



Figure S2. Manhattan plots of SNP-wise scores for each selection test statistics (**A**: CSS, **B**: F_{ST} , **C**: XP-EHH, **D**: ΔDAF) for double muscle cattle (dataset B). 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. The square dots are in dark brown colour in B plot as the highest F_{ST} signals is more than 3 Mb upstream from the known candidate region on chromosome 2.