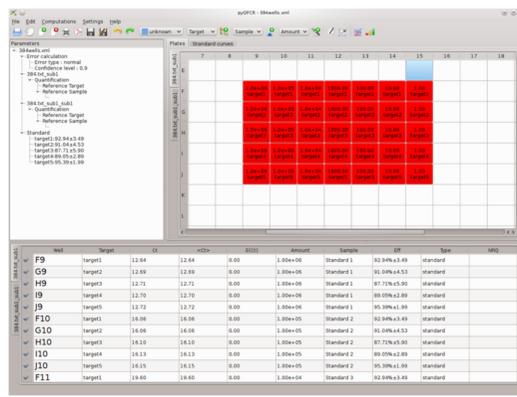


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. Results at the root of the AUC parameter can be approximated in relative terms. Examples are the numbers of molecules per cell or per mL of the blood sample. It is as simple as a comparison of the Ct-values. Gag-probe is able to bind simultaneously to the episome and the genomic DNA, where during the amplification process the bound genes can be amplified more efficiently due to their proximity. Thus, the efficiency is greater than that achieved with general primer pairs [15]. One of the important aspects of Gag-probe is the significantly lower variability of the qPCR Ct-values compared to the traditional dPCR method [8]. However, Gag-probe enables the reliable detection of all the viruses types (N-RTI and N-NNRTI) using a single primer pair [15]. The unique primer design of the Gag-probe makes it possible to identify the mutations that have occurred in NNRTI-resistant HIV-1. It is also possible to measure the selection of resistant mutations based on the geometric mean of Ct-values [15]. Due to the high sensitivity of Gag-probe, it is possible to detect almost all the cell-associated HIV-1 in any given sample. Several studies have demonstrated the stability and reproducibility of Gag-probe [16]–[18]. In addition, the results of the amplification reaction with Gag-probe are stable over time, which makes it possible to reliably detect viral loads. Interestingly, with the Gag-probe it is possible to amplify the samples more efficiently and reliably compared to dPCR. Gag-probe has a high signal-to-noise ratio. The number of the detected molecules is more than tenfold higher compared to the other methods used to detect HIV-1. The results obtained with Gag-probe are comparable to the results obtained using ViroSeq® Assay [19], [20], which uses a more specific probe. In addition, Gag-probe uses a single probe that can amplify all HIV-1 types and thus Gag-probe is more versatile and applicable to all HIV-1 types. Conclusion [10] ===== 82157476af

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