resDNASEQ NS0 Residual DNA Quantitation System

Integrated sample preparation and real-time PCR assay for the quantitation of NS0 host cell DNA

- Highly sensitive quantitation using proven Applied Biosystems™ TaqMan® real-time PCR technology (Figure 1)
- Manual and automated sample preparation, optimized for quantitative recovery from complex sample matrices (Table 1)
- Consistent performance across the expected range of DNA fragment sizes (Figure 2)
- Integrated system from sample to results, with sample preparation kit, master mix, TaqMan primer/probe mix, and genomic DNA standard

Table 1. DNA recovery using the manual protocol for the Applied Biosystems™ PrepSEQ™ Residual DNA Sample Preparation Kit. Assay performance data were determined from 10 pg NS0 genomic DNA spiked into 6 test samples.

Genomic DNA	Mean recovery	Mean CV
NS0	77%	7%

The Applied Biosystems™ resDNASEQ™ NS0 Residual DNA Quantitation System is a quantitative PCR (qPCR)-based system for the detection of host cell DNA from NS0 (mouse myeloma) cells, an expression system commonly used for the production of monoclonal antibodies. Reliable and rapid, the system enables sensitive (limit of quantitation = 1.5 pg DNA per mL of test sample, Figure 1) and specific (Figure 3) quantitation of NS0 DNA, typically in less than 4 hours. This performance helps ensure a high degree of confidence in quantitation data obtained from a broad range of sample types—from in-process samples to final product—whether the sample contains high molecular weight or sheared DNA (Figure 2).

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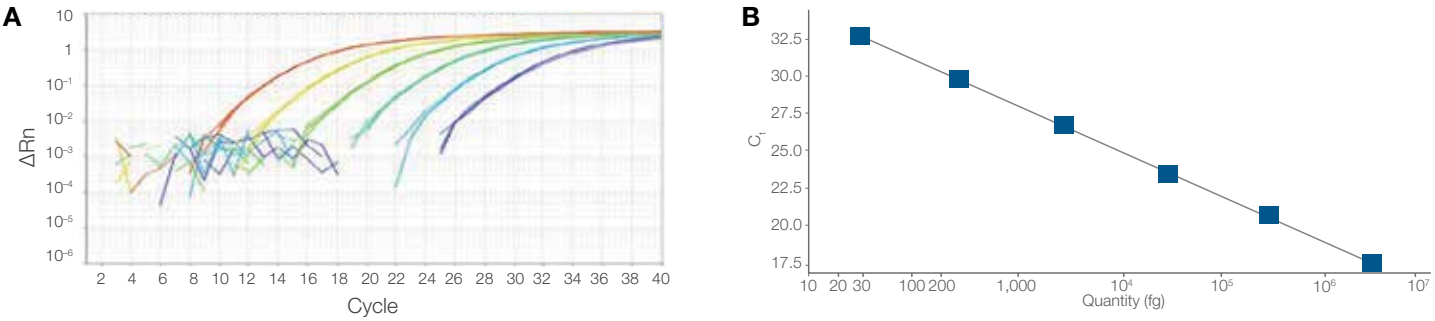

Figure 1. High sensitivity and broad dynamic range using the resDNASEQ NS0 Residual DNA Quantitation System. (A) The amplification plots were generated using 10-fold serial dilutions (containing 3 ng to 30 fg) of NS0 genomic DNA, provided in the kit. **(B)** Standard curve of the 10-fold dilution series. Data were analyzed using Applied Biosystems™ AccuSEQ™ Real-Time PCR Software.

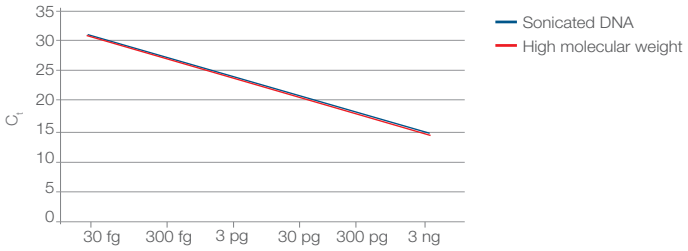

Figure 2. Consistent quantitation across a broad range of fragment sizes. Standard curves were generated using 10-fold serial dilutions of high molecular weight or fragmented DNA, from 3 ng to 30 fg. Fragmented DNA was generated by sonicating total NS0 genomic DNA. Fragmentation of the DNA was confirmed by agarose gel analysis.

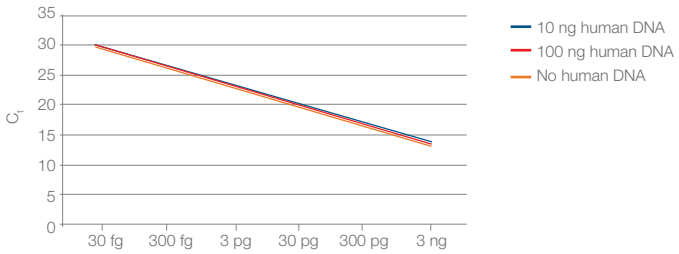

Figure 3. Assay specificity. Standard curves were generated using 10-fold serial dilutions of NS0 genomic DNA in the presence of 100 ng, 10 ng, or no human DNA.

Ordering information

Product	Quantity	Cat. No.
resDNASEQ Quantitative NS0 DNA Kit	100 reactions	4458441
resDNASEQ Quantitative NS0 DNA Kit with PrepSEQ Residual DNA Sample Preparation Kit	100 reactions	4460364
Sample preparation and automation		
PrepSEQ Residual DNA Sample Preparation Kit	100 reactions	4413686
Pharma KingFisher Flex 96 Deep-Well Magnetic Particle Processor	1 instrument	A31508
Real-time PCR system		
7500 Fast Real-Time PCR System	1 instrument	4365464
Software		
AccuSEQ Real-Time PCR Software	1 license	4443420
Service		
7500 Fast IQ/OQ Service		4365572

Find out more at **thermofisher.com/resdnaseq**

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