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Publisher Correction: A Computational Method to Quantify the Effects of Slipped Strand Mismatching on Bacterial Tetranucleotide Repeats

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This Article contains a typographical error in the Introduction section.

“Where this postulate holds true, the fractional base compositions (FBC, the proportion of the number of A, C, G, or T relative to the total number of bases in the SSR) for a base in SSM-mediated SSR length variants are necessarily nearly identical and essentially independent of the total length of the SSR, given the SSR > RU length.”

should read:

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