DropSense16 App – DNA mammalian

Quantification of mammalian DNA using cDrop

Fig 1. *App button on the DropSense16 app selection screen*

Introduction

An app for precise quantification of mammalian DNA is available on DropSense16. Trinean's proprietary cDrop software is used to analyse the UV/VIS spectral shape of the sample to isolate the profile of the desired analyte (here DNA) from interfering contaminants. The specific DNA profile is then used to determine the correct DNA concentration. In this note we describe how to use this application and how to interpret its results.

App description

This cDrop app is specifically designed to quantify genomic DNA from mammalian origin. The sample source can vary, including: human or animal blood, saliva, tissue or cell lines. This app is fit to use in combination with most extraction methods or commercial kits for DNA isolation. For proper use of this application, always use pure water as blank(s) on DropSense16 slides.

Fig 2. *Illustrations of the results display*

Results

The cDrop algorithms in this app will analyse the measured UV/VIS spectrum (white curve) to extract specific profiles (see figure 2):

- ***DNA*** *(blue) = molecule of interest. This profile is specific for dsDNA (40-45 %GC)*
- ***Impurities*** *(orange) = non-DNA molecules that also absorb in the UV-region. By tapping on the impurities info, additional data appears on the presence of RNA residue, thiocyanate salts, Buffer components and phenol respectively.*
- ***Background*** *(grey) = profile combining intrinsic sample turbidity. By tapping on the background info, additional info on contaminants causing scatter like beads and haemoglobin/heme (absorbance max at 405 nm) is shown. This background spectrum is subtracted from the measurement prior to cDrop analysis.*
- ***Residue*** *(yellow) = unidentified part of the measured spectrum, also shown as % of the measured spectrum (white curve)*

In certain cases, a measurement doesn't allow specific quantification of the dsDNA fraction: **(1)** samples with A260 below 0.5 OD (10mm) after background correction or **(2)** samples with residue is above 2.5% due to an unknown component. In these circumstances, a total nucleic acids spectrum will be displayed instead of the DNA profile. The concentration is calculated using the A260 value of this profile multiplied by the concentration factor of dsDNA (= 50).

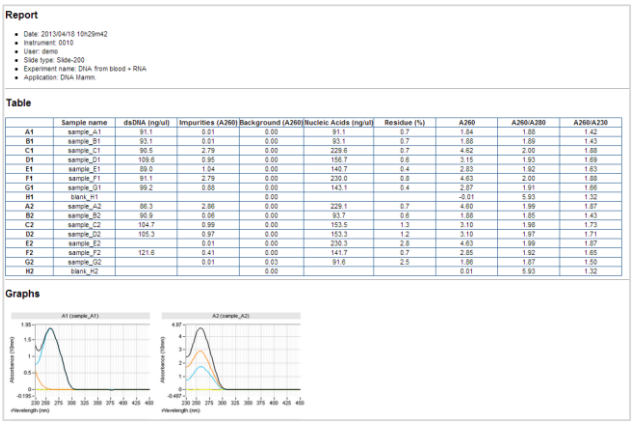

Fig 3. *Example of HTML report*

Report

Two report types are generated: an HTML file and a CSV file (opens in Windows excel). Both reports include a table containing all cDrop information as shown on the results screen as well as the classic spectrometry data like A260, 260/230 and 260/280 absorbance data (see figure 3). In addition, the HTML report also contains an illustration of all cDrop curves of each separate sample (figure 3).

These reports can be exported from DropSense16 using a USB key or the network connection. A folder is exported containing both reports and the DropSense16 specific measurement file (.bin).

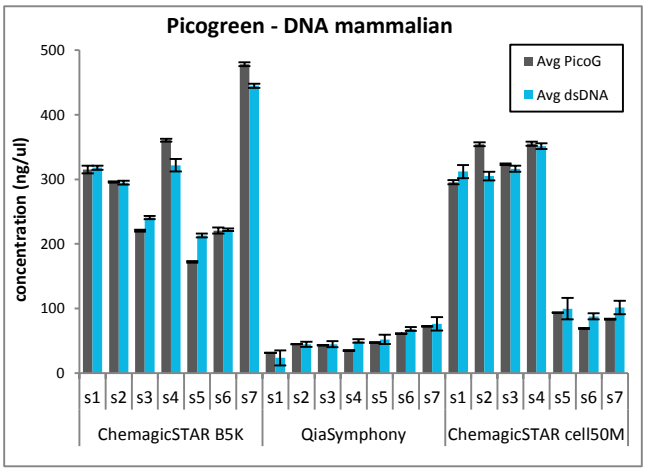

Fig 4. *Comparative data Picogreen – DropSense16 DNA mammalian application*

Results

In figure 4 DNA samples were quantifed using the Picogreen assay and compared to dsDNA data measured by the DNA mammalian application on DropSense16. The DNA samples are isolated using different methods (ChemagicSTAR and QiaSymphony) and originate from different sources (blood and cells). As shown, the DropSense16 results have a close resemblance to the dsDNA specific picogreen results (Quant-iT™ PicoGreen® dsDNA Assay Kit, life technologies).

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