sparQ Fast Library Quant Kit (for Q)

Fastest qPCR-based library quantification in 40 minutes

40 min

FEATURES & BENEFITS:

- Faster time to results – 50% shorter run time than traditional cycling protocols
- Accurate, reliable quantification of NGS libraries of various sizes and GC-content
- High amplification efficiency across a wide linear dynamic range
- Stabilized, ready-to-use sparQ Fast Mastermix to reduce pipetting steps
- Superior run to run uniformity ensuring highly precise measurements

DESCRIPTION:

sparQ Fast Library Quant Kit provides rapid and accurate quantification of libraries prepared for sequencing on Illumina® NGS platforms. Accurate quantification of the number of amplifiable library molecules prior to loading onto a flow cell is a critical step in the NGS workflow and it ensures optimal cluster generation and cost-effective use of sequencing capacity. The sparQ Fast Library Quant Kit uses real-time quantitative PCR (qPCR) to specifically quantify the number of library molecules that possess the appropriate adapter tag at each end.

Accurate library quantification in 40 minutes

This kit is optimized for the Q qPCR instrument which uses a magnetic induction technology to rapidly heat samples coupled with fan forced air for cooling to acquire data more rapidly. The combination of the sparQ Fast Library Quant Kit and the Q instrument enables fast cycling, reducing qPCR run time by 50% compared to traditional cycling protocols.

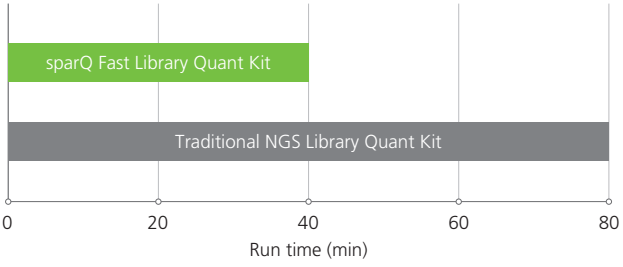

Figure 1 **Comparison of average qPCR run time for library quantification.** sparQ Fast Library Quant Kit uses fast cycling protocol, allowing results to be achieved in 40 minutes versus 1 hour and 20 minutes with the traditional NGS Library Quant Kit.

Complete library quantification solution with unmatched convenience

sparQ Fast Library Quant Kit contains six stabilized, pre-diluted DNA standards, ready-to-use 1.25x mastermix pre-mixed with primer sets containing Illumina P5 and P7 sequences, and an optimized buffer for diluting NGS library samples. This unique formulation minimizes pipetting steps and ensures precise qPCR results.

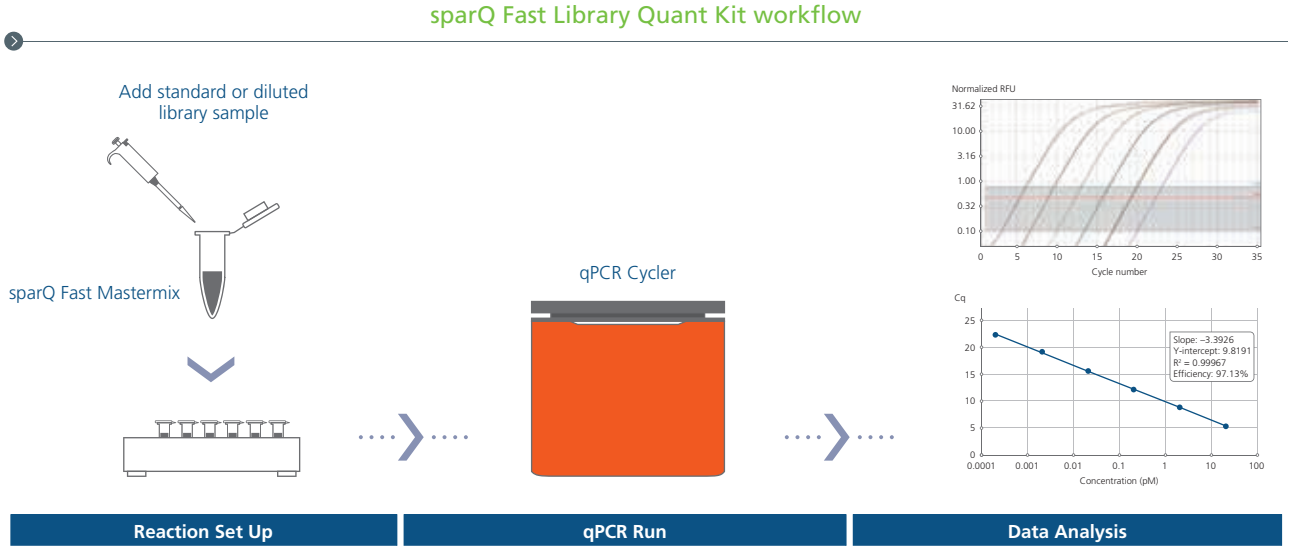

Figure 2 **Illustration of sparQ Fast Library Quant Kit workflow.** Reactions are prepared by simply adding standard or diluted library sample. Optimized protocols with fast cycling condition are provided for both 10 µl or 20 µl reaction volumes.

qPCR as the most accurate method for library quantification

Real-time quantitative PCR is the most sensitive and precise method for quantifying adapter-ligated DNA molecules. Other methods based on spectrophotometry, fluorometry, or microfluidic electrophoresis (e.g. nanodrop, Qubit, or Bioanalyzer) are acceptable for estimating the appropriate dilutions to use for library quantification. These methods, however, are prone to variabilities and inaccuracies due to factors such as sensitivity to contaminants or measurement of unsequenceable fragments. The qPCR-based sparQ Fast Library Quant Kit measures only library DNA fragments containing the appropriate adapter sequences on both ends and thus serves as the most accurate method for library quantification, which in turn facilitates optimal loading onto sequencing flow cells.

Figure 3 **Comparison of commonly used methods for measuring library concentration.**

High amplification efficiency across a wide linear dynamic range

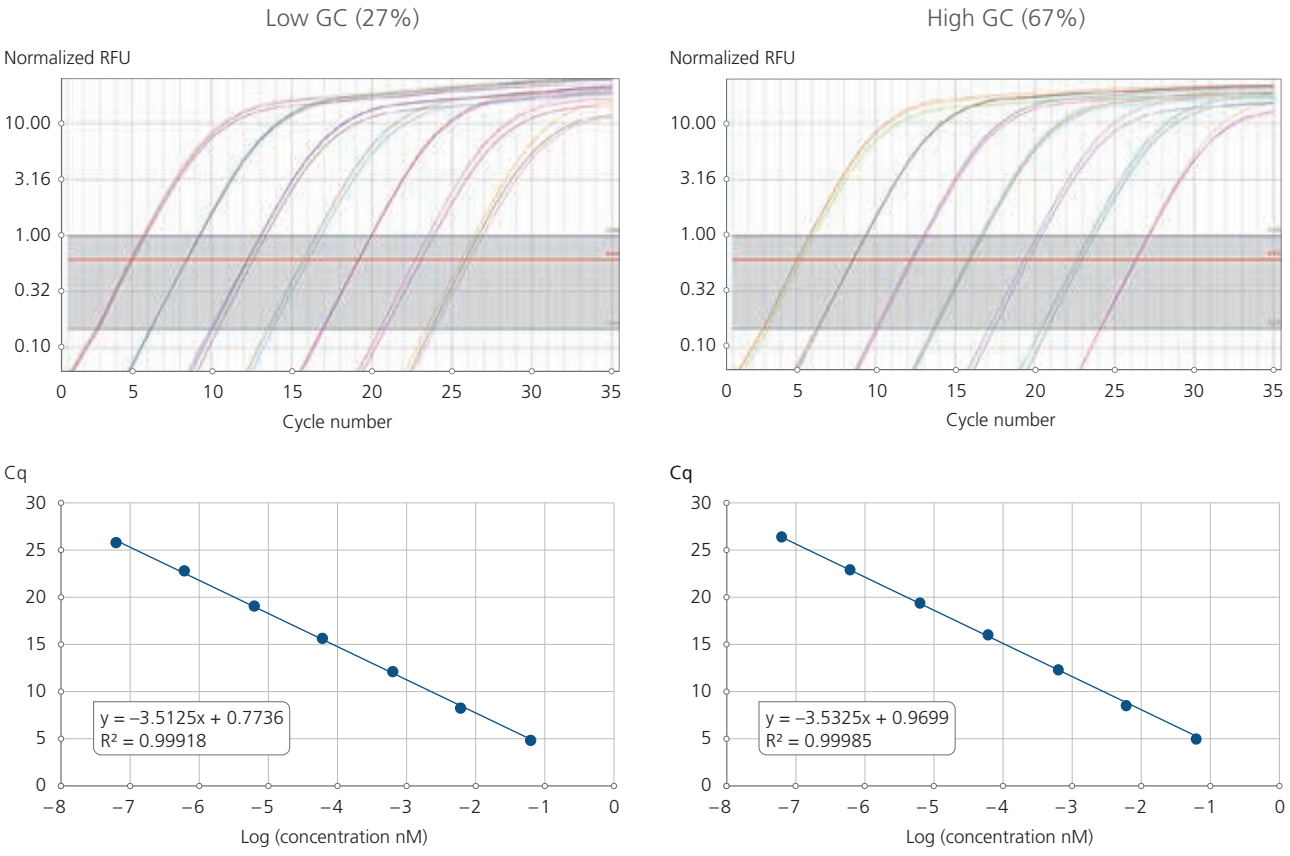

Figure 4 **sparQ Fast Library Quant Kit provides high amplification efficiency across a wide linear dynamic range.** A 10-fold dilution series was prepared from libraries of low (27%) and high (67%) GC-content and amplified under fast conditions on the Q using the sparQ Fast Mastermix. The slopes of the Cq vs Log (concentration) plots and the individual sample reactions measured by the LinRegPCR algorithm indicated superb amplification efficiencies.

Outstanding repeatability of multiple runs

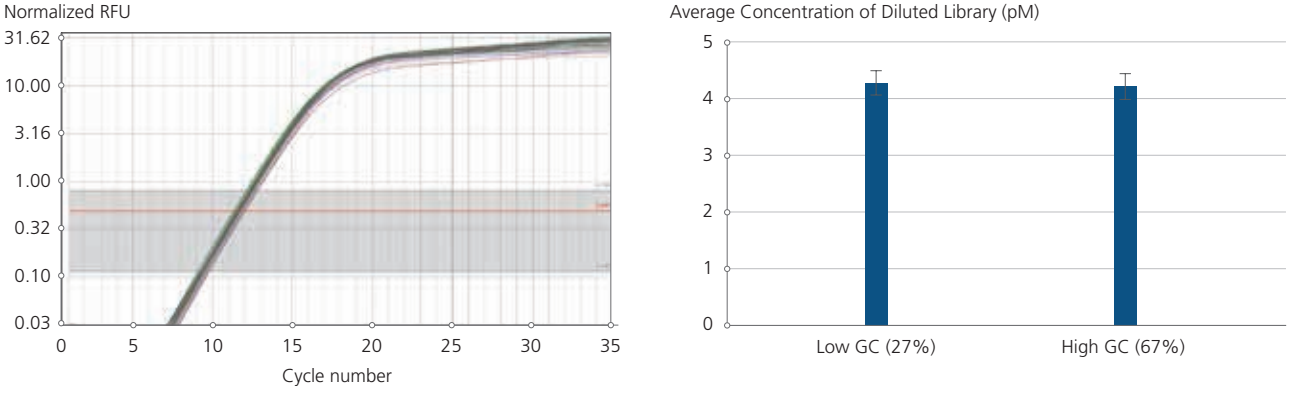

Figure 5 **Multiple runs using sparQ Fast Library Quant Kit resulted in similar quantification values.** Two NGS library preparations with high and low GC-contents were amplified and quantified in five distinct runs. Plots of the Normalized fluorescence vs Cycles and average quantification values show the high repeatability of measurements with the sparQ Fast Library Quant Kit under fast cycling on the Q.

Equivalent performance with 50% faster run time

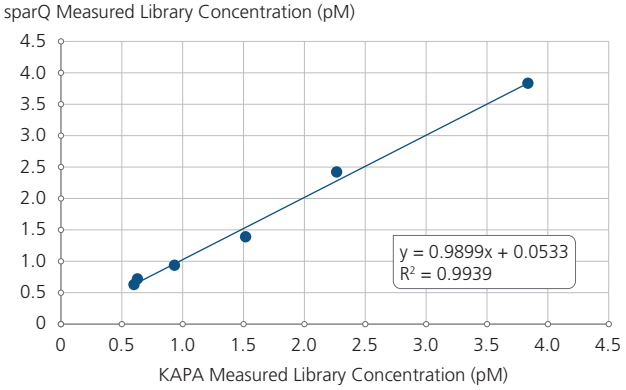

Figure 6 Results from sparQ and Roche KAPA Library Quant Kits were highly correlated. Concentrations of six different diluted libraries were determined using either the sparQ Fast Library Quant Kit on Q or the Roche KAPA Library Quantification Kit on Bio-Rad CFX following the manufacturer's recommended protocol. Run times, including melt curves, were 40 minutes for sparQ and 80 minutes for KAPA.

Lot-to-lot consistency of sparQ DNA Standards

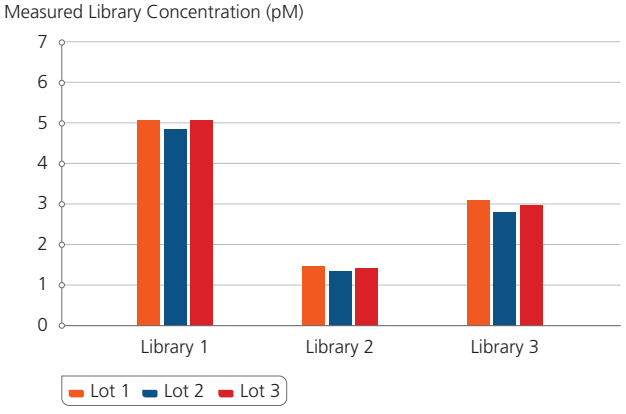

Figure 7 sparQ Fast Library Quant Kits are manufactured with high lot to-lot consistency. Concentrations of diluted libraries with low GC (library 1), high GC (library 2), or balanced GC-content (library 3) were determined using 3 different lots of sparQ DNA Standards. Each library sample was tested in quadruplicate reactions with each lot of sparQ DNA Standards. Standard deviations of average quantification values were all <0.13 pM.

ORDER INFO

Product Name	Quantabio Catalog Number	Size*
sparQ Fast Library Quant Kit - 50	95197-050	50 rxns
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*** Based on 20 µl reaction volume.**

MK-SF-0032 REV 01 sparQ Fast Library Quant 0419