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d_CM016578.1:28521418 : TGGCATTCCCAAGTCTCTTACAGTGTCTTAAGAAGATCTCTCCAGGATCCCTGGGTGGCGCAGCGGTTTGGCGCCTGCCTTTGGCCCAGGGCGCGATCC

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s_CM021969.1:53495922 : GTATAGTTTCTTTGATGATTTTTTGTTTTTAAAGCTTCTGTCTT
d_CM016576.1:53100186 : GTATAGTTTCTTTGATGATTTTTTGTTTTTAAAGCTTCTGTCTT
s_CM022000.1:124513739 : AATTTTCATGTACTGGACAGACTAATTTCTAAAATTTCCCATTCAG
d_CM016607.1:122259922 : AATTTTCATGTACTGGACAGACTAATTTCTAAAATTTCCCATTCAG
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chr29 Can : TGGAGACCCGGGATCGAATCCACGTCGGGCTTT--CCGGTGCATGGAGCCTGCTTCTCCCTCTGCCTATGTCTCTGC---CTCTCTCTCTCTCTCACTG

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b_CM000023.4:38752119	:	TGGAGACCCGGGATCGAATCCACGTCGGGCTTT	--	CCGGTGCATGGAGCCTGCTTCTCCCTCTGCCTGTGTCTCTGC	CTCT	CTCTCTCTCTCTCTCTCACTG
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b_CM000034.4:41229417	:	TGGAGACCCGGGATCGAATCCACGTCGGGCTTT	--	CCGGTGCATGGAGCCTGCTTCTCCCTCTGCCTGTGTCTCTGC	CTCT	CTCTCTCTCTCTCTCTCACTG
d_CM016602.1:32172425	:	TGGAGACCCGGGATCGAATCCACGTCGGGCTTT	--	CCGGTGCATGGAGCCTGCTTCTCCCTCTGCCTGTGTCTCTGC	CTCT	CTCTCTCTCTCTCTCTCACTG
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 b_CM000027.5:10401007 : TGTGCCTATCATAAATAAAT-----AAAAAATT-AAAAAAAAAATTCATTATATCTTAGGAATAACATAGACATGTTTCTCTCTCTCTGTTTCTCTC
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Figure S6. Members of the Can_b2 tribe 1 in the three dog breeds. The upper sequence “chr29 Can” (chr29:16532880-16533057, German Shepherd) was used as the search query. The letter prefix in sequence names indicates the genome where they are

present (s, German Shepherd; d, Great Dane; and b, Boxer). Sequence names are given in black if present in all three breeds, while those available in one or two genomes are given in blue and violet, respectively. Rudimentary terminators (TT and TTT) are marked green; TSDs are underlined. Notice that no copies contain a functional terminator ($T_{>3}$) in the proper place, which indicates that their retrotransposition proceeds without polyadenylation of pol III transcripts. Can copies from orthologous loci were not combined to demonstrate their sequence conservation and absence of terminators in either breed.