# xGEN™ PRE-HYBRIDIZATION CAPTURE NORMALASE™ MODULE

Fast pre-hybridization capture library normalization

**Eliminates tedious library concentration adjustments with equal volume pooling**

**Improved library balance compared to conventional methods**

**Reduced hands-on time that seamlessly integrates into NGS sample preparation workflows**

## NOVEL ENZYMATIC NORMALIZATION TECHNOLOGY FOR PRE-HYBRIDIZATION CAPTURE LIBRARIES

The xGen Pre-Hybridization Capture Normalase Module generates equimolar library pools and balanced sample representation for hybridization capture. This method eliminates the need for individual library quantification and pooling of variable volumes. Instead, equal volumes of each library are pooled during the Normalase workflow.

The xGen Pre-Hybridization Capture Module workflow can be easily integrated into standard DNA and RNA library preparation and hybridization capture protocols to improve turnaround time and loading accuracy for NGS. Indexing and Normalase library conditioning can occur in a single reaction, meaning a second PCR reaction may not be required.

## BETTER NORMALIZATION COMPARED TO CONVENTIONAL METHODS

Libraries normalized using xGen Pre-Hybridization Capture Normalase Module have more uniform read distribution compared to library pools generated using qPCR quantification and fluorometric assays (Figure 1). Using the xGen Pre-Hybridization Capture Normalase Module, researchers can select a broad range of library inputs into hybridization capture (100–500 ng), across multiple insert sizes (150–350 bp), while supporting multiplexing of 4–24 libraries per pool.

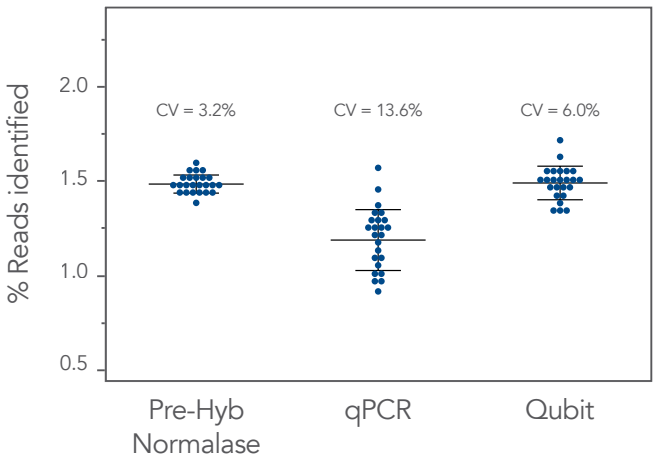


**Figure 1. xGen Pre-Hybridization Capture Normalase Module generates better balanced coverage into hybridization capture.** Twenty-four xGen DNA EZ libraries were generated with 10 ng NA12878 and amplified with xGen Normalase UDI primers using 11 cycles of PCR and normalized to 250 ng for hybridization capture. Libraries were normalized and pooled prior to hybridization capture based on one of the three methods - xGen Pre-Hybridization Capture Normalase Module, qPCR quantification, or Qubit™ (Thermo Fisher) quantification. After hybridization capture, the libraries were sequenced on a single Illumina® MiniSeq (300 cycle) run, and the coefficient of variation (CV) of the reads was measured. The coefficient of variation (CV) for the xGen Pre-Hyb Normalase Module pool was 3.2% showing robust normalization of multiplexed pools compared to standard quantification methods (13.6% for qPCR and 6.0% for Qubit).

## FAST NORMALIZATION THAT INTEGRATES INTO NGS SAMPLE PREPARATION WORKFLOWS

The xGen Pre-Hybridization Capture Normalase Module can be seamlessly integrated into library preparation and hybridization capture workflows to reduce hands-on time (HOT) and improve loading accuracy for NGS research. Compared to conventional methods, this novel enzymatic normalization technology has reduced HOT for high throughput applications (Figure 2).

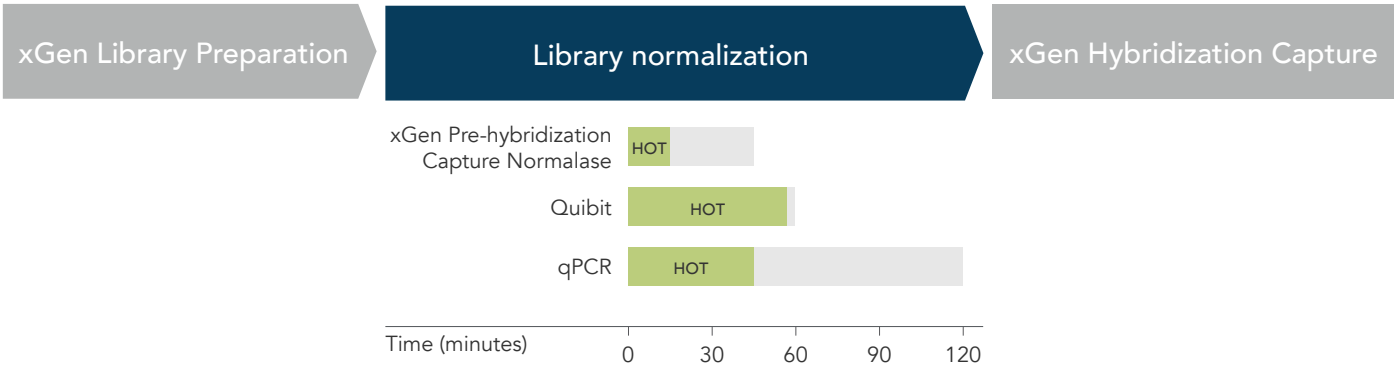


**Figure 2. xGen Pre-Hybridization Capture Normalase Module reduces hand-on time (and total workflow time compared to standard library normalization methods).** Hands-on time (green box) and total workflow time (gray box) were compared for *n* = 24 libraries across xGen Pre-Hybridization Capture Normalase Module, Qubit, and qPCR-based normalization methods. xGen Pre-Hybridization Capture Normalase Module had the shortest hand-on time (15 min) and total workflow time (45 min).

## ORDERING INFORMATION

| Product | Size | Catalog # |
|---|---|---|
| xGen™ Pre-Hyb Normalase™ Module | 96 rxn | 10017913 |

> FOR MORE INFORMATION, VISIT **WWW.IDTDNA.COM/NGS**