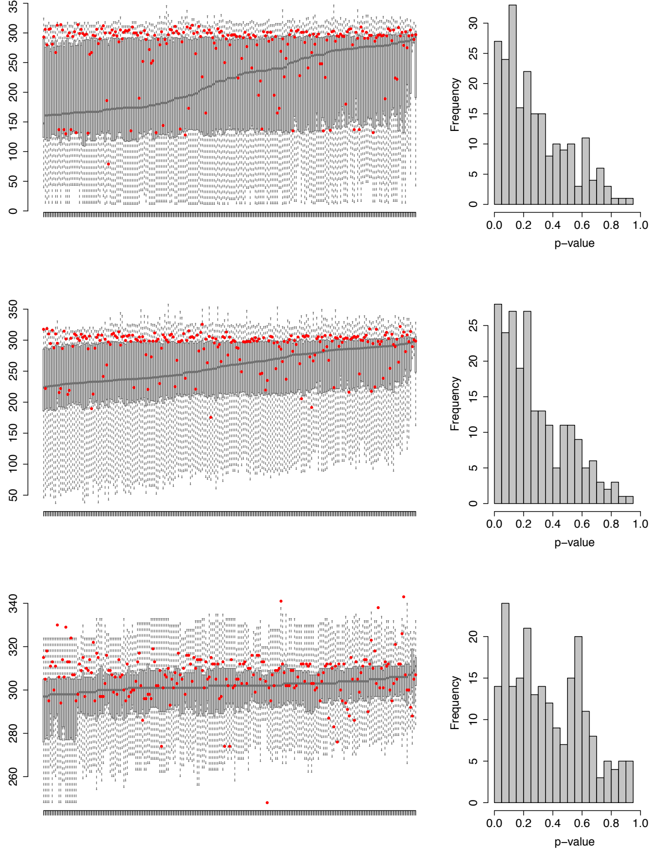
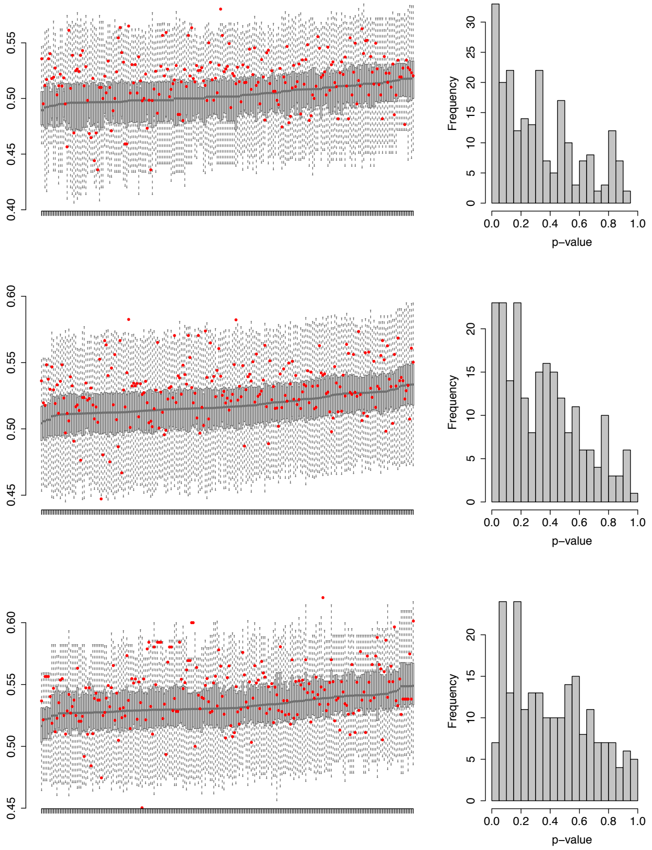
Supplemental Fig S5. The difference between CNV-*Alu* pairs and Ctrl-*Alu* pairs in pairwise features. For each feature of *Alu* sequence, including *Alu* length, GC percentage, max. matching score of A Boxes in active *Alu*s, max. matching score of B Boxes in active *Alu*s, length of the poly(A) tail, max. matching score of PRDM9 binding motif, number of PRDM9 binding motif and *Alu* density, three panels are presented with respect to the minimum, mean and maximum value of each pair. For the genomic characteristics including replication timing, average methylation score and the percentage of methylated region, one more panel is plotted showing the absolute difference value of each pair besides the three panels.

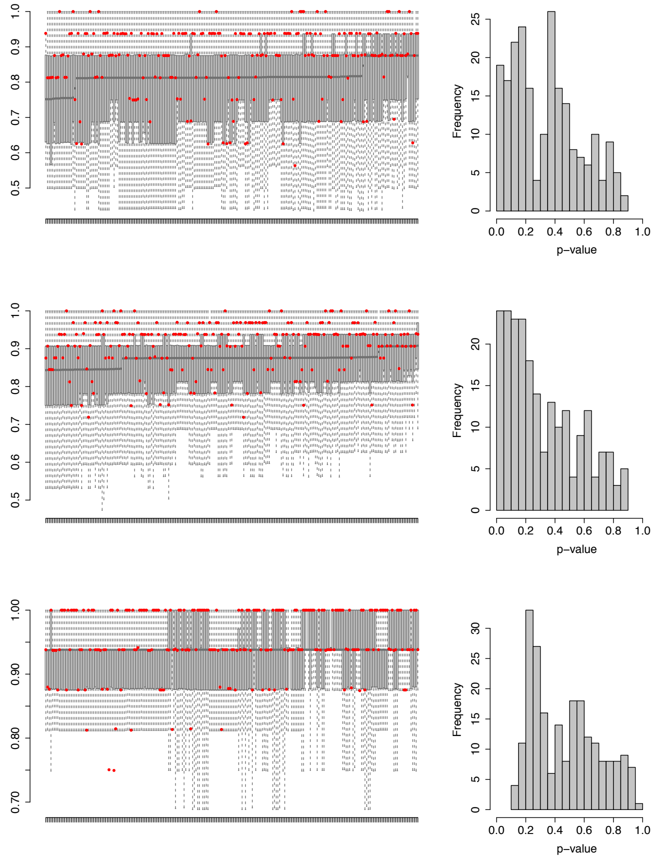
Length of an *Alu* element



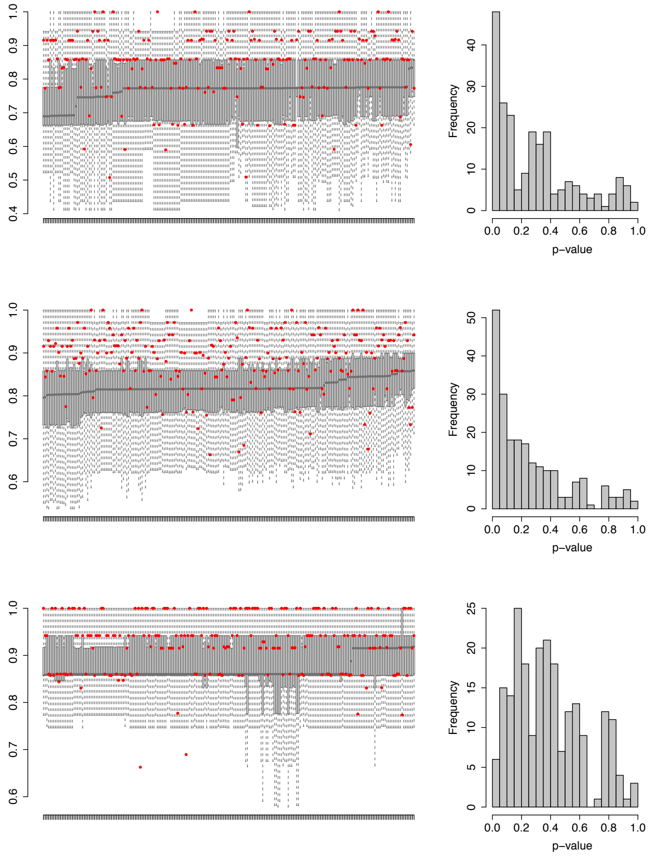
GC percentage



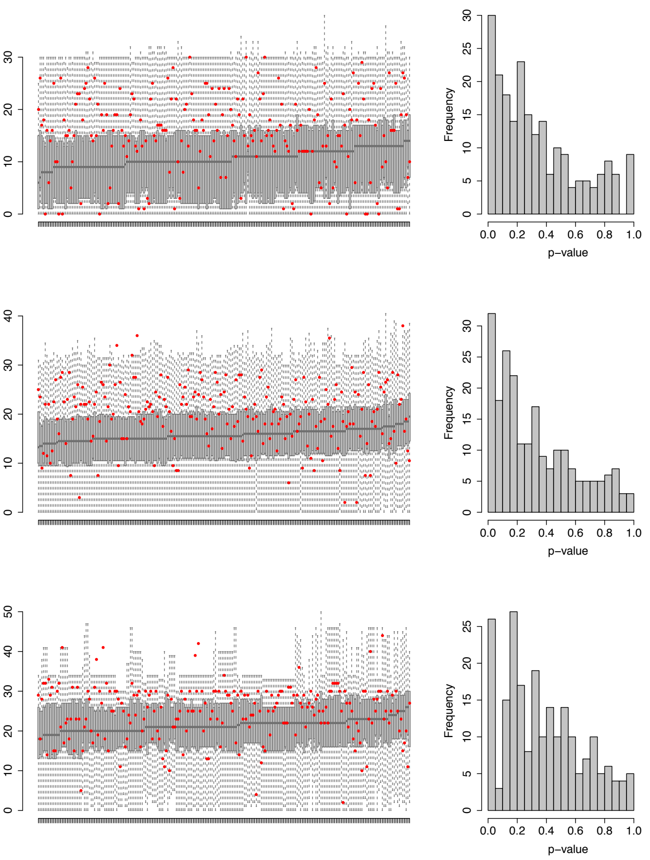
Max. Matching score of A Boxes in active *Alu*s



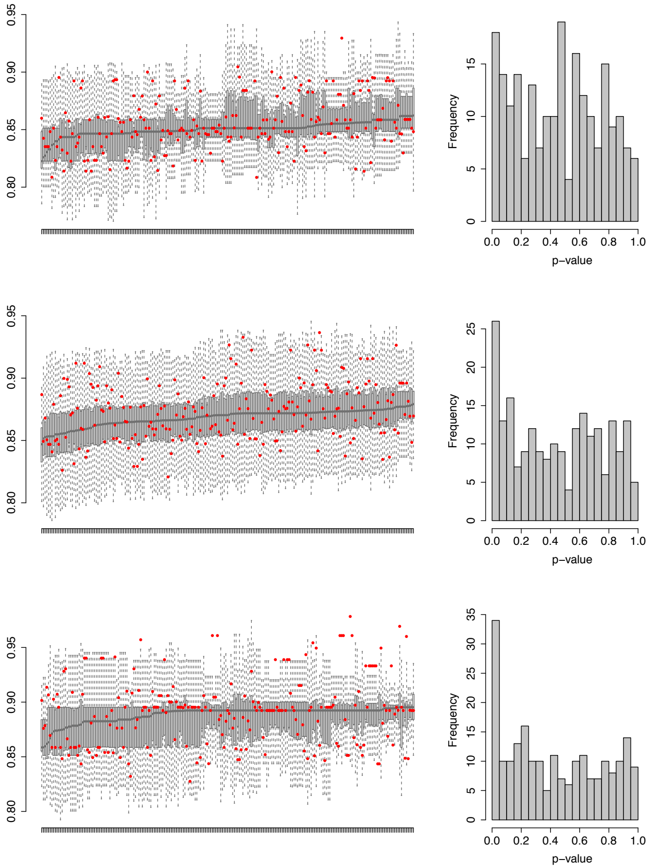
Max. Matching score of B boxes in active *Alu*s



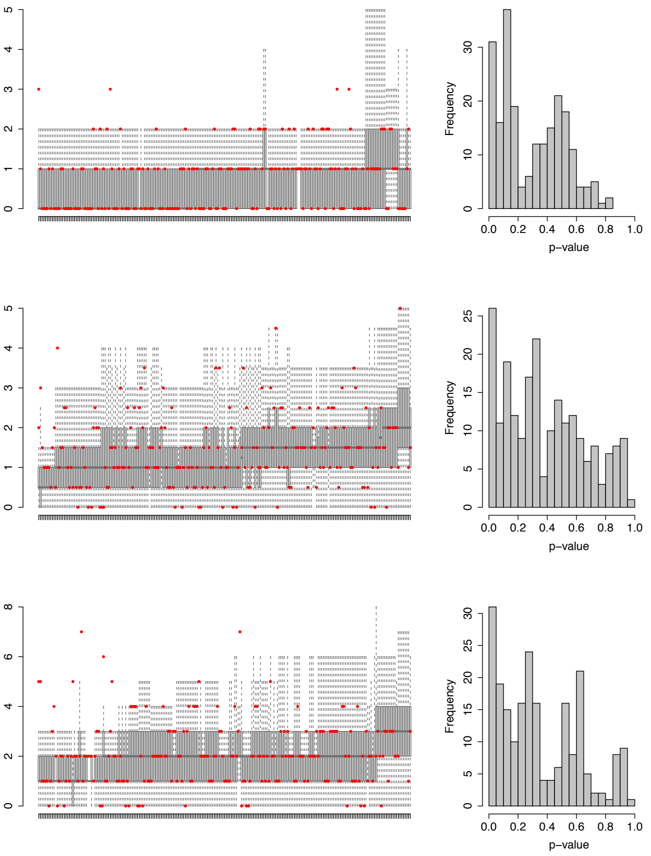
Length of the poly(A) tail



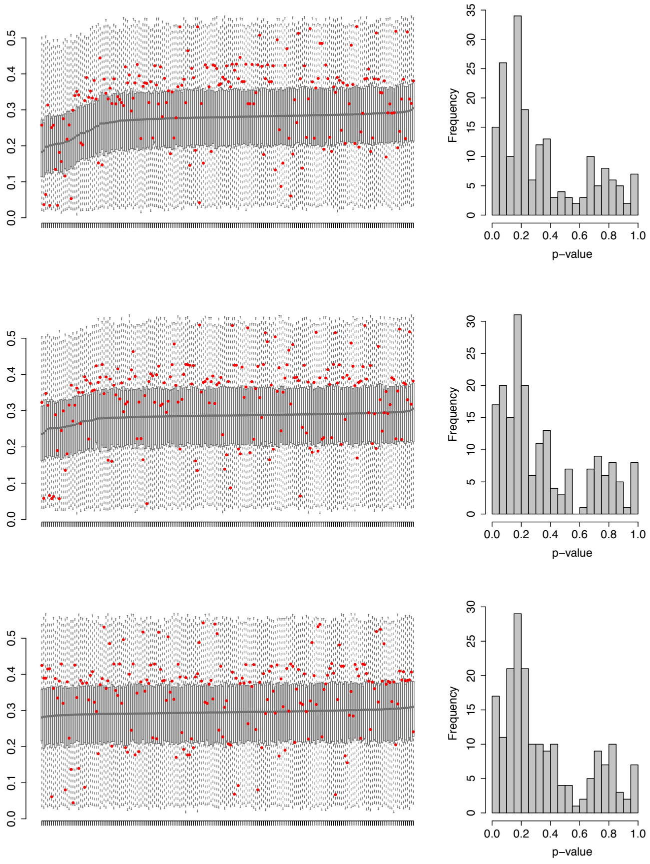
Max. matching score of PRDM9 binding motif



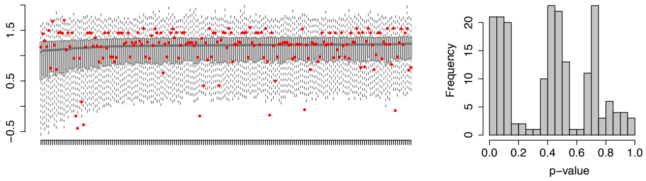
Number of PRDM9 binding motif

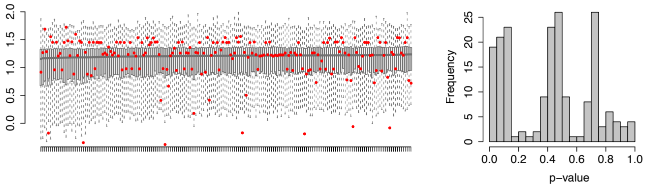


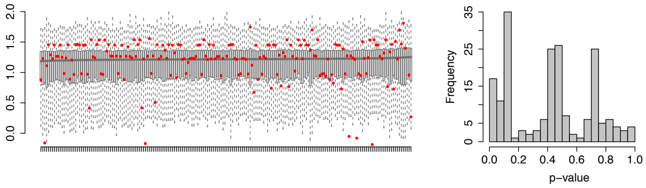
Alu density

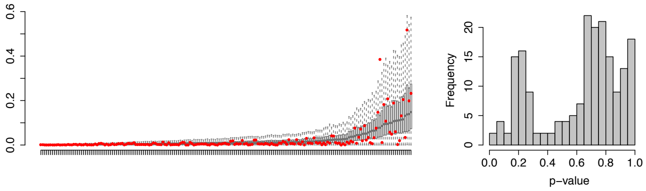


Replication timing

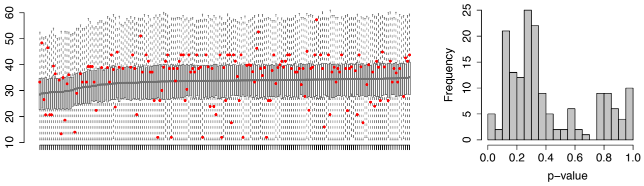


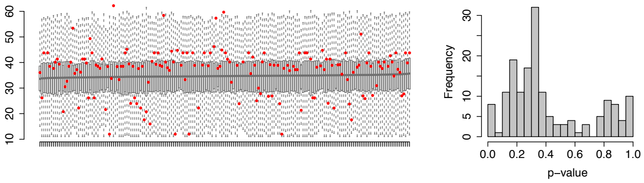


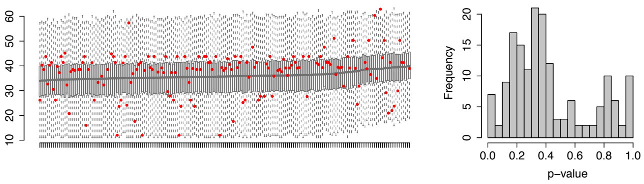


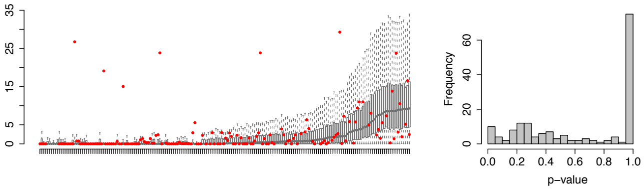


Average methylation level









Percentage of methylated region