LEXOGEN
The RNA Experts

QuantSeq 3′ mRNA-Seq Library Prep

The most cited reason for doing RNA sequencing is to investigate gene expression. Whilst differential expression may be addressed by conventional mRNA sequencing, this method requires high read depth sequencing and complex data analysis.

QuantSeq 3′ mRNA-Seq offers a much faster and more cost-efficient way to get expression analysis done with the added benefits of high-multiplexing capability and the robustness to deal with the most difficult of samples!

The most cost-efficient way to study differential gene expression

3′ mRNA-Seq requires a vastly lower number of reads per sample, saving you money by multiplexing a higher number of samples on a single sequencing lane.

Fast, easy, and robust library prep in under 4.5 hours

QuantSeq only requires 5 major steps and no RNA pre-processing, saving you time and allowing you to go from sample to sequencing in a single day.

Vast species, quantity, and quality compatibility, even ideal for FFPE samples

The robust protocol generates RNA-Seq libraries from any sample type, including degraded RNA. This facilitates your work with the broadest range of samples.

Free and simple data analysis

Every QuantSeq read is counted for expression profiling, thus complementary access to our easy data analysis platform allows you to analyse your data personally without bioinformatic support.

Introduction

QuantSeq 3′ mRNA-Seq generates only one fragment per transcript at the 3′ end instead of covering the full length of the transcript with read as conventional mRNA-Seq (Fig. 1).

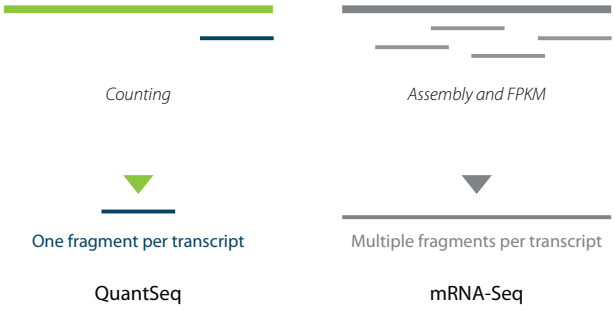

Figure 1 | In contrast to common mRNA-Seq methods, QuantSeq generates only one fragment per transcript at the very 3′ end.

The most cost-efficient way to study differential gene expression

Since QuantSeq generates only one fragment per transcript, gene expression studies with QuantSeq require a vastly lower number of reads per sample (we recommend 3-5 M reads for standard applications) than with conventional mRNA-Seq (usually 20-50 M reads recommended). This means that more samples can be pooled and sequenced on one single lane, reducing the cost per sample drastically (Fig. 2).

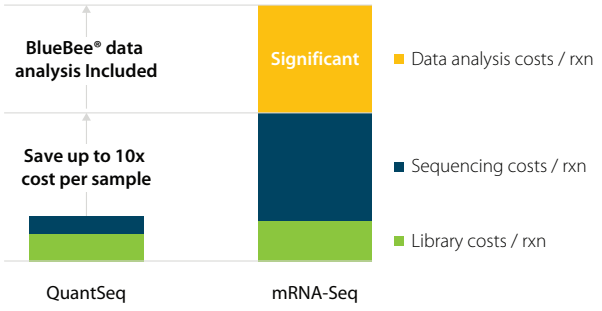

Figure 2 | Comparison of cost per sample of conventional mRNA-Seq and QuantSeq 3′ mRNA-Seq for a complete gene expression profiling experiment.

Fast, easy, and robust library prep in under 4.5 hours

In contrast to conventional mRNA-Seq, QuantSeq only requires 5 major steps and can be completed in about 4.5 hours! QuantSeq does not require any pre-processing of the RNA, such as poly(A) RNA selection or ribosomal RNA depletion since the protocol intrinsically selects only poly(A) RNA. This saves time and makes the protocol very robust (Fig. 3).

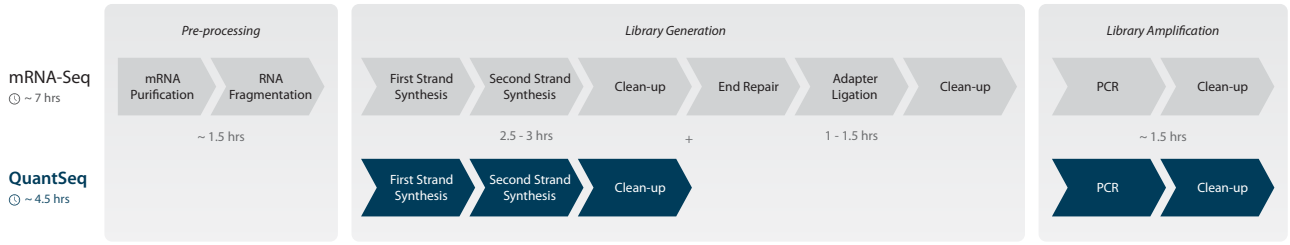

Figure 3 | Workflow comparison of conventional mRNA-Seq and QuantSeq 3′ mRNA-Seq for gene expression profiling.

Vast species, quantity, and quality compatibility, even ideal for FFPE samples

QuantSeq's 3′ capture approach successfully generates fragments even from degraded RNA, such as RNA derived from FFPE samples. The technology is less sensitive to variations in RNA quality than conventional mRNA-Seq which requires high-quality RNA for mRNA enrichment.

Free and simple data analysis

With QuantSeq, the number of reads mapped to a given gene is directly proportional to its expression. 3′ mRNA-Seq does not rely on correct isoform annotation and identification for determining unambiguous gene expression values. Thus, the data analysis of QuantSeq reads is simple and requires only a short time. Researchers lacking bioinformatics expertise can access the user-friendly data analysis pipeline on the BlueBee Genomics Platform, free with the purchase of a QuantSeq Kit.

Type d'indexage	Référence	Désignation	Conditionnement
Kits avec "Unique Dual Indexing "	LEX191.24	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Set A1, (UDI12A_0001-0024)	24 rxns
	LEX191.96	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Set A1, (UDI12A_0001-0096)	96 rxns
	LEX193.384	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Sets A1-A4, (UDI12A_0001-0384)	384 rxns
	LEX194.96	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Set A2, (UDI12A_0097-0192)	96 rxns
	LEX195.96	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Set A3, (UDI12A_0193-0288)	96 rxns
	LEX196.96	QuantSeq 3′ mRNA-Seq V2 Library Prep Kit FWD with UDI 12 nt Set A4, (UDI12A_0289-0384)	96 rxns
Kit pour étude en haut débit	LEX139.96	QuantSeq-Pool Sample-Barcoded 3′ mRNA-Seq Library Prep Kit for Illumina	96 rxns
Produits complémentaires	**Référence**	**Désignation**	**Conditionnement**
Détermination du nombre de cycles PCR à effectuer lors de la préparation de banques	LEX020.96	PCR Add-on Kit for Illumina	96 rxns
Unique Molecular Identifiers	LEX081.96	UMI Second Strand Synthesis Module for QuantSeq FWD (Illumina, Read 1)	96 rxns

Multiplexage QuantSeq : jusqu'à 384 échantillons - Multiplexage QuantSeq-Pool : jusqu'à 36 864 échantillons