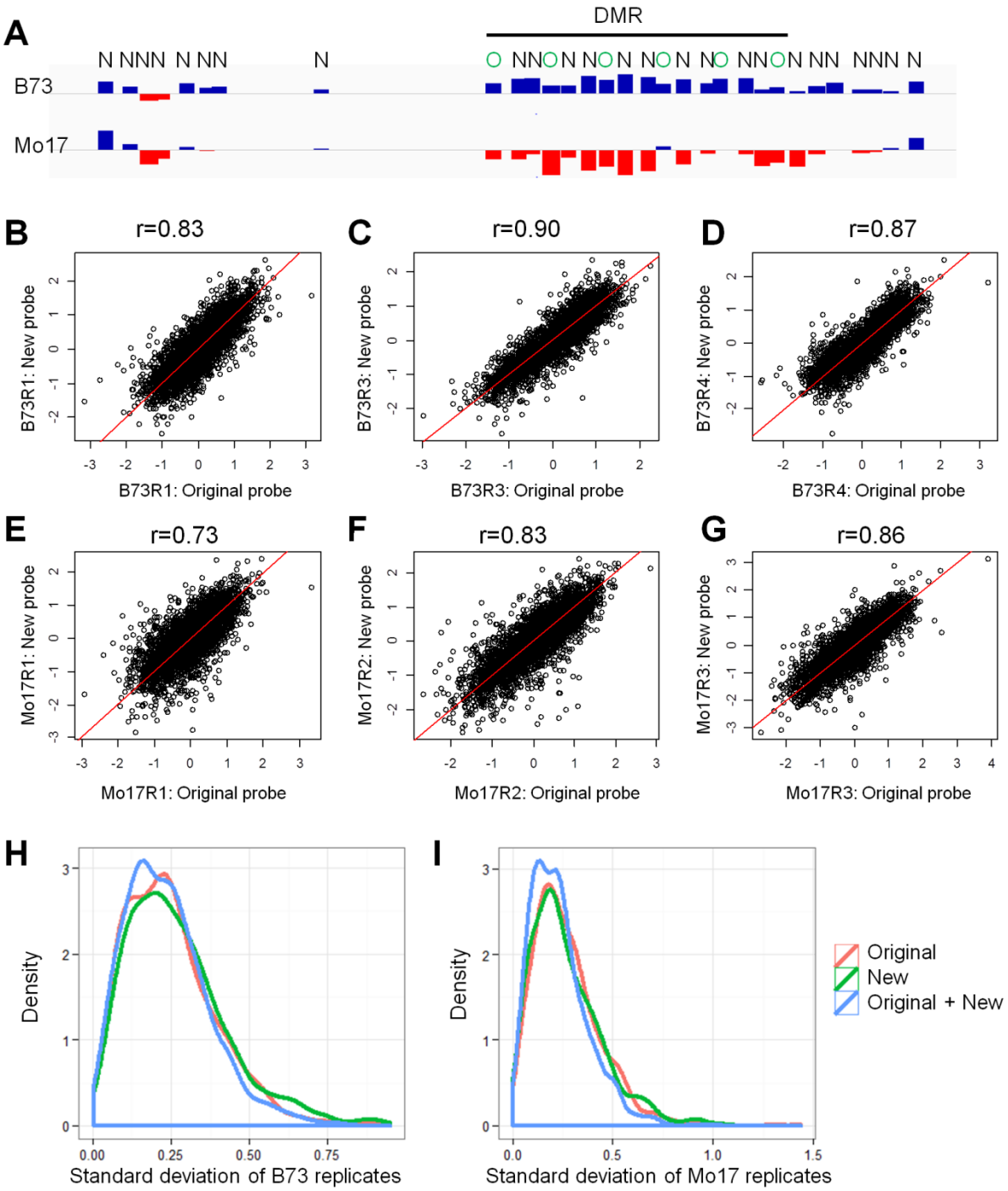

Figure S1 Comparison between Original and New probes for B73 and Mo17. (A) New (N) probes were designed to fit in-between Original (O) probes, and around the DMR. (B-G) Correlation between Original and New probes for inbred lines B73 and Mo17. The red line represents y=x. The correlation coefficient was shown on the top of each plot. Shown here are the 3 biological replicates of each inbred line. From these figures, we can see that the original probes and the new probes show high consistency of DNA methylation measurement. (H-I) Distribution of standard deviation across 3 biological replicates of B73 (H) or Mo17 (I) when the methylation level of each DMR was calculated using Original probes, or New probes or both types of probes within the DMR. From (H) and (I), we can see that variances between replicates of both B73 and Mo17 were slightly reduced when using the combined set of probes. Therefore, we used the average of both new and original probes to represent methylation level in this study.

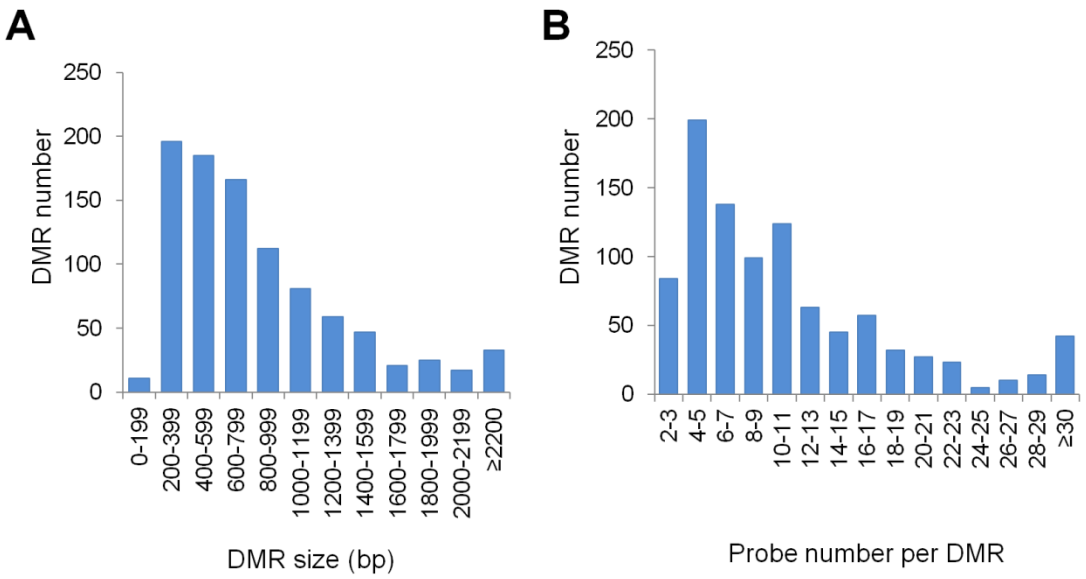

Figure S2 Characteristics of DMRs used in this study. (A) Size distribution of 962 DMRs used in this study. (B) Distribution of probe numbers per DMR. Both Original and New probes were included.

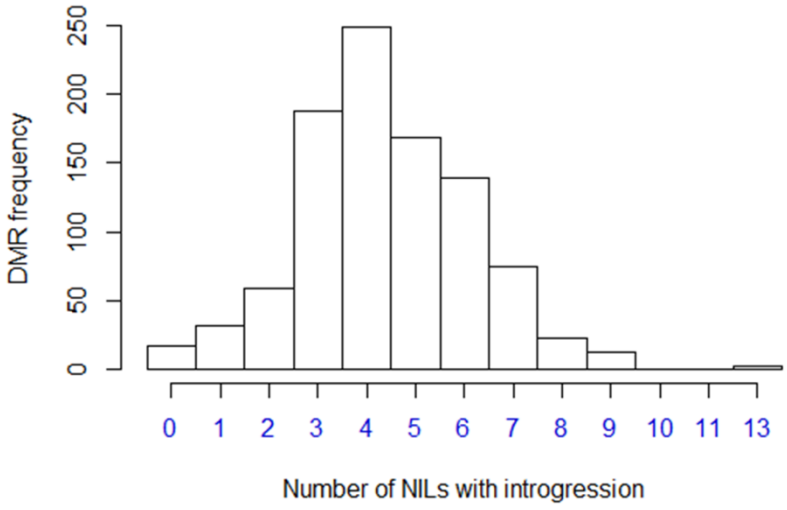

Figure S3 Distribution of informative NIL number per DMR. Note: the majority of DMRs have 3-6 NILs with introgressions. All 962 significant DMRs between B73 and Mo17 were included.

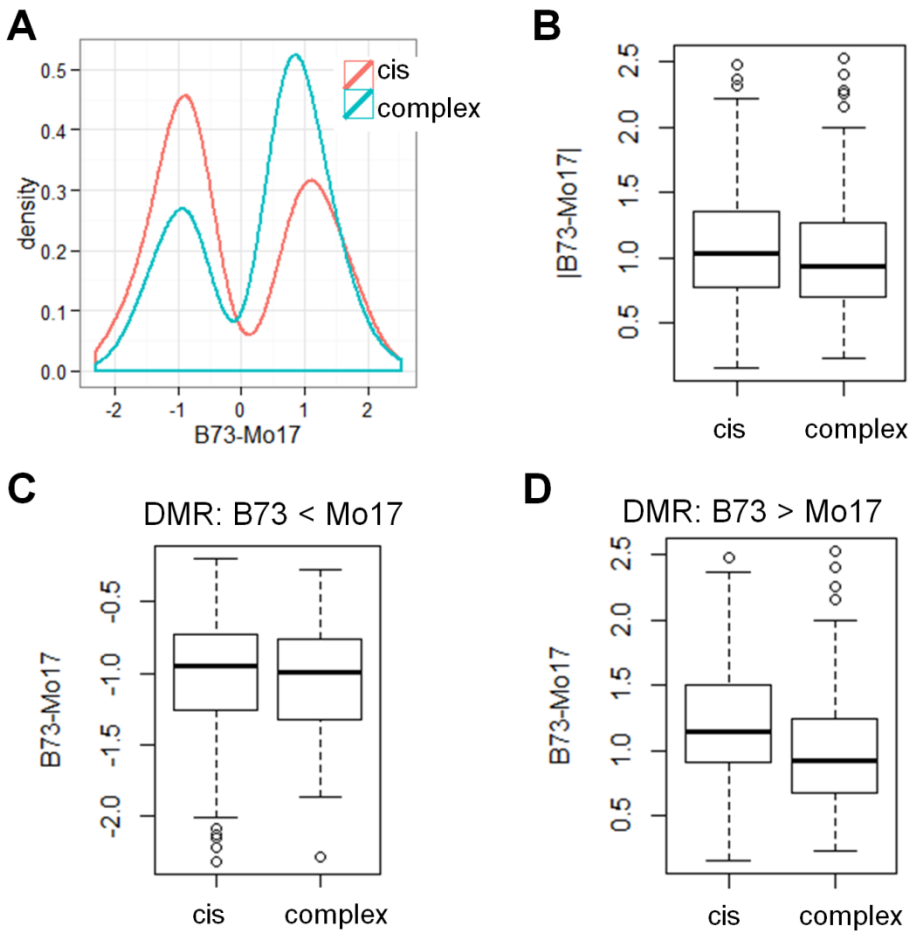

Figure S4 Comparison of parental difference between cis DMR and complex DMR. (A) Distribution of parental difference for DMRs showing cis or complex inheritance pattern. (B) Boxplot showing the absolute value of parental difference for cis and complex DMR. (C-D) Comparison of parental methylation difference between cis and complex DMR. In C, only DMRs with Mo17 having higher methylation level than B73 were included. In D, only DMRs with B73 having higher methylation level than Mo17 were included.

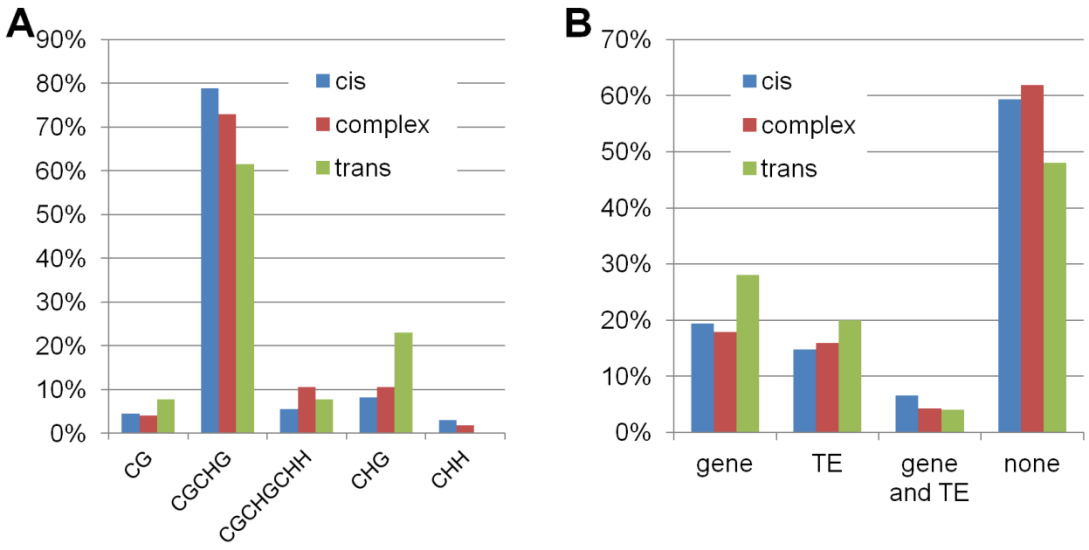

Figure S5 Association between DMR inheritance patterns and DMR types (A) or different genomic features (B). (A) Percentage of DMRs with different methylation contexts for each DMR inheritance pattern. We classified DMRs with Whole-Genome Bisulfite Sequencing data into 5 context categories: CG, CHG, CHH, CGCHG and CGCHGCHH based on the methylation difference between B73 and Mo17. For CG and CHG, we used a cutoff of 20% difference; and for CHH, we used a cutoff of 5% difference. DMRs that have methylation difference greater than the cutoff of the respective sequence context (i.e., CG, CHG, and CHH) are defined as DMRs of that sequence context. For example, CG-DMRs showed more than 20% methylation difference in CG, less than 20% in CHG and less than 5% in CHH. (B) Percentage of DMRs overlapping different genomic features for each DMR inheritance pattern. The DMR position was compared with the gene annotation (version: 5b) or transposable element (TE) annotation (version: 5a_MTEC). DMRs that don't overlap any of these annotated features were classified into the "none" group.

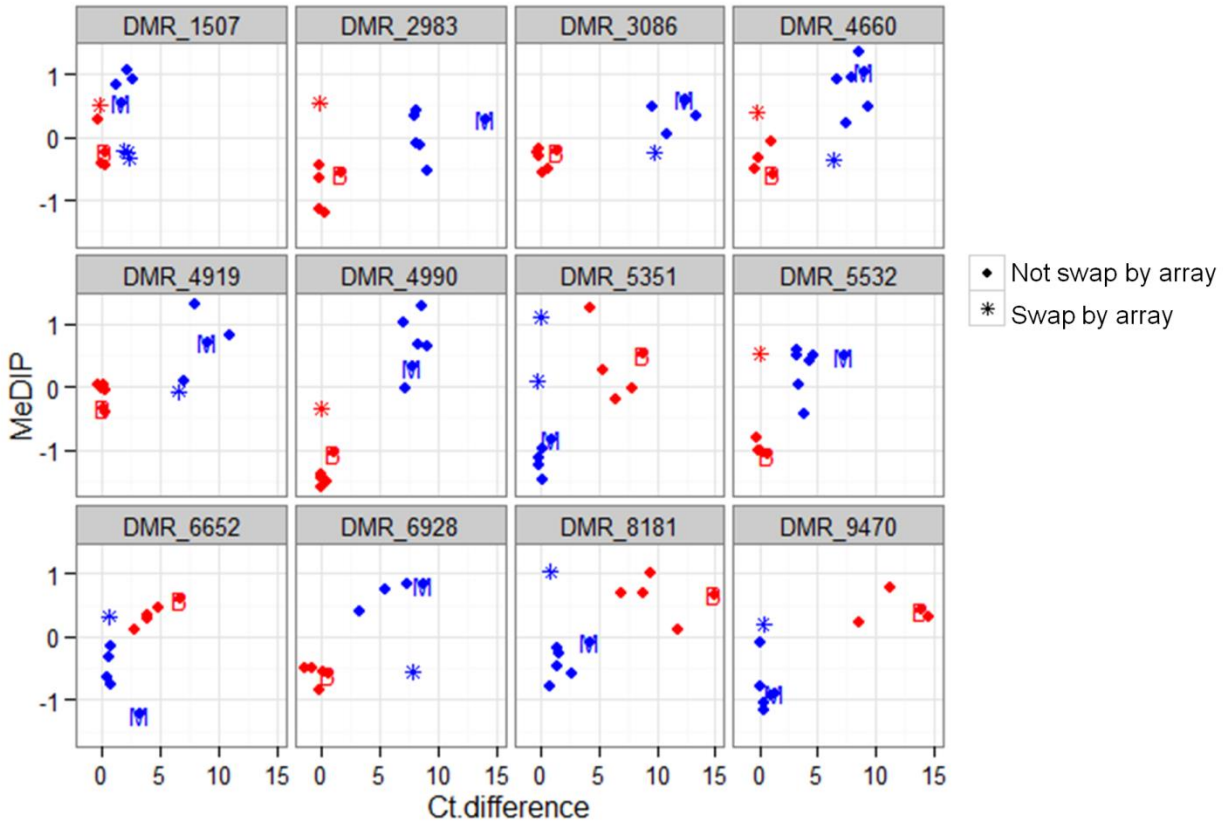

Figure S6 qPCR validation of DMR inheritance pattern and swaps (i.e. unstable inheritance relative to genotype). For each panel, the x axis is methylation level based on qPCR, big numbers represent higher methylation level; the y axis is methylation level based on array, with positive and negative values representing higher and lower methylation, respectively. The dot/star within each panel represent either B73 inbred (B) or Mo17 inbred (M), or one NIL, with B73-like and Mo17-like lines colored as red or blue, respectively. For all the 12 DMRs tested, the inheritance pattern (cis) was confirmed, while the swaps was only supported by array and not by qPCR.

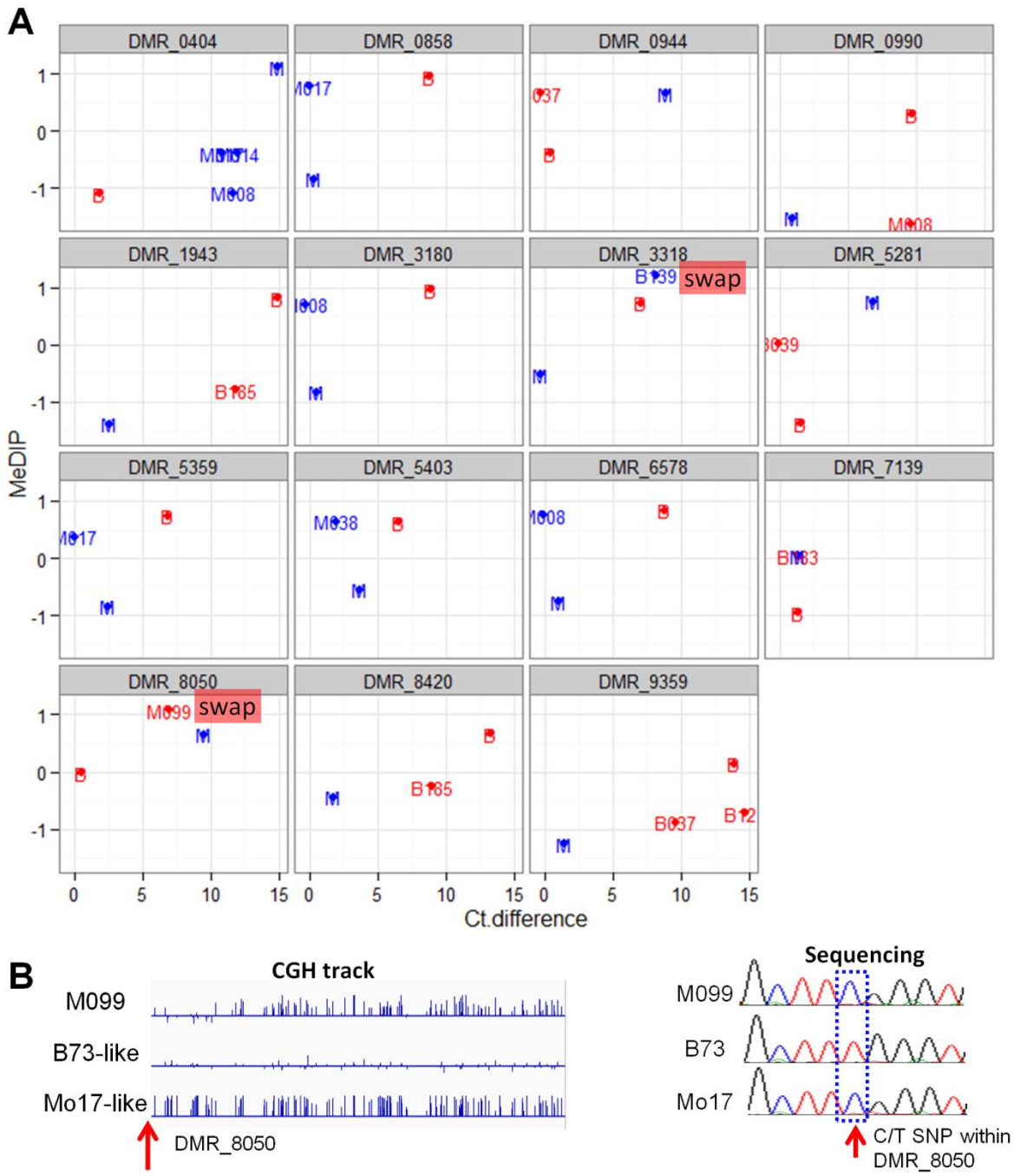

Figure S7 qPCR validation of high-confident swaps. (A) Each panel was shown in the same way as in Figure S6 except that the swaps were labeled using the NIL name (Bxxx, or Mxxx) instead of a star. For the 15 tested DMRs, parental difference (B73 vs Mo17) were confirmed in all of them except one (DMR_7139). 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).

Table S1 Primers used in this study

Name	Forward sequence	Reverse sequence
DMR_0404	ACCCTGGTGGCATTGTTCTAGT	TCCCCTCTCTTCAAGCAGAAAC
DMR_0858	ATCGCCCTAGGACAGCTAACAG	ACTCCCTTCGGTTCTCCCTATC
DMR_0944	GGACTCCTAGGGGAGAGGGATA	TAGATCTCGGGTCAGGAGGAAG
DMR_0990	ACTCTCTGCGACGTTTCTCAGTT	ACGTCTTCAACCAAACTCCTCTG
DMR_1507	TGTCTCGGTGATCATGGTGT	TGAGACATACTACTAGCACACTGCTG
DMR_1943	CCGACCAACAAGTGTAAAGTGA	AGTCTCGAGAAGGTTGCCATAG
DMR_2983	TTTGGAAAGCGAGGAACAAAAT	CCCGATTAAATTCCGGTGATAA
DMR_3086	TAGGTTAGGGTTTGTCGGTGCT	TATCTTTTCATGCCTTGCTGGA
DMR_3180	AAGAGAAAAGGTTTCCCTGAGC	GTGGAAGAGTACCATCTGGTTTG
DMR_3318	TGCACTCGAACAGTTAGAAATCAG	GCAGAACCTGGAAACAGAAAAA
DMR_4660	GTTGTAGCGTAGCAGCATCTTCA	TTCTCTATCCTTGCACCTTCCTG
DMR_4919	CGATCAACCGTGTTCTGGTTTC	ATGAAGGGGGATCAAGCTGAAG
DMR_4990	GCTACGTAACTGTGCTGCCTGT	ATCGAGGTTGGAGGGTCTCATA
DMR_5281	TGCCTGGTGATTGATTCCAC	ATCCACCTGCTACACCGACTTC
DMR_5351	CATTTCTATGCTCGGCTACATGA	GAACGGTCATGGTGAATTGCT
DMR_5359	ATGCAGTGAGCTCTAGGGTTACG	CAAATAGCACAACCGCTTTCTCT
DMR_5403	AAGAATTAAGGTTGTGGGTGTGC	TCGTATGTGCCATTTGGTAAGG
DMR_5532	ACGAGTCCAATTCCATGTTCCT	TCATCGAACTTCAACTGCCCTA
DMR_6578	AACGCAACAGCACAACATTAGG	TGTTTTGACAAGTGCATCGAGA
DMR_6652	GTTTACAGAGGCTGAGGGCAAG	CTCCCTATCGAAGCACCACTG
DMR_6928	GTTAAGGGGGCAAGAAGAAAGA	ACCCATGTCTACATCACGAACC
DMR_7139	CCACTCGGCATCTAGTCAACAC	GTAGAAACGAGAGCCTGCGACT
DMR_8050	TCTTCAACGCTGACTTCTTTGC	GTGTGCTGAAGGTGATTTGGAG
DMR_8181	TACAGCACCGTAGATTGCCAGT	GCGGAGTTTTGGATAACTTTGG
DMR_8420	AATTTCTCGTCGGAGATCGAAG	GACTTGACCATGCCGACATTT
DMR_9359	TAGCCGCAGATCAAGAATTCAA	CGTTCCTCATTGGGAGTACACA
DMR_9470	ACGGCGGACCTAACTATACACC	CCAATCGTGTGTCGGTTATTCT

Tables S2-S3 are available for download as Excel files at
http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.158980/-/DC1

Table S2 DMR inheritance pattern in NIL population

Table S3 DMR inheritance pattern in RIL population