

**Supplementary Information File S1A.** Experimental details on the genetic analysis.

<b>Primer and probe sequences</b>	<b>Amplicon information</b>
1F: 5'-CAAGTTTGGCTCCGGCGCTGC-3' (EX1) 1R: 5'-AGCGCTTGTCGGCGATGTGC-3' (EX2)	Transcript variant validation (cDNA) X3 (canonical): 360 bp; X1: 535 bp
2F: 5'-TGAGCCGTTCTCCGTCACACGTC-3' (EX1a) 2R: 5'-GGCGGTCGCATCCGTTCTGC-3' (EX1b)	Transcript variant validation (cDNA) X2: 140 bp (231 bp gDNA)
3F: 5'-GGTGGCTAGGAGTTGGCTGGA-3' (IN1) 3R: 5'-TCGCCCTCTTTGGTCTGGTG-3' (EX2)	Variant detection (gDNA): 742 bp
4F: 5'-GCCATCGTGCTTCTGATTGC-3' (EX2) 4R: 5'-GCAGGGGACACTGGAAGGAA-3' (3'-UTR)	Variant detection (gDNA): 900 bp
5F: 5'- TCTGGGGCTACGAGTTC-3' (EX2) 5R: 5'-ACGACTCCTCCA ACTTGA-3' (EX2) 5W: 5'-FAM-TGACTTCAGCCTTTTTGACCA-BHQ1-3' 5M: 5'-TR-ACTTCAGCCCTTTTTGACCAG-BHQ2 -3'	Genotyping assay with dual labelled probes 165 bp (gDNA) 5W: Wt-probe 5M: Mt-probe
<b><u>PCR mix (1-4):</u></b> 5,7 µl H <sub>2</sub> O 1,0 µl 10x Key buffer 1,0 µl Primers (5 µM each) 0,2 µl dNTPs (10 mM each) 0,1 µl Tempase HS DNA polymerase (5 U/µl) <u>2,0 µl Template</u> 10,0 µl Total volume	<b><u>PCR program (1-4):</u></b> 14'30" - 95°C 00'30" - 95°C ] 00'30" - 65°C ] 35x 01'00" - 72°C ] 04'00" - 72°C Hold - 15°C
<b><u>qPCR mix (5):</u></b> 4,7 µl H <sub>2</sub> O 1,0 µl 10x Key buffer 1,0 µl Primers (5 µM each) 1,0 µl Probes (5 µM each) 0,2 µl dNTPs (10 mM each) 0,1 µl Tempase HS DNA polymerase (5 U/µl) <u>2,0 µl Template</u> 10,0 µl Total volume	<b><u>qPCR program (5):</u></b> 14'30" - 95°C 00'20" - 95°C ] 00'40" - 60°C ] 40x Plate read ]
<b><u>Sequencing mix:</u></b> 3,0 µl H <sub>2</sub> O 2,0 µl 5x SEQ-buffer 1,0 µl GC-rich 0,5 µl RR-mix 1,5 µl Sequencing primer (2 µM) <u>2,0 µl Template</u> 10,0 µl Total volume	<b><u>Sequencing program:</u></b> 2'00" - 95°C 0'20" - 95°C ] 0'10" - 60°C ] 30x 4'00" - 65°C ] Hold - 15°C

**Supplementary Information File S1B.** Coding and protein sequence of canine KCNJ10. The c.986T>C (p.(Leu329Pro)) variation is shown in red.

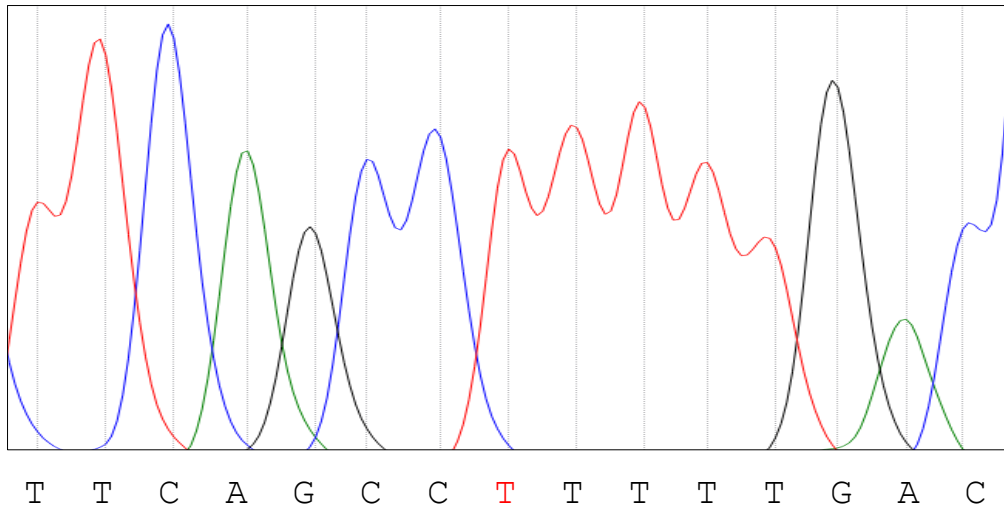
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1 M T S V A K V Y Y S Q T T Q T E S R P L
1 atgacgtctgtcgcgaaggtgtactacagccagaccactcagacggagagccggcccctc
21 V G P G V R R R R V L T K D G R S N V R
61 gtgggcccaggggtccggcgccgggtcctgaccaaggacggccgcagcaacgtgagg
41 M E H I A D K R F L Y L K D L W T T F I
121 atggagcacatcgccgacaagcgcttcctctacctcaaggacctgtggaccaccttcac
61 D M Q W R Y K L L L F S A T F A G T W F
181 gacatgcagtgggcgctacaagctgctgctcttctcggcgacctttgcaggcacctgggtc
81 L F G V V W Y L V A V A H G D L L E L G
241 ctcttcggcgtggtgtggtatctggtggctgtggccccacggggacctgctggagctcggc
101 P P A N H T P C V V Q V H T L T G A F L
301 cccccggccaaccacacccccctgctggttacaggtgcacacgctcacgggggccttcctc
121 F S L E S Q T T I G Y G F R Y I S E E C
361 ttctccctcgaatcgcagaccaccatcggctacggcttccgctacatcagtgaggagtgc
141 P L A I V L L I A Q L V L T T I L E I F
421 ccgctggccatcgtgcttctgattgccagctggtgctcaccaccatcctggaaatcttc
161 I T G T F L A K I A R P K K R A E T I R
481 atcacggggaccttcctggcaaagatcgcccggcccaagaagcgggcgagaccatccgg
181 F S Q H A V V A A H N G K P C L M I R V
541 ttcagccagcacgcggtcgtcgcggccccacaacgggaagccctgcctcatgatccgagtc
201 A N M R K S L L I G C Q V T G K L L Q T
601 gccaacatgcggaagagcctcctcatcggctgccaggtgacgggcaagctgcttcagacc
221 H Q T K E G E N I R L N Q V N V T F Q V
661 caccagaccaaagagggcgagaacatccggctcaaccaggtcaacgtgactttccaggtc
241 D T A S D S P F L I L P L T F Y H V V D
721 gacacggcctcggacagcccccttcctcattctgcccctgaccttctaccacgtggtagat
261 E T S P L K D L P L R S G E G D F E L V
781 gagaccagtccttgaaagacctccccctgcgccagtgggcgaggggtgacttcgagctggtg
281 L I L S G T V E S T S A T C Q V R T S Y
841 ctgatacctcagtgggacgggtggagtccaccagtgccacctgccaggtgcgccagctcctac
301 L P E E I L W G Y E F T P A I S L S A S
901 ctgccggaggagatcctctggggctacgagttcaccgccatctcgtgtccgccagc
321 G K Y I A D F S L F D Q V V K V A S P G
961 ggcaaatacatcgctgacttcagcctttttgaccaggtggtgaaagtggcctcccctggc
341 G L R D S A V R Y G D P E K L K L E E S
1021 ggctccgcgacagcgtgtccgctacggagaccctgagaagctcaagttggaggagtgc
361 L R E Q A E K E G S A L S V R I S N V *
1081 ttaagggaaacaagcgggagaaggaggggcagcgcctgagcgtgcgcatcagcaacgtctga
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**Supplementary Information File S1C. KCNJ10 protein BLAST alignment between human (Acc. No. NP\_002232.2) and dog (Acc. No. XP\_545752.3).**

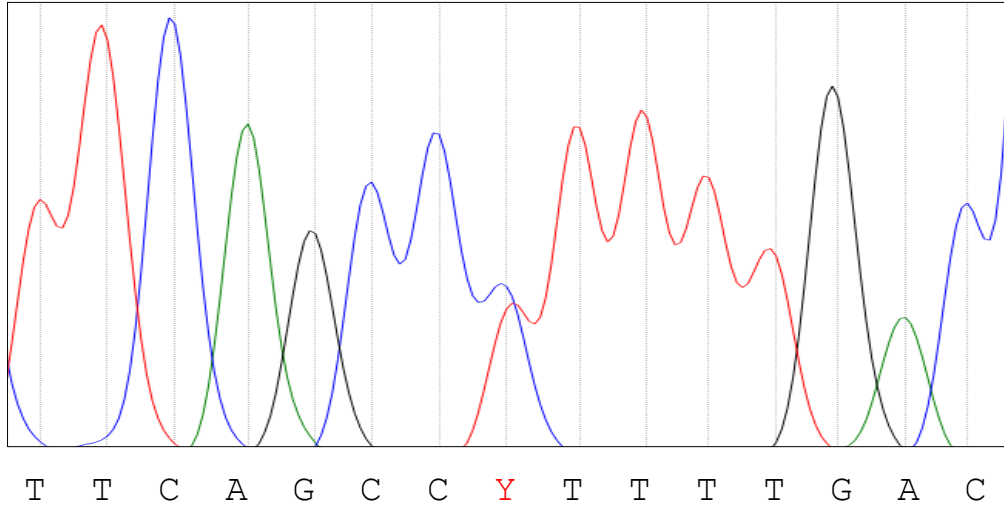
Score	Identities	Positives	Gaps
771 bits (1992)	374/380 (98%)	377/380 (99%)	0/380 (0%)
Human 1	MTSVAKVYYSQTTQTESRPLMGPGIRRRRVLT KDGRSNVRMEHIADKRFLYLKDLWTTFI		60
Dog 1	MTSVAKVYYSQTTQTESRPL+GPG+RRRRVLT KDGRSNVRMEHIADKRFLYLKDLWTTFI		60
Human 61	DMQWRYKLLLF SATFAGTWFLFGVWVYLVAVAHGD LLELDPPANHTPCVVQVHTLTGAFL		120
Dog 61	DMQWRYKLLLF SATFAGTWFLFGVWVYLVAVAHGD LLEL P PANHTPCVVQVHTLTGAFL		120
Human 121	FSLESQTTIGYGFRYI SEECPLAIVLLIAQLVLT T T I L E I F I T G T F L A K I A R P K K R A E T I R		180
Dog 121	FSLESQTTIGYGFRYI SEECPLAIVLLIAQLVLT T T I L E I F I T G T F L A K I A R P K K R A E T I R		180
Human 181	FSQHAVVASHNGK PCLMIRVANMRKSL L I G C Q V T G K L L Q T H Q T K E G E N I R L N Q V N V T F Q V		240
Dog 181	FSQHAVVA+HNGK PCLMIRVANMRKSL L I G C Q V T G K L L Q T H Q T K E G E N I R L N Q V N V T F Q V		240
Human 241	DTASDSPFLILPLTFYHVVD ETSPLKDLPLRS GEGDFELVLILSGTVESTSATCQVRTSY		300
Dog 241	DTASDSPFLILPLTFYHVVD ETSPLKDLPLRS GEGDFELVLILSGTVESTSATCQVRTSY		300
Human 301	LPEEILWGYEFTPAISLSASGKYIADFS LFDQVVKV ASPGLRDSTVRYGDPEK LKLEES		360
Dog 301	LPEEILWGYEFTPAISLSASGKYIADFS LFDQVVKV ASP GLRDS VRYGDPEK LKLEES		360
Human 361	LREQAEKEGSALSVRISNV*	380	
Dog 361	LREQAEKEGSALSVRISNV*	380	

**Supplementary Information File S1D.** Chromatogram of the region containing the c.986T>C (p. (Leu329Pro)) variation (in red) in a (1) homozygous wild type, (2) heterozygous and (3) homozygous mutant animal.

1



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