ZYMO RESEARCH

The Beauty of Science is to Make Things Simple®

Zymo-Seq SwitchFree™ 3′ mRNA Library Kit

- **Simplest protocol:** RNA to library in less time with easy handling driven by the SwitchFree™ technology.
- **High performance:** Built-in Unique Molecular Identifiers (UMIs) allow for accurate deduplication maximizing unique reads.
- **Low input compatible:** Utilize as little as 10 ng total RNA without prior mRNA enrichment.

Simple and Streamlined Workflow

Zymo-Seq SwitchFree™ 3′ mRNA Library Kit enables NGS library preparation in ~ 4 hours. Starting directly with total RNA as input, the 3-section protocol includes reverse transcription of poly(A)+ RNAs, adapter ligation, and library amplification with unique dual-indexed PCR primers. The procedure requires approximately 2.5 hours of thermal cycler programs and 1.5 hours of hands-on time, **streamlined for same-day library preparation.**

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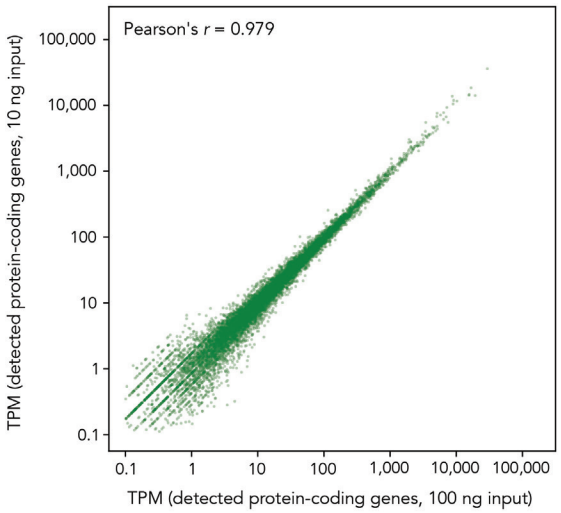
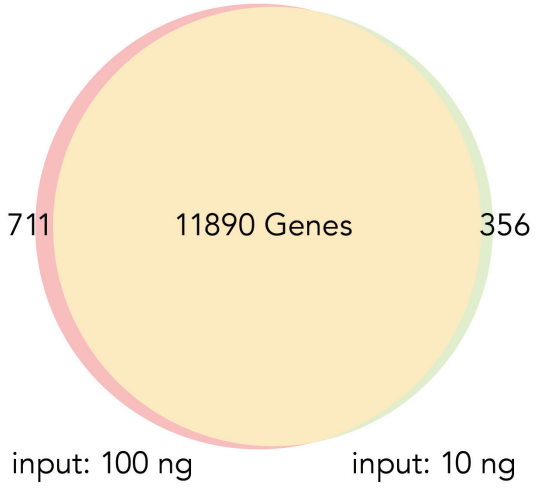
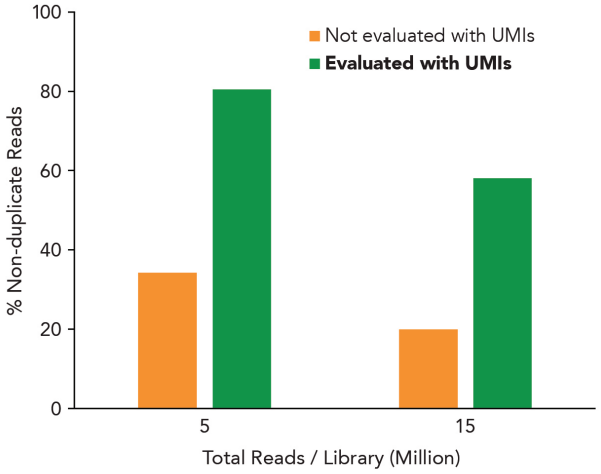
High Consistency at Different Input Amounts





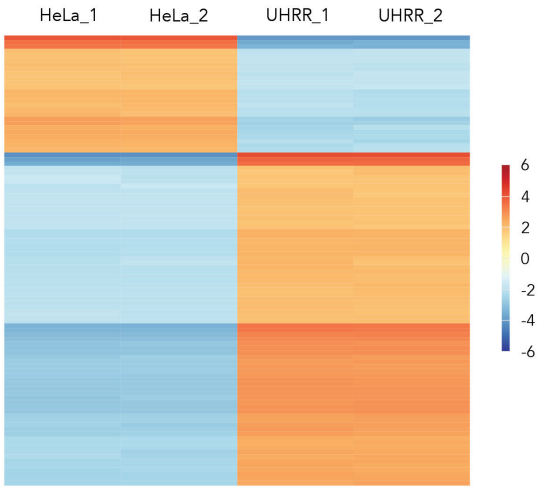
High consistency achieved in protein-coding gene detection (unique Ensembl GRCh38 gene IDs, TPM > 0.1). Zymo-Seq SwitchFree™ 3′ mRNA libraries were prepared with 100 ng and 10 ng of input HeLa RNA (RIN > 8), respectively. **Left:** TPM correlation between libraries. Pearson's r calculated on log-transformed TPM values. **Right:** Overlap of detected protein-coding genes between libraries. 5 million reads per library (read length of 150 bp) were used for the shown analysis. TPM: Transcripts Per Million.

Accurate Duplicate Evaluation



Accurate evaluation of duplicate rate obtained with the built-in UMIs. Zymo-Seq SwitchFree™ 3′ mRNA libraries were prepared with 100 ng of Universal Human Reference RNA (UHRR) (RIN > 8). UMI-tools and MarkDuplicates (Picard) were used to evaluate duplicate rates with and without UMIs, respectively.

Great Tool for DGE Analysis



Differential gene expression (DGE) identified among Zymo-Seq SwitchFree™ 3′ mRNA libraries. Heatmap included the top 100 genes with the highest variance between the two groups (HeLa and UHRR, n = 2). Each row represented one gene and each column represented one sample. 5 million reads per library were used for the shown analysis.

Product	Cat. No.	Size
Zymo-Seq SwitchFree™ 3′ mRNA Library Kit	R3008 R3009	12 prep 96 prep

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