

Introducing NEBNext[®] for MGI[®] sequencing

NEBNext library prep reagents are now available for MGI sequencing applications. Kit components and protocols have been optimized for the production of high-quality libraries from DNA ([NEB #BE9705](#)) and RNA ([NEB #BE9710](#)). The NEBNext Library Prep Kits for MGI are used in conjunction with NEBNext Multiplex Oligos for MGI (Dual Index Primer Pairs Set 1) ([NEB #BE9725](#)) and libraries are circularized using the NEBNext Circularization Module for MGI ([NEB #BE9720](#)) before sequencing.



Fast workflows



High library yields



Broad input ranges



Uniform transcript & GC coverage



Minimized adaptor-dimers

Ordering Information

PRODUCT	NEB #	SIZE
NEBNext FS DNA Library Prep Kit for MGI	BE9705S/L	24/96 rxns
NEBNext RNA Library Prep Kit for MGI	BE9710S/L	24/96 rxns
NEBNext Multiplex Oligos for MGI (Dual Index Primer Pairs Set 1)	BE9725S/L	24/96 rxns
NEBNext Circularization Module for MGI	BE9720S	24 rxns



“*We have been using MGI sequencing systems since 2020 and we observed a significant improvement with NEB’s NEBNext solutions for MGI in both library prep performances and sequencing quality metrics reaching impressive Q40 results.*”

– Davide Cacchiarelli, PhD
University of Naples, Italy



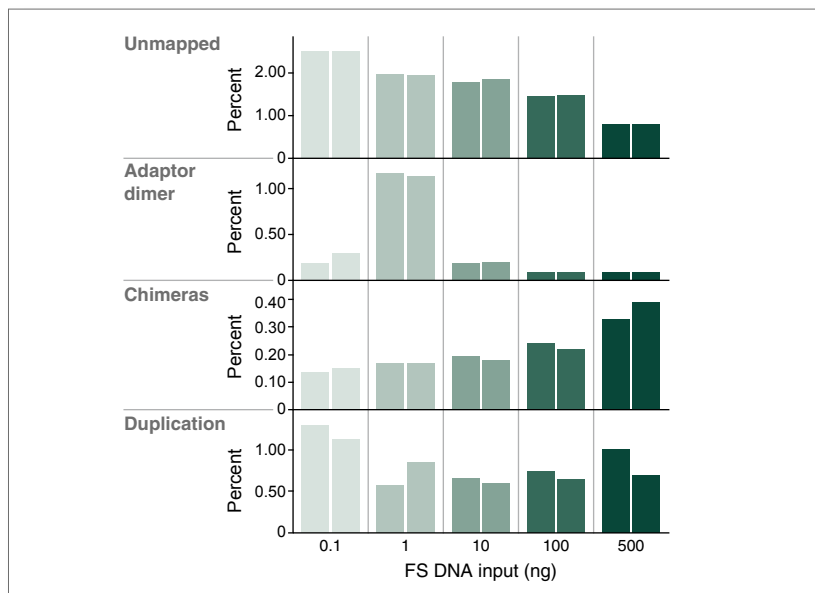
Introducing NEBNext for MGI sequencing

NEBNext FS DNA Library Prep Kit for MGI NEB #BE9705

- Incorporates enzymatic DNA fragmentation and a streamlined workflow
- Enables production of high-quality libraries from 0.1–500 ng input DNA

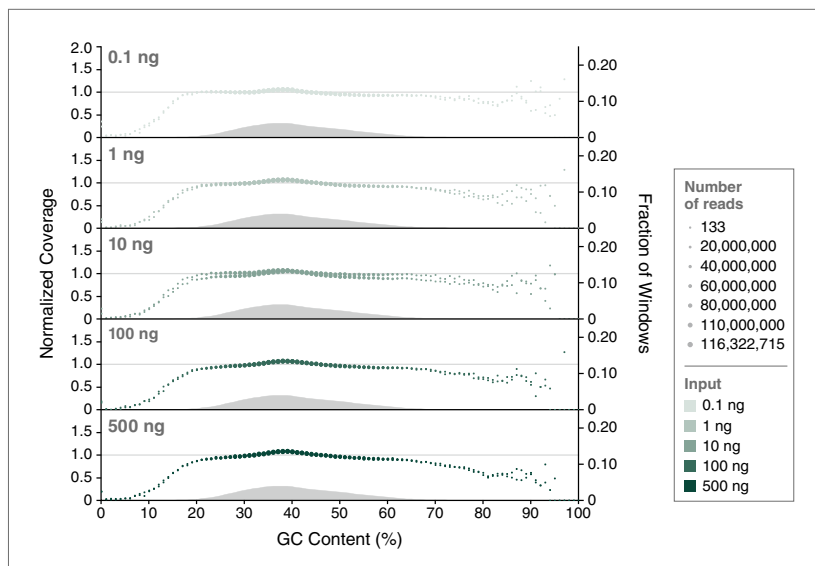


The NEBNext FS DNA Library Prep Kit for MGI produces high-quality libraries with excellent sequencing metrics across the input range



Libraries were prepared in duplicate from 0.1–500 ng of NA12878 gDNA (Coriell Institute for Medical Research), sequenced on an MGI G99 platform with PE100 and downsampled to 3.5 million paired-end reads. Reads were mapped using Bowtie2 (version 2.3.2.2) to the GRCh38 reference, and duplicates were marked using Picard MarkDuplicates (version 1.56.0). Library quality metrics were assessed using Picard Alignment Summary Metrics (version 1.56.0). High mapping rates, low chimera rates, and low adaptor-dimer rates were obtained for all libraries. A slightly higher adaptor-dimer presence (~1%) was observed with the 1 ng input for this specific experiment, and this can be optimized with adaptor dilution. Stock adaptor concentration was used for all input levels except for 0.1 ng, where a 10-fold dilution of the stock was applied.

The NEBNext FS DNA Library Prep Kit for MGI produces high-quality libraries with uniform GC coverage across the input range

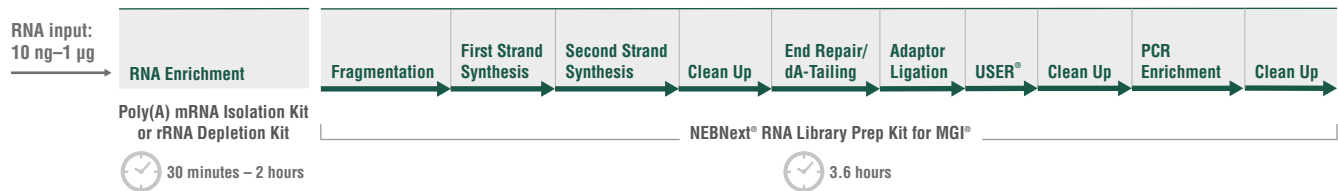


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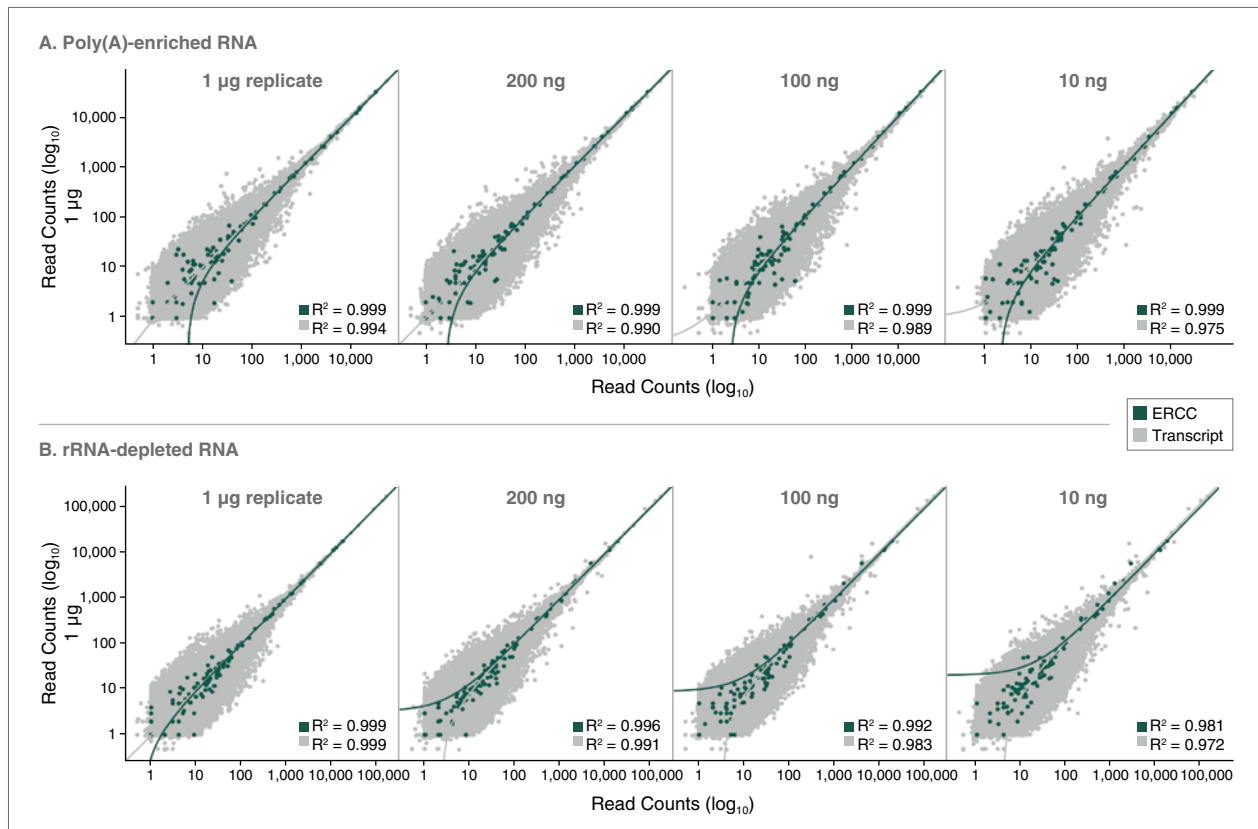
Introducing NEBNext for MGI sequencing

NEBNext RNA Library Prep Kit for MGI NEB #BE9710

- Compatible with rRNA depletion or poly(A) enrichment protocols (including the Express protocol for the NEBNext Poly(A) mRNA Magnetic Isolation Module – NEB #BE7490)
- Optimized for the production of high-quality directional RNA libraries from 10 ng–1 µg total RNA



The NEBNext RNA library prep kit for MGI provides excellent transcript correlation between inputs and replicates



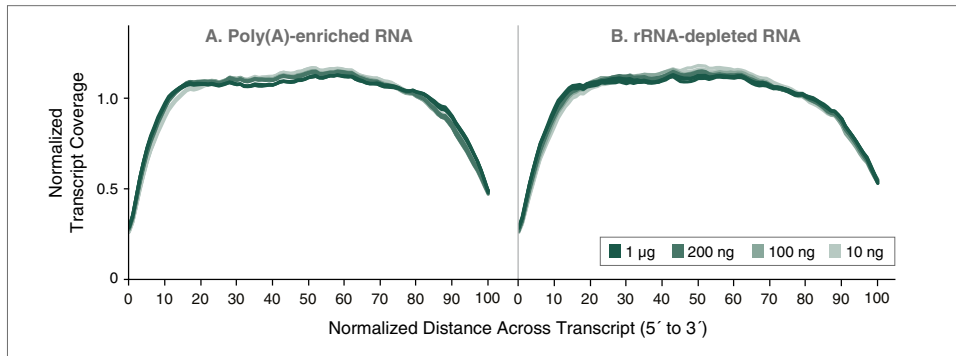
A. Poly(A)-containing mRNA was isolated from Universal Human Reference RNA (UHRR) (Agilent[®]), using the NEBNext Poly(A) mRNA Magnetic Isolation Module (NEB #E7490). Libraries were prepared using the NEBNext RNA Library Prep Kit for MGI. The NEBNext RNA Library Prep Kit for MGI was used using the recommendations for adaptor dilution and PCR cycles included in the kit protocol.

B. Ribosomal RNA (rRNA) was depleted from UHRR (NEBNext rRNA Depletion Kit v2 (Human/Mouse/Rat), NEB #BE7400) and libraries were prepared using the NEBNext RNA Library Prep Kit for MGI, following the recommendations for adaptor dilution and PCR cycles included in the kit protocol. Libraries were sequenced on an MGI DNBSQ[®]-G400 (2 × 100 bases). 10 million reads were sampled and libraries were correlated for transcript expression levels across inputs using Salmon v1.5.1 quantification of all gencode v38 transcripts and ERCCs. Each data point represents a transcript, with the \log_{10} abundance in Read Counts with 1 µg total RNA input on the y-axis compared to a replicate at 1 µg followed by 200 ng, 100 ng and 10 ng on the x-axis. The number of transcripts detected have very high correlation across the different inputs and replicates.

Introducing NEBNext for MGI sequencing

NEBNext RNA Library Prep Kit for MGI NEB #BE9710

The NEBNext RNA Library Prep Kit for MGI provides consistent transcript coverage



A. Poly(A)-containing mRNA was isolated from Universal Human Reference RNA (UHRR) (Agilent), using the NEBNext Poly(A) mRNA Magnetic Isolation Module (NEB #E7490). Libraries were prepared using the NEBNext RNA Library Prep Kit for MGI using the recommendations for adaptor dilution and PCR cycles included in the kit protocol.

B. Ribosomal RNA (rRNA) was depleted from UHRR (NEBNext rRNA Depletion Kit v2 (Human/Mouse/Rat), NEB #E7400) and libraries were prepared using the NEBNext RNA Library Prep Kit for MGI, following the recommendations for adaptor dilution and PCR cycles included in the kit protocol.

Libraries were sequenced on an MGI DNBSEQ-G400 (2 x 100 bases). 10 million reads were sampled and mapped to the hg38 reference genome using RNA STAR v2.7.8a and 5' to 3' transcript coverage was calculated from the top 1,000 transcripts using the CollectRnaSeqMetrics (Picard) tool v2.18.2.2. Even and consistent coverage was observed across all input amounts.

NEBNext Multiplex Oligos for MGI (Dual Index Primer Pairs Set 1) NEB #BE9725

NEBNext Multiplex Oligos for MGI (Dual Index Primer Pairs Set 1) enables high-yield, multiplexed MGI library production. The carefully selected pairs of index primers (following a combinatorial dual indexing scheme) are provided pre-mixed in a 96-well plate for ease of use in multiplexing up to 120 samples.



NEBNext Circularization Module for MGI NEB #BE9720

The NEBNext Circularization Module for MGI is optimized for the circularization of dsDNA MGI-compatible libraries to create single-stranded circular DNA libraries for sequencing on the MGI platform.



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