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Correction to: Silencing of a BAHD acyltransferase in sugarcane increases biomass digestibility

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After the publication of the article [1], it was brought to our attention that the GenBank Accession number for the EF1 is missing in Methods section. Please find the accession number in the erratum below.

Expression analysis of SacBAHD genes in sugarcane leaves

Top leaves (a pool of four fully expanded leaves) of 3- and 8-month-old SP80-3280 sugarcane variety were collected for expression analysis of the identified SacBAHD genes (SacBAHD01, 03, 05 and 09) from three different plants. Total RNA was isolated using TRIzol reagent (Invitrogen, Grand Island, NY) and treated with RNaseFree RQ1 DNase (Promega, San Luis Obispo, CA) according to the manufacturer's instructions. cDNA was synthesized from one µg of RNA using SuperScript® III kit (Invitrogen). The expression level was normalized against the sugar-Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and Elongation factor 1-alpha (EF1) genes by gRT-PCR. The reactions were performed with SYBR Green Master Mix (Applied Biosystems) under the following conditions: 95 °C for 3 min denaturation, 40 cycles at 95 °C for 10 s, and 58 °C for 45 s. Amplification specificity was verified by melt curve analysis from 55 to 95 °C. SacBAHD expression levels were calculated using the $2^{-\Delta\Delta Ct}$ method [59]. The primers' sequences used for GAPDH (CA254672), EF1 (EF581011.1), and SacBAHDs (SacBAHD1: MK614571; SacBAHD3: MK614570; SacBAHD5: MK614573; SacBAHD9: MK614572) amplifications are listed in Additional file 6: Table S3.

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