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Corrigendum

Corrigendum: A statistical learning method for simultaneous copy number estimation and subclone clustering with single-cell sequencing data

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Fei Qin, Guoshuai Cai, Christopher I. Amos, and Feifei Xiao

^{OA}Open Access paper



Cover Just as runway lights guide airplanes to the correct runway, short sequences guide ribosomes to identify the correct translation initiation sites. A recent study has revealed that ribosomes can recognize novel CU-rich motifs along mRNAs, which enable them to initiate translation at both AUG and nonAUG initiation sites. These CU-rich motifs have been found in dicots, monocots, humans, and viruses, suggesting their evolutionary importance for initiation activity across different species. (Cover illustration by Ying Wang, <https://www.ywangstudio.com>. [For details, see Wu et al., pp. 272–285.]