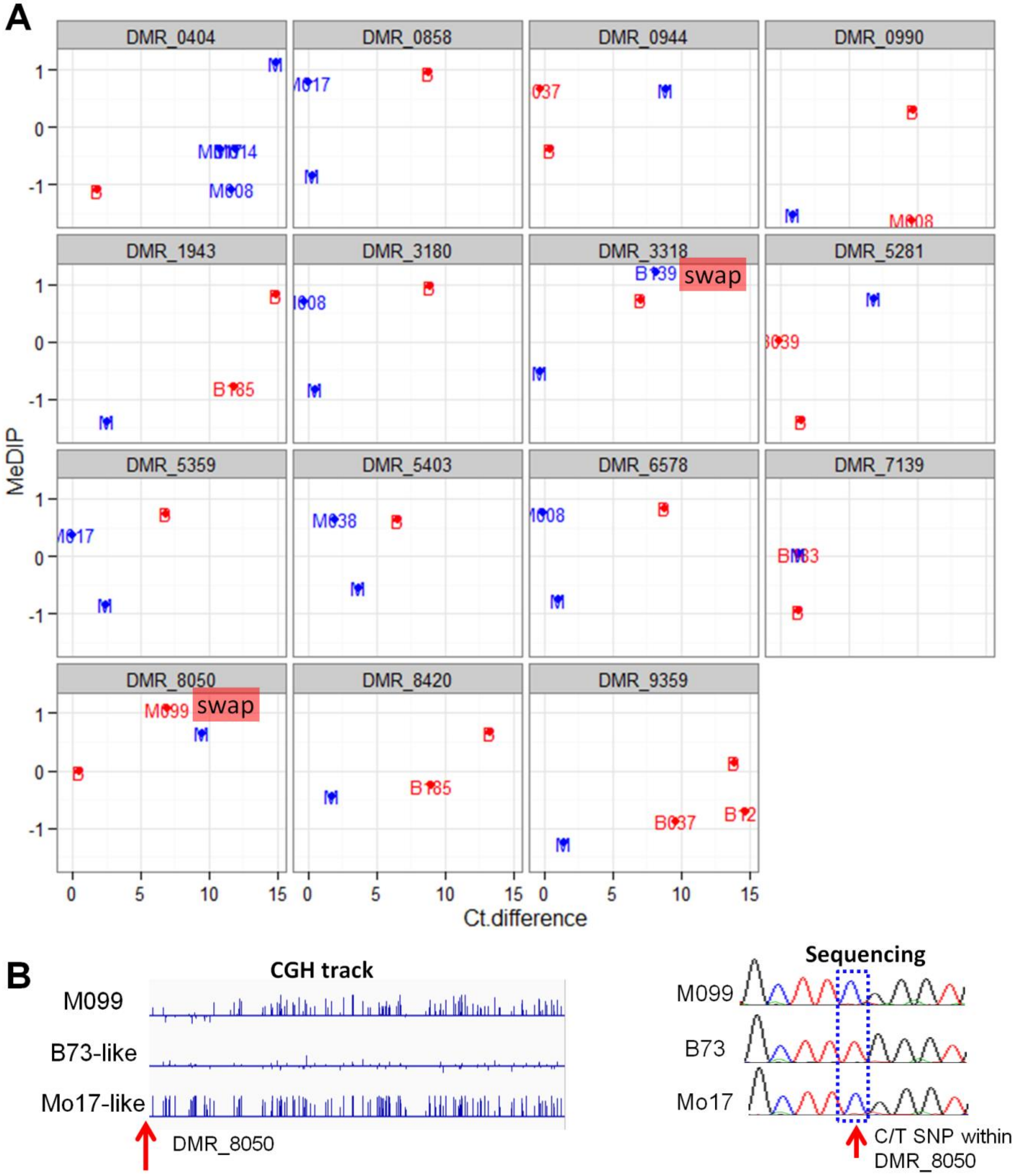

Figure S7 qPCR validation of high-confident swaps. (A) Each panel was shown in the same way as in Figure S6 except that the swaps were labeled using the NIL name (Bxxx, or Mxxx) instead of a star. For the 15 tested DMRs, parental difference (B73 vs Mo17) were confirmed in all of them except one (DMR_7139). Two DMRs showed swaps based on both array and qPCR (DMR_3318 and DMR_8050). Further checking (panel B) showed that the swap at DMR_8050 was caused by miscalled genotype instead of methylation change (i.e. M099 was called to have a swap because it had methylation level same as Mo17, but with a B73 genotype (CGH track). Subsequent Sanger sequencing showed that M099 had Mo17 genotype instead of B73).