Rice

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Correction: Alternative polyadenylation and metabolic profiling in young panicle development of hybrid rice and its parents

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In this article (Wu et al. 2025), the section of library construction and sequencing methods in Materials and Methods contains repetitive text and inaccurate descriptions. The erroneous original wording and the corrected version are listed below.

Incorrect Paragraph

Tissue collection and high molecular weight RNA extraction

Total RNA was extracted using the Trizol method (Meng and Feldman 2010). mRNA libraries were constructed using ONT's library preparation kits (Ip et al. 2015). The libraries were sequenced using high-throughput Oxford Nanopore Technology (Stancu et al. 2017; Alonge et al. 2020).

Library construction and long-read RNA sequencing

Libraries for Oxford Nanopore sequencing were constructed using high-quality high molecular weight (HMW) RNA (Wang et al. 2021). RNA was sheared to ~20 kb and purified using a 1× AMPure XP bead cleanup. Next, RNA size selection was performed using the Short Read Eliminator kit. Library preparation was performed with 1.5 µg of size-selected HMW RNA, using the Ligation Sequencing Kit SQK-LSK109 (Oxford Nanopore Technologies) following the manufacturer's guidelines. Libraries were loaded on PromethION flow cells and sequenced according to standard protocols. Runs were basecalled with Guppy v2.1 (Samarakoon et al. 2023). Basecalling was performed using the PromethIONr9.4.1 model using the recommended settings for theSQK-LSK109 kit and FLO-PRO001.

Correct Paragraph

RNA extraction

Total RNA was extracted using the Trizol reagent according to the manufacturer's instructions (Meng & Feldman, 2010).

Library construction and long-read RNA sequencing

Libraries were prepared using the Ligation Sequencing Kit SQK-PCS111 (Oxford Nanopore Technologies) following the manufacturer's protocols (Ip et al. 2015). Briefly, ligate reverse transcription adapters to 0.2 ug of the end of total RNA, and reverse transcription primers were added to the reaction solution from the previous step, followed by reverse transcription and PCR amplification. The resulting cDNA was purified using

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0.8×AMPure XP beads. Subsequently, the purified cDNA was ligated to sequencing adapters. The final library was loaded onto an R9.4.1 sequencing chip and sequenced for 48–72 h on a PromethION sequencer (Oxford Nanopore Technologies, Oxford, UK) (Alonge et al. 2020; Wang et al. 2021). The sequencing was performed by Wuhan Benagen Technology Co., Ltd., Wuhan, China. Basecalling of the raw Nanopore sequencing data was conducted using GUPPY (version 5.0.16) software (Samarakoon et al. 2023).

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Reference

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