

Figure S1. Sequences of *SLC22A17* methylated DNA hotspot. (A) Bisulfite-converted sequence of *SLC22A17* and primers used for the PCR amplification and Sanger sequencing. Underlined sequence represents the *SLC22A17* hotspot analyzed in the present study. (B) *SLC22A17* sequence used to generate DNA unmethylated and methylated controls and to analyze the *SLC22A17* methylation status using the standard MSRE and the MSRE-droplet digital PCR protocols. (C) Sequence of Custom methCTRL. Primers and probes were highlighted in each sequence. MSRE, methylation-sensitive restriction enzyme.

A

SLC22A17 bisulfite-converted sequence (Assembly: GRCh37/hg19 - chr14:23,821,176-23,821,349)

SLC22A17 Prom2 Forward
GTGAGTATAGGAAGGTTATTATAGTTTTAATTTTTGAGGTAATGGTTGAAGTTCGGCGGGGCGAAGTCGT
 TGTACGAGGGGTCGGTATTGGTGGCGATACGGTTGGCGGCGTTGGTTGTTAGGGTAGCGTTGGCGACGTT
 SLC22A17 Prom2 Reverse
 GACGTCGTTGGTATTGGGAGGTTGTTTTTAGTTA

B

SLC22A17 sequence (Assembly: GRCh37/hg19 - chr14:23,821,170-23,821,445)

SLC22A17 cloning Forward
TTGGTGGTGAGCACAGGAAGGCCATTATAGTCCCAATCCTTGAGGCAATGGTTGAAGTTCGGCGGGGCGA
 SLC22A17 Forward methDNA hotspot
 SLC22A17 probe
AGCCGCTGCACGAGGGGTCGGTACTGGTGGCGACACGGCTGGCGGCGCTGGCTGCTAGGGCAGCGCTGGC
 SLC22A17 Reverse
 GACGCTGACGCCGCTGGCATTGGGAGGCTGCTCCCAGCCAGAGGCATTAGGGGGGAAGGCCCCGTAGTGG
 SLC22A17 cloning Reverse
 CAATGCAGCGGGGCGCCAGCGTGAAGATGGGGTCCGAGGCCATGCCCAGAGCCACGAAGAGCACC

C

Methylation Internal Control sequence (methCTRL)

T7 Forward
TAATACGACTCACTATAGGGAGACCCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTG
 MethCTRL Forward
 TGCTGGAATTCTGGCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTTCGAGCT
 MethCTRL probe
 MethCTRL Reverse
 GGACGGCGACGTAAACGGCCACAAGTTCAGCGTCCGCGGCGAGGGCGAGG
 EGFP-N bis
GCGATGCCACCAACGGCAAG

Figure S2. Bisulfite sequencing of the *SLC22A17* hotspot in SK-MEL-23, A375 and A2058 cells. (A-C) Sanger sequencing chromatogram of the *SLC22A17* methylated DNA hotspot obtained from bisulfite-converted DNA of (A) SK-MEL-23, (B) A375 and (C) A2058 cells. The peak relative to internal cytosine of CCGG sequence within the *SL22A17* sequence is highlighted in red. The unconverted cytosine indicates complete methylation, while the conversion of cytosine to thymine (C>T) is indicative of hypomethylation of CpG dinucleotide. Bisulfite-converted sequence of *SLC22A17* is detailed in Fig. S1A.

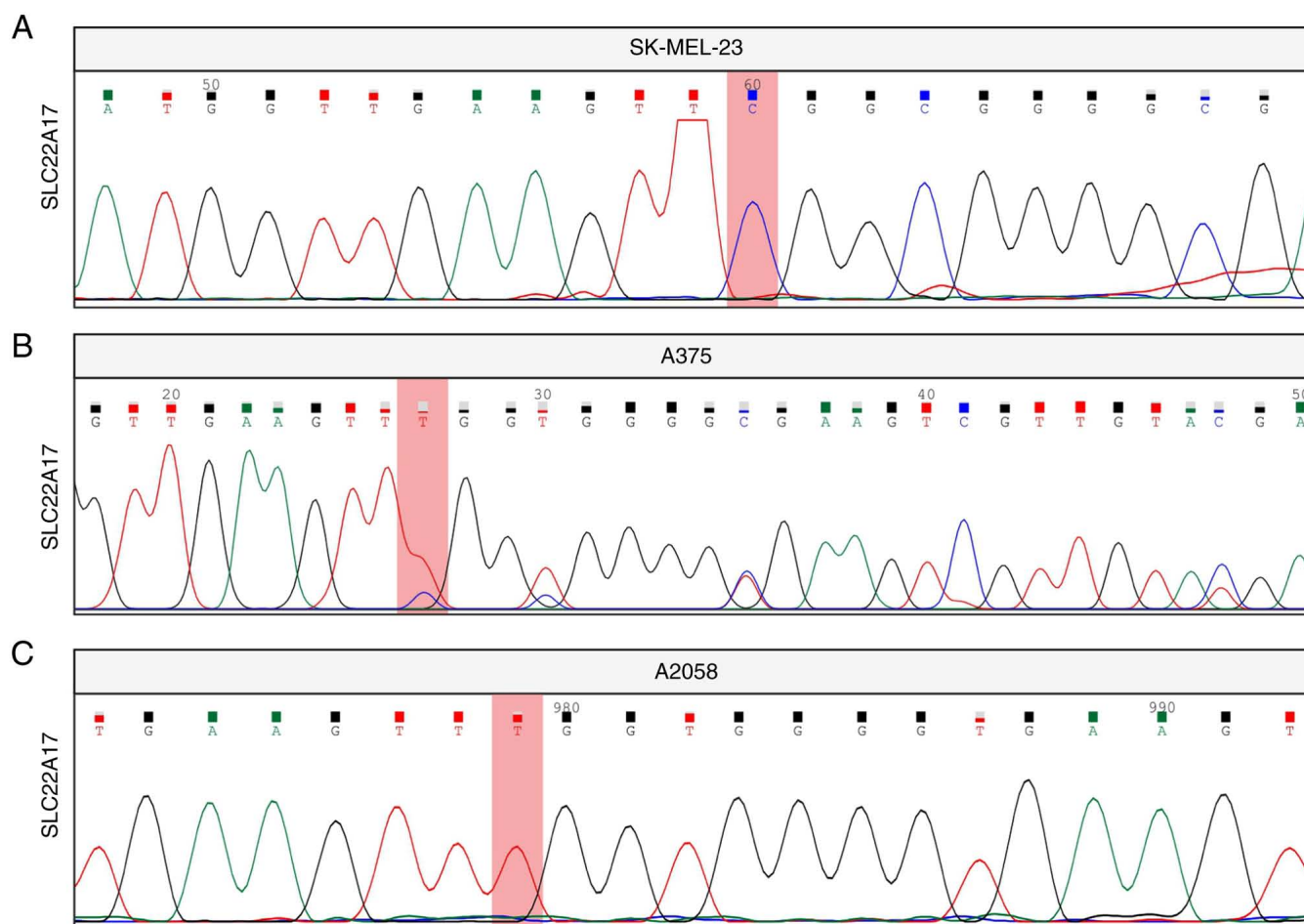


Figure S3. ddPCR amplification of the *SLC22A17* methDNA hotspot on standard MSRE-digested gDNA from SK-MEL-23. (A) FAM amplitude of *SLC22A17* hotspot detected in undigested, *HpaII* and *MspI* mix. (B) HEX amplitude of methCTRL. All experiments were performed in duplicate. For SK-MEL-23 MSRE mix (200 ng of gDNA in 10 μ l final reaction volume), 1 μ l of each digested sample was added to the ddPCR mix, while 5 μ l of SK-MEL-23 diluted MSRE mix (20 ng of gDNA in 10 μ l final reaction volume) were used for the following ddPCR amplification. ddPCR, droplet digital PCR; meth-, methylated; MSRE, methylation-sensitive restriction enzyme.

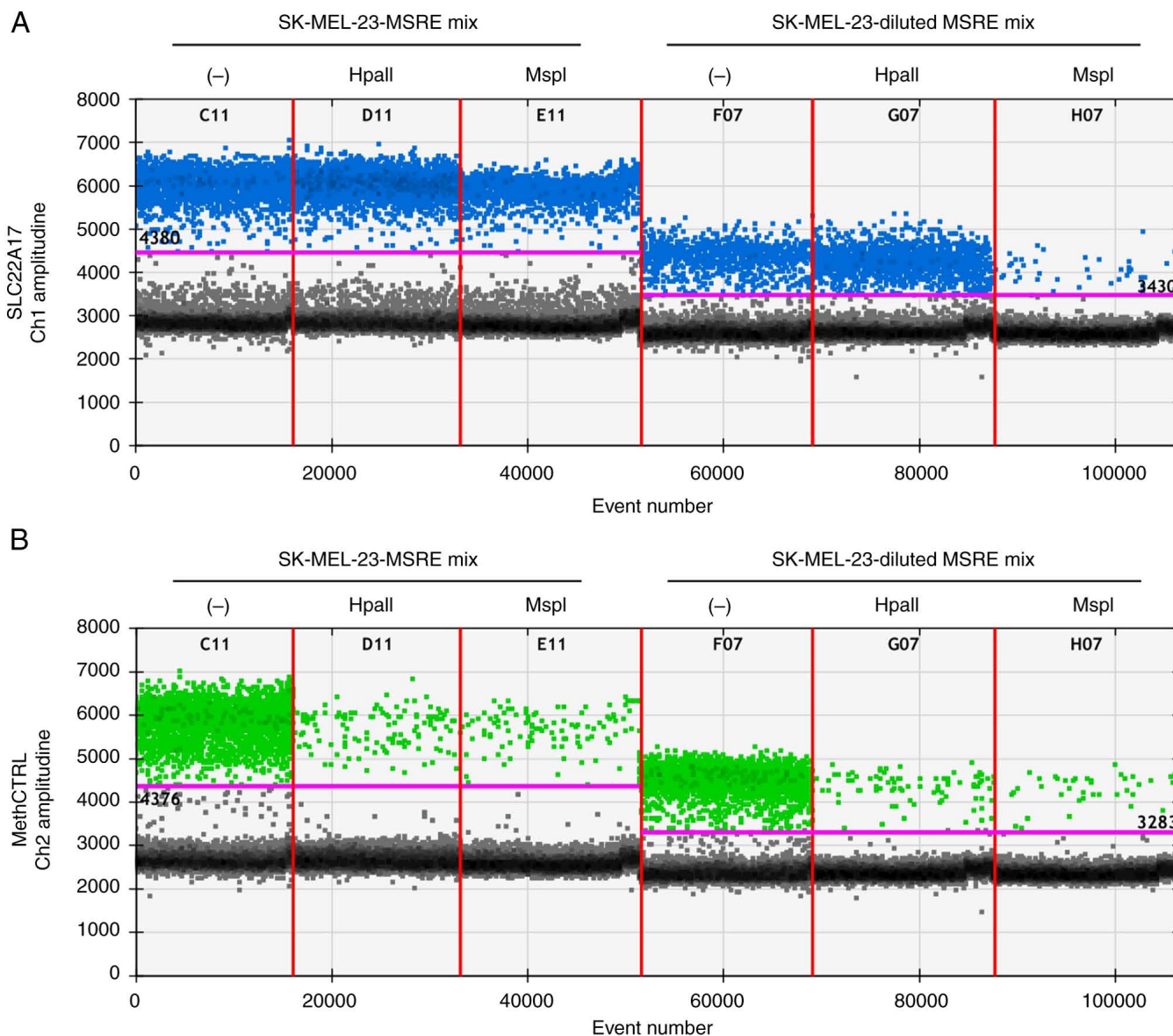


Figure S4. Methylation-sensitive restriction enzyme digestion buffer interference on droplet digital PCR amplification efficiency. (A) FAM amplitude of *SLC22A17* target. (B) HEX amplitude of methCTRL. (C) Amplitude plot of channel 1 (*SLC22A17*). (D) Amplitude plot of channel 2 (methCTRL). All experiments were performed in duplicate. meth-, methylated.

