



June 2022

QIASymphony® DSP Circulating DNA Kit

Instructions for Use (Performance Characteristics)

Version 2



For In Vitro Diagnostic Use

For use with QIASymphony DSP Circulating DNA Kit



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Performance Characteristics available electronically and can be found under the resource tab of the product page on www.qiagen.com.

General introduction

The QIAAsymphony DSP Circulating DNA system constitutes a ready-to-use in vitro system for the qualitative purification of circulating cell-free DNA (ccfDNA) from human plasma and urine.

The QIAAsymphony DSP Circulating DNA Kit is intended to be used only in combination with the QIAAsymphony SP instrument.

The QIAAsymphony DSP Circulating DNA Kit provides reagents for fully automated and simultaneous purification of ccfDNA from a broad range of human plasma types (with ccfDNA profile stabilizers, e.g., Cell-Free DNA BCT® from Streck® as well as without ccfDNA profile stabilizers, e.g., EDTA tubes) and human urine (with and without ccfDNA profile stabilizers). However, a performance characteristic for every blood collection tube has not been established and must be validated by the user.

The purified ccfDNA is compatible with a wide range of downstream applications, such as PCR chemistries, fluorescence-based quantification assays or NGS.

The QIAAsymphony SP performs all steps of the purification procedure. Up to 96 samples, in batches of 24, are processed in a single run. Urine samples may require manual sample pretreatment.

Note: Performance Characteristics highly depends on various factors and relates to the specific downstream application. It has been established for the QS DSP Circulating DNA Kit in conjunction with exemplary downstream applications. However, methods for isolating nucleic acids from biological specimen are used as a front-end for multiple downstream applications, performance parameter, for example, cross contamination and run precision need to be established for any such workflow as part of the downstream application development. Therefore, it is the responsibility of the user to validate the whole workflow to establish appropriate performance parameters.

Basic performance

The basic performance for the QIAAsymphony DSP Circulating DNA Kit was evaluated using 48 single donors for ccfDNA extraction from 4 ml Streck plasma as well as 4 ml stabilized urine. The ccfDNA yield has been determined with an in-house real-time PCR assay for the 18S ribosomal RNA coding sequence.

The difference in yields (\log_{10} copies/ml) in Figure 1 (4 ml plasma) and Figure 2 (4 ml urine) reflect the strong donor-dependent concentrations of ccfDNA typically found in the same volume of the respective sample material.

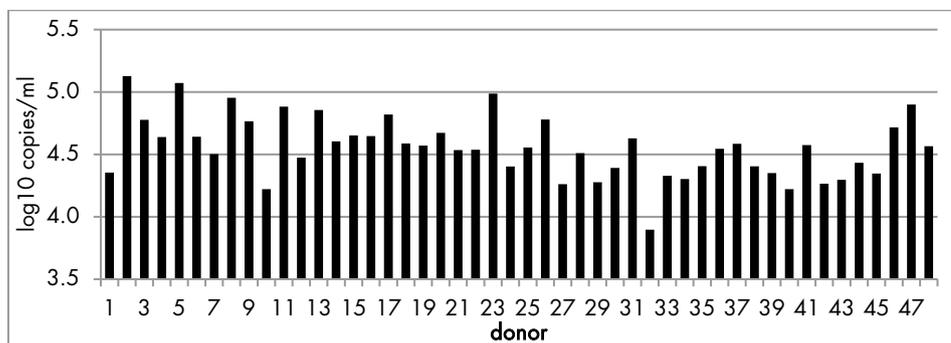


Figure 1. The ccfDNA yield from plasma from 48 single donors. Blood donation from 48 single donors was made in Cell-Free DNA BCT (Streck). CcfDNA was extracted from 4 ml plasma using the QIAAsymphony DSP Circulating DNA Kit. CcfDNA yield was quantified using an in-house real-time PCR assay for the 18S coding sequence. The results were calculated as target copies per milliliter plasma input.

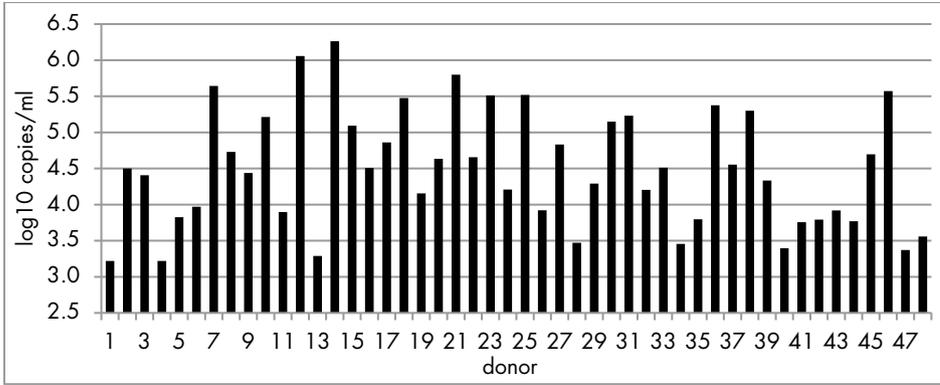


Figure 2. The ccfDNA yield from urine from 48 single donors. Urine collected from 48 single donors was stabilized using Cell-Free DNA Urine Preserve® (Streck). CcfDNA was extracted from 4ml urine using the QIAasymphony DSP Circulating DNA Kit. CcfDNA yield was quantified using an in-house real-time PCR assay for the 18S coding sequence. Results were calculated as target copies per milliliter urine input.

Run precision

Coefficients of variations (CVs) were determined for the extraction of human ccfDNA from EDTA plasma. For precision analysis, ccfDNA was quantified using an in-house real-time PCR assay for the 18S ribosomal coding sequence. In total, 10 QIAasymphony runs were performed each in 4 batches (8 replicates per batch). The precision data are shown in Table 1.

Table 1. Analysis of precision estimates

Precision	CV (%)
Within batch	11.67
Repeatability	13.14
Intermediate precision	13.14
Total precision	14.12

Equivalent performance of 2 and 4 ml protocols

Equivalent performance of protocols for 2 and 4 ml sample input was evaluated for the QIAasymphony DSP Circulating DNA Kit using endogenous ccfDNA extracted from a human EDTA plasma pool. In total, 8 independent QIAasymphony runs were performed each in 4 batches with 8 replicates per batch. The linear range of the QIAasymphony DSP Circulating DNA Kit procedure has been determined for the 18S coding sequence with an in-house real-time PCR assay (Figure 3). The ratio of difference for the 2 and 4 ml protocols is shown in Table 2 (The reference protocol is 4 ml sample input).

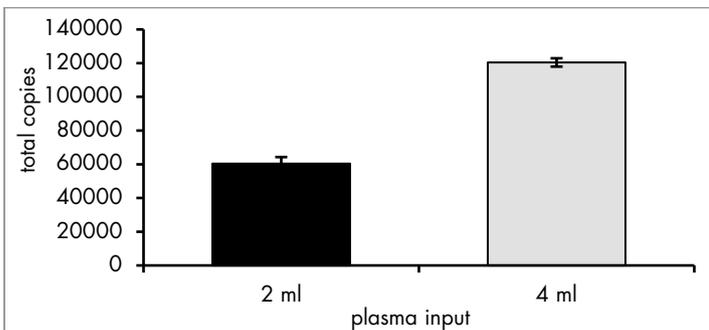


Figure 3. Equivalent performance using the 2 and 4 ml sample input protocol. The linear range of the ccfDNA protocol was determined using the 2 and 4 ml protocols. The ccfDNA yield was quantified using an in-house real-time PCR assay for the 18S coding sequence. Results were calculated as total copies per protocol.

Table 2. Difference between 2 and 4 ml protocols (N= 256)

Parameter	Value
Estimated ratio of geometric mean in calculated copies/ml	1.01
Lower 95% confidence limit	0.92
Upper 95% confidence limit	1.11
Total precision	14.12

The performance of protocols for 2 and 4 ml sample input is equivalent, measured in calculated copies per milliliter.

Size distribution

To evaluate the size distribution of sample output, ccfDNA from a sample input of 4 ml was extracted using the QIAAsymphony DSP Circulating DNA Kit, eluted in 75 μ l and then 1 μ l of eluate was subjected to size analysis with the Agilent® 2100 Bioanalyzer using an Agilent High Sensitivity DNA Chip. A total of 5 independent replicates was performed. One representative DNA profile is shown for plasma in [Figure 4](#) and for urine in [Figure 5](#).

The electropherogram for plasma in [Figure 4](#) shows the frequently observed peak at approximately 165 bp, ranging from 145 to 196 bp, which is in the range of the length of the histone-bound DNA in the nucleosome. The electropherogram for urine in [Figure 5](#) shows that the predominant peak at approximately 160 bp is broader, ranging from approximately 145 to 250 bp. In addition, for urine a second peak ranging from approximately 20 to 100 bp (at the level of the lower marker peak) is present indicating a ccfDNA fraction with a higher degree of fragmentation. Moreover, [Figure 5](#) shows a high number of long DNA fragments from approximately 2 kb. High abundance of such genomic DNA fragments is often found in urine sample most likely due to genomic DNA release from cells present in urine.

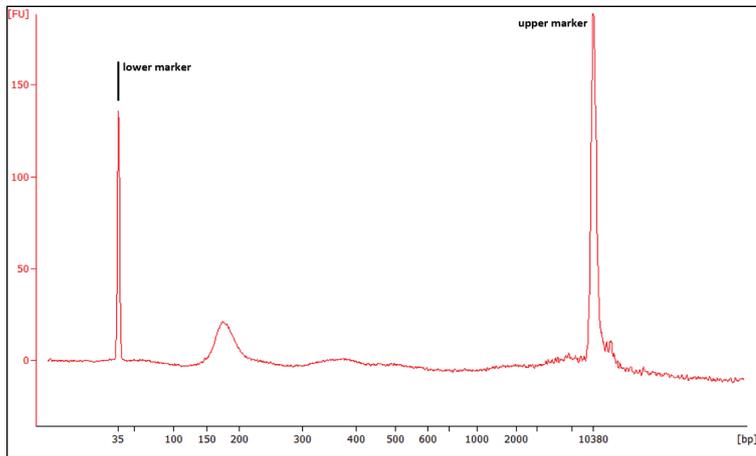


Figure 4. Size distribution of ccfDNA from plasma (Bioanalyzer profile). The ccfDNA was extracted from 4 ml EDTA plasma using the QIAAsymphony DSP Circulating DNA Kit; 1 μ l eluate was subjected to an Agilent High Sensitivity DNA Chip analysis. x axis: base pair size (bp); y axis: fluorescence units (FU).

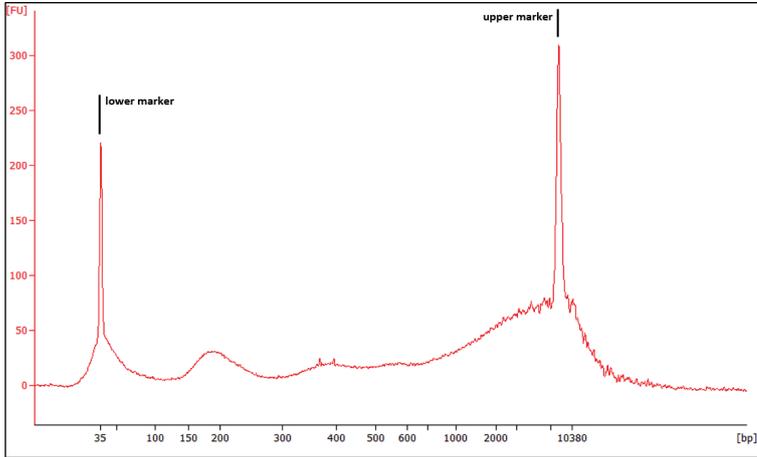


Figure 5. Size distribution of ccfDNA from urine (Bioanalyzer profile). The ccfDNA was extracted from 4 ml urine using the QIAasymphony DSP Circulating DNA Kit; 1 µl eluate was subjected to an Agilent High Sensitivity DNA Chip analysis. x axis: base pair size (bp); y axis: fluorescence units (FU).

Eluate stability

Eluate stability for the QIAasymphony DSP Circulating DNA Kit was evaluated, using extracted ccfDNA from a human EDTA plasma pool. Eluates were stored in 2 different elution rack formats: QIAGEN® EMTR (Elution Microtubes CL 96; cat. no. 19588) and 1.5 ml Eppendorf® LoBind® Snap Cap Safe-Lock tubes. Eluates were analyzed in replicates of 8. Stability of DNA in eluates was determined with an in-house real-time PCR assay for the 18S ribosomal RNA coding sequence.

Eluate stability at 2–8°C was not affected by duration of the storage period up to one month, or by storage format (Figure 6). Stability of DNA in LoBind tubes was not affected by storage at –15°C to –30°C that included 3 freeze–thaw cycles after 7 days, one month and two months (Figure 7).

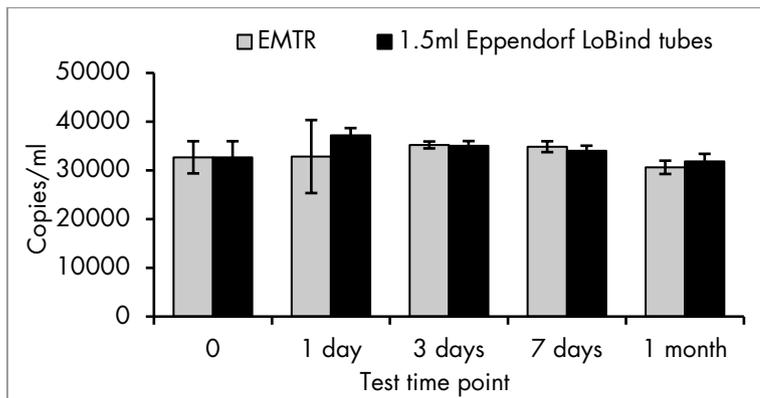


Figure 6. Stability of ccfDNA in eluates stored at 2–8°C in 2 tube formats. The ccfDNA was extracted from EDTA plasma using the QIAasymphony DSP Circulating DNA Kit and stored at 2–8°C for different test time points. The yield of ccfDNA was quantified using an in-house real-time PCR assay for the 18S coding sequence. The results were calculated as target copies per milliliter plasma input.

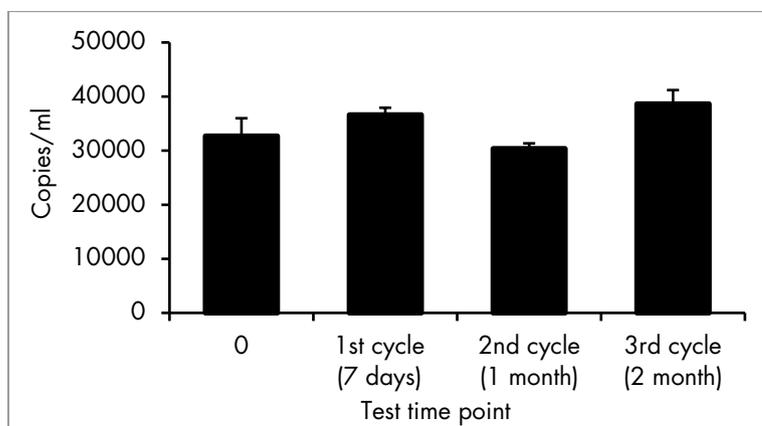


Figure 7. Stability of ccfDNA in eluates stored at -15°C to -30°C including 3 freeze-thaw cycles. The ccfDNA was extracted from EDTA plasma using the QIAAsymphony DSP Circulating DNA Kit and stored at -15°C to -30°C in 1.5 ml Eppendorf LoBind tubes. The yield of ccfDNA was determined at 3 test time points by using the same eluate at 3 freeze-thaw cycles. The yield of ccfDNA was quantified using an in-house real-time PCR assay for the 18S coding sequence. The results were calculated as target copies per milliliter plasma input.

Interfering substances

Human plasma and urine were spiked with different potential interfering substances (see Table 3) to test their impact on the ccfDNA extraction performance of the QS DSP Circulating DNA Kit and subsequent compatibility to exemplary downstream assays. Eluates were analyzed with an in-house real-time PCR for the 18S coding sequence and with the Qubit® Fluorometer using an High Sensitivity dsDNA assay.

Table 3. Test concentrations of potential interfering substances

Interfering substances	Plasma	Urine
Bilirubin	200 mg/liter*	200 mg/liter*
Hemoglobin	2 g/liter ¹	-
BSA and Gamma-Globin	Up to 120 g/liter*	1 g/liter [†]
Triglycerides	5 g/liter*	-
Glucose	10 g/liter*	10 g/liter*
Blood	-	1% [†]
pH	-	pH 4 and pH 9 [†]

* CLSI EP7-A2 Vol. 25 No. 27

[†] FDA Draft Guidance (11.05.2011)

None of the substances listed in Table 3 are interfering, except plasma samples with high concentrations of gamma-globulin (>30 g/liter) may lead to reduced recovery of circulating cell-free DNA.

Note: Testing was done using exemplary downstream applications for an assessment of the quality of the extracted nucleic acids. However, different downstream applications may have different requirements with respect to purity (i.e. absence of potential interfering substances), so the identification and testing of relevant substances also needs to be established as part of the downstream application development for any workflow involving the QIAAsymphony DSP Circulating DNA kit.

Cross-contamination

The risk of cross-contamination of the QIAasympphony DSP Circulating DNA system was analyzed by performing three 96 sample runs on the QIAasympphony SP instrument with alternating checkerboard batches (positive and negative samples alternating). Female plasma (negative sample) and female plasma spiked with sheared male gDNA of a concentration of $1.0E+05$ copies of SRY1 gene per milliliter plasma (positive sample) were used as sample materials for a model system. Sample preparation was performed using the 4 ml protocol that includes two separate sample transfers of each 2 ml volume. A potential contamination of the negative female plasma samples during the extraction runs was evaluated by subsequent analysis of the eluates using a real-time PCR for the Y-chromosome specific gene SRY1. No cross-contamination was detected for a sample to sample, batch to batch, or run to run carry over.

Compatibility to different downstream applications

Exemplary downstream applications were utilized during the development of the QIAasympphony DSP Circulating DNA kit to demonstrate that the isolated nucleic acids are compatible to a wide range of different downstream application technologies, including Real Time-PCR (see Figure 1, Figure 2, Figure 3, Figure 6, and Figure 7), Qubit Fluorometer (protein assay and high sensitivity dsDNA assay), Library (see Figure 8), and Next Generation Sequencing (NGS).

The electropherogram in Figure 8 shows an example for a successful adapter ligation and subsequent amplification of ccfDNA. Next to the prominent peak at 300 bp for the nucleosomal ccfDNA (approx. 165 plus approx. 70 bp for each adapter), also the di-nucleosomal peak at approx. 470 bp is visible.

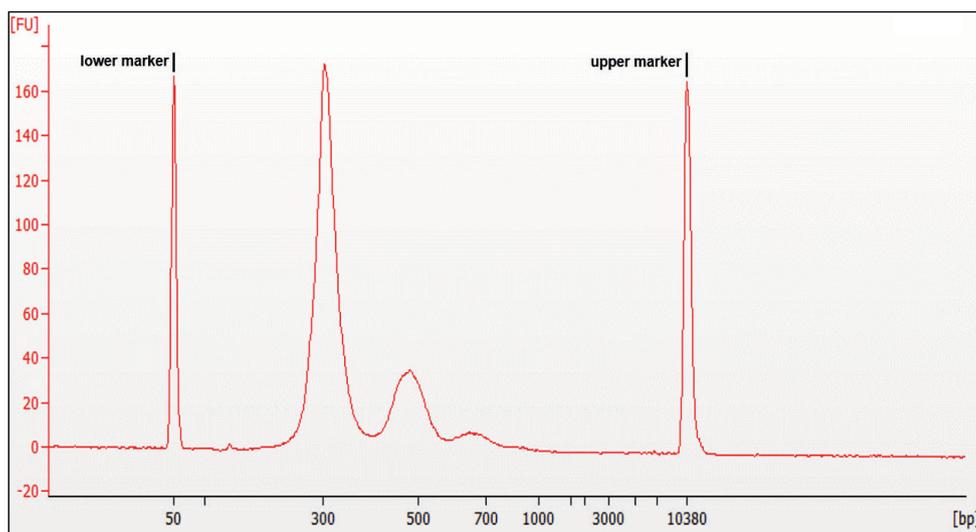
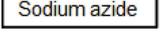


Figure 8. DNA Library of ccfDNA (single donor) extracted with the QIAasympphony DSP Circulating DNA Kit. The ccfDNA was extracted from Streck plasma using the 4 ml protocol and subsequently 35 μ l eluate was transferred into the NEBNext[®] Ultra DNA Library Prep Kit (Biolabs). After amplification and AMPure XP cleanup 1 μ l eluate was analyzed with the Agilent 7500 DNA Kit.

Symbols

The following symbols appear in the instructions for use or on the packaging and labeling:

Symbol	Symbol definition
	Contains reagents sufficient for <N> reactions
	Use by
	This product fulfills the requirements of the European Regulation 2017/746 for in vitro diagnostic medical devices.
	In vitro diagnostic medical device
	Catalog number
	Lot number
	Material number (i.e., component labeling)
	Components
	Contains
	Number
	Global Trade Item Number
Rn	R is for revision of the Instructions for Use and n is the revision number
	Temperature limitation
	Manufacturer
	Consult instructions for use
	Warning/caution
	Proteinase K
	Well number (i.e., reagent cartridge well)
	Reagent cartridge
	Sodium azide

Symbol**Symbol definition****EtOH**

Ethanol

UDI

Unique device identifier

Revision History

Revision	Description
R1, June 2022	Version 2, Revision 1 <ul style="list-style-type: none">Update to version 2 for compliance to IVDRSection for Interfering substances, Cross contamination and Compatibility to downstream applications added

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Trademarks: QIAGEN®, Sample to Insight®(QIAGEN Group); Cell-Free DNA Urine Preserve®, Cell-Free DNA BCT®, Streck® (Streck); Agilent®, Bioanalyzer® (Agilent Technologies, Inc.); Eppendorf®, LoBind® (Eppendorf AG); NEBNex® (New England Biolabs, Inc.); Qubit® (Thermo Fisher Scientific or its subsidiaries). Registered names, trademarks, etc. used in this document, even when not specifically marked as such, are not to be considered unprotected by law.

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