# Correction to: The cytidine deaminase under-representation reporter (CDUR) as a tool to study evolution of sequences under deaminase mutational pressure 

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## Correction

Following publication of the original article [1], the authors reported that Figs. 1 and 3 were interchanged. The original article has been corrected.
The correct versions of the figures are given below:

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## Reference

1. Shapiro $M$, et al. The cytidine deaminase under-representation reporter (CDUR) as a tool to study evolution of sequences under deaminase mutational pressure. BMC Bioinformatics. 2018;19:163. 10.1186/s12859-018-2161-y

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Fig. 1 gc3 shuffle method. The choice of codons in the 4th nucleotide in the sequence (lle) was determined by the probabilities as follows: since there is an overall GC content of $60 \%$ at the 3 rd position of the codons in the subject sequence, the ATC codon will be chosen with 0.6 probability. Since the AT content is then 0.4 , the other two codons ATT and ATA are chosen randomly with equal probability, conditional on the $40 \%$ AT content. Note that the shuffling occurs iteratively throughout sequence, not just one codon at a time


Fig. $\mathbf{3}$ dn23 shuffle method. First the dinucleotide frequency is calculated for the 2 nd and 3 rd codon positions of the original sequence. Then for each amino acid, codons are chosen based on the appropriately normalized probabilities for the dinucleotides available for that amino acid


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