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db_CM016599.1:10739390 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAAAAAAAAAATAAAAAAAAAAATAAAAAAATAAAAAAATAAAATAGCTTTTGGGGTGCC
sd_CM021982.1:9291573 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAACTTTTAAAAAATAAAAAATAAAAAATAAAAAATAAAAGAAAGACATCAGAGAATAAAA
sb_CM021983.1:23192950 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATAAAATAAAATCTATAAAATTACAAAAAACTTCATTGCAAGACGCTGA
sd_CM021974.1:14210188 : TGC-----CTTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAAAGCTATCCTTTAAAAAATAAAATAAAATAAAATAAAAGGATGAGC
sb_CM021962.1:91468831 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTTAAATAAAAAATTTTATAGAGTGGGGCAGGAGCAGAAATCGCAGTAGCTCCGTGT
sd_CM021987.1:2619279 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTTAAAAAATAAAAAAGAGAATAAACAAAGATTCAAGAATGTTCTGAACAGAAGGAACAA
sb_CM021972.1:53963274 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTTGAAATTTTGTAGCTTAAATGGATGAATGAGTGAATGAATGAATGAATGAATGAAT
sd_CM021968.1:19720283 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATAAAATAAAATAAAATGAGATGATCTTTGTTTTGAACAATATCCTACTTTTCCA
db_CM016582.1:53132597 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATAAGAGAAGGTACATATAGGATAGTATACATATAGGATACATATAAAGGAC
sb_CM022000.1:62922866 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAAAAAAAAAAAAAGAAACACAGGCAGAGGAGAAGCAGGTTCCATCAGGGAGCTCGA
sb_CM021981.1:39092485 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTAATAAAAAATAAACAGTAAGGAGGGAAGACTGCCTGACATGCGGTACACACCATGC
sb_CM021971.1:65017672 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAAAAAAAAAAAAGAAATGATGGTGGCATAGATCAAAGTGGTGGCAGTGGGACGAGTT
sd_CM021978.1:60626329 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAAAAAAAAAGAAAGCATGTTCTGTTTTGATTATTAATAACACATGGCTATTGCA
sd_CM021977.1:50395861 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAATAAGGAGAGAACACAGGTGCTGTATGACAAAATAAAAAATGGGACATCATA
sb_CM021984.1:20467312 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAATTTAAAAAATAAAATACTTAATGACAAACAAATGTACCTCCCTCAAATGTGAAAC
sb_CM021962.1:120114565 : TGC-----CTCTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAATAAAAAAAAAAGAAAGAAAGATGGATCTGAAATCAGTAATTTGGTGAGGGCTATCCT
sd_CM021988.1:40175605 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--AAAAATTTAAAAAATAAAAGTATTTATCACCATGACCAACCAAGTGGGATTTATTTCTAGGGGTGCAAGGG
sb_CM021965.1:62540357 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAATTTAAAAAATAAAAGAAATTTTTCAGAAATTTATGTTATATGCTAAATATAGATTTCTCAG
db_CM016591.1:19458397 : TGC-----CTCTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATGTATCTCATTTGCGGTCTAAAAAAGCATTGCTTCAATTTCTAAAGGAGTTGAACATA
sb_CM021997.1:8473338 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTTTAAAAAATAAAAAAAAAAAAAAATGAAGAGAGGCTGTAGAGAAAATCAT
sd_CM022000.1:2743930 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTTAAAAAATAAAAAAAAAAAAAAAGAAATGGATTCCCAAGGAGATGTGAAGAA
sb_CM021982.1:12879397 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTAAAAAATAAAATTTAAAAAATAAAATGAATGATCTGGAACTTTAACCAAGGTTT
sd_CM021997.1:996683 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTAAAAAATAAAAAATAAATAACCAGCTACCTGTTCCGTGGAATGCCATTATCACCCA
sb_CM021994.1:1406069 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTAAAAAATAAAAAAGAACTGTATTGTGTATAGAAATTTGTTTCGGTTGAGAATAAACAA
sd_CM022000.1:17338555 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTAAAAAATAAGAGAAATTAATCAATTAAGTGCTAAGAAATGAGAGAAAATAA
db_CM016582.1:35939277 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTAAAAAATAAAAAAATAAATATGCCCCTCTATTTTATGACAGGTTGCAATTTTCT
sd_CM021970.1:56114063 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAATAAAAAAAGATCAGCAACTGAAAGAAAGCAGCACCATTCACTCAGGTGGTTTGGGTA
sd_CM021983.1:35095652 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATAAGTTAATAAACTGTATATGTAATGGGTTAAGCATACACCTCTTCCCATAGTCTTC
sd_CM021966.1:16793607 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATCTTTAAAAAAGATGTGTTCATTGTTACCAGGGAATGTGGTACTCCAGTCTGCGAAT
sb_CM021978.1:51394651 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAATTCATTGAGGAAGAGAGGATTTTGAACATAAGATCTTTCTCAGGCTGCAGTGATTA
sb_CM021975.1:32570287 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAGAAATTAATGTTGCTTACTTAAATAAGACTTAATTTTTCATCTTTGTTCA
sd_CM021982.1:33169530 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--AAAAAATAAAAAAAGAAATATACAGTCTCTCCAATAAATTTAGCATGTAATTTAATTTTTTTTTTTAAT
db_CM016574.1:21486827 : TGC-----CTTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAATAAAAAAAGAACTGAGTTGGACAAATCTAAGTCCCTGGTTCGAGGTCACCAACC
sb_CM021988.1:23669522 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATAAAAAAATAAAAAAATAAAAAATGCCTTGTATGTGTAATCTTTACACAATC
sb_CM021991.1:29058659 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTAAAAAAATAAACAGTAAATAAGACATTAACATTTATTT
sd_CM021964.1:56205731 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAATAAAAAATGACAAATACCACCATTTGCTTCAACGTGGATGGAACGTGAGGGATATAT
sd_CM021963.1:13103183 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAAATTTATATATAATTTATTAGTTTGTGTTGCTTAACATTTCCAGGAAGCCTCTGTCTCTTA
sd_CM021963.1:77390505 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAAGAAATCTTGAAGGTTAAAAAACCATTAAACATAAATCCTTAGCCTCATTATT
sb_CM021985.1:42396960 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAACTTTAAAAAATAAAAAAGACAGGGTGAGAGGCCAGGATGAGGTTGAGGTGAGGT
db_CM016569.1:117729902 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAAGTAAATCTGAAGAATCTGGGCTCTCTAGCATTTAAGCTCAGTCAGTATGTGGAT
sd_CM021966.1:40387236 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTTAAAGTTGGCACTGCGAGTCTTCAACTTTGTTCTTCTTTTCAAGATTGTTTGTAT
sb_CM021995.1:10269465 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTTAAAAAATAAATAAATAAATAAATTTACTGTATATCAAACTAGACTGTTGATTGGGATTTTCATTATGAT
sd_CM022000.1:4949772 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAACTTTAAAAAATAAAAAAGATGCTCAATAACTCAGACATGAAACTGTAATCAACTTTTAT
db_CM016585.1:2698746 : TGC-----CTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTAATATCATATAATATCTTCTTTTAAAAAATAGTAATTAACAAAAAACAGC
db_CM016583.1:17007826 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATCATGGGCTCTTTGTGTCAGTGATTCTTGGAGGGTCAGCTGAGTTTGAAGGTCCAACCT
sb_CM021968.1:10922333 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATAAAACCTTCTAATATTCCTCTCTGACTCTTCTGATAGCTTCTCTATATTACAC
db_CM016597.1:28379392 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAATTTGCTCACACAAGCATTTATGAGAGTTAAGACAGGCTGCTGAGGTCAAAGTTGGAAC
sd_CM021962.1:5942164 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATAAGTCTTTGTCAACCAATGCGCCACTGCGCTCTCTGGGAGGAGAGCTAAGAAG
db_CM016581.1:33919269 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT- AAATAAATAAAAA--TTAAAAAATAAAAAATTAAGTGCATATTAATGAACAGTGTGCTTCTAGCAAGAGGAGGAGCAACCAAGAGAA

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s_CM021999.1:1302320 : TGC-----CTCTCTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTTAAAAAAAAAAAAAAAAAAAAAAAAAATCCATCAGGTAACCTCCAAACACTGGACTCACACATGATCCTC
d_CM016585.1:39244977 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATTTGAAGGTGGTACTAACTGCTGAGCCACCCGGGCTGCCATGTTTGGATGTTCTT
s_CM021974.1:2158052 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAAAACAAGTATAAAAAAAAAAATAAAAAAAAAAAGGAACTGTATTAG
s_JAAHU010001567.1 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAAGTCCAGGTGAGACCCAGGTGGCGAC
s_CM021992.1:33557050 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATTTAAAAAAAAAAAAAAAAAAAAAGAAAGGAACCTTGCTATTTTCCGTTGCCAAGCTGTGT
s_CM021964.1:30379999 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAGTCAAAAAAAAAAGAAACACGGTGTGAGCCACTTTCCTACCAACTGGGACGCCAGTCA
s_CM021983.1:39843791 : TGC-----CTCTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATGAATTGTTAAGAGGATTGAAAAACCTTTAATCTGGAATTTTATTTCCATAAAA
d_CM016602.1:37922450 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAGTCCAGATACTAAATATGTTGGTAGCTTTGAGGGCCACGGGGTCTCTTTCA
s_CM021975.1:44948071 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAGGAAGGCCAAGGGGAGAGTCAGGCCCTTCTCTTTAAAAAAAAAAAAAAAAAAAA
b_CM000015.4:12045115 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----AATTTAAAAAAATTTAAAAAAAAAAAAAAAAAAAAAAAAAATCTTTCTTACTTTTAAGGATGTGTCTGAGAA
d_CM016593.1:25664656 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----AAAAATAAAATAAAAAAAAAATAGAACTTCATAGCTAGATAGAAGAAGTCATTGCCTAGCTTCAAAGCTTTG
s_CM021979.1:3998940 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAATAAAAATAAAAAAATAAACAGGGAAGCAGACACAATGAGAAAAGGAACCTCAGGGGA
d_CM016595.1:17341917 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATTTAAAAAGGGGGGAGGAGGGAAGCTTGAGGTTACTAATTTAAGTAAGAAGAAAGGG
b_CM000008.4:45177897 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAGCCACCCAGTCTATGATATAGTTCCTCTTCTTCTATGAGGGAATCTTTGGAGTTCTTG
s_CM021968.1:70022581 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATATGACATCTGGTGTGGTCTTGTACATTTTGGGTAGTTTTTCCCGAATTTCTGTCT
b_CM000026.4:29896458 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----AAAAAAAAAAGAAAGCCAAATTCAGAAGCACTATTATACAGCACTGCTGCTAGAAAAAGCATA
b_CM000037.4:499477 : TGC-----CTCTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAATCTTTTAAAAAAAAAAAAAAACAATTCAATGTCAGAAAGCCAATTCAGAAGCATTATTATACAG
b_CM000004.4:83154346 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAAAATTTCCCTGGCTATTCGGGGTCTTTTCTGATTCCACACAATCTTAAATATA
s_CM021966.1:24511004 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAATTTTAAAAAAAAAAAAATATAATATCTGACTACTAATTATGTGTCTAGGTACTATTTTAAATATT
s_CM021985.1:13731355 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAATTTTAAAAAAATAAAACAATTTCTCTGTATCATTTACCACCAGCAATTTTATAGTTCA
d_CM016584.1:49524041 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAAAATTTACAGATTTATTTGCTATCTTAAGCCTCAGGGTCTTTTCTGCCACATATTC
b_CM000013.4:4729652 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAATATATATATATAAATGGAGAAGGGGCAGGCCAAGTACTATGGGAGAAGCATTTCTTCTCCC
b_CM000019.4:44555175 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----AAAAATTTAAAAAAATATATAATATGTATGTGTTTTATCTTCTATCACTCCACATGTACCTTCTACTCTACTCTA
s_CM021965.1:38018467 : TGC-----CTCTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTTAAAAAAATAAATAAATAAGCACAGTCCAGCAGTTTCTGCTGAAGAAACAATAATGAGCTGCCA
s_CM021989.1:34192529 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAATTTAAACAAAGGACAAAGTTCAACAAGTGTATGTTGTCTCTGTTCAAGTCCATAATCC
d_CM016578.1:31768031 : TGC-----CTCTCTCTCTCTCTCTCTGTGACTATCAT--AAATAAATAAAAA-----TTAAAAAAAAAAATTTAAATTTCTGGGTCCAGTCCAGGCCACAGAATCTGGGACTCTGGGAACGGGGTC

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Figure S7. Analysis of 3'-terminal regions of Can_b2 sequences of the tribe 2. The upper copy (chr9:16208268-16208630) was used as the search query (marked blue in the sequence above). 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. The letter prefix in sequence names indicates the genome where they are present (s, German Shepherd; d, Great Dane; and b, Boxer). Only the 3'-terminal Can and flanking sequences are presented; the missing 5'-terminal sequences are identical in these 265 copies. Rudimentary terminators (TT and TTT) are marked green, while functional ones are marked red (T₃) or brown (TCTTT). A-stretches are marked yellow and T residues within TA₃₋₅ repeats are marked purple; TSDs are underlined.