

Figure S14: Manhattan plot summarizing results of the genome scan for footprints of selection among 18 European cattle breeds based on the XtX statistics under the core model (A), the STD model with the population morphology covariable (B), the piebald coloration covariable (C) and both covariables (D). The dotted horizontal lines represent the 0.1% POD significance thresholds. The vertical dotted lines indicate the positions of the footprints of selection. The underlying candidate genes are explicitly given in A.