









## Author Correction: A systems view of spliceosomal assembly and branchpoints with iCLIP

Michael Brieese, Nejc Haberman, Christopher R. Sibley , Rupert Faraway, Andrea S. Elser, Anob M. Chakrabarti, Zhen Wang, Julian König, David Perera, Vihandha O. Wickramasinghe, Ashok R. Venkitaraman, Nicholas M. Luscombe , Luciano Saieva, Livio Pellizzoni , Christopher W. J. Smith , Tomaž Curk  and Jernej Ule 

Correction to: *Nature Structural & Molecular Biology* <https://doi.org/10.1038/s41594-019-0300-4>, published online 30 September 2019.

In the version of this article initially published, in the Methods section “Mapping of Sm iCLIP reads,” it was incorrectly stated that iCLIP data were mapped to the GRCh38 primary assembly and GENCODE v.27 gene annotations using STAR (v.2.2.1). The iCLIP data were mapped to hg19 gene annotations using bowtie2. At the end of this section, the following text was missing: “The raw and processed data are available here: <https://imaps.genialis.com/iclip/search/collection/spliceosome-in-encode-lines-and-hek293>”. Also in the Methods, in the section “Identification of RBPs overlapping with spliceosomal peaks,” the following text was missing: “Because eCLIP data have been mapped to hg38, BPs were lifted over from hg19 to the hg38 genome for all analyses of eCLIP overlaps.” The errors have been corrected in the HTML and PDF versions of the article.

In the supplementary information originally posted for this article, in the description for Supplementary Data 2, it stated that “This table contains genomic positions of all 4 BP groups....” The correct description is “This table contains hg19 genomic positions of all 4 BP groups....” In the description for Supplementary Data 3, it stated “Each row represents a unique BP genomic position....” The correction description is “Each row represents a unique BP hg19 genomic position....” The errors have been corrected online.

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