

Figure S3 Estimated insertion ages for BosERV retrotransposon subfamilies. The x-axis represents insertion age in million years (Mya), and the y-axis indicates the percentage of the bovine genome occupied by each BosERV subfamily.

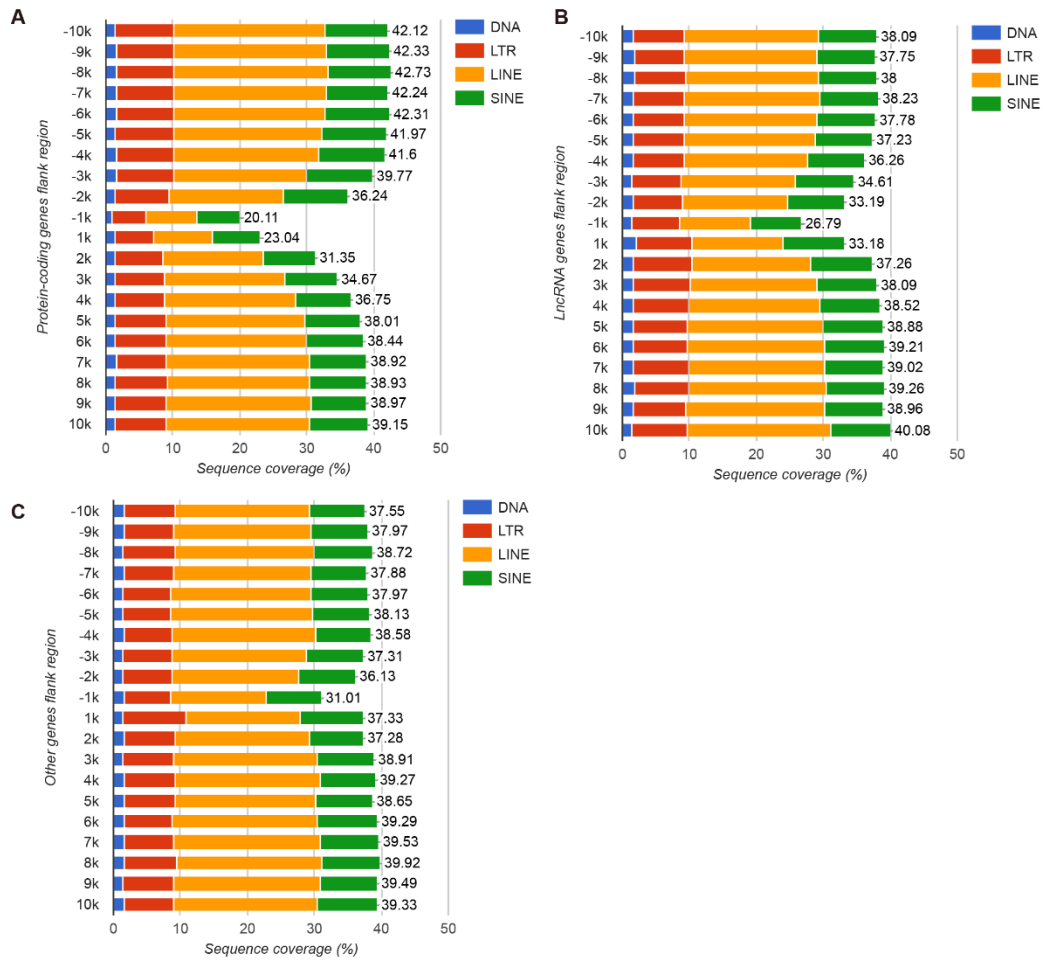


Figure S4 Density of retrotransposon elements in the flanking regions of protein-coding genes (A), lncRNA (B) and other genes (C). The ordinate axis represents the position relative to the gene, negative and positive numbers representing upstream and downstream of the gene, respectively.

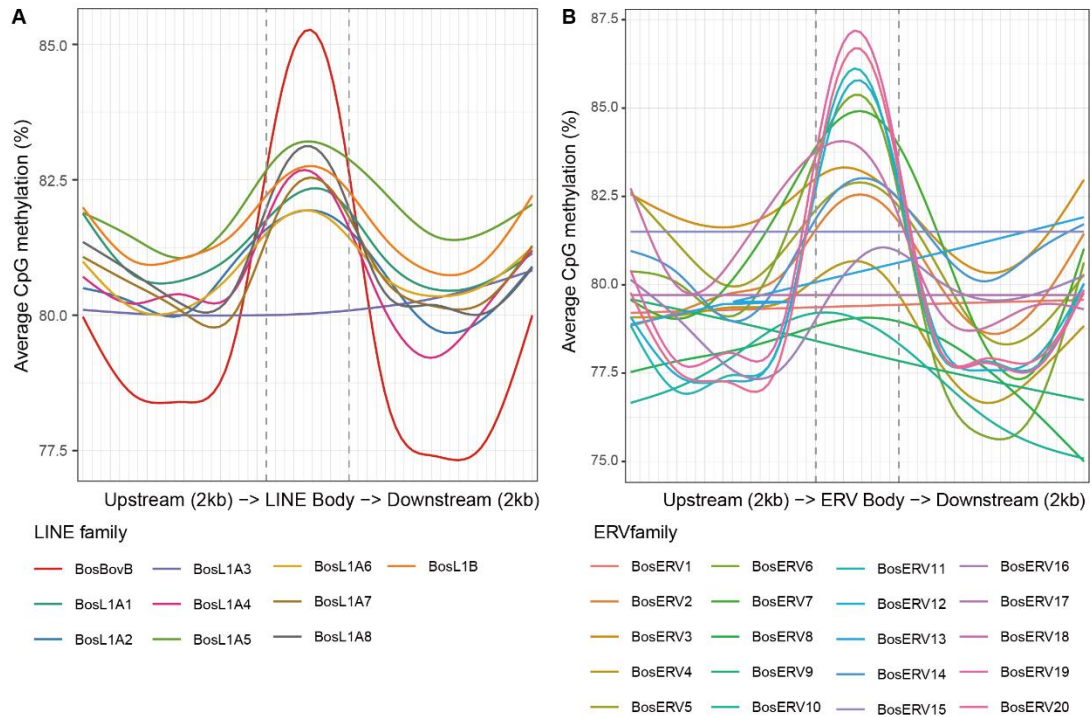


Figure S5 DNA methylation profiles across LINE (A) and ERV (B) subfamilies.

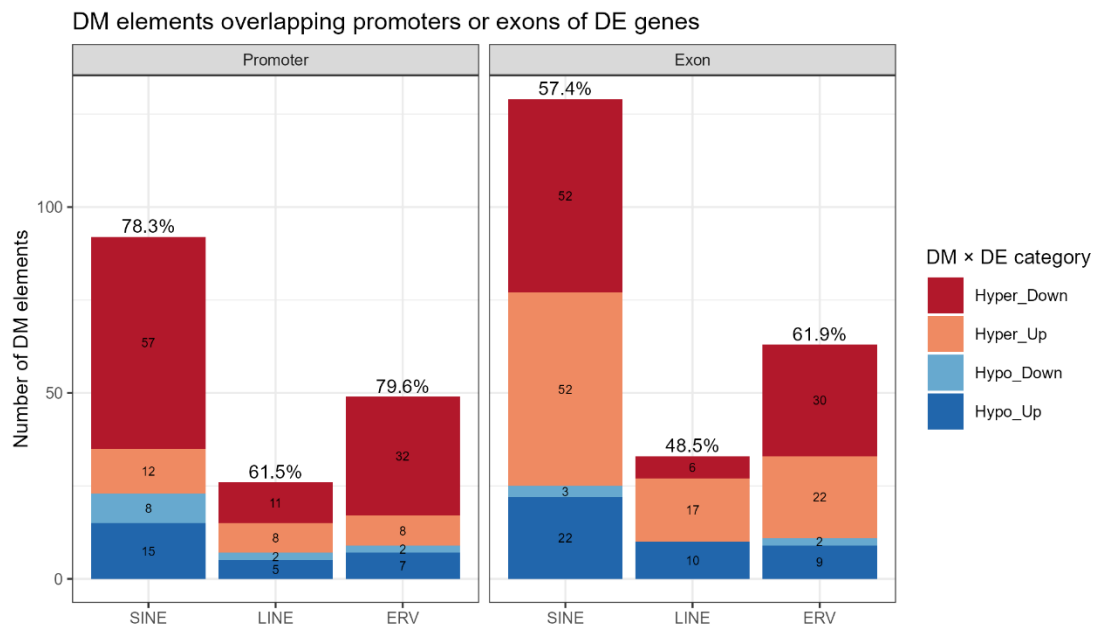


Figure S6 Number of differentially methylated (DM) retrotransposons overlapping the promoter or exons of differentially expressed (DE) genes. “Hyper” and “Hypo” indicate higher or lower DNA methylation in cows with *Staphylococcus aureus*-induced subclinical mastitis (SA) compared with healthy control (CT) cows. “Up” and “Down” indicate genes that are up- or down-regulated in the SA group relative to the CT group. The number above each bar represents the percentage of DM retrotransposons showing an inverse relationship with gene expression, defined as the sum of “Hyper_Down” and “Hypo_Up”.