CORRECTION

Correction to: XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites

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The original version of this article contained errors in Table 5 and the description about Fig. 3. The authors apologize for this oversight. The corrected Table 5 and the description about Fig. 3 can be found below.

"As shown in Fig. 3, when the 54, 97, and 90 optimal features were used, the best predictive accuracies of 66.1%, 73.4%, and 71.1% were obtained for identifying Ψ sites in *H. sapiens*, *M. musculus*, and *S. cerevisiae*, respectively."

Table 5 The performance of the model for identifying Ψ sites in each species

Species	Acc (%)	Sn (%)	Sp (%)	Mcc
H. sapiens	66.05	63.45	68.65	0.32
M. musculus	73.42	77.35	69.48	0.47
S. cerevisiae	71.10	65.92	76.30	0.43

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