, 200 nM of each partzyme A, 200 nM of each partzyme B, 400 nM of each substrate SEQ ID NO 3 and 200 nM of substrate SEQ ID NO 11, 1x SensiFAST Probe
 5 No-ROX Mix (Bioline), 2 mM MgCl₂ (Bioline), 0.2 U/μL RiboSafe RNase Inhibitor (Bioline), 0.2 μL of Reverse Transcriptase enzyme (Bioline) and nuclease free water (Ambion) in a total volume of 20 μL. All reactions were performed in triplicate on a BioRad® CFX96 thermocycler. The cycling parameters were 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (with a 0.5°C
 10 decrease in temperature per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. The reactions contained either 5 μL of TNA template (1/100 dilution) or no target (dH₂O).

5.6 Results

15 Chlamydia DNA and RNA from 2 regions within the omp1 gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified in single RT-PCR from TNA extracted from viable untreated cells and from cells incubated with antibiotic at concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC) (Figure 5 panel ii). Table 5 shows the threshold cycle (Ct) values measured for NED, and for the
 20 combined signals from GAT1 and GAT2 (GAT1/2), in each sample. The ΔCt was calculated as the differences between the Ct values of the NED and GAT1/2. In turn, the fold change (ratio of GAT to NED) which would theoretically lead to those ΔCt values was estimated as 2^{ΔCt} and shown in Table 5. The VITA Indices were calculated by dividing the FC by the TR, in this instance 2. The results were then compared to the
 25 viability in each cell population.

Table 5: Results of triplex RT-PCR analysis of TNA from treated and untreated samples

Sample	Threshold (Ct)		ΔCt	FC	TR 2xGAT/1xNED	VITA Index
	GAT1/2	NED				
No Antibiotic	9.23	11.71	2.48	5.57	2	2.79
< MIC	11.30	14.17	2.87	7.32	2	3.66
MIC	20.83	22.15	1.32	2.49	2	1.25
> MIC	20.83	22.16	1.33	2.52	2	1.26
No TNA	No Ct	No Ct				

Analysis of results shows that when TNA samples, extracted from untreated or treated samples below the MIC, were amplified the Ct value for GAT1/2 was lower than the NED (Table 5) consistent with active transcription. For GAT1/2 and NED from TNA
 5 treated with at the MIC level or above, the differences in Ct value were small (Table 5) indicating little or no transcription. The fold change and VITA Indices were calculated for the four sample types. Since two genes and their transcripts were used to calculate the GAT1/2, and only a single non-transcribed region was used to calculate NED, then the fold change is divided by the TR to calculate the VITA Indices (Table 5).

10 The ability to incorporate multiple primers sets capable of amplifying both DNA and its associated RNA transcripts is in fact highly desirable, as specific genes may only be expressed during certain stages in the development cycle of, for example, bacteria. An assay containing multiple genes expressed, preferably at high levels under different conditions, could ensure expression will consistently be detectable in desperate
 15 conditions.

Example 6 - Use of VITA PCR on clinical specimens

The following example estimates levels of GAT relative to NED in a clinical sample. The urine sample was obtained from a symptomatic patient with successive
 20 treatment failures to the first line antibiotic azithromycin. TNA was extracted from the sample and tested alongside reference material extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D) confirmed to be alive/viable (Positive reference) or dead (Negative reference). Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts to measure
 25 GAT. Another region of *Chlamydia* DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed to measure NED. The levels of GAT and NED were determined and used to calculate the VITA Indices.

6.1 VITA PCR analysis of GAT1, GAT2 and NED

30 Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 5 (5.1, 5.2 and 5.3 respectively).

6.2 Preparation of TNA

Clinical sample:

RNA and DNA (TNA) were co-extracted from a clinical specimen of urine, that had been obtained from a patient with successive treatment failure to first line antibiotic treatment. A total of 8mL of urine was pelleted, followed by extraction of nucleic acids, performed using the FireMonkey PuriSpin extraction kit, as described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B), following the manufacturer's instructions for the simultaneous extraction of both DNA and RNA.

Reference material:

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been obtained through in-vitro methods, cultured in HEp-2 cells, treated with high dose of azithromycin antibiotic (0.512 $\mu\text{L/mL}$) and confirmed to be "Dead" or Not treated and confirmed to be "Alive", as described in example 1. The viability status of these reference samples had been confirmed through Immunofluorescence staining. Extraction was performed as a liquid-liquid extraction (LLE) technique, using phenol:chloroform:isoamyl, also described in example 1, (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A)

6.3 Reaction components

The RT-PCR conditions used were as described in Example 5 (5.5) with the following modifications; 0.1 μL of Reverse Transcriptase enzyme (Bioline) was added in a total reaction volume of 10 μL , which contained either 2.5 μL of TNA extracted from clinical sample (neat), 2.5 μL of each reference TNA sample (1/100 dilution) or no target (dH_2O).

6.4 Results

Chlamydia DNA and RNA from 2 regions within the *omp1* gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified and detected in single RT-PCR from TNA extracted from a clinical sample of urine (Figure 6 panel i). Amplification of the clinical sample was compared to reference samples derived from *chlamydia* cultures, either "Alive CT" (samples not treated) or "Dead CT" (treated with high doses of azithromycin) (Figure 6 panel ii). The ΔCt was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔCt values was estimated as $2^{\Delta\text{Ct}}$ and shown in Table 6.

It would be predicted that the clinical sample, being derived from a symptomatic patient would contain viable bacteria. In turn this expectedly would result in a similar

VITA Index between the clinical sample and the Alive CT reference (Positive), since both would contain higher levels of transcript present.

Analysis of results shows that when the clinical sample, extracted from urine, was amplified the Ct value for GAT1/2 was lower than the NED (Table 6). This is consistent with active transcription and similar to that observed with the reference sample, Alive CT (positive) (Table 6). For all three Dead CT reference samples (Negative 1-3), the Ct values for GAT1/2 and NED were more similar (Table 6). The Δ Ct, fold change and VITA Index were calculated for all the samples (Table 6). Since two genes and their transcripts were used to calculate the GAT1/2, and only a single non-transcribed region was used to calculate NED, then the fold change is double that of the VITA Indices (Table 6). Comparison of VITA indices of the clinical sample and the Alive CT demonstrated no difference, correlating with detection of a viable population (Figure 6 panel ii). Contrary, comparison of VITA indices of the clinical sample and Dead CT samples, demonstrated a difference in the VITA indices. These were higher for the clinical sample than the dead CT samples (Figure 6 panel ii) consistent with decreased or no transcriptional activity in the Dead CT samples which had been treated with high dose of azithromycin and confirmed to not be viable.

The data from this example demonstrated that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. The comparison between VITA indices of the clinical sample and those of the reference material, demonstrated an accurate call on viability of cells in the clinical sample. This indicates the positive performance of the technology on clinical specimens and its applicability in a clinical setting. The ability to differentiate between dead and alive cells could have application in determining whether a patient has successfully cleared an infection or not following treatment with antibiotics. The tests could provide an initial diagnosis or a “Test of Cure”.

Table 6: Results of a triplex RT-PCR analysis of TNA from a clinical specimen in comparison to reference material

Sample	Threshold (Ct)		Δ Ct NED - GAT	FC	TR 2xGAT/1xNED	VITA Index
	GAT1/2	NED				
Clinical sample	14.33	16.56	2.23	4.86	2	2.34
Positive	9.16	11.44	2.28	4.68	2	2.43

(Alive CT)						
Negative 1 (Dead CT 1)	20.96	21.83	0.88	1.83	2	0.92
Negative 2 (Dead CT 1)	22.38	23.73	1.35	2.55	2	1.27
Negative 3 (Dead CT 1)	21.72	22.95	1.23	2.35	2	1.17
No TNA	No Ct	No Ct				

Example 7 - Antibiotic susceptibility testing using VITA PCR

The following example estimates the change of GAT levels in TNA samples, extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells, which at an exponential growth phase, 24 hours post infection, were either treated with antibiotic at the MIC or not treated (control), as described in example 1, Treatment B (1.1.2). Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the *omp1* gene and its transcripts to measure GAT. Another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed to measure NED. The levels of GAT and NED were estimated and used to calculate VITA Index.

7.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 5 (5.1, 5.2 and 5.3 respectively). The RT-PCR reaction conditions used were as described in Example 5 (5.5). These reactions contained either 5 µL of TNA template (1/1000 dilution) or no target (dH₂O).

7.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.2 Treatment Protocol B). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA))

extraction, 1.3.1 Extraction Protocol A) with the following modification; cell debris pelleting step was not performed during extraction of the samples in this example.

7.3 Results

5 Chlamydia DNA and RNA from 2 regions within the *omp1* gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified and detected in single RT-PCR from TNA extracted from chlamydia cultures. These cultures were treated with antibiotic or left untreated (control) at an exponential growth phase and harvested at 1 and 6 hours post treatment (Figure 7 panel i). Table 4 shows the threshold cycle (Ct) values
10 measured for the GAT1/2 and NED in each sample. The ΔC_t was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔC_t values was estimated as $2^{\Delta C_t}$ and shown in Table 7. The results were then compared between no treatment reactions (control) and those treated with antibiotic at
15 each time point (Figure 7 panel ii).

It would be predicted that cells susceptible to antibiotic treatment would have a decrease in levels of transcription, as the presence of antibiotic would be anticipated to disrupt the normal functioning of the cells. In turn this would result in a decrease in the VITA Index of these cells compared to control (non-treated cells).

20 Analysis of results shows that when TNA samples, extracted from untreated and treated groups, were amplified the Ct value for GAT1/2 was lower than the NED (Table 7). This is consistent with active transcription in all four samples. The fold change and VITA Indices were calculated for the samples and different time points post treatment (Table 7). Since two genes and their transcripts were used to calculate the GAT1/2, and
25 only a single un-transcribed region was used to calculate NED, then the fold change is double that of the VITA Indices (Table 7). Comparison of VITA indices of the untreated and treated samples, at both time points, demonstrated a difference in the VITA indices for treated samples, being lower than untreated samples (Figure 7 panel ii) consistent with decreased transcriptional activity in the presence of antibiotic. The $\Delta VITA$ Ratio is
30 calculated by dividing the VITA Index (no antibiotic) by the VITA Index with antibiotic.

The data from this example demonstrates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. The comparison between VITA indices of treated and untreated cells, calculated as $\Delta VITA$ ratio, demonstrated a response to the presence of antibiotic. This indicates antibiotic
35 susceptibility of the cells. Further, it shows this susceptibility can be ascertained at various time points including at 1h or 6h post treatment.

Table 7: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, harvested at different time points post treatment (PT)

Sample		Threshold (Ct)		ΔC_t	FC	VITA Index	$\Delta VITA$ A/B
		GAT1/2	NED				
1h	A No Antibiotic	12.95	18.39	5.44	43.51	21.76	3.77
PT	B Plus Antibiotic	11.76	15.29	3.53	11.55	5.78	
6h	A No Antibiotic	10.88	16.81	5.93	60.83	30.41	2.12
PT	B Plus Antibiotic	12.69	17.53	4.84	28.71	14.35	

Example 8 - Antibiotic susceptibility testing with Azithromycin using VITA PCR with shorter incubation time

The following example estimates the change of GAT levels relative to NED in TNA samples extracted from HEp-2 cells which had been infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells, which had been either treated with antibiotic at the MIC, or not treated (control), at 24 hours post infection whilst in an exponential growth phase. Treatment was as described in example 1, Treatment B (1.1.2) using Azithromycin (0.128 $\mu\text{g/mL}$). To obtain a GAT measure, Chlamydia DNA and RNA were amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts. To measure NED, another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate VITA Index. Further to this the VITA Indices of treated and untreated samples were used to calculate the $\Delta VITA$ ratio.

8.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 5 (5.1, 5.2 and 5.3 respectively). The RT-PCR conditions used were as described in Example 5 (5.5) and reactions contained either 5 μL of TNA template (1/1000 dilution) or no target (dH₂O).

8.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.2

Treatment Protocol B). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A) with the following modification; cell debris pelleting step was not performed during extraction of the samples in this example.

5

8.3 Results

Chlamydia DNA and RNA from 2 regions within the omp gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified and detected in single RT-PCR from TNA extracted from chlamydia cultures. These cultures were treated with antibiotic or left untreated (control) at an exponential growth phase and harvested at 30 min or 1 hour post treatment with 0.128 µg/mL of Azithromycin (Figure 7 panel i). Table 8 shows the threshold cycle (Ct) values measured for the GAT1/2 and NED in each sample. The ΔC_t was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔC_t values was estimated as $2^{\Delta C_t}$ and shown in Table 8. The results were then compared between no treatment reactions (control) and those treated with antibiotic at each time point (Figure 7 panel iii).

Table 8: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, harvested at different time points post treatment (PT)

20

		Threshold (Ct)					
Sample		GAT1/2	NED	ΔC_t	Fold Change	VITA Index	$\Delta VITA$ Ratio A/B
30 min PT	A No Antibiotic	14.14	22.18	8.04	263.20	133.44	1.4
	B Plus Antibiotic	14.00	21.55	7.55	187.40	94	
1h PT	A No Antibiotic	14.18	22.11	7.93	243.88	121.67	2.5
	B Plus Antibiotic	13.79	20.41	6.62	98.36	49.20	

Analysis of results shows that when TNA samples, extracted from untreated and treated groups, were amplified the Ct value for GAT1/2 was lower than the NED (Table

8) indicating there was active transcription in all samples. The fold change and VITA Indices were calculated for all samples at all time points post treatment (Table 8). Since two genes and their transcripts were used to calculate the GAT1/2, and only a single untranscribed region was used to calculate NED, then the fold change is double that of the VITA Indices (Table 8). Comparison of VITA indices, between the untreated and treated samples at each time point, demonstrated a difference in the VITA indices (Figure 7 panel iii). This is consistent with a disruption to the transcription activity of cells in the presence of antibiotic. The Δ VITA Ratio is calculated by dividing the VITA Index (no antibiotic) by the VITA Index with antibiotic.

As per example 7, the data from this example demonstrates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. A response to the presence of antibiotic was detected, through comparison between VITA indices of treated and untreated cells and calculated as Δ VITA Ratio. This reflects the antibiotic susceptibility of the cells. It further demonstrates that susceptibility can be established at various time points including at 30 min or 1h post antibiotic treatment with Azithromycin.

Example 9 - Antibiotic susceptibility testing with rifampicin VITA PCR and shorter incubation time

The following example estimates the change of GAT levels relative to NED in TNA samples extracted from HEP-2 cells which had been infected with *Chlamydia trachomatis* strain 1 and strain 5 (serovar D lab strain and serovar L2 strain resistant to rifampicin respectively). TNA was extracted from cells, which had been either treated with the antibiotic Rifampicin at a concentration of 0.256 μ g/mL, or not treated (control), at 20 hours post infection whilst in an exponential growth phase. Treatment was as described in example 1, Treatment C (1.1.3). To obtain a measure GAT, Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the *omp1* gene and its transcripts. To measure NED, another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate VITA Index. Further to this the VITA Indices of treated and untreated samples were used to calculate the Δ VITA Ratio.

9.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzymes were designed to assemble into two active MNazymes when they bound to amplicons generated by amplification of either the *omp1* gene or *omp1* transcripts. These

two MNazymes were capable of binding to two different amplicons derived by amplification of two separate regions of omp1 (a GAT1 and a GAT2 region). Once assembled, both MNazymes could cleave the same reporter substrate Sub102(20)-FB. A third pair of partzymes was designed to assemble into an active MNazymes when bound to amplicons generated by amplification of a non-transcribed DNA region denoted infA_IGR thus providing a measure of NED. Once assembled, this MNzyme could cleave the reporter substrate Sub72-A1B. The sequences of Partzyme A and Partzyme B for each MNzyme are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNzyme and bases in italic refer to sequence which hybridizes to the substrate.

SEQ ID NO: 18 Partzyme A for GAT1 CTomp1T_3A4/102-P
ATTGAACGACATGTTCTCGATTAAACAACGAGGGACGTCGA/3Phos/
 SEQ ID NO: 19 Partzyme B for GAT1 CTomp1T_3B5/102-P
CGGTAGAGGAGGCTAGCTGGCTGCTTTTACTTGCAAGACA/3Phos/
 SEQ ID NO: 20 PartzymeA for GAT2 CTomp1L_A4/102-P
CTTGCACCACTTGGTGTGACGACAACGAGGGACGTCGA/3phos/
 SEQ ID NO: 21 Partzyme B for GAT2 CTomp1L_B5/102-P
CGGTAGAGGAGGCTAGCTCTATCAGCATGCGTGTGGGTTA/3phos/
 SEQ ID NO: 8 Partzyme A for NED CTinfAIGR_A4/72-P
TCGACTAAACAGAAAATGTCAAAAACAACGAGAGGCGTGAT/3Phos/
 SEQ ID NO: 9 Partzyme B for NED CTinfAIGR_B5/72-P
CTGGGAGGAGAGGCTAGCTCAACTTGTCAAAAACAGAAGG/3Phos/

9.2 Reporter substrates

In the current example, two different reporter substrates were used, each labelled with distinct fluorophores. Sub102(20)-FB was end-labelled at the 5' end with 6-FAM and with IABkFQ at the 3' end, and its cleavage was monitored at 516 nm with excitation at 492 nm. Sub72-A1B was labelled with ATTO™ Rho101 at the 5' end and with IAbRQSp at the 3' end, and its cleavage was monitored at 609nm with excitation at 592 nm. The reporter substrates for this example are shown below with the sequence, 5' to 3'. The lower case bases represent RNA and the upper case bases represent DNA.

SEQ ID NO: 10 for GAT1 and GAT2 Sub102(20)-FB
 TCGACGTCCCguCCTCTACCG
 SEQ ID NO: 11 for NED Sub72-A1B
 ATCACGCCTCguCTCCTCCCAG

9.3 PCR primers for amplification of GAT1, GAT2 and NED

In vitro amplification of TNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse primers were used to amplify two regions of the omp1 gene and transcripts (GAT1 and GAT2) and infA_IGR DNA (NED) by RT-PCR. All sequences are written 5' to 3'.

5	SEQ ID NO: 4	Forward primer for GAT1	5omp1
	CTTCTTCCTGGGACGAACG		
	SEQ ID NO: 22	Reverse primer for GAT1	3omp1_2
	CAATTAATGGCCTGAGGAATGTC		
	SEQ ID NO: 16	Forward primer for GAT2	5CTomp1_1
10	TTTCGGCGGAGATCCTTGCGATCC		
	SEQ ID NO: 17	Reverse primer for GAT2	3CTomp1_2
	CGAAAACAAAGTCACCGTAGTAACC		
	SEQ ID NO: 12	Forward primer for NED	5CTinfAIGR_2
	GAGAGAGTGATTATATCGACTAA		
15	SEQ ID NO: 23	Reverse primer for NED	3CTinfAIGR_3
	GCAAAAACCTCAAGAGAGAATGTC		

9.4 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.3 Treatment Protocol C). Extraction was performed using the FireMonkey PuriSpin Extraction kit, as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B) and following manufacturer's instructions for simultaneous extraction of DNA and RNA.

9.5 Reaction components

All reactions contained 40 nM of each Forward primer, 200 nM of each Reverse primer, 200 nM of each partzyme A, 200 nM of each partzyme B, 400 nM of substrate SEQ ID NO 10 and 200 nm of substrate SEQ ID NO 11, 1x SensiFAST Probe No-ROX Mix (Bioline), 2 mM MgCl₂ (Bioline), 0.2 U/μL RiboSafe RNase Inhibitor (Bioline), 0.2 μL of Reverse Transcriptase enzyme (Bioline) and nuclease free water (Ambion) in a total volume of 20 μL. All reactions were performed in triplicate on a BioRad® CFX96 thermocycler. The cycling parameters were 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (with a 0.5°C decrease in temperature per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. The reactions contained either 5 μL of TNA template (1/1000 dilution) or no target (dH₂O).

9.6 Results

Chlamydia DNA and RNA from 2 regions within the *omp1* gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified and detected in single RT-PCR from
5 TNA extracted from chlamydia cultures. These cultures were treated with antibiotic or left untreated (control) at an exponential growth phase. They were incubated for either 5 minutes at 37°C (Figure 7 panel iv) or 15 minutes at room temperature (Figure 7 panel v). The antibiotic used for treatment was Rifampicin, at a concentration of 0.256 µg/mL, equivalent to 32 times more than the MIC for susceptible strains and 32 times less than
10 the MIC for resistant strains. Table 9 shows the threshold cycle (Ct) values measured for the GAT1/2 and NED in each sample. The ΔC_t was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔC_t values was estimated as $2^{\Delta C_t}$ and shown in Table 9. The results were then compared between no
15 treatment reactions (control) and those treated with antibiotic at each time point (Figure 7 panel iv and v).

Table 9: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, harvested at different time points post treatment (PT) 5min with incubation at 37°C with 5% CO₂ and 15 minutes with incubation at room temperature.

			Threshold (Ct)						
Sample			GAT 1/2	NED	ΔCt	Fold Change	VITA Index	ΔVITA Ratio A/B	p value
5min incubation PT At 37°C with 5% CO ₂	Susceptible strain (strain 1)	A No Antibiotic	13.96	18.11	4.16	17.81	8.91	1.90	< 0.0001 ****
		B Plus Antibiotic	15.07	18.30	3.23	9.37	4.69		
	Resistant strain (strain 5)	A No Antibiotic	14.75	19.32	4.58	23.86	11.91	1.07	0.2573
		B Plus Antibiotic	14.28	18.76	4.48	22.37	11.18		
15 min incubation PT At room temperature	Susceptible strain (strain 1)	A No Antibiotic	14.93	18.92	3.99	15.91	7.95	1.80	<0.0001 ****
		B Plus Antibiotic	15.34	18.48	3.14	8.82	4.41		
	Resistant strain (strain 5)	A No Antibiotic	14.82	19.19	4.37	20.65	10.33	0.91	N/A
		B Plus Antibiotic	14.55	19.06	4.51	22.81	11.41		

5

Analysis of results shows that when TNA samples, extracted from untreated and treated groups, were amplified the Ct value for GAT1/2 was lower than the NED (Table 9) indicating there was active transcription in all samples. The fold change and VITA Indices were calculated for all samples at all time points post treatment (Table 9). Since two genes and their transcripts were used to calculate the GAT1/2, and only a single untranscribed region was used to calculate NED, then the fold change is double that of the VITA Indices (Table 9). Decreases in VITA indices, between the untreated and treated samples were analysed using the unpaired t-test, at each time point and incubation condition.

10

Results showed a significant decrease in the VITA indices of the susceptible strain 1 (Table 9, $p < 0.0001$) following 5 minutes incubation with Rifampicin at 37°C (Figure 7 panel iv). This is consistent with a disruption to the transcription activity of cells in the presence of antibiotic and confirms the susceptibility profile of this particular serovar.

Contrastingly, the VITA Index of the resistant strain (strain 5) did not demonstrate a significant difference between treated and untreated samples under these same conditions (Table 9, Figure 7 panel iv) confirming the resistant profile of this particular serovar. In a parallel experiment, a decrease in the VITA indices of replicates of the susceptible strain 1 (Table 9, $p < 0.0001$) was observed following 15 minutes incubation with Rifampicin at room temperature (Figure 7 panel v). The VITA Index of the resistant strain 5 did not decrease in the presence of Rifamycin under the same conditions, and in fact showed a small increase.

The data from this example demonstrates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. A response to the presence of antibiotic was detected, through comparison between VITA indices of treated and untreated cells and calculated as Δ VITA Ratio. This can be used to accurately reflect the antibiotic susceptibility or resistance profiles of cells and further demonstrates that susceptibility can be established after short incubation times. Differentiation between susceptibility and resistance to antibiotics can be detected as early as 5 minutes post antibiotic treatment. It was also demonstrated that the need for incubation at a stable 37°C is not necessary, with incubation at room temperature correctly distinguishing susceptible and resistant organisms.

Example 10: Antibiotic susceptibility testing using VITA PCR – dose dependent response using Extraction Protocol A

The following example estimates the change of GAT relative to NED in TNA samples, extracted from HEp-2 cells which had been infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells, which were either untreated (control) or treated with antibiotic (azithromycin) at varying doses; specifically, at a concentration four times the MIC (0.128 µg/mL), six times the MIC (0.192 µg/mL) and eight times the MIC (0.256 µg/mL). Antibiotic was added at 24 hours post infection when cells were in exponential growth phase, as described in example 1, Treatment D (1.1.4). To measure GAT, chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts. To measure NED, another region of chlamydia DNA was co-amplified in the same RT-PCR using primers

targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate the VITA Indices. Further to this the VITA Indices of treated and untreated samples were used to calculate the Δ VITA Ratio.

5 **10.1 VITA PCR analysis of GAT1, GAT2 and NED**

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 5 (5.1, 5.2 and 5.3 respectively). The RT-PCR conditions used were as described in Example 5 (5.5) and reactions contained either 5 μ L of TNA template (1/1000 dilution) or no target
10 (dH₂O).

10.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.4
15 Treatment Protocol D). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.1 Extraction Protocol A) with the following modification; cell debris pelleting step was not performed during extraction of the samples in this example.

20 **10.3 Results**

Chlamydia DNA and RNA from 2 regions within the *omp1* gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified and detected in a single RT-PCR using TNA extracted from *chlamydia* cultures. These cultures were treated with serial doses of antibiotic or left untreated (control) during the exponential growth phase
25 and harvested after a 1-hour incubation (Figure 8 panel i). Table 10 shows the threshold cycle (Ct) values measured for the GAT1/2 and NED in each sample. The Δ Ct was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those Δ Ct values was estimated as $2^{\Delta\text{Ct}}$ and shown in Table 10. The
30 results were then compared between no treatment reactions (control) and those treated with the different doses of antibiotic (Figure 8 panel ii).

Table 10: Results of a triplex RT-PCR analysis of TNA from untreated samples and samples treated with serial doses of antibiotic, harvested at 1h post treatment

Sample	Threshold (Ct)		ΔCt	FC	TR 2xGAT/ 1xNED	VITA Index	$\Delta VITA$ Ratio control/treated		
	GAT 1/2	NED							
A No Antibiotic	12.30	20.26	7.96	249.58	2	124.87			
B Plus Antibiotic dose 1	12.38	19.86	7.48	178.53	2	89.28	A/B 1.4		
C Plus Antibiotic dose 2	12.63	19.77	7.14	141.37	2	70.74		A/C 1.8	
D Plus Antibiotic dose 3	12.20	18.05	5.85	57.81	2	28.91			A/D 4.3

It was predicted that cells susceptible to antibiotic treatment would have a decrease in levels of transcription in the presence of antibiotic since this would be anticipated to disrupt the normal functioning of the cells. Further, it was predicted that higher doses of antibiotic would lead to greater disruption to normal functioning and consequently transcription levels. This example was performed to demonstrate this and to establish whether the decrease in the VITA Indices of the treated cells correlates to the dose of antibiotic used.

Analysis of results shows that when TNA samples, extracted from untreated and treated groups, were amplified the Ct values for GAT1/2 was lower than the NED (Table 10), consistent with active transcription in all four samples. The fold change and VITA Indices were calculated for each sample (Table 10). Since two gene and transcript regions were used to calculate the GAT1/2, and only a single un-transcribed region was used to calculate NED, then the fold change is double that of the VITA Indices (Table 10). Comparison of VITA indices of the untreated and treated samples demonstrated a difference (Figure 8 panel ii). The difference was significant for untreated (No drug) and treated (Plus drug dose 1) ($p=0.0005$, using an unpaired t-test). For all treated samples, being not only lower than untreated samples, they were also sequentially lower the higher

the dose of antibiotic used during incubation (Figure 8 panel ii). In this experiment there was a correlation between the dose and the decrease the VITA Indices ($R^2 = 0.9775$, Figure 8 panel ii). This is consistent with a decrease in transcriptional activity in the presence of antibiotic, and the higher the dose of antibiotic given, the greater the disruption to transcriptional activity was observed. The Δ VITA Ratio is calculated by dividing the VITA Index (no antibiotic) by the VITA Index of samples treated with each dose of antibiotic (plus antibiotic dose1, dose 2 and dose 3, Table 10, Figure 8 panel ii) .

The data from this example demonstrates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. The comparison between VITA indices of treated and untreated cells, calculated as Δ VITA Ratio, demonstrated a response to the presence of antibiotic. That response to antibiotics was also greater when serially higher doses of antibiotic were used, indicating a dose dependent response. This further demonstrated the ability to use VITA Indices to examine whether cells are susceptible to an antibiotic and that a 1-hour incubation can be sufficient to determine this. The response to a drug in a dose dependent manner may find application in drug discovery or drug screening programs

Example 11 - Antibiotic susceptibility testing using VITA PCR – dose dependent response using Extraction Protocol B

The following example estimates the change of GAT relative to NED in TNA samples, extracted from HEp-2 cells which had been infected with *Chlamydia trachomatis* (serovar D). TNA was extracted from cells, which were either untreated (control) or treated with the antibiotic azithromycin at varying doses; specifically, at a concentration four times the MIC (0.128 μ g/mL), six times the MIC (0.192 μ g/mL), eight times the MIC (0.256 μ g/mL) and sixteen times the MIC (0.512 μ g/mL). Antibiotic was added at 20 hours post infection when cells were in exponential growth phase, as described in example 1, Treatment D (1.1.4). To measure GAT, Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts. To measure NED, another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate the VITA Indices. Further to this the VITA Indices of treated and untreated samples were used to calculate the Δ VITA Ratio.

11.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 9 (9.1, 9.2 and 9.3 respectively). The RT-PCR conditions used were as described in Example 9 (9.5) and reactions contained either 5 μ L of TNA template (1/1000 dilution) or no target (dH₂O).

11.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.4 Treatment Protocol D). Extraction was performed using the FireMonkey PuriSpin Extraction kit, as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B) and following manufacturer's instructions for simultaneous extraction of DNA and RNA.

11.3 Results

Co-amplification of Chlamydia DNA and RNA from 2 regions (GAT1 and GAT2), and one NED region, were monitored in a single RT-PCR using TNA extracted from chlamydia cultures. These cultures were treated with serial doses of antibiotic or left untreated (control) during the exponential growth phase and harvested at 1-hour post treatment (Figure 8 panel i). Table 11 shows the threshold cycle (Ct) values measured for the GAT1/2 and NED in each sample. The Δ Ct was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those Δ Ct values was estimated as $2^{\Delta\text{Ct}}$ and shown in Table 11. The results were then compared between no treatment reactions (control) and those treated with the different doses of antibiotic (Figure 8 panel iii).

Table 11: Results of a triplex RT-PCR analysis of TNA from untreated samples and samples treated with serial doses of antibiotic, with 1h incubation post treatment

		Threshold (Ct)						
Sample		GAT 1/2	NED	ΔCt	FC	TR 2xGAT/ 1xNED	VITA Index	ΔVITA Ratio
A	No	15.71	19.25	3.54	11.66	2	5.83	

Antibiotic							
B Plus Antibiotic dose 1	16.08	19.24	3.16	8.94	2	4.47	A/B 1.30
C Plus Antibiotic dose 2	16.01	19.07	3.06	8.36	2	4.18	A/C 1.39
D Plus Antibiotic dose 3	16.37	19.35	2.98	7.91	2	3.95	A/D 1.47
E Plus Antibiotic dose 4	16.56	19.31	2.74	6.70	2	3.35	A/E 1.74

In the same way as described in example 10, it is expected that cells susceptible to antibiotic treatment would have a reduction in transcription levels as the presence of antibiotic would be anticipated to disrupt the normal functioning of the cells. It is predicted that the disruption caused could correlate to the dose of antibiotic and as such, it would be likely that the higher the dose of antibiotic the greater the disruption to normal functioning, transcription levels and resulting VITA Indices.

Analysis of results shows that when TNA samples, extracted from untreated and treated groups, were amplified the Ct value for GAT1/2 was lower than the NED (Table 11). This is consistent with active transcription in all samples. The fold change and VITA Indices were calculated for the samples (Table 11). The fold change is double that of the VITA Indices (Table 11), since two gene and corresponding transcript regions were used to calculate the GAT1/2, and only a single non-transcribed region was used to calculate NED. Comparison of VITA indices, of the untreated (No Drug) and treated sample (Plus drug dose 1), demonstrated a significant difference (Figure 8, panel iii, $p < 0.05$ generated using an unpaired t-test). All remaining treated samples were also different to the untreated (Figure 8, panel iii). The treated samples displayed VITA Indices that were lower than untreated samples. Further, as the treatment dose increased the VITA Indices decreased (Figure 8 panel iii). This is consistent with a decrease in transcriptional activity in the presence of antibiotic and further evident that the more antibiotic used the greater the disruption to transcriptional activity was observed. This trend also generated a linear correlation ($R^2 = 0.8325$) between VITA Index and antibiotic dose (Figure 8 panel iii,

Table 11). The Δ VITA Ratio is calculated by dividing the VITA Index (no antibiotic) by the VITA Index of samples treated with each dose of antibiotic (plus antibiotic dose1, dose 2, dose 3 and dose 4). The Δ VITA Ratio displayed an increase in value correlating with the increase in antibiotic dose (Table 11).

5 The data from this example further elucidates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. The comparison between VITA indices of treated and untreated cells, calculated as Δ VITA Ratio, demonstrated a response to the presence of antibiotic. The response to antibiotics was linearly correlated with the dose used for treatment, indicating a dose dependent
10 response. This was independent of the extraction method used to obtain the TNA samples. This further established, as seen in example 10, the ability to use VITA Indices to examine whether cells are susceptible or resistant to an antibiotic and that a 1-hour incubation is sufficient. The capacity of the VITA PCR to monitor response to a drug in a dose dependent manner may find application in drug discovery or drug screening
15 programs.

Example 12 - Antibiotic susceptibility testing with Azithromycin and Doxycycline using VITA PCR

 The following example analyses the susceptibility of bacteria to a given drug, by
20 estimation of the change of GAT levels relative to NED in TNA samples. These were then compared between samples treated with antibiotic and not treated (control). Samples were obtained from HEP-2 cells which had been infected with different *Chlamydia trachomatis* strains, known to be susceptible to both drugs tested, Azithromycin and Doxycycline. TNA was extracted from cells, which had been either treated with a single
25 dose of either antibiotic (0.256 μ g/mL), or not treated (control) 20 hours post infection whilst in an exponential growth phase and incubated for one hour post-treatment. Treatment was as described in example 1, Treatment E (1.1.5). To obtain a measure GAT, Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the omp1 gene and its transcripts. To measure NED, another region
30 of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate VITA Index. Further to this the VITA Indices of treated and untreated samples were used to calculate the Δ VITA Ratio.

12.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 9 (9.1, 9.2 and 9.3 respectively). The RT-PCR conditions used were as described in Example 9 (9.5) and reactions contained either 5 µL of TNA template (1/1000 dilution) or no target (dH₂O).

12.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from different strains of *Chlamydia trachomatis*, which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.5 Treatment Protocol E). Extraction was performed using the FireMonkey PuriSpin Extraction kit, as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B) and following manufacturer's instructions for simultaneous extraction of DNA and RNA.

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12.3 Results

Chlamydia DNA and RNA from 2 GAT regions and one NED region, were co-amplified and detected in single RT-PCR from TNA extracted from chlamydia cultures. These cultures were treated with antibiotic or left untreated (control) at an exponential growth phase and harvested at 1 hour post treatment. Table 12a and 12b display the threshold cycle (Ct) values for each sample (treated or untreated) for each individual strain and antibiotic used for treatment, namely Azithromycin and Doxycycline respectively. The ΔC_t was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔC_t values was estimated as $2^{\Delta C_t}$ and shown in Table 12a and 12b. The results were then compared between no treatment reactions (control) and those treated with antibiotic for each strain. Antibiotics tested were Azithromycin (Table 12a, Figure 9 panel i) and Doxycycline (Table 12b, Figure 9 panel ii).

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Since all strains tested had previously been characterised as being susceptible to both antibiotics used in this example, a difference between the VITA Indices of treated and non-treated samples would be expected. The VITA Index of treated samples would be predicted to be lower than the untreated samples, as the presence of antibiotic would cause a disruption to normal transcriptional activity of cells. Subsequently, all samples indicated they were alive and actively transcribing regardless of treatment. This was

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observed from the amplification of TNA samples, extracted from untreated and treated groups, which displayed Ct values lower for GAT1/2 than the NED, independent of antibiotic used (Table 12a and 12b).

The fold change and VITA Indices were calculated for all samples at all time points post treatment, for each of the drugs used (Table 12a and 12b). Comparison of VITA indices, between the untreated and treated samples at each time point, demonstrated a significant difference, with VITA Indices for treated samples being lower than untreated, for all strains and antibiotics tested ($p < 0.01$ using an unpaired t-test for each group; Table 12a and 12b, Figure 9, panel i and ii). This is consistent with the predicted results, evidencing the susceptibility of the strain to the drugs used for treatment and resulting in the disruption to the transcriptional activity. The Δ VITA Ratio, calculated by dividing the VITA Index (no antibiotic) by the VITA Index with antibiotic, also displayed similar results between each strain tested with the same antibiotic, and between antibiotics also (Table 12a and 12b).

This experiment, by the results obtained, demonstrates that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices and Δ VITA Ratios. The individual responses obtained from each strain tested was consistent with its predicted susceptibility to both antibiotics used, obtained through analysis of the VITA Indices of treated vs non-treated. This further highlighted the ability to utilise VITA Indices to examine the antibiotic susceptibility of cells with a short incubation in the presence and absence of the drug of interest.

Table 12a: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, harvested one hour post treatment (PT) with Azithromycin.

		Average Threshold (Ct)							
	Sample	GAT 1/2	NED	Δ Ct	FC	TR	VITA Index	Δ VITA Ratio A/B	P value
Strain 1	A No Antibiotic	15.71	19.25	3.54	11.66	2	5.83	1.47	0.0073 **
	B Plus Antibiotic	16.37	19.35	2.98	7.91	2	3.95		
Strain 2	A No Antibiotic	15.43	19.03	3.60	12.10	2	6.05	1.42	0.0005 ***

	B Plus Antibiotic	16.33	19.43	3.09	8.53	2	4.27		
Strain 3	A No Antibiotic	17.48	21.38	3.90	14.88	2	7.44	1.31	0.0008 ***
	B Plus Antibiotic	17.85	21.35	3.50	11.33	2	5.66		
Strain 5	A No Antibiotic	17.24	21.08	3.84	14.29	2	7.14	1.30	0.0006 ***
	B Plus Antibiotic	17.69	21.15	3.46	11.00	2	5.50		

Table 12b: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, harvested 1 hour post treatment (PT) with Doxycycline.

		Average Threshold (Ct)						Δ VITA Ratio A/B	P value
	Sample	GAT 1/2	NED	Δ Ct	FC	TR	VITA Index		
Strain 1	A No Antibiotic	18.17	21.22	3.05	8.25	2	4.13	1.48	<0.0001 ****
	B Plus Antibiotic	18.87	21.35	2.48	5.59	2	2.80		
Strain 2	A No Antibiotic	15.61	18.89	3.28	9.71	2	4.86	1.24	0.008 ***
	B Plus Antibiotic	16.22	19.19	2.97	7.84	2	3.92		
Strain 3	A No Antibiotic	17.48	21.38	3.90	14.88	2	7.44	1.32	< 0.0001 ****
	B Plus Antibiotic	17.13	20.62	3.50	11.27	2	5.64		
Strain 5	A No Antibiotic	17.24	21.08	3.84	14.29	2	7.14	1.43	< 0.0001 ****
	B Plus Antibiotic	18.21	21.53	3.33	10.02	2	5.01		

Example 13: Antibiotic susceptibility testing with Rifampicin using VITA PCR using resistant and susceptible strains

The following example analyses the susceptibility of bacteria to a given drug, by estimation of the change of GAT levels relative to NED in TNA samples. These were then compared between samples treated with antibiotic and not treated (control). Samples were obtained from HEp-2 cells which had been infected with different *Chlamydia trachomatis* strains, previously characterized in culture to be either susceptible to the drug Rifampicin (total of four strains: serovar D, lab strain (strain 1), serovar L2, Wild Type lab strain (strain 2), serovar L2, Trimethoprim resistant strain (strain 3) and serovar L2, Spectinomycin resistant strain (strain 4)); or resistant to Rifampicin (serovar L2, Rifampicin resistant strain (strain 5)). TNA was extracted from cells, which had been either treated with a high dose of antibiotic, or not treated (control), 20 hours post infection whilst in an exponential growth phase. Treatment was as described in example 1, Treatment E (1.1.5), using a single concentration of Rifampicin (0.256 µg/mL), equivalent to 32 fold greater than MIC of susceptible trains and 32 fold below the MIC of the resistant strain. To obtain a measure GAT, Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the *omp1* gene and its transcripts. To measure NED, another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed. The levels of GAT and NED were estimated and used to calculate VITA Index. Further to this the VITA Indices of treated and untreated samples were used to calculate the Δ VITA.

13.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 9 (9.1, 9.2 and 9.3 respectively). The RT-PCR conditions used were as described in Example 9 (9.5) and reactions contained either 5 µL of TNA template (1/1000 dilution) or no target (dH₂O).

13.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from all different *Chlamydia trachomatis* strains (strain 1, 2, 3, 4 and 5) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.5 Treatment Protocol E). Extraction was performed using the FireMonkey PuriSpin Extraction kit, as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B) and following manufacturer's instructions for simultaneous extraction of DNA and RNA.

13.3 Results

Chlamydia DNA and RNA from 2 GAT regions and one NED region, were co-amplified and detected in single RT-PCR from TNA extracted from chlamydia cultures. These cultures were treated with antibiotic (Rifampicin) or left untreated (control) during the exponential growth phase and harvested at one hour post treatment. Table 13 displays the threshold cycle (Ct) values for the components in each sample, for each individual strain. The ΔCt was calculated as the differences between the Ct values of the NED and GAT1/2 signals. In turn, the fold change (difference between the GAT1/2 and NED) which would theoretically lead to those ΔCt values was estimated as $2^{\Delta Ct}$ and shown in Table 13. The results were compared between no treatment reactions (control) and those treated with antibiotic for each strain (Figure 9 panel iii); and results were compared for susceptible versus resistant strains. The fold change and VITA Indices were calculated for all samples at one hour post treatment (Table 13).

Comparison of VITA indices, between the untreated and treated samples presented a significant difference in the VITA indices for strains 1 – 4 ($p < 0.0001$, using an unpaired t-test, Table 13). This is consistent with a disruption to the transcription activity of cells susceptible to the antibiotic used for treatment and visible in Figure 9 panel iii. Comparison of VITA Indices for strain 5, between untreated and treated samples, showed no significant difference, with VITA Indices being similar (Figure 9, panel iii, Table 13). This is indicative of resistance to the antibiotic rifampicin when incubated at 37°C for 1h, consistent with little or no disruption to the transcription of this strain.

The $\Delta VITA$ Ratio is calculated by dividing the VITA Index (no antibiotic) by the VITA Index with antibiotic. $\Delta VITA$ Ratio was significantly lower for strain 5, the resistant strain (Table 13), further demonstrating the reduced amount of difference between the treated and untreated samples. The $\Delta VITA$ Ratio for all other strains was in all instances > 2.93 (Table 13). Graphing of the $\Delta VITA$ Ratio demonstrates visually the difference between the $\Delta VITA$ Ratio of susceptible and resistant strains (Figure 9 panel iv). These differences were also determined as statistically different ($p < 0.0001$, unpaired Welch's t-test). A threshold $\Delta VITA$ value of 1.63 allowed susceptible and resistant strains to be distinguished with 95% confidence (Figure 9, panel iv).

Results from this experiment demonstrate that the GAT1/2 and NED can be measured in a single reaction and results of this used to calculate VITA indices. Alongside this, the comparison between VITA indices of treated and untreated cells, calculated as $\Delta VITA$ Ratio, further correlated with either a response or lack thereof to the presence of antibiotic. The individual responses obtained from each strain tested was

consistent with its predicted susceptibility to the antibiotic used, whilst a lack of response was linked with the resistance profile of the strain tested. This further highlighted the ability to utilise VITA Indices to examine the antibiotic susceptibility or resistance of cells with a short incubation in the presence and absence of the drug of interest.

- 5 ***Table 13: Results of a triplex RT-PCR analysis of TNA from treated and untreated samples, with antibiotic Rifampicin, harvested 1 hour post treatment (PT) with comparison between susceptible and resistant strains.***

		Average Threshold (Ct)							
Strain	Sample	GAT1/2	NED	ΔCt	FC	TR	VITA Index	ΔVITA Ratio A/B	P value
1	A No Antibiotic	18.17	21.22	3.05	8.25	2	4.13	3.54	<0.0001 ****
	B Plus Antibiotic	20.32	21.54	1.22	2.33	2	1.17		
2	A No Antibiotic	15.61	18.89	3.28	9.71	2	4.86	2.93	<0.0001 ****
	B Plus Antibiotic	17.49	19.22	1.73	3.31	2	1.66		
3	A No Antibiotic	17.48	21.38	3.9	14.88	2	7.44	4.70	<0.0001 ****
	B Plus Antibiotic	18.81	20.47	1.66	3.16	2	1.58		
4	A No Antibiotic	16.24	20.54	4.30	19.72	2	9.86	5.86	<0.0001 ****
	B Plus Antibiotic	18.66	20.41	1.75	3.37	2	1.68		
5	A No Antibiotic	17.24	21.08	3.84	14.29	2	7.14	1.06	0.1813
	B Plus Antibiotic	17.41	21.16	3.75	13.42	2	6.71		
	No TNA	No Ct	No Ct						

Example 14 - Exemplary Antibiotic susceptibility testing using VITA PCR

The following example describes a process, illustrated in Figure 10, which could be used as a general screen for infections, including sexually transmitted infections and their antibiotic resistance/susceptibility status. A clinical specimen could be taken from a patient suspected of having a sexually transmitted infection such as *Neisseria gonorrhea* (GC), *Chlamydia trachomatis* (CT) or *Mycoplasma genitalium* (MG). The specimen could be split into subsamples, one of which is not incubated with any antibiotic, whilst the other could be incubated in the presence of a range of antibiotics used in the treatment of one or more of GC, CT and MG. Following incubation, total nucleic acid could be analysed in a multiplex VITAPCR assay with primers targeting GAT and NED specific for GC and/or CT and/or MG. Positive GAT and NED signal for a specific organism could allow diagnosis of an STI and comparison of VITA indices in the presence or absence of drugs could reveal which therapy, or therapies, may be used to treat the patient.

Further, one could analyse a large series of samples and establish threshold VITA Indices for each organism in the assay. This threshold value could then be used as a tool to diagnose these sexually transmitted infections and/or provide a method for Test of Cure following treatment with an appropriate antibiotic. Further, analysis of a large series of samples in the presence or absence of each antibiotic could allow determination of a Δ VITA Ratio Threshold capable of distinguishing sensitivity or resistance of each organism to each antibiotic. The Δ VITA Ratio Threshold could then be used as a tool to predict response to specific antibiotic in a format which would no longer require a subsample of the specimen or sample to serve as an untreated, control comparator. Further, since example 7 has shown that sensitivity and resistance can be determined following as little as a 5 minutes incubation, coupling the incubation to rapid amplification protocol could make it suitable as a rapid point of care test. Finally, since example 7 also demonstrated that incubation with the drug can be performed at room temperature, such a test should not require additional equipment beyond that required for extraction and amplification.

Example 15 - Use of VITA PCR on different loads of viable material

The following example estimates levels of NED and GAT in samples with varying loads of viable to dead bacteria. TNA was extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D), either not treated (Alive CT) or treated with a high dose 0.512 ug/ml for 40 hours of the antibiotic azithromycin (Dead CT). Upon harvesting these were mixed in different ratios to obtain different viable loads of 0%, 0.1%, 0.2%,

0.5%, 1%, 10%, 20%, 50% and 100%, as described in example 1, Treatment F (1.1.6). Chlamydia DNA and RNA was amplified by RT-PCR using primers targeting two different locations of the *omp1* gene and its transcripts to measure GAT. Another region of Chlamydia DNA was co-amplified in the same RT-PCR using primers targeting a region of genomic DNA which is not transcribed to measure NED. The levels of GAT and NED were estimated and used to calculate VITA Index.

15.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzyme oligonucleotides, Reporter substrates and PCR primers used for amplification and detection of GAT1, GAT2 and NED were as per example 9 (9.1, 9.2 and 9.3 respectively). The reverse primer for NED (SEQ ID NO 23) was substituted in this example for the following.

SEQ ID NO: 13 Reverse primer for NED 3CTinfAIGR_1
CAAGAGAGAATGTCAAAAGATAC

The RT-PCR conditions used were as described in Example 9 (9.5) and reactions contained either 5 µL of TNA template (1/100 dilution) or no target (dH₂O).

15.2 Preparation of TNA

RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.6 Treatment Protocol F). Extraction was performed using the FireMonkey PuriSpin Extraction kit, as defined in example 1 (1.3 Total Nucleic Acid (TNA) extraction, 1.3.2 Extraction Protocol B) and following manufacturer's instructions for simultaneous extraction of DNA and RNA.

15.3 Results

Chlamydia DNA and RNA (GAT), or DNA only (NED), were co-amplified in single RT-PCR from TNA extracted from a mixture of viable untreated cells (Alive CT) and cells treated with a high dose of antibiotic (Dead CT) to generate varying loads of viable chlamydia. Table 14 show the threshold cycle (Ct) values measured for each viability load, using either GAT1 or GAT1/2 in the reaction. The ΔC_t was calculated as the differences between the Ct values of the NED and GAT signals. In turn, the fold change (ratio of GAT to NED) which would theoretically lead to those ΔC_t values was estimated as $2^{\Delta C_t}$ and plotted in Table 15 and VITA Indices were plotted in Figure 11 panel i. The results were then compared to the percentage of viability in each mixture.

Analysis of viability, through infectivity and immunofluorescent staining, was performed to confirm the accuracy of load in each mixed sample. This visually confirmed the increase in Chlamydial inclusions as the percentage of viability increased (data not included).

5 Theoretically, low loads of viable cells would have lower levels of transcripts detectable in a background of genomic DNA derived from non-viable cells. If DNA is not degraded during treatment, the amount of DNA detected could be anticipated to be greater than the amount of RNA, since DNA is inherently more stable than RNA. In samples with high loads of viable cells, it is expected that higher amounts of transcripts
10 would be present.

Analysis of results showed that when TNA extracted from a 0% viable load sample was amplified, the ΔC_t value for GAT and NED was small (Table 14) indicating little or no active transcription. For all samples with 0.2% or more viable load the C_t value for GAT was lower than the NED (Table 14) consistent with active transcription.
15 The fold change and VITA Indices were calculated for all the viable loads (Table 14). The VITA indices were significantly different for sample with 0% viable load compared to those with 0.2% or greater of viable load (Figure 11 panel i, Table 14, $p < 0.05$). Significant differences were not observed between mixtures containing viable loads greater than 0.2% (Table 14, $p > 0.05$). Viability loads of 0.1% were also tested and VITA
20 Index was found to be significantly different to the VITA Index of 0% viable loads, but was also significantly different to viable loads greater than 0.2% (data not shown).

As expected, the different viable loads also lead to a difference in C_t values for the GAT and NED reactions, as the C_t values would correlate to chromosomal copies of *Chlamydia trachomatis* in each mixture. Since cells, from dead CT, were incubated with
25 drug for 40 hours this suggests there may not have only been a halt in active transcription of RNA but also of active replication of the bacteria, affecting the concentration of DNA. It is also likely that there was degradation of both DNA and RNA during this time. As such, higher loads of viable bacteria showed lower C_t values (earlier detection) than lower viability loads (detection in later PCR cycles) (Figure 11 panel ii). This also
30 correlates with the analysis of chlamydial viability from the mixtures (Figure 11 panel i).

The data from this example demonstrates that the VITA Indices correlate with the measure of viable and non-viable populations, as evidenced by the differentiation between viable populations with as low load as 0.1% and non-viable populations. This example demonstrates that GAT and NED can be measured in a single reaction and the
35 results can be used to calculate VITA Indices which correlate with the observed viability, as low as 0.1% viable load and its distinction from non-viable populations. Finally, this

example demonstrates a major advantage of VITA PCR in that it is not necessary to quantify the amount of TNA which is added to the VITA PCR as the method determines the ratio of GAT to NED regardless of the amount of starting material. Evidence for this is the fact that no significant difference is observed between viable loads, over the broad
 5 range investigated in this example.

Table 14: Results of a Triplex RT-PCR analysis of TNA from samples containing different viability loads

	Threshold (Ct)							
Sample % viable	GAT1/2	NED	ΔCt	FC	TR 2xGAT to 1xNED	VITA Index	P value	
0%	21.45	22.80	1.35	2.55	2	1.27	0.0035	
0.2%	19.16	21.77	2.60	6.08	2	3.04	**	0.1911
0.5%	17.76	20.26	2.50	5.66	2	2.83		
1%	17.06	19.52	2.47	5.53	2	2.76		
10%	13.44	16.13	2.69	6.47	2	3.23		
20%	12.28	14.85	2.57	5.95	2	2.98		
50%	11.25	13.72	2.47	5.53	2	2.76		
100%	10.24	12.66	2.42	5.36	2	2.68		
No TNA	No Ct	No Ct						

10

Example 16 – Influence of amplicon size and other RT-PCR parameters on VITA Indices

The following example estimates levels of NED and GAT in TNA samples extracted from HEp-2 cells infected with *Chlamydia trachomatis* (serovar D). TNA was
 15 extracted from cells which were not incubated with antibiotic (untreated, viable cells), and from cells incubated with antibiotic at a concentration eight times below the MIC (<MIC), at the MIC (MIC) or at 8 times greater than the MIC (> MIC), as described in example 1, Treatment Protocol A (1.2.1). Chlamydia DNA and RNA (GAT) was amplified by RT-PCR using primers targeting two different locations of the omp1 gene
 20 and its transcripts (GAT1/2). The two primer pairs used to amplify the two omp1 GAT targets in this experiment (section 16.3 SEQ ID NO4 and 24; SEQ ID NO 16 and 25) generated longer amplicons than those generated using the two GAT primer pairs used in previous examples including example 5 (section 5.3 SEQ ID NO 4 and 5, SEQ ID NO 16

and 17). The resultant amplicons were 215 bp and 311 bp long for GAT1 and GAT2 respectively. Chlamydia DNA only (NED) was co-amplified in the same RT-PCR mix using primers targeting a region of genomic DNA designated InfA_IGR which is not transcribed. The Ct values of GAT1/2 and NED were estimated for the RT-PCR for all treatments.

16.1 VITA PCR analysis of GAT1, GAT2 and NED

Partzymes were designed to assemble into two active MNazymes when they bound to amplicons generated by amplification of either the omp1 gene or omp1 transcripts. These two MNazymes were capable of binding to two different amplicons derived by amplification of two separate regions of omp1 (a GAT1 and a GAT2 region). Once assembled, both MNazymes could cleave the same reporter substrate Sub102(20)-FB. A third pair of partzymes was designed to assemble into an active MNazymes when bound to amplicons generated by amplification of a non-transcribed DNA region denoted infA_IGR thus providing a measure of NED. Once assembled, this MNzyme could cleave the reporter substrate Sub72-A1B. The sequences of Partzyme A and Partzyme B for each MNzyme are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNzyme and bases in italic refer to sequence which hybridizes to the substrate.

SEQ ID NO: 6 Partzyme A for GAT1 omp1_A4/102-P
TGGTCTCGAGCATTGAACGAACAACGAGGGACGTCGA/3Phos/
 SEQ ID NO: 7 Partzyme B for GAT1 omp1_B5/102-P
CGGTAGAGGAGGCTAGCTCATGTTCTCGATTAAGGCTG/3Phos/
 SEQ ID NO: 20 PartzymeA for GAT2 CTomp1L_A4/102-P
CTTGCACTTGGTGTGACGACAACGAGGGACGTCGA/3phos/
 SEQ ID NO: 21 Partzyme B for GAT2 CTomp1L_B5/102-P
CGGTAGAGGAGGCTAGCTCTATCAGCATGCGTGTGGGTTA/3phos/
 SEQ ID NO: 8 Partzyme A for NED CTinfAIGR_A4/72-P
TCGACTAAACAGAAAATGTCAAAAACAACGAGAGGCGTGAT/3Phos/
 SEQ ID NO: 9 Partzyme B for NED CTinfAIGR_B5/72-P
CTGGGAGGAGAGGCTAGCTCAACTTGTCAAAAAACAGAAGG/3Phos/

16.2 Reporter substrates

In the current example, two different reporter substrates were used, each labelled with distinct fluorophores. Sub102(20)-FB was end-labelled at the 5' end with 6-FAM and with IABkFQ at the 3' end, and its cleavage was monitored at 516 nm with excitation at 492 nm. Sub72-A1B was labelled with ATTO™ Rho101 at the 5' end and with IAbRQSp at

the 3'end, and its cleavage was monitored at 609nm with excitation at 592 nm. The reporter substrates for this example are shown below with the sequence, 5' to 3'. The lower case bases represent RNA and the upper case bases represent DNA.

SEQ ID NO: 10 for GAT1 and GAT2 Sub102(20)-FB

5 TCGACGTCCCguCCTCTACCG

SEQ ID NO: 11 for NED Sub72-A1B

ATCACGCCTCguCTCCTCCCAG

16.3 PCR primers for amplification of GAT1, GAT2 and NED

10 In vitro amplification of TNA template extracted from cells infected with *Chlamydia trachomatis* was performed using the primers listed below. The Forward and Reverse primers were used to amplify two regions of the omp1 gene and transcripts (GAT1 and GAT2) and infA_IGR DNA (NED) by RT-PCR. All sequences are written 5' to 3'.

SEQ ID NO: 4 Forward primer for GAT1 5omp1

15 CTTCTTCCTGGGACGAACG

SEQ ID NO: 24 Reverse primer for GAT1 3omp1_2Lhp3

GAGCTATAATTAGCTCTCTTTGTGCTC

SEQ ID NO: 16 Forward primer for GAT2 5CTomp1_1

TTTCGGCGGAGATCCTTGCGATCC

20 SEQ ID NO: 25 Reverse primer for GAT2 3CTomp1_6

GATATCCACTGGTGGCTCCTAA

SEQ ID NO: 12 Forward primer for NED 5CTInfAIGR_2

GAGAGAGTGATTATATCGACTAA

SEQ ID NO: 23 Reverse primer for NED 3CTinfAIGR_3

25 GCAAAACTCAAGAGAGAATGTC

16.4 Preparation of TNA

30 RNA and DNA (TNA) were co-extracted from *Chlamydia trachomatis* (serovar D) which had been obtained through in-vitro methods, cultured in HEp-2 cells, as described in example 1 (1.1 Culture, 1.1.1 Treatment Protocol A). Extraction was performed as a LLE technique, using phenol:chloroform:isoamyl, also described in example 1 (1.3 Total Nucleic Acid (TNA) extraction).

16.5 Reaction components

35 All reactions contained 40 nM of each Forward primer, 200 nM of each Reverse primer, 200 nM of each partzyme A, 200 nM of each partzyme B, 400nm of substrate

SEQ ID NO 10, 200 nM substrate SEQ ID NO 11, 1x SensiFAST Probe No-ROX Mix One-Step (Bioline), 2 mM MgCl₂ (Bioline), 0.2 U/μL RiboSafe RNase Inhibitor (Bioline), 0.2 μL of Reverse Transcriptase enzyme (Bioline) and nuclease free water (Ambion), in a total volume of 20 μL. All reactions were performed in triplicate on a
 5 BioRad® CFX96 thermocycler. The cycling parameters were 48°C for 10 minutes, 95°C for 2 min, 10 cycles of 95°C for 5 seconds and 61°C for 30 seconds (with a 0.5°C decrease in temperature per cycle), and 30 cycles of 95°C for 5 seconds and 52°C for 50 seconds. The reactions contained either 5 μL of TNA template (1/1000 dilution) or no target (dH₂O).

10

16.6 Results

Chlamydia DNA and RNA from 2 regions within the omp gene and transcripts (GAT1 and GAT2), and one NED region, were co-amplified in single RT-PCR from TNA extracted from viable untreated cells and from cells incubated with antibiotic at
 15 concentrations below (<MIC), equal to (MIC) or above the MIC (>MIC). Table 15 shows the threshold cycle (Ct) values measured for NED, and for the combined signals from GAT1 and GAT2 (GAT1/2), in each sample. The ΔCt was calculated as the differences between the Ct values of the NED and GAT1/2. In turn, the fold change (ratio of GAT to NED) which would theoretically led to those ΔCt values was estimated as 2^{ΔCt} and shown
 20 in Table 15. The VITA Indices were calculated by dividing the FC by the TR. The results were then compared to the viability in each cell population.

Primer pairs used in this example generated longer amplicons than that observed in previous examples. Amplicon lengths were 215 bp and 311 bp for GAT1 and GAT2 respectively. The use of longer amplicons may be expected to provide more accurate and
 25 stringent estimation of the viability of the organism in question, because these primer sets will amplify less of short, residual fragments associated with dead cells or cells where expression is decreased by the presence of an antibiotic. The use of longer versus shorter amplicons for the GAT would therefore be expected to alter the absolute values obtained for VITA Indices for each of the samples tested (untreated or treated with different doses
 30 of antibiotic) but would not be expected to alter the correlation between cell viability as measured by immunofluorescent staining (**Figure 3 panel i and ii**) or the information that can be inferred by examination of the VITA Indices (Table 15, Figure 12)

35

Table 15: Results of triplex RT-PCR analysis of TNA from treated and untreated samples, amplified using primer pairs creating long amplicon lengths for GAT1 and GAT2

Sample	Threshold (Ct)		ΔC_t	FC	TR 2xGAT/1xNED	VITA Index
	GAT1/2	NED				
No Antibiotic	19.20	20.65	1.45	2.73	2	1.37
< MIC	21.06	22.67	1.61	3.05	2	1.53
MIC	30.54	30.82	0.28	1.21	2	0.61
> MIC	29.21	29.21	-0.33	0.80	2	0.40
No TNA	No Ct	No Ct				

Analysis of results shows that when TNA samples extracted from untreated or treated samples below the MIC, were amplified the Ct value for GAT1/2 was lower than the NED (Table 15) consistent with active transcription in both sample types. For GAT1/2 and NED from TNA treated at the MIC level or above, the differences in Ct value were very low (< 1) (Table 15) indicating DNA is not being actively transcribed. The fold change and VITA Indices were calculated for the four sample types (Table 15). Since two genes and their transcripts were used to calculate the GAT1/2, and only a single untranscribed region was used to calculate NED, then the fold change is divided by the TR to calculate the VITA Indices (Table 15). The data demonstrates that long GAT amplicons translated into lower VITA Indices (Figure 12) comparatively to shorter amplicons used for detection as seen in example 5 (Figure 5 panel ii). This indicates that fewer partially degraded transcript fragments are being detected by the GAT primers that generate longer amplicons.

The results from this example demonstrate that GAT and NED can be measured in a single reaction and the results used to calculate VITA Indices which correlate with the observed viability of cells. It further displays differences in VITA Indices between viable and non-viable samples, with VITA Indices being lower than that observed with short amplicons for GAT1 and GAT2. Despite the different parameters used in this example the ultimate distinction between viable and non-viable cells is accurately called, with similar trends observed for all samples comparatively to VITA Indices with shorter amplicons for GAT1 and GAT2.

Example 17 – Exemplary Test of Cure and Antibiotic susceptibility testing for *Neisseria gonorrhoeae* using VITA PCR

5 The following example describes an assay targeting GAT and NED used for diagnosis, TOC and AST for *Neisseria gonorrhoeae* (GC). The assay would estimate the change of GAT relative to NED in TNA samples. To measure GAT, gonorrhoeae DNA and RNA would be amplified by RT-PCR using primers targeting locations of a gene and its transcripts or multiple genes and their transcripts. To measure NED, another region of
10 gonorrhoeae DNA would be co-amplified in the same RT-PCR reaction using primers pairs targeting a region of genomic DNA which is not transcribed. Potential GAT and NED targets can be screened as per example 3. The levels of GAT and NED would be estimated and used to calculate the VITA Indices. The VITA indices generated would allow the determination of viability of the organism in any given sample (e.g. urine,
15 vaginal swab, rectal swab or throat swab). Further to this, the sample could also be used for Antibiotic susceptibility testing by splitting the sample and incubating it in the presence and absence of a desired drug or multiple drugs. The levels of GAT and NED would be estimated and used to calculate the VITA Indices for each condition. Further to this the VITA Indices of treated and untreated samples would be used to calculate the
20 Δ VITA, ultimately determining the susceptibility or resistance profile of the organism. This would aid in the guidance of therapy, with the best choice antibiotic being given at first presentation of symptoms.

Potential target genes and respective sequences of MNazymes, reporter substrates and primer pairs used for their amplification are listed in the following sections (17.1,
25 17.2 and 17.3). Reporter substrates are different to those tested for GAT and NED assays targeting *Chlamydia trachomatis*, allowing for the potential to multiplex all targets together, as embodied in example 14, Figure 10. Further target organisms may also be further included (example 14, Figure 10). This would permit identification, confirmation of status of infection and antibiotic susceptibility testing, in a single reaction for both
30 organisms.

17.1 Candidate targets for GAT1, GAT2 and NED for VITA PCR analysis

Partzymes have been designed to assemble into two active MNazymes when they bound to amplicons generated by amplification of different genes, the ompA or cysK
35 gene or transcripts. These two MNazymes are designed to bind to two different amplicons derived by amplification of the two separate genes, representing GAT1 and

GAT2 respectively. Once assembled, both MNazymes could cleave the same reporter substrate Sub97(20)-JB. A third pair of partzymes has been designed to assemble into an active MNzyme when bound to amplicons generated by amplification of a non-transcribed DNA region denoted IGR1109 which is a candidate for measuring NED.

5 Once assembled, this MNzyme would be capable of cleaving the reporter substrate Sub84(20)-CB. The sequences of partzyme A and Partzyme B for each MNzyme are listed below, from 5' to 3'. Bases in bold hybridize with the target, underlined bases form part of the catalytic core in the assembled MNzyme and bases in italic refer to sequence which hybridizes to the substrate.

10 SEQ ID NO: 26 Partzyme A for GAT1 NGompA_3A4/97-P
GGTTGCCTACTATCTGCAGAACAACGAGAGGACTAGG/3Phos/
 SEQ ID NO: 27 Partzyme B for GAT1 NGompA_3B5/97-P
GACGTGAGGAGGCTAGCTCGCGCGGCGTGGCGGCT/3Phos/
 SEQ ID NO: 28 Partzyme A for GAT2 NGcysK_3A4/97-P
 15 **ACGACAGCATTGCCAAAGTGACAACGAGAGGACTAGG**/3Phos/
 SEQ ID NO: 29 Partzyme B for GAT2 NGcysK_3B5/97-P
GACGTGAGGAGGCTAGCTCCGAACGAAGCGGCTTTTG/3Phos/
 SEQ ID NO: 30 Partzyme A for NED NG1109IGR_A4/84-P
TGCTTTTGCTGTGAAAAAGGGACAACGAGAGGGTTCGAG/3Phos/
 20 SEQ ID NO: 31 Partzyme B for NED NG1109IGR_B5/84-P
GGACGAGGGAGGCTAGCTCTGAAATTGCCAACAATCCTG/3Phos/

17.2 Reporter substrates

In the current example, two different reporter substrates, labelled with distinct
 25 fluorophores would be useful in detection in systems incorporating the partzymes/MNzyme listed above. These substrates are Sub97(20)-JB end-labelled at the 5' end with 5-JOEN and IABkFQ at the 3' end, the cleavage of which could be monitored at 555 nm with excitation at 529 nm and Sub84(20)-CB labelled with 5Cy5 at the 5' end and with IABRQSp at the 3' end, the cleavage of which could be monitored at 668nm with
 30 excitation at 648 nm. These reporter substrates are shown below with the sequence, 5' to 3' where lower case bases represent RNA and the upper case bases represent DNA.

SEQ ID NO: 32 for GAT1 and GAT2 Sub97(20)-JB
 CCTAGTCCTCguCCTCACGTC
 SEQ ID NO: 33 for NED Sub84(20)-CB
 35 CTCGACCCTCguCCCTCGTCC

17.3 PCR primers for amplification of GAT1, GAT2 and NED

Amplification of TNA could be performed using the primers listed below. The Forward and Reverse primers are designed to amplify two separate genes and transcripts, ompA and cysK (GAT1 and GAT2) as well as IGR1109 DNA (NED) by RT-PCR. All sequences are written 5' to 3'.

5	SEQ ID NO: 34	Forward primer for GAT1	5NGompA_1
	CGGCACGCAAATCGAAATCC		
	SEQ ID NO: 35	Reverse primer for GAT1	3NGompA_L1
	TGCGCGCGGCCTTCAACC		
10	SEQ ID NO: 36	Forward primer for GAT2	5NGcysK_3W3g
	CTTGGTGGACGCTCATGCA		
	SEQ ID NO: 37	Reverse primer for GAT2	3NGcysK_2W3a
	GCCTTCTTTTCCGCCATTACA		
	SEQ ID NO: 38	Forward primer for NED	5NG1109IGR_1
15	GTTTTACGCCTGCTTTTGC		
	SEQ ID NO: 39	Reverse primer for NED	3NG1109IGR_1
	GACGCTCAAAACGCGGACGA		

Primers for GAT for additional candidate genes including *porB* and *rpmB* can be screened using the method outlined in example 3.

Example 18 – Influence of amplification efficiency, sensitivity, inclusivity and specificity on VITA Indices

The following example discusses parameters that can further influence the absolute values observed for the VITA Indices obtained for a specific multiplexed assay. The amplification efficiencies of GAT and NED assays included in the VITA PCR analysis should ideally be high and equal for GAT and NED. The amplification efficiencies of GAT1, GAT2 and NED targeting *Chlamydia trachomatis*, used in several examples, including Example 5, were estimated using synthetic target sequences serially diluted and found to be similar to each other, with efficiencies close to 100%, with $R^2 > 0.998$ (data not shown). When all components of the reaction are efficient and comparable to each other, the VITA indexes obtained have been shown to allow accurate differentiate between viable and non-viable cells, as evidenced in example 5 (figure 5 panel ii).

Another important factor is the length of the amplicons generated by amplification with the GAT and NED primers. As previous shown (example 16) VITA PCR systems generating longer amplicons may have lower observed values for VITA Indices,

compared to systems generating shorter amplicons. However, whilst the absolute values of the VITA Indices can change, the correlation between the observed values and viability is maintained.

Factors affecting the power of VITA PCR to provide a versatile tool for basic
5 research and clinical investigations include the sensitivity, inclusivity and specificity. Sensitivity impact the ability to detect target, specifically at the lower limit of detection, such as <10 copies. Inclusivity would relate to the ability to detect all strains and serovars, within the same species of organism, with the same efficiency. Specificity would relate to the detection of target being specific only to the organism of interest. Detection of “off
10 target”, but related species, could cause increased VITA Indices not reflective of the viability of the cell, organism or virus of interest.

It has also been discussed that the target used for GAT and NED must be chosen carefully. Example 3 shows a method for determining if a specific sequence meet the criteria ie GAT must target DNA region which is expressed, while NED primers must
15 target a region which is not expressed. The examples in this document have shown that it is possible to use more than one GAT in a particular VITA PCR. This is in fact highly desirable, as specific genes may only be expressed during certain stages in the development cycle of, for example, bacteria. An assay containing multiple genes expressed, preferably at high levels under different conditions, could ensure expression
20 will consistently be detectable in various conditions.

Finally, the choice of GAT targets is predicted to be dependent on the organism and the antibiotic under investigation. For example, studies by other groups have shown that the *porB* and *rpmB* transcripts of *Neisseria gonorrhoeae* are highly expressed and change in expression levels in response to the antibiotic ciprofloxacin. The *Chlamydia*
25 *trachomatis* *omp1* gene and its transcripts has been shown (example 9) to be suitable for discriminating resistance or susceptibility to rifampicin, and able to reflect viability of the organism.

CLAIMS

1. A method for normalising quantitative data obtained by amplification of nucleic acids from a cell, organism, or virus, the method comprising:

- (i) obtaining quantitative data
 - from amplification of genomic DNA from a first gene and RNA transcribed from the first gene, and
 - from amplification of a sequence of non-transcribed DNA in the cell, organism, or virus; and

(ii) using the quantitative data to derive a normalised value (nV) representative of the relative amounts of:

- said genomic DNA and RNA transcripts of the first gene, to
 - said genomic DNA that is not transcribed, present within the nucleic acid sample prior to said amplification;
- wherein said genomic DNA from the first gene and RNA transcribed from the first gene, and said sequence of non-transcribed DNA, are co-amplified in the same reaction.

2. The method of claim 1, wherein the quantitative data is amplicon copy number, and the method comprises:

- obtaining a value A (vA) representing total amplicon number generated from the amplification of said genomic DNA and RNA transcripts of the first gene, and a value B (vB) representing total amplicon number generated from the sequence of non-transcribed DNA;
- calculating a normalised value (nV) using the equation:
$$vA/vB = nV$$
or an equivalent form thereof.

3. The method of claim 1, wherein the quantitative data is amplicon copy number, and the method comprises:

- obtaining a value X (vX) representing total amplicon number generated from: the amplification of genomic DNA and RNA transcripts from the first gene, and amplification of genomic DNA and RNA transcripts from at least one additional gene;
- obtaining a value B (vB) representing total amplicon number generated from the sequence of non-transcribed DNA,
- calculating a normalised value (nV) using the equation:

$$vX / (vB \times (X+1)) = nV$$

or an equivalent form thereof,

wherein X is the number of said additional gene(s).

4. The method of claim 2 or claim 3, wherein the amplification is digital polymerase chain reaction (dPCR).

5. The method of claim 1, wherein the quantitative data is threshold value (Ct), and the method comprises:

- obtaining a cycle threshold value CtA from the amplification of said genomic DNA and RNA transcripts of the first gene,
- obtaining a cycle threshold value CtB from the amplification of the sequence of non-transcribed DNA; and
- calculating a normalised value (nV) using the equation:

$$2^{CtB - CtA} = nV$$
or an equivalent form thereof.

6. The method of claim 1, wherein the quantitative data is threshold value (Ct), and the method comprises:

- obtaining a cycle threshold value CtX from: the amplification of said genomic DNA and RNA transcripts of the first gene, and from amplification of genomic DNA and RNA transcripts from at least one additional gene;
- obtaining a cycle threshold value CtB from the amplification of the sequence of non-transcribed DNA; and
- calculating a normalised value (nV) using the equation:

$$2^{CtB - CtX} / (X + 1) = nV$$
or an equivalent form thereof,
wherein X is the number of said additional gene(s).

7. The method of claim 5 or claim 6, wherein the amplification is quantitative polymerase chain reaction (qPCR).

8. The method of any one of claims 1 to 7, wherein the sequence of non-transcribed DNA is genomic DNA.

9. The method of any one of claims 1 to 8, further comprising conducting said amplification of the nucleic acids from the cell, organism, or virus.
10. The method of any one of claims 1 to 9, wherein the nucleic acids from the cell, organism, or virus are an extract of total nucleic acids.
11. The method of any one of claims 1 to 10, wherein any said amplification is conducted using: polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), strand displacement amplification (SDA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), recombinase polymerase amplification (RPA), helicase dependant amplification (HDA), strand invasion based amplification (SIBA), transcript-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), or any combination thereof.
12. The method of any one of claims 1 to 11, further comprising using the normalised value (nV) to assess the level of transcriptional activity in the cell, organism, or virus.
13. The method of any one of claims 1 to 12, further comprising:
- obtaining a transcription-negative normalised value (nV-) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity; and
 - comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the transcription-negative normalised value (nV-), to thereby assess the level of transcriptional activity in the cell, organism, or virus.
14. The method of claim 13, wherein the transcription-negative normalised value (nV-) is a mean value generated from said series of said normalised values (nV).
15. The method of claim 13 or claim 14, wherein:
- the transcription-negative normalised value (nV-) is used as a base value for assessing a presence or an absence of transcriptional activity in the cell, organism or virus; and

- an absence of transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or below the transcription-negative normalised value (nV-); or

- transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is above the transcription-negative normalised value (nV-).

16. The method of any one of claims 13 to 15, wherein said transcription-negative normalised value (nV-):

- incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known not to have transcriptional activity; and/or

- is provided with a confidence interval that said transcription-negative normalised value (nV-) is predictive of a presence or an absence of transcriptional activity in the cell, organism or virus.

17. The method of claim 16, wherein the confidence interval is more than 90%, or more than 95%.

18. The method of any one of claims 13 to 17, further comprising:

- obtaining a transcription-positive normalised value (nV+) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the transcription-positive normalised value (nV+), to thereby assess the level of transcriptional activity in the cell, organism, or virus.

19. The method of claim 18, wherein the transcription-positive normalised value (nV+) is a mean value generated from said series of said normalised values (nV).

20. The method of claim 18 or claim 19, wherein:

- the transcription-positive normalised value (nV+) is used as a base value for transcriptional activity in the cell, organism or virus; and

- a lack or absence of transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is below the transcription-positive normalised value (nV+); or

- transcriptional activity is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or above the transcription-positive normalised value (nV+).

21. The method of any one of claims 18 to 20, wherein said transcription-positive normalised value (nV+):

- incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to have transcriptional activity; and/or

- is provided with a confidence interval that said transcription-positive normalised value (nV+) is predictive of a presence or an absence of transcriptional activity in the cell, organism or virus.

22. The method of claim 21, wherein the confidence interval is more than 90%, or more than 95%.

23. The method of claim 13, further comprising:

- obtaining a transcription-negative normalised value (nV-) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known not to have transcriptional activity;

- obtaining a transcription-positive normalised value (nV+) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to have transcriptional activity; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to:

- (i) the transcription-negative normalised value (nV-) and to the transcription-positive normalised value (nV+), or

- (ii) to a combined transcription normalised value (nV[±]) intermediate to the transcription-negative normalised value (nV-) and the transcription-positive normalised value (nV+),

to thereby assess the level of transcriptional activity in the cell, organism, or virus.

24. The method of claim 23, wherein the combined transcription normalised value ($nV^{\pm}$) is calculated using the equation:

$$(nV^{+}) + (nV^{-}) / 2 = (nV^{\pm})$$

or an equivalent form thereof.

25. The method of claim 24, wherein said combined transcription normalised value ($nV^{\pm}$):

- incorporates statistical variation in said series of transcription-negative normalised value (nV^{-}) and/or said transcription-positive normalised value (nV^{+}); and/or
- is provided with a confidence interval that said combined transcription normalised value ($nV^{\pm}$) is predictive of a presence or an absence of transcriptional activity in the cell, organism or virus.

26. The method of claim 25, wherein the confidence interval is more than 90%, or more than 95%.

27. The method of any one of claims 12 to 26, wherein the level of transcriptional activity in the cell, organism, or virus is assessed for the purpose of determining any one or more of:

- viability of the test cell or the test organism;
- whether the test cell, organism or virus is alive or dead;
- transcriptional perturbation within the test cell, organism, or virus.

28. The method of any one of claims 1 to 11, further comprising using the normalised value (nV) to assess the level of drug resistance or drug sensitivity in the cell, organism, or virus, wherein:

- said cell, organism, or virus has been treated with a drug prior to said amplification of nucleic acids, and
- said normalised value (nV) is compared to a control normalised value (cnV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to be:

- (i) resistant to the drug; or
- (ii) sensitive to the drug,

to thereby assess the level of drug resistance or drug sensitivity in the cell, organism, or virus.

29. The method of any one of claims 1 to 11 or 28, further comprising:

- obtaining a drug-sensitive normalised value (dsV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to be sensitive to the drug; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the drug-sensitive normalised value (dsV), to thereby assess the level of drug resistance or drug sensitivity or in the cell, organism, or virus, wherein the cell, organism, or virus has been treated with a drug prior to said amplification of nucleic acids.

30. The method of claim 29, wherein the drug-sensitive normalised value (dsV) is a mean value generated from said series of said normalised values (nV).

31. The method of claim 29 or claim 30, wherein:

- the drug-sensitive normalised value (dsV) is used as a base value for assessing a presence or an absence of resistance or sensitivity to the drug in the cell, organism or virus; and

- resistance to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is above the drug-sensitive normalised value (dsV); or

- sensitivity to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or below the drug-sensitive normalised value (dsV).

32. The method of any one of claims 29 to 31, wherein said drug-sensitive normalised value (dsV):

- incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to be sensitive to the drug; and/or

- is provided with a confidence interval that said drug-sensitive normalised value (dsV) is predictive of a presence or an absence of:

- (i) resistance to the drug in the cell, organism or virus; or
- (ii) sensitivity to the drug in the cell, organism or virus.

33. The method of claim 32, wherein the confidence interval is more than 90%, or more than 95%.

34. The method of any one of claims 1 to 11 or 28, further comprising:

- obtaining a drug-resistant normalised value (drV) generated using a series of said normalised values (nV) obtained from individuals of a population of the cells, organisms, or viruses known to resistant to the drug; and

- comparing the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus to the drug-resistant normalised value (drV), to thereby assess the level of drug resistance or drug sensitivity or in the cell, organism, or virus, wherein the cell, organism, or virus has been treated with a drug prior to said amplification of nucleic acids.

35. The method of claim 34, wherein the drug-resistant normalised value (drV) is a mean value generated from said series of said normalised values (nV).

36. The method of claim 34 or claim 35, wherein:

- the drug-resistant normalised value (drV) is used as a base value for assessing a presence or an absence of resistance or sensitivity to the drug in the cell, organism or virus; and

- resistance to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is equal to or above the drug-resistant normalised value (drV); or

- sensitivity to the drug is indicated when the normalised value (nV) obtained by said amplification of nucleic acids from the cell, organism, or virus is below the drug-resistant normalised value (drV).

37. The method of any one of claims 34 to 36, wherein said drug-resistant normalised value (drV):

- incorporates statistical variation in said series of normalised values (nV) from individuals of the population of the cells, organisms, or viruses known to be resistant to the drug; and/or

- is provided with a confidence interval that said drug-resistant normalised value (drV) is predictive of a presence or an absence of:

- (i) resistance to the drug in the cell, organism or virus; or

(ii) sensitivity to the drug in the cell, organism or virus.

38. The method of claim 37, wherein the confidence interval is more than 90%, or more than 95%.

39. The method of one of claims 1 to 11, further comprising using the normalised value (nV) to assess the level of drug resistance or drug sensitivity in the cell, organism, or virus, wherein:

- a first population of said cell, organism, or virus which has been treated with a drug prior to said amplification of nucleic acids, is used to generate a first said normalized value (nV),

- a second population of said cell, organism, or virus which has not been treated with a drug prior to said amplification of nucleic acids, is used to generate a second said normalized value (nV),

- said first normalized value (nV) and said second normalized value (nV) are compared to assess the level of transcriptional activity in the cell, organism, or virus with or without drug treatment, and thereby assess the level of drug resistance or drug sensitivity in the cell, organism, or virus.

40. The method of claim 39, wherein said drug sensitivity is indicated when said first normalized value (nV) is lower than said second normalized value (nV).

41. The method of any one of claims 28 to 40, wherein the drug is an antimicrobial.

42. The method of any one of claims 28 to 41, wherein the drug is an antimicrobial of a class selected from: Aminoglycosides, ansamycins, carbacephem, carbapenems, cephalosporins, glycopeptides, macrolidespenicillins, monobactams, polypeptides, quinolones, sulphonamides, tetracyclines.

43. The method of any one of claims 28 to 42, wherein the drug is Ciprofloxacin, Azithromycin, Rifampicin, or Doxycycline.

44. The method of any one of claims 28 to 43, wherein the first gene is a gene from a *Chlamydia* species (e.g. *Chlamydia trachomatis*), a *Gonorrhea* species, or a mycoplasma species (e.g. *Mycoplasma genitalium*).
45. The method of claim 44, wherein said reaction comprises using reverse transcriptase.
46. The method of any one of claims 1 to 45, wherein the cell is a mammalian cell, a human cell, an animal cell, a plant cell, a bacterial cell, a host cell infected by viruses, or a host cell of infected by bacteria.
47. The method of any one of claims 1 to 46, wherein the organism is a mammal, a human, a plant, a bacterium, a virus, a fungus, an alga, an archaeon or a protozoan.