

BrightBox Quantitation Assay

The BrightBox Assay is a novel method to quantitate your NGS libraries

Library quantitation can be a lengthy, costly and inaccurate process where variability can lead to unequal library loading and wasted time and money.

The BrightBox Assay is a quick and simple method to accurately quantitate any NGS libraries.

Get results quickly by shortening your current library preparation and instrument loading workflow.



Why Use BrightBox

✓ FAST

Save time with reactions done in just 5 minutes.

✓ EASY

Reduce manual errors and save time with premixed Assay Mix and prediluted standards stored in the fridge.

✓ ACCURATE

Improve data with consistent pooling based on actual molarity.

✓ FLEXIBLE

Quantitate any library with attached P5 and P7 adapters.

Faster than current workflows.
Preparation and incubation times for the BrightBox assay are a fraction of the times for other methods.

Aliquot Assay Mix
Add Libraries
Incubate and read
- 5 minutes!
BrightBox

15 minutes

**26 libraries per
96 well-plate**

Mix Library with Dye
Load one sample
at a time onto Qubit
Mass Analysis

25 minutes

**16
libraries**

Estimate Mass
- 1 hour
Dilute Library
Prime
Run on instrument
- 1 hour
Fragment Analysis

2 hours

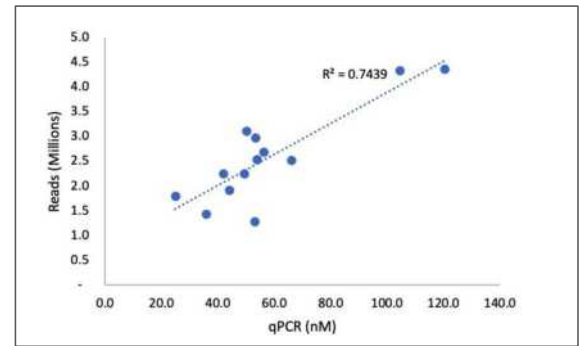
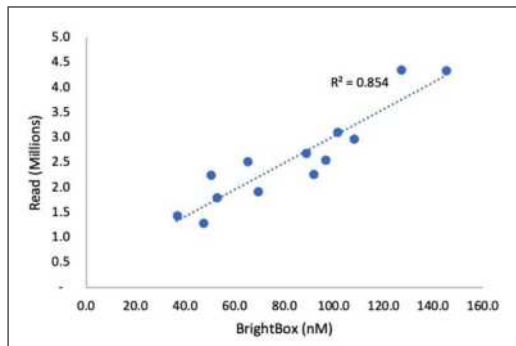
**11 - 96
libraries**

Dilute Libraries
- 1 hour
Thaw Master Mix
Assemble Master Mix
Aliquot Master Mix
Add Libraries
Cycle and read - 1 hour
qPCR

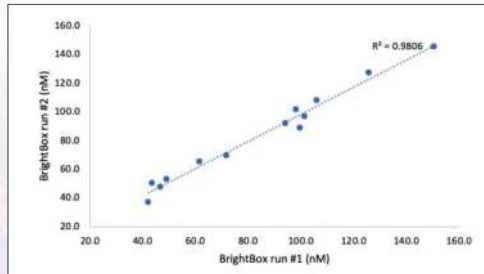
2.5 hours

**12 libraries per
96 well-plate**

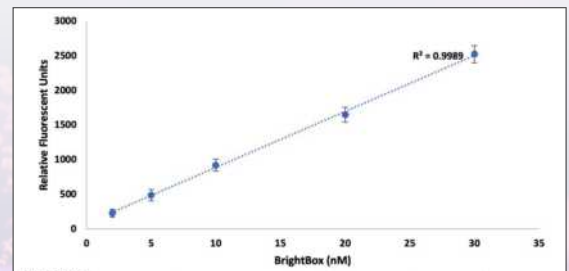
Quantitation is correlated to read numbers. Molarity was calculated for 13 libraries with the BrightBox assay and a commonly used qPCR library quantitation kit. Equal volumes of each library were loaded onto a MiSeq and read numbers were plotted against calculated molarity.



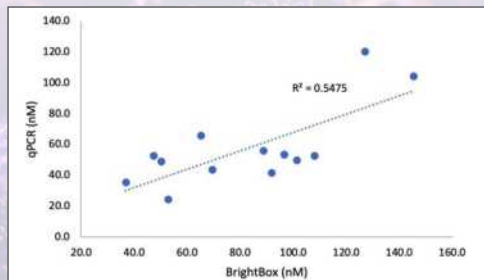
Reproducible results. 16 different libraries were repeatedly run using the BrightBox assay on a qPCR instrument



Quantitation is linear and reproducible. Standards from the BrightBox kit were run 12 different times on a qPCR instrument and show high linearity and low variability.



Correlation between methods. 16 different libraries were quantitated with the BrightBox assay and a qPCR library quantitation kit. Outlying points are due to an inaccurate estimation of average fragment size during qPCR quantitation



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