Natural selection supports escape from concerted evolution of a recently duplicated CEACAM1 paralog in the ruminant CEA gene family

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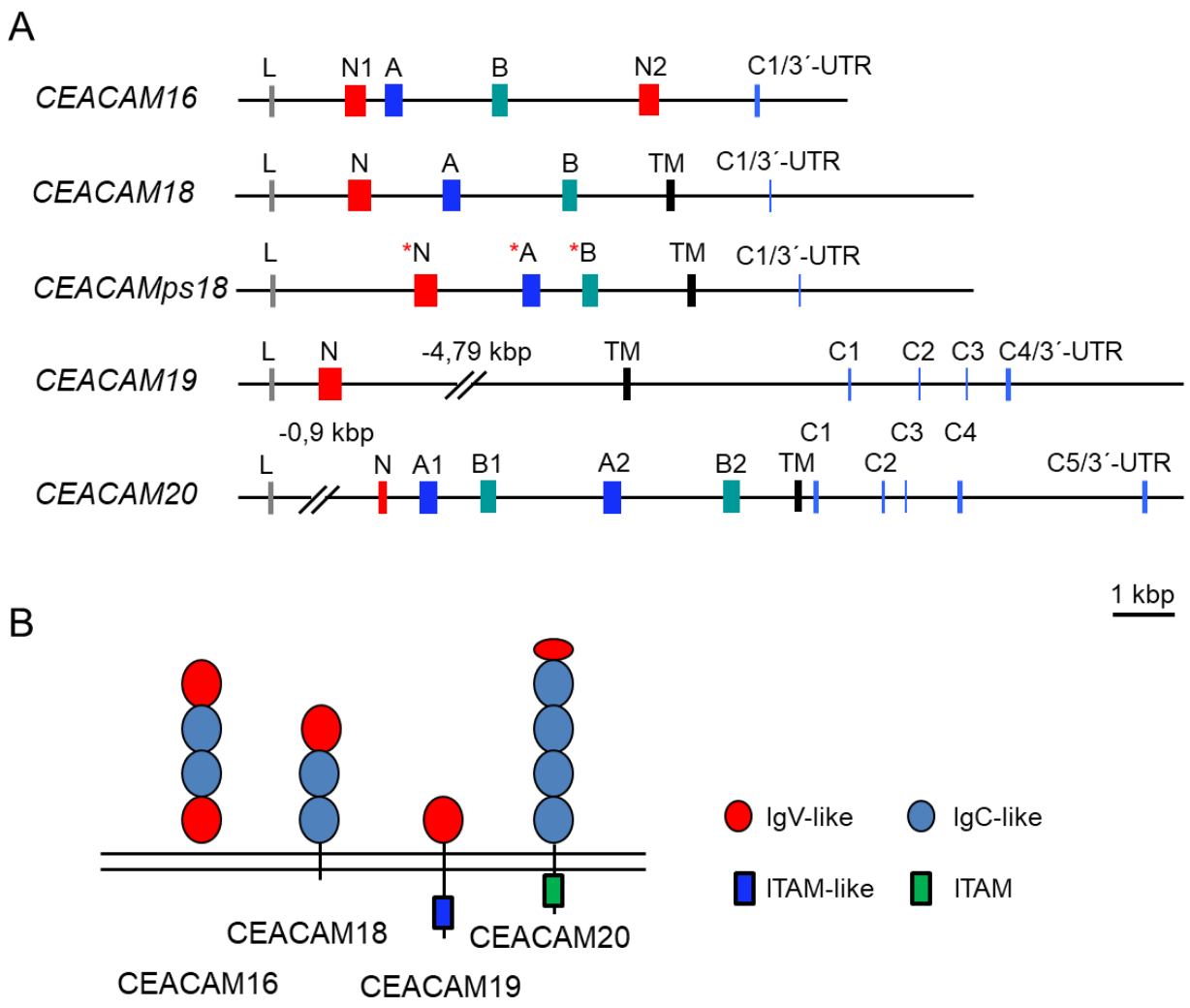
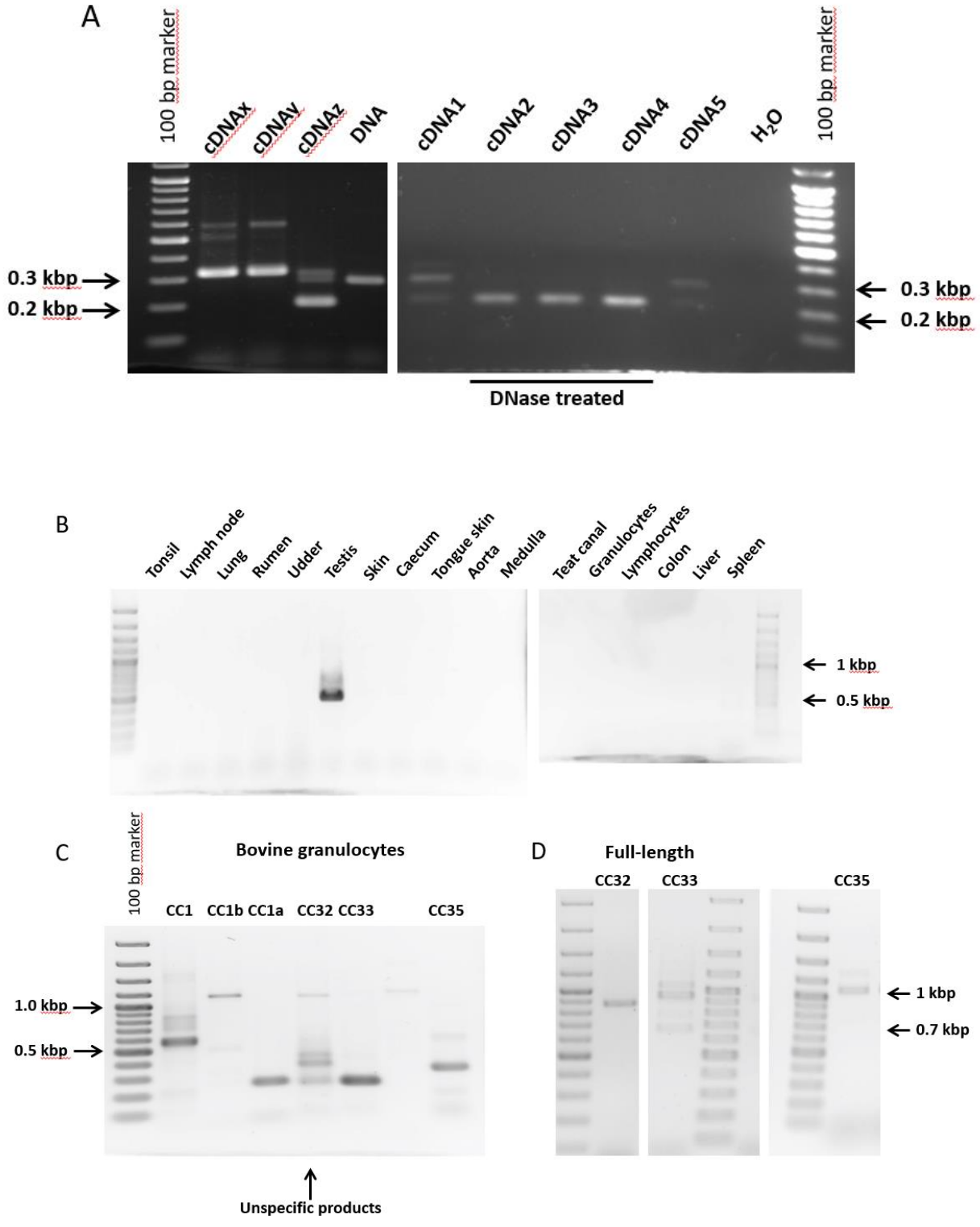
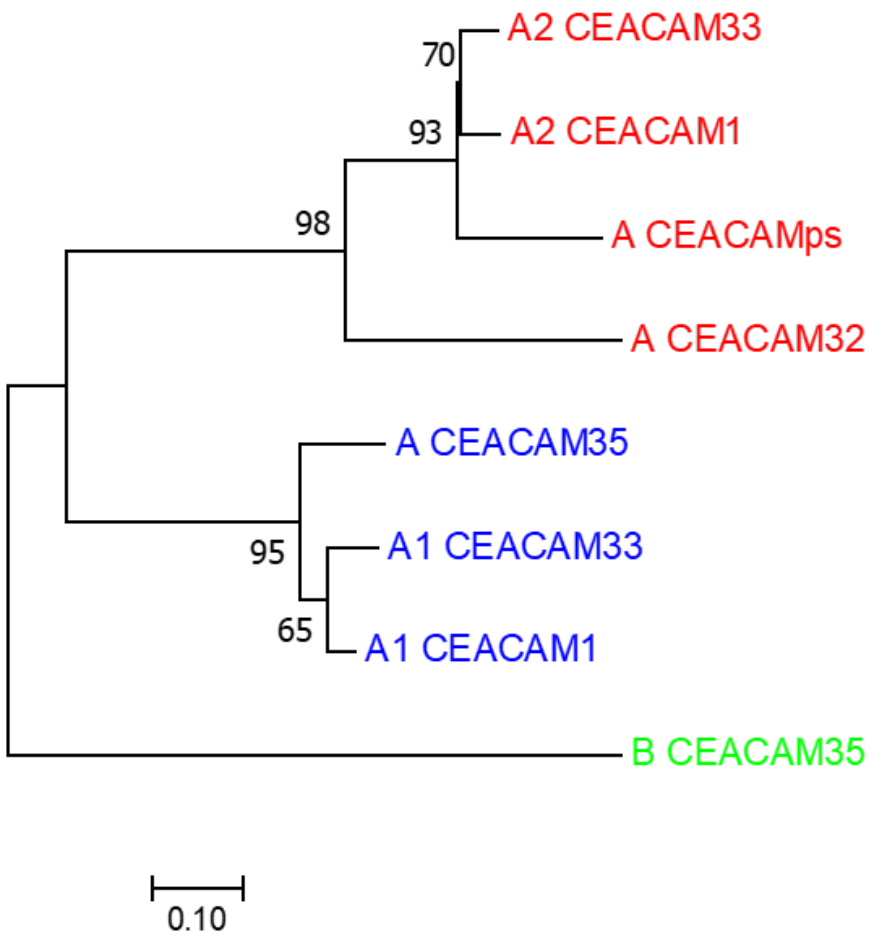


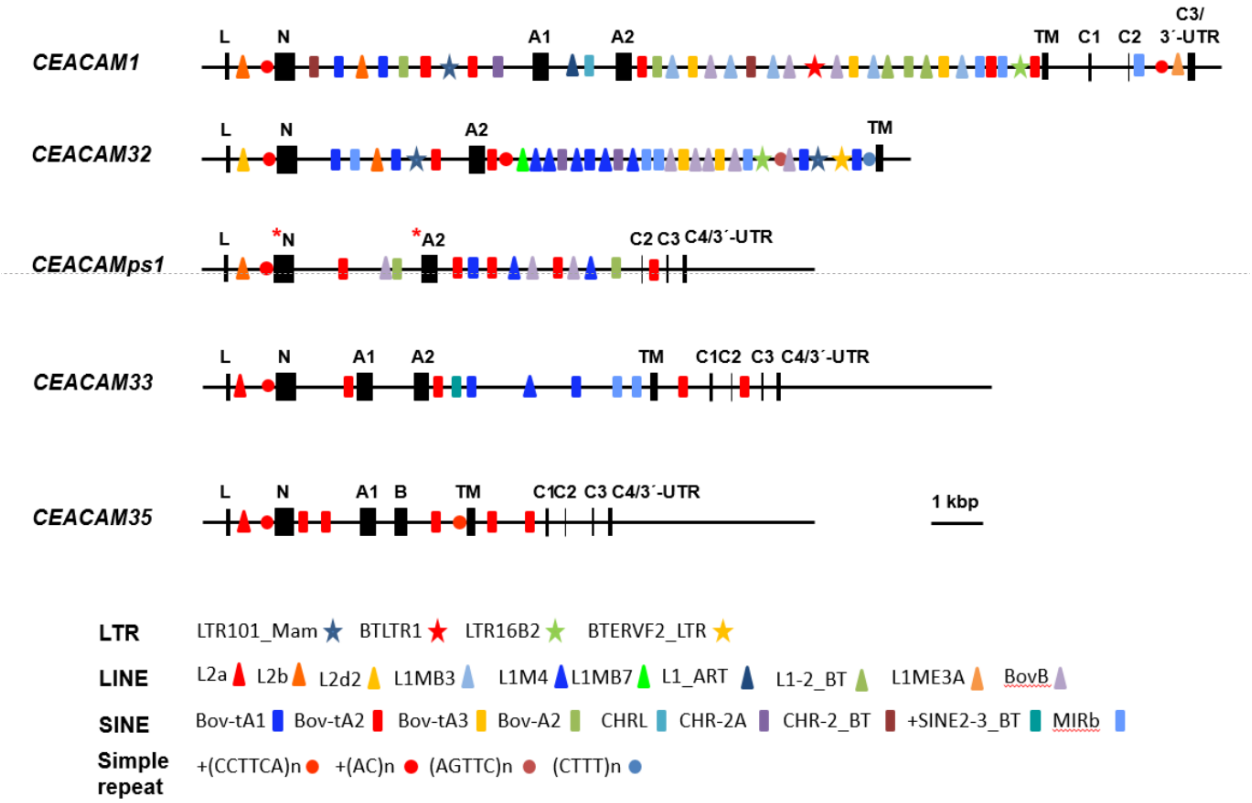
Supplementary Figure 1 - Conserved bovine CEA gene family members. (A) Exon arrangement of conserved bovine CEACAM genes. The exon types are indicated by differently colored boxes. Leader sequences are shown as gray, IgV-like domain exons as red, IgC-like domain exons as blue (A type) and green (B type) transmembrane domain exons as black boxes. The exons encoding the cytoplasmic domain with an ITAM-like or an ITAM motif are shown in blue and green, respectively. The presence of deletions/insertions in exons causing reading frame shifts is indicated by an asterisk. **(B)** The domain organization of bovine conserved CEACAMs. The signaling motifs in the cytoplasmic domains are schematically shown as green (immunoreceptor tyrosine-based activation motifs; ITAM), blue (ITAM-like motif, no acidic amino acid present at position -1 to -3 from first Y in consensus motif E/Dx0-2YxxL/Ix6-8YxxL/I).



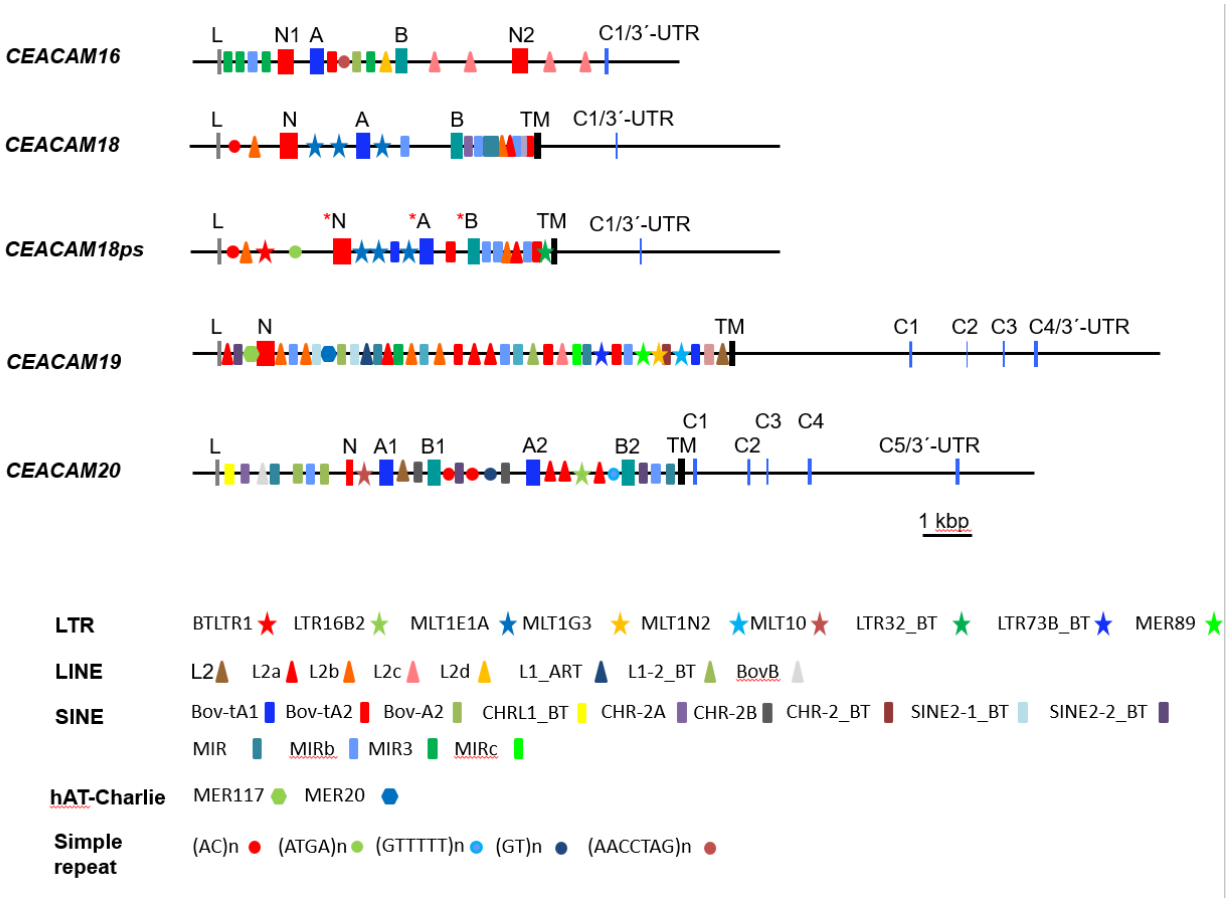
Supplementary Figure 2 - 'Full-length' gels used in Figure 1 A, B, C, D. These uncropped images are labeled as in the main text.



Supplementary Figure 3 – Phylogenetic relationship of IgC-like domains of CEACAM1 paralogs. The Phylogenetic tree was constructed using nucleotide sequences and the maximum likelihood (ML) method with bootstrap testing (500 replicates). Numbers at the nodes indicate the percentage of trees in which the associated taxa clustered together.



Supplementary Figure 4 – Mobile elements within bovine CEACAM1-related CEACAMs. Mobile elements and low complexity DNA sequences within bovine CEACAM1-related genes were identified using the RepeatMasker software. LTR (stars), Lines (triangles), Sines (rectangles) and simple sequences (discs) were placed in the corresponding order into introns.



Supplementary Figure 5 – Mobile elements within bovine conserved *CEACAM* genes. Mobile elements and low complexity DNA sequences within bovine *CEACAM* genes were identified using the RepeatMasker software. LTR (stars), Lines (triangles), Sines (rectangles) and simple sequences (discs) were placed in the corresponding order into introns.

Supplementary File 1 – predicted coding sequences of bovine conserved CEACAMs

(Exon sequences are indicated by different colors)

>CEACAM16 [Bos taurus]

ATGGTCTCAGGGAAGGGAGGGGAGCCTGGGGAGGGAAGATCCGCGATCCTGAGTGCGGGGGCCGAGATCATTATCACC
CCCGAGCCTGCCCAGCCAGCCGAGGGCGACAACGTCACTCTGGCTGTCCAAGGGCTTTCGGGGGAACTGCTGGCCTAC
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GGCCCAGCCCACACGGGGCGGGAGGCTGTGCGCCCCGACGGTGGCCTGGACATCCAGGGTGCCCTGCCTGGGCACTCG
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GGCCGGGTGCTGACCCGGCATGGCATCCGCAGGGAGGAGGCCGGCGCCTACCAGTGTGAGGTCTGGAACCCTGTCAGT
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CGCACAGGCTGCACCATCAAAGTCGACTTCAACACGTCCCTCACGCTGTGGTGTGTGTCCCGGTCCTGCCCGGAGCCC
GAGTACGTGTGGACCTTCAATGGGCGGGCCTTAAAGAGCGACCAAGACCACCTGAACATCAGTAGCATGACAGCCACC
CAGGAGGGCACGTACACGTGTATTGCTAAGAACCCCAAGACCCTGCTCTCTGGATCTGCCTCAGTGGTGGTCAAACTC
TCTGCGGCCACGGTCATCATGACCATCGTTCCGGTGCCCACCCGGCCAATGGAGGGCCAGGACGTGACACTGACCGTC

CAGGGCTACCCCAAGGATCTGCTGGTCTATGCCTGGTACCGTGGGCCTGCCTCCGAGCCCAACCGGCTTCTCAGCCAA
CTTCCTTCCGGGAACTGGATCGCAGGCCCTGCGCACACAGGCCGGGAGGTGGGCTTCCCCAACTGCTCACTGCTGGTG
CAGAAGCTGAACCTCACAGATGCCGGCCGCTACACCCTCAAGACCGTCACGCTGCAGGGCAAGACAGAGACACTGGAA
GTGGAGCTGCAGGTGGCCCTCCTGGAGTAG

>CEACAM18ps[Bos taurus]

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CAGGCCTCCAGCCAAATGTACATCAGCCCAGACCCATTCACAGGTTTGAAGGGATACCGGAGCCTCCTGATTTTCAAC
AATGCCCATAAAAATGTTCAGGAGTATAGTTGGCACCAGGGTACAAATGACACTGAGGAAAATCTTATTATCAGCTAC
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CAAGTGAAGATGGAGTATCTTTCTGATGGCAGACCGCAAATCAAGTACCACTGGATCCACAATATCTCTGTCCTGAGC
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ACACTGCTCCTGAACTTCCTCATGACGTGGTCAATCTTGGGCTATGTCTTCCTCTTTACACTCATCCTTCTGGGCCTC
ATCAGATGTTATTCCACCAGTAAATAGGATTCCAACTTCTCCACTTCCTTAACCTGACCCTGTGGGACCATCAGAGAG
GCTGCAAATATGCCCCATCTCAGCATCGCCAGTAA

>CEACAM18 [Bos taurus]

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>CEACAM19 [Bos taurus]

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>CEACAM20 [Bos taurus]

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