ERRATUM

Erratum to: Transcriptomics analysis of hulless barley during grain development with a focus on starch biosynthesis

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The original version of this article, unfortunately, contained errors.

The errors and their correct form are given in the following.

Under Plant Materials and RNA isolation:

1. Zhangqing2000 (Q) has a higher amylose content (68.5%) and β -glucan content (6.88%) as compared to 08–1127 (C2), which has almost 100% amylose content and 11.23% β -glucan (data collected from 2012 to 2013 in Chengdu).

The correct sentence is: Zhangqing2000 (Q) has a higher amylose content (31.5%) and β -glucan content (6.88%) as compared to 08–1127 (C2), which has little amylose(almost 100% amylopectin)content and 11.23% β -glucan (data collected from 2012 to 2013 in Chengdu).

The online version of the original article can be found at <http://dx.doi.org/10.1007/s10142-016-0537-5>.

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Under Discussion:

1. For starch synthase (GBSS), *GBSS1a* (*Hvulgate_GLEAN_10032543*) showed much higher expression level in 08–1127 (C2) than Zangqing 2000 (Q), contrary to *GBSS1b* (*Hvulgate_GLEAN_10049996*)

The correct sentence is: For starch synthase (GBSS), *GBSS1a* (*Hvulgate_GLEAN_10032543*) showed a much higher expression level in Zangqing 2000 (Q) than 08–1127 (C2), contrary to *GBSS1b* (*Hvulgate_GLEAN_10049996*).

Under Reads processing and identification of differentially expressed genes:

1. After alignment, normalized gene-level expression values expressed as fragments per kilobase pair of exon model per million fragments mapped (FPKM) were determined using RSEM version 0.9.3 (Trapnell *et al.* 2010).

The correct sentence is: After alignment, normalized gene-level expression values expressed as fragments per kilobase pair of exon model per million fragments mapped (FPKM) were determined using Cufflinks (Trapnell *et al.* 2012).