



Figure S1. Manhattan plots of SNP-wise scores for each selection test statistics (**A**: CSS, **B**: F_{ST} , **C**: XP-EHH, **D**: ΔDAF) for polled cattle (dataset A). Gray dots in the background show raw scores and blue and orange dots in the foreground show smooth scores, averaged over SNPs within 1 Mb sliding windows. Red dotted lines indicate a threshold of top 0.1 percentile of the genome-wide smoothed scores for each of the selection test statistics. Red square dots in each plot show the genome-wide highest raw signals.