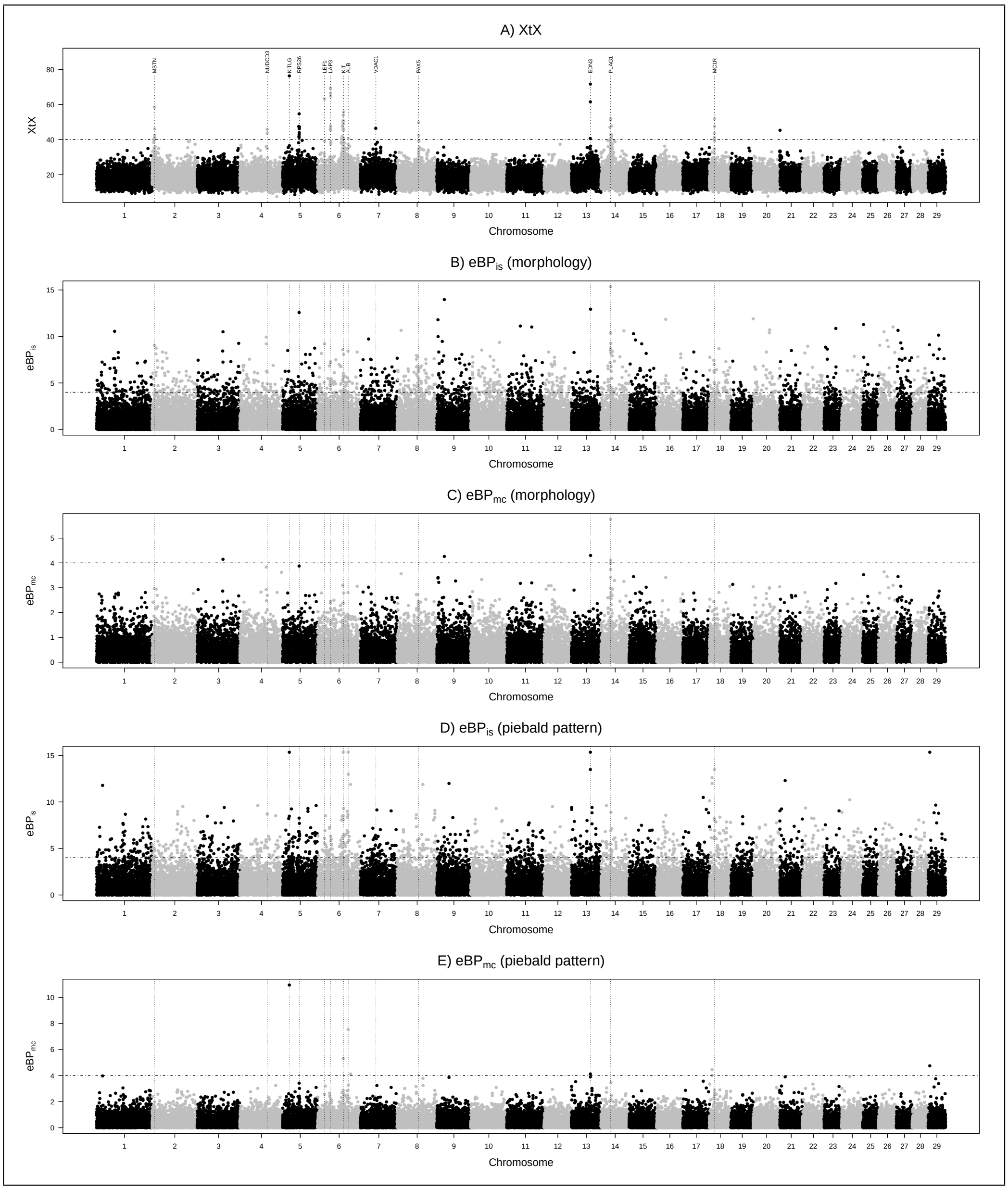

Figure S13: Manhattan plot summarizing results of the genome scan for footprints of selection based on the XtX statistics (A) and association with the synthetic morphological traits (B and D) and piebald coloration pattern (C and D) among 18 European cattle breeds. For the association analyses, eBP were derived from an Importance Sampling algorithm (B and C) or from the MCMC output of the STD model (D and E). The dotted horizontal lines represent the 0.1% POD significance thresholds (A) and the threshold of $eBP = 4$ (B, C, D and E). The vertical dotted lines indicate the positions of the footprints of selection. The underlying candidate genes are explicitly given in A.