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Author Correction: The *Seminavis robusta* genome provides insights into the evolutionary adaptations of benthic diatoms

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In the original version of this Article, under the Methods subsection “DNA extraction and genome size estimation”, the availability of the benthic diatoms used in this study and the accession number of the genome-sequenced strain were omitted. The first sentence, “Both Illumina and PacBio technologies were used for sequencing of *S. robusta* D6 strain mating type plus (MT+) to take advantage of short-read (better quality) and long-read (better contiguity) sequencing approaches”, should be replaced by “The *S. robusta* D6 reference strain (accession number DCG 0498) and the 48 additional strains used in this study are available from the BCCM/DCG diatom culture collection at Ghent University (<http://bccm.belspo.be/about-us/bccm-dcg>). Both Illumina and PacBio technologies were used for sequencing of the D6 strain (mating type plus (MT+)) to take advantage of short-read (better quality) and long-read (better contiguity) sequencing approaches”. This has been corrected in both the PDF and HTML versions of the Article.

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