



Correction to High Sensitivity Detection and Quantitation of DNA Copy Number and Single Nucleotide Variants with Single Color Droplet Digital PCR

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The caption for Figure 5 reads: One-color SNV quantification. (A) Primers are designed with the single nucleotide variant at the 3' end of the complementary region. Noncomplementary tails of varying lengths are then added to the 5' end and amplified with a universal reverse primer. (B) 1:4 mixture of MUT/WT BRAF template amplified with mutant primers with the short tail and wild-type primers with the long tail. (C) Swap: 1:4 mixture of MUT/WT BRAF template amplified with wild-type primers with the short tail and mutant primers with the long tail. (D) Serial dilution of mutant BRAF template (LS411N) into wild-type (Human male control). Theoretical % mutant was calculated from TaqMan measured concentrations of mutant and wild-type template. The assay was performed with the EvaGreen primer mix from (B). (E) The red border regions provide a magnified view of three data points on the lower end of the dilution series from (D).

However, the caption for Figure 5 should read: One-color SNV quantification. (A) and (B) Primers are designed with the single nucleotide variant at the 3' end of the complementary region. Noncomplementary tails of varying lengths are then added to the 5' end and amplified with a universal reverse primer. (C) 1:4 mixture of MUT/WT BRAF template amplified with mutant primers with the short tail and wild-type primers with the long tail. (D) Swap: 1:4 mixture of MUT/WT BRAF template amplified with wild-type primers with the short tail and mutant primers with the long tail. (E) Serial dilution of mutant BRAF template (LS411N) into wild-type (Human male control). Theoretical % mutant was calculated from TaqMan measured concentrations of mutant and wild-type template. The assay was performed with the EvaGreen primer mix from (C). (F) The red border regions provide a magnified view of three data points on the lower end of the dilution series from (E).

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