Corrigendum: MIPSTR: a method for multiplex genotyping of germline and somatic STR variation across many individuals

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Corrigendum

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Corrigendum: MIPSTR: a method for multiplex genotyping of germline and somatic STR variation across many individuals

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Five measures of reagents reported in the Methods section of the paper are incorrect. When mixing 750 ng genomic DNA with the MIPs mixture, we added 2 fmol of MIPs mixture (1 μL of 2 nM MIPs mixture), not 2 pmol as stated in the text. In the extension and ligation reaction, we added 2.5 nmol dNTPs (1 μL of 2.5 mM dNTPs), not 2.5 pmol. After the exonuclease was added, the final reaction volume was 24 μL, not 19 μL. Finally, during the PCR reaction of library construction, we added 12.5 nmol of dNTPs (5 μL of 2.5 mM dNTP) and 25 pmol of the forward and reverse primers (5 μL of 5 μM stock solution of each forward and reverse primer), not 12.5 pmol of dNTPs and 25 μmol primers as reported.

The authors thank Joseph Christopher and Doug Winton for using the method and pointing out these errors. These errors do not affect any of the conclusions of the paper, but could prevent others from successfully using the method. The authors sincerely apologize for any inconvenience these errors may have caused.

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