

Figure S3 Sequences of the bovine *APOB* alleles. Sequences shown in black font correspond to BTA 11: 77958946-77959194 (bovine genome assembly version UMD3.1). The exon 5 of *APOB* is highlighted in yellow. The precise location (breakpoint) of the insertion is indicated with a blue vertical bar and submitted to dbVar (<http://www.ncbi.nlm.nih.gov/dbvar>) under accession NSTD119. The sequence of the 1299 bp insertion in the affected cattle is shown in blue. The binding sites of the 3 PCR primers used for genotyping are shown underlined. Diagnostic PCR primer sequences are given below.

Wild type allele:

GGTGACCATCCTCTCTCTGCACCAGGTACGACCTCAAGCTGGCTGTTCC | TGAAGGCAAGCA
 AGTTCTACTTTACCCAGAGAAAGAAGAGCCTAAACACATCCTCAACATCAAGAGGGGCATCA
 TCTCTGCCCTCCTGCTTCCCCCAGAAACAGAAGAGGCTAAGCAAGTGTTATTTCTGGTGAGA
 ATTTTAAAAGCTGATAATAGTGGTCCTTTGAACTCCTCTTCATATAATGGAGCTGGGTTCCA
CT

Mutant (with insertion) allele:

GGTGACCATCCTCTCTCTGCACCAGGTACGACCTCAAGCTGGCTGTTCC | TGAGGTGCGGGG
 AGCCGGTGAGGCATTCCACTCGTGACAAAGGTCATGAGGAAGGAGGCTCGGCATACGCAAAG
 GCGGGATCGAGCCTCAGGAGTCCCCCGGATATTCTCGAGCATTTCCCCCAAAAAACCAGA
 GTCTGCCTACTTTATTGCTTTGTGCTCTCACCTCTGACTTTACTGGGGGCTGTCCCCTACCA
 CCGTCTCTCTCTCTCTGTGTCAAAGAGTTAACTTACAGCTCCAATTAATAAAGTTCTGGGC
 AATTAGGAGTGTTTAAATCCAAACCCTCTGATGGCTCTCTAACTCGCCTGACAAGTTTACC
 CGGACTCCTGCAGCTATGCATACGATTGTTTACAGTCTCCAGCCTCGAGAGGCATGGGAAG
 CTTAAGATATTCAAATAGCTTAGAGCCTCTCAGAGAGTTAAAACTGTGAGAATAAACTAGT
 AAAGGATTTTCATTGATGAGTCAATGCTTGTGTTGCCAAGTTTTTCACATCCCCTGAATTGTATCC
 TTGAATATGTATCAATTAATAGTGGGTATGTAGAAAAAATAAGTAGTGGCCCTTGGTGTTA
 GTAACTTTAGACCCTTAAGGTAATAAATTCTTTCTTTGTTGTAAACCCATTACACATCCGCC
 CTATAGGAATGCAATTTTATCTTTGGAAGATGGTGCCAAACCCTTGAAATAAATTAATCTTAG
 AGAAAAGTAAAGTCTTTGTTGATAAGTCTTGTCAAGAGTCATAAAATGTTTAGTAGGCCTT
 CTGGCCAGAAGATGATGTAAATCACCTAAACCATTGTATACGATAACATTTGCAGGAAAGAA
 ACCTTGTTTTTTGATAAGAATCAAAGACTGCTGACTTTGCATCCCCCTATTATCCTCTATGT
 GTAACTTAGGGTATAAAAGCCCCTGTTAAAAATAAAGCTACGGGCCTTGCTCACCAACGCTT
 GGTCTCCCCATGTCATTCTTTAACTTCCAGCTGAGTCTCCATCTGGAGCGCGGAACCCACC
 ACGCTTACTAATCATGCCTGGGCTTCTAAGACCCACTCGAGAAGGTGTCTAGGGTGAGACAC
 CTTCCGCTATTCGAGAGGGCGCCTGCGGCCTACGTAAGTGGTGCAAACCTTCTTGTCTTGAAG
 TTTTATTGGTCTCCGCGTAAACCAAGCTACTCAGCTTCTTTTCTCCACTGAAATTTCTTAC
 TGAGCTATCCTCATTCTATTGTTCTCTATATCCCTAATTAGCATATAAATAGTCGCCGACGC
 CGTCTCCCCTTCGAATACCCTGGATCAGCCGGGGCTGGTCCTCGGCA | TGAAGGCAAGCAAG
 TTCTACTTTACCCAGAGAAAGAAGAGCCTAAACACATCCTCAACATCAAGAGGGGCATCATC
 TCTGCCCTCCTGCTTCCCCCAGAAACAGAAGAGGCTAAGCAAGTGTTATTTCTGGTGAGAAT
 TTTAAAAGCTGATAATAGTGGTCCTTTGAACTCCTCTTCATATAATGGAGCTGGGTTCCACT

Diagnostic PCR primers:

Wild type forward primer	5' -GGTGACCATCCTCTCTCTGC-3'
Wild type reverse primer	5' -AGTGGAACCCAGCTCCATTA-3'
Mutant forward primer	5' -CACCTTCCGCTATTCGAGAG-3'