Figure S1: A) Methylation state classification for each genotype based on alignment to their respective genome assemblies. Each 100bp bin of the genome was assigned a methylation state based on CG, CHG, and CHH methylation. Any bin with less than 2 cytosines was labeled "No Sites" and any bin with < 3x coverage was labeled "Missing Data". For all other bins, context-specific cutoffs of methylation were used to classify CHH, CG only, CG/CHG, Intermediate and Unmethylated status. The proportion of each domain category for all bins in the respective genome are shown. B) The proportion of all bins for the B73 and non-B73 (Mo17, W22, Oh43) samples aligned to the B73v4 genome assembly that have coverage (black) or bins without enough coverage to be assessed (grey).
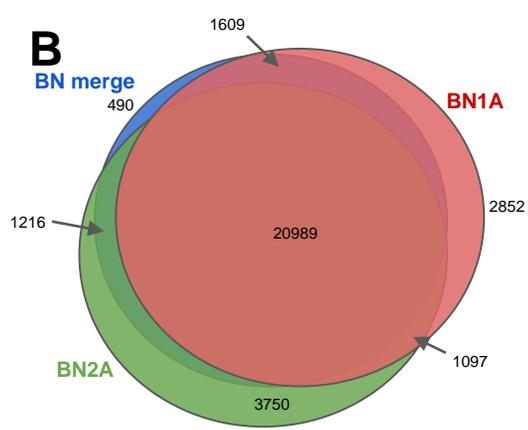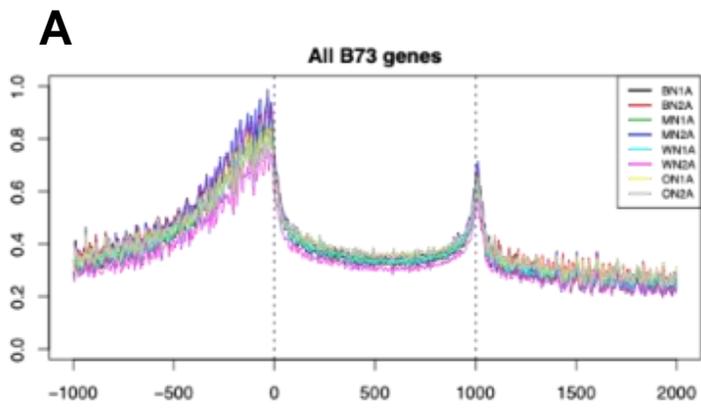
Figure S2: B73 ATAC-seq reproducibility. A) Metaplot of ATAC-seq coverage over annotated B73 genes for all ATAC-seq tissue samples aligned to the B73v4 genome assembly. The gene space was normalized to a 1kb region (represented in the middle of the metaplot) with the flanking upstream and downstream 1kb based on gene transcript direction. B) ATAC-seq was performed on two replicates for each genotype and ACR calls were generated for each sample individually (BN1A and BN2A) as well as the merged alignment file (BM merge). The venn diagram represents the overlap in defined ACRs for individual and merged samples for B73.
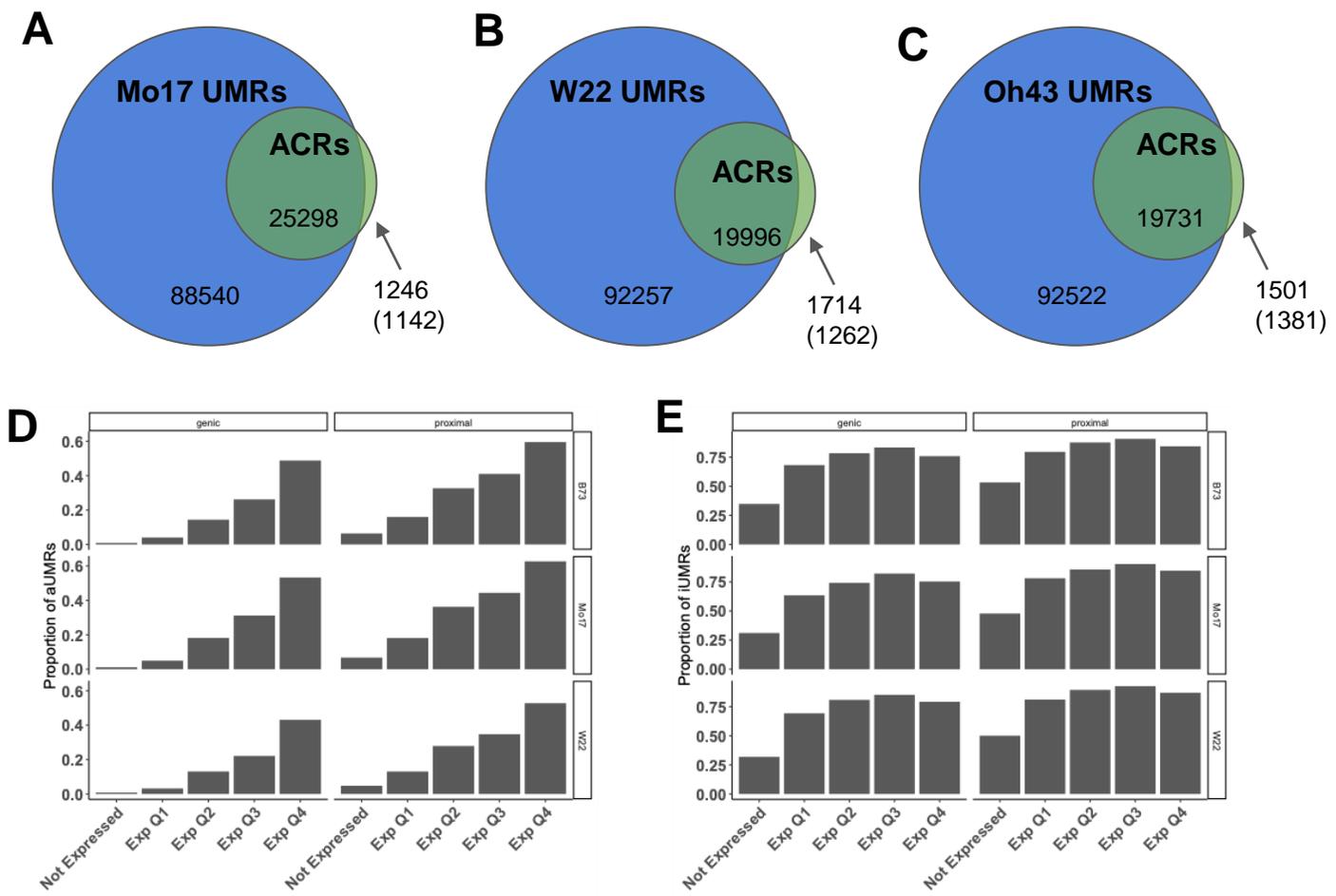
Figure S3: Overlap between ACRs and UMRs. The overlap between the Mo17 (A), W22 (B) and Oh43 (C) UMRs (blue) and ACRs (green) defined based on alignments to the B73v4 genome. Non-UMR ACRs that are defined as methylated are shown in parentheses below ACR count. RNAseq data for the same tissue sample was used to classify all B73 genes as not expressed (CPM <1) or into expression quantiles of lowest expression (Q1) to highest expression (Q4). For each category of gene, the proportion of genes with aUMRs (D) and iUMRs (E) that are overlapping the gene or proximal to the gene(<2kb) was calculated.
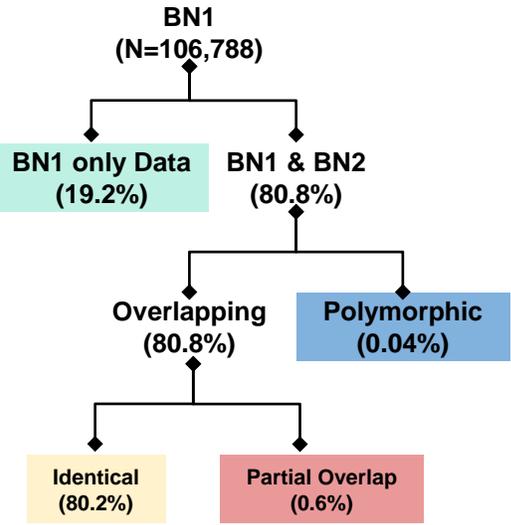
Figure S4: Stability of UMRs across replicates. The stability of UMRs was assessed among different B73 samples. There are two biological replicates of B73 WGBS data labeled as BN1 and BN2. There are 106,788 UMRs identified in BN1. We assessed the proportion of these regions that have sufficient coverage in BN1 and BN2 and then classified the proportion that have overlapping or polymorphic UMRs in BN2. The proportion of the overlapping UMRs that are identical or partial were determined. All percentages are relative to the total number of UMRs identified in BN1.