

File S3 - BLAST comparison of the sub-telomeric region of chromosome 6 with the homologous region of the cattle genome.

As the sheep genome assembly is still ongoing, we wished to determine if a region of reduced linkage disequilibrium within an otherwise complete LD haplotype block at the sub-telomeric region on chromosome 6 was the consequence of the region being assembled incorrectly. We compared DNA sequence from a 2.7Mb region of cattle chromosome 6 (positions 107,699,493 to 110,430,052, cattle genome vUMD3.1) homologous to the 2.1Mb sub-telomeric region of sheep chromosome 6 (positions 115,000,000 to 117,031,472, sheep genome Oar_v3.1) containing candidate regions associated with recombination rate (see main text results and Figure 5). Sequence comparison was carried out using BLAST v2.2.27+ with the default parameters and a word size of 20. BLAST hits of < 2000 bases and < 80% match were discarded. Regions with more than two hits per ~2000bp window were also discarded as they were indicative of repetitive sequence. Our results indicate that a sheep region from 116.725Mb to 116.823Mb is likely to have been incorrectly assembled, and is likely to occur at a position between 116.30 Mb and 116.36Mb (Figure 1, Table S7).

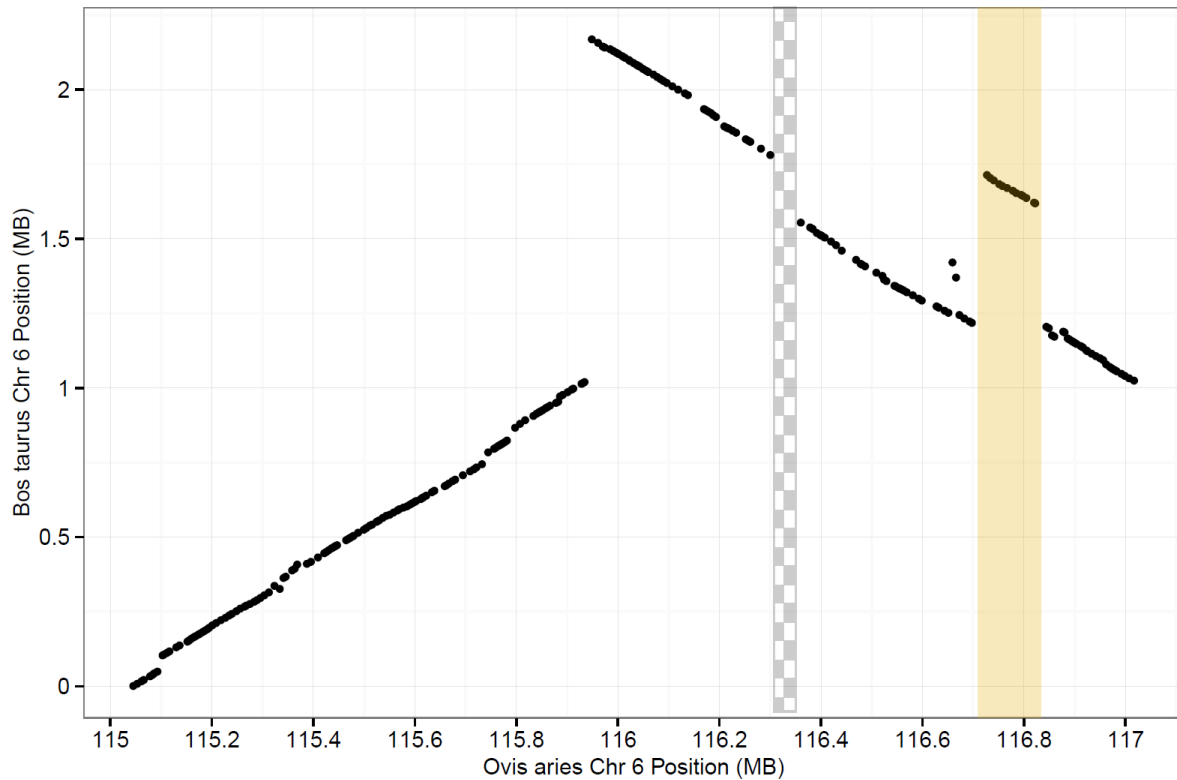


Fig 1. BLAST results comparing a 2.7Mb region of cattle chromosome 6 (*Bos taurus*, positions 107,699,493 to 110,430,052, cattle genome vUMD3.1) with a homologous 2.1Mb sub-telomeric region of sheep chromosome 6 (*Ovis aries*, positions 115,000,000 to 117,031,472, sheep genome Oar_v3.1). Points indicate the mid position of each BLAST hit on their respective query sequence. The beige block indicates the position of a fragment on the sheep genome which is likely to have been incorrectly placed – its most likely position is indicated by the grey chequered block. BLAST results are provided in Table S7.