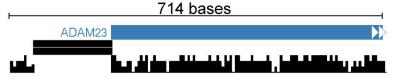
## Chr37 14996659-14997373 bp canfam3.1

sequence gap GC percent



## ADAM23 5' 190 bp gap region

CCCTTGCCTCCGCGGCGACGCATGCGCAGTGCCCCGTGCCCGGCACT AGCCACAGCGTCGGGACCGGCGTCGGCGCAGCATCAGGACCCG**CGGC** CCCCGCGCCCCGCGCCCCCCCCGCGCGCGCGCTCGCCCGCGCCC TCTCAGCATCCTCAGCCCCGGCGGCAGCCCCCGCAGCTGCTGGAGCGGC CGCGCCGCCGCAGGGAGGAGGAGCATCTGGGGCGGCTCCAAGTTGGC GGAGCCGCCGGGACCCCCGGACTCCTCCGCGGCCCCCGGGAGGGGCGG GCCCGAGCCCTGCCCTGCCCTGCCCCTGCCCCTGCCCCTGCCCCT CAGCCTCCCGCAGCCTCCCCGGCGCTGTCGCCGGCCACACCGAGCGG CGCCCGGGAGCTATGAGCCATGAAGCCGCCCGGCAGCAGCTCCCGGCGG CCGCCCGCGCGGCTCCAGCCGCCCCCGCGCCTCCCGCGCCCCCGCG GCGGCCCGCCGGCCGGTGCCCGCCCGCACGCCCCTGCCGCCTGCT CCTCGTCCTTCTCCTGCTGCCTCCTCTCGCCACCTCGTCGCGGCCCCGC GCCTGGGGGGCGCCCAGCG

## ADAM23 exon 1

Additional Figure 4.Overview of the *ADAM23* 5'- region and DNA sequence. Canine BAC clone CHORI82\_R4\_266G10 spanning the ADAM23 region was sequenced using PacBio sequencing to uncover the genomic sequence of the unknown sequence 5' of *ADAM23*. The newly-identified 190-bp sequence is shown here along with *ADAM23* exon 1 genomic sequence. The translation starts at ATG highlighted in red. Both the newly-identified sequence and exon 1 have GC content above 80 percent and contain simple repetitive elements, highlighted in bold.