

CORRECTION

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Correction to: A new primer construction technique that effectively increases amplification of rare mutant templates in samples

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Correction to: BMC Biotechnol (2019) 19:62
<https://doi.org/10.1186/s12896-019-0555-1>

Following publication of the original article [1], the author informed us that the legend for Fig. 2 was incorrect.

Fig. 2 legend has been corrected in the original article.

The correct legend for Fig. 2 is given below:

Mutant sequence enrichment using stutmmer PCR. The abilities of stutmers to detect four different mutation scenarios (single nucleotide mutation, two different single nucleotide mutations, and a deletion mutation) were tested under three different sample conditions (only wild-type, 90:10 ratio of wild-type:mutant, and 99:1 ratio of wild-type:mutant). In all cases, the stutmers were able to detect the mutations even when the mutant templates were present in only 1% of the tested samples. The wild-type template was completely inhibited in the T790 M point mutation (a) and exon 19 deletion mutation (b). The arrow indicates where the deletion mutation occurred

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Published online: 12 November 2019

Reference

1. Huang JK, et al. A new primer construction technique that effectively increases amplification of rare mutant templates in samples. *BMC Biotechnol.* 2019;19:62. <https://doi.org/10.1186/s12896-019-0555-1>.

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