Figure S12: 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, Bayes Factor were derived from an Importance Sampling algorithm (B and C) or under the AUX model (D and E). The dotted horizontal lines represent the 0.1% POD significance thresholds (A) and the threshold of $BF = 20$ dB (B, C, D and E) that corresponding to decisive evidence according to the Jeffreys' rule. The vertical dotted lines indicate the positions of the footprints of selection and the underlying candidate genes are explicitly given in A (see the main text).