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Correction to: Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome

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Following publication of the original article [1], the authors reported an error in Additional file 1. The updated Additional file 1 is given below.

Additional file

Additional file 1 Description of MCC-Seq capture panel. This file contains: (1) summary of CpGs and genomic regions targeted by the MCC-Seq capture panel design (.xlsx Excel spreadsheet format), and (2) a list of the targeted regions (.bed text file). (ZIP 4405 kb)

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