

Appendix 1. A list of members of 99 Lives Cat Genome Sequencing Consortium, and detailed information on magnetic resonance imaging sequences, whole genome sequencing, fibroblast cell culture, feline *COL6A1* cDNA analysis, and histopathology and transmission electron microscopic analysis.

A list of members of 99 Lives Cat Genome Sequencing Consortium (Domestic cat analysis – whole genome sequencing data from 362 cats and whole exome sequencing data from 52 cats)

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Magnetic resonance imaging sequences obtained for the brain and spinal cord

The sequences for brain magnetic resonance imaging (MRI) obtained are as follows: T2-weighted, fluid-attenuated inversion recovery, T1-weighted, and contrast-enhanced T1-weighted images in sagittal, dorsal, and transverse planes. The spinal MRI sequences obtained were as follows: T2-weighted and T1-weighted images in sagittal and transverse planes, and transverse sections were obtained at levels between the T4–T12 vertebrae.

Detailed information regarding whole genome sequencing and its analysis

DNA was extracted from heparinized whole blood using Genra Puregene Blood Kit (Qiagen, Hilden, Germany) and submitted to Macrogen Japan (Tokyo, Japan), where DNA library preparation and whole genome sequencing (WGS) were performed. In brief, DNA library was prepared using TruSeq DNA PCR-Free (Illumina, San Diego, CA, USA) with 350 bp of the target insert size. Then WGS was conducted for the case using illumina HiSeq X Ten system (Illumine) with 2×150 base paired-end reads. Read mapping, realignment, and variant calling were carried out as described (1), with respect to a feline genome assembly (Felis_catus_9.0) (2) and RefSeq 104 annotation. The sequence data was included in the 99 Lives Cat Genome Sequencing Consortium (<http://felinegenetics.missouri.edu/99lives>) and submitted to the NCBI

short read archive under BioProject: PRJNA614458; BioSample: SAMN14425582. The 99 Lives Cat Genome Sequencing Consortium members are listed at the top of this file.

Approximately 25× genomic coverage was generated for this cat. This case's WGS data were compared with the 99 Lives Cat Genome Sequencing Consortium dataset was conducted using VarSeq v2.2.5 software (Golden Helix, Bozeman, Montana, USA), which included 362 cats' WGS and 52 cats' whole exome sequencing data. Variants affecting the coding sequence of genes or existing in 10 bp regions flanking exons in this cat were filtered, for which the cat is privately homozygous; heterozygosity in up to one additional cat was permitted. After that, unique candidate gene variants were assessed, including previously known causative genes of human or animal Ehlers-Danlos Syndromes (EDS) or congenital scoliosis based on the published literature. Those for EDS initially included the following 20 orthologous candidate genes: *COL5A1* (XM_023242950.1), *COL5A2* (XM_003990962.4), *COL1A1* (XM_003996699.4), *COL3A1* (XM_003990961.3), *COL1A2* (XM_003982764.5), *ADAMTS2* (XM_023254116.1), *PLOD1* (XM_003989499.3), *FKBP14* (XM_003982902.4), *TNXB* (XM_023254711.1), *COL12A1* (XM_019830870.1), *CHST14* (XM_003987275.4), *DSE* (XM_019831105.2), *B4GALT7* (XM_023254211.1), *B3GALT6* (XM_011279777.2), *SLC39A13* (*ZIP13*) (XM_023239820.1), *ZNF469* (XM_023245050.1), *PRDM5* (XM_023252840.1), *C1R* (XM_019834454.2), *C1S* (XM_006933467.4), *AEBP1* (*ACLP*) (XM_023250110.1) (3,4). Those for congenial scoliosis included the following 37 orthologous candidate genes, including *DLL3* (XM_003997806.5), *MESP2* (XM_019833746.2), *LFNG* (XM_023246563.1), *HES7* (XM_003996191.4), *NOTCH2* (XM_011285094.3), *NOTCH3* (XM_023246608.1), *SLC35A3* (XM_003990360.4), T (*TBXT*) (XM_003986708.3), *TBX6* (XM_011290514.3), *FBNI* (XM_023255387.1), *SHH* (XM_023242357.1), *SOX9* (XM_023243815.1), *FLNB*

(XM_019823423.2), *PTK7* (XM_003986191.4), *HSPG2* (XM_023258277.1), *KIAA1217* (XM_023256446.1), *DCC* (XM_019815281.2), *DVL3* (XM_023260347.1), *FGFR3* (XM_023253489.1), *RECQL4* (XM_019823278.2), *ROBO3* (XM_019811488.2), *WNT7A* (XM_011280231.3), and *CHRNA3* (XM_003991260.4), all which or some of which were previously used elsewhere (5,6), and recently reported candidate gene, named *FGFR1* (XM_011281522.3) (7). Subsequently, the number of genes studied was expanded to 55, including hereditary connective tissue disorders overlapping phenotype genes in addition to genes associated with EDS (8). Those 55 orthologous genes were the following: *ADAMTS2* (XM_023254116.1), *B3GALT6* (XM_011279777.2), *CHST14* (XM_003987275.4), *COL1A1* (XM_003996699.4), *COL1A2* (XM_003982764.5), *COL3A1* (XM_003990961.3), *COL5A1* (XM_023242950.1), *COL5A2* (XM_003990962.4), *DSE* (XM_019831105.2), *FKBP14* (XM_003982902.4), *PLOD1* (XM_003989499.3), *TNXB* (XM_023254711.1), *COL12A1* (XM_019830870.1), *C1R* (XM_019834454.2), *C1S* (XM_006933467.4), *SLC39A13* (XM_023239820.1), *ZNF469* (XM_023245050.1), *PRDM5* (XM_023252840.1), *LZTS1* (XM_003984723.4), *FLNA* (XM_023249411.1), *COL4A1* (XM_023253172.1), *COL6A1* (XM_011285711.3), *COL6A2* (XM_023238595.1), *COL6A6* (XM_011286221.3), *ELN* (XM_019820582.2), *FBLN5* (XM_019833518.1), *FBNI* (XM_023255387.1), *LOX* (XM_023254614.1), *MYH11* (XM_023246707.1), *RYR1* (XM_023245508.1), *SEPNI* (XM_023258321.1), *SGCB* (XM_023253126.1), *myosin-7 (MYH7)* (XM_006932746.4), *TTN* (XM_023259509.1), *SMAD2* (XM_023241966.1), *SMAD3* (XM_023255153.1), *COL2A1* (XM_023256993.1), *COL11A1* (XM_023258940.1), *COL11A2* (XM_003985999.5), *COL9A1* (XM_003986294.4), *COL9A2* (XM_023258522.1), *COL9A3* (XM_023251026.1), *MED12* (XM_004000604.5), *FLNB* (XM_019823423.2), LOC105261197 (*CANT1*) (XM_019818343.2),

SLC2A10 (XM_006929697.2), *ABCC6* (XM_011290585.3), *GGCX* (XM_011281186.3), *ENPPI* (XM_023254376.1), *AEBPI* (XM_023250110.1), *SKI* (XM_023257965.1), *TGFB2* (XM_003999507.5), *TGFB3* (XM_003987851.3), *TGFBRI* (XM_023242499.1), *TGFBRI2* (XM_023260647.1). Furthermore, the presence of a *HES7* variant (XM_003996191.5; c.5A>G; p.Val2Ala [NC_058381.1:chromosome E1:g.2918735A>G]) and *T* variants (XM_003986708.3; c.1196del,c.1166del,c.995delT,c.[995_1011dup;1011_1014del] [NC_058372.1:chromosome B2:g.152019395del, g.152019424del, g.152021379del,g.{152021360_152021362del;152021363_152021379dup}}) were checked, which were known to cause kinked-tail phenotype in Japanese Bobtail cats and Manx cats, respectively (9,10). Those genes and corresponding phenotypes were summarized in **Table S1**.

Method of fibroblast cell culture

Fibroblasts, derived from skin biopsy samples, were grown in Dulbecco's Modified Eagle's Medium - low glucose (Sigma-Aldrich, St. Louis, MO, USA) supplemented with 10% fetal bovine serum and 1% penicillin-streptomycin-amphotericin B at 37 °C and 5% CO₂.

Skin biopsy from healthy cats for cDNA sequence analysis, histopathology, and transmission electron microscopic analysis

Ethical approval for the skin biopsy from healthy cats was obtained from the Animal Care and Use Committee of Nippon Veterinary and Life Science University (Accession No. 2019S-32, S2019S-32). Healthy cats were part of another study by the Laboratory of Veterinary Radiology, Nippon Veterinary and Life Science University (Accession Nos. 2019K-2, S2019K-2).

For cDNA analysis, a skin biopsy was performed on 1 healthy cat (sex: female; age: 57 mo; body weight: 5.9 kg) from the caudal cervical region. The skin sample was cut into pieces and immediately snap-frozen in liquid nitrogen. For histopathology, and transmission electron microscopic analysis, a skin biopsy was conducted on another healthy cat (sex: female; age: 106 mo; body weight: 3.6 kg) from the caudal cervical region. The skin biopsies in each cat were performed under general anesthesia or sedation, respectively.

Methods of RNA extraction, reverse transcription PCR, and cDNA sequence analysis of feline *COL6A1*

Reverse transcription PCR (RT-PCR) and Sanger sequencing were performed to validate the in-frame deletion in *COL6A1* in the affected cat. Cultured cells established from the affected cat's dermal fibroblast were used as material for RNA extraction.

Total RNA of the affected cat and the healthy cat was extracted from the cultured cells and a skin sample using a FastGene RNA Premium Kit (NIPPON Genetics, Tokyo, Japan). RT-PCR was performed using ReverTra Ace (TOYOBO, Osaka, Japan) with the Oligo(dT)20 Primer (TOYOBO). Then, PCR was conducted using the synthesized cDNA, the primer sets, and Tks Gflex DNA Polymerase (Takara Bio, Shiga, Japan) with a 3-step PCR protocol, following the manufacturer's instructions. The PCR conditions and the primer sequences used are summarized in **Table S5**. Purification of PCR products and the subsequent Sanger sequencing was performed as described (11).

Sanger sequencing of the cDNA confirmed that the affected cat had an in-frame 3-bp deletion predicted to delete one amino acid residue (XM_011285711.3:c.1678_1680del; XP_011284013.1:p.Asn560del) in *COL6A1*, which suggested that the affected cat had a 1026

amino acid sequence (3081 nucleotides) whereas a normal cat had a 1027 amino acid sequence (3084 nucleotides). The *COL6A1* coding sequences of both the affected cat and a normal cat were submitted to the DNA Data Bank of Japan (DDBJ) (Accession Nos. LC750709 and LC750710, respectively).

Methods of histopathology and transmission electron microscopic analysis

For histopathological analysis, skin biopsy samples were fixed in 10% neutral buffered formalin, processed routinely, and embedded in paraffin wax. Sections (4 μ m) were stained with hematoxylin and eosin (H&E) and Masson's trichrome. For transmission electron microscopy analysis, small pieces of cat skin samples were prefixed in 4% paraformaldehyde and 1% glutaraldehyde in 0.1 M phosphate buffer, postfixed in 1% osmium tetroxide in 0.1 M phosphate buffer, dehydrated through a graded ethanol series, transferred to 100% acetone, and then embedded in epoxy resin. Using a transmission electron microscope (JEM1011; JEOL, Tokyo, Japan), ultrathin sections were examined after staining with uranyl acetate and lead citrate.

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B4: 119 334 703 D4: 269 302 19 B3: 207 175 1 X:4 109 184 3 A2: 119 192 88 C2: 838 840 A1: 188 662 224 A1: 711 263 0 B1: 844 872 37 C1: 104 653 076 X:4 617 580 9 C1: 103 358 745 A1: 599 017 8 B4: 416 271 64 A2: 122 664 33 C1: 557	PASS,VQS RTrancheS NP99.00to9 9.90	3	0.003 62319	82 8	1	1	2	<i>CCDC38</i>	missense_ variant	Misse nse	XM_011284 160.3	XM_011284160.3:c. 269T>C	p.Phe90Se r	1	0.20	20	60
	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>CD4H9 orf153</i>	missense_ variant	Misse nse	XM_019815 828.2	XM_019815828.2:c. 553G>A	p.Gly185 Arg	1	0.20	20	60
	PASS	2	0.002 41546	82 8	0	1	1	<i>CEMIP</i>	missense_ variant	Misse nse	XM_023254 807.1	XM_023254807.1:c. 382G>A	p.Val128Il e	1	0.21	21	63
	VQSRTran cheSNP99. 90to100.00	2	0.002 41546	82 8	0	1	1	<i>CHST7</i>	missense_ variant	Misse nse	XM_023248 942.1	XM_023248942.1:c. 559A>C	p.Thr187P ro	1	0.5	5	15
	VQSRTran cheSNP99. 00to99.90	3	0.003 62319	82 8	1	1	2	<i>CIB3</i>	missense_ variant	Misse nse	XM_023241 207.1	XM_023241207.1:c. 469G>C	p.Gly157 Arg	1	0.14	14	42
	PASS	3	0.003 62319	82 8	1	1	2	<i>COL6A 1</i>	inframe_de letion	Misse nse	XM_011285 711.3	XM_011285711.3:c. 1678_1680delAAC	p.Asn560d el	1	0.20	20	60
	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>GABRG 2</i>	missense_ variant	Misse nse	XM_003981 341.5	XM_003981341.5:c. 8C>T	p.Pro3Leu	1	0.12	12	36
	VQSRTran cheSNP99. 90to100.00	2	0.002 41546	82 8	0	1	1	<i>GTF3A</i>	missense_ variant	Misse nse	XM_011282 105.2	XM_011282105.2:c. 1247G>A	p.Cys416 Tyr	1	0.19	19	57
	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>HHIP</i>	missense_ variant	Misse nse	XM_003984 977.5	XM_003984977.5:c. 590A>G	p.Asp197 Gly	1	0.29	29	87
	PASS	2	0.002 41546	82 8	0	1	1	<i>ITGA10</i>	missense_ variant	Misse nse	XR_0021612 63.2	XR_002161263.2:n.88C>T		1	0.25	25	75
	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>KDM5 C</i>	missense_ variant	Misse nse	XM_023249 335.1	XM_023249335.1:c. 4060G>A	p.Gly1354 Arg	1	0.8	8	24
	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>LOC10 109353 7</i>	missense_ variant	Misse nse	XM_006935 036.4	XM_006935036.4:c. 2557A>G	p.Met853 Val	1	0.29	29	87
	PASS	2	0.002 41546	82 8	0	1	1	<i>LOC10 109677 9</i>	missense_ variant	Misse nse	XM_019821 051.2	XM_019821051.2:c. 883A>T	p.Ile295Le u	1	0.18	18	54
	PASS	3	0.003 62319	82 8	1	1	2	<i>LOC10 950143 8,NCA PD2</i>	missense_ variant	Misse nse	XR_0021594 88.2, XM_01 9834405.2	XR_002159488.2:n. 82+2075C>T, XM_0 19834405.2:c.4141 G>A	,p.Asp138 IAsn	1	0.16	16	48
	PASS	3	0.003 62319	82 8	1	1	2	<i>MED26</i>	missense_ variant	Misse nse	XM_023246 873.1	XM_023246873.1:c. 301G>A	p.Ala101T hr	1	0.25	25	73
	PASS	3	0.003 62319	82 8	1	1	2	<i>MIER1</i>	missense_ variant	Misse nse	XM_019837 205.1	XM_019837205.1:c. 812G>A	p.Cys271 Tyr	1	0.28	28	84

334																				
58																				
B4:																				
167																				
369				0.003	82															
66	A/G	PASS	3	62319	8	1	1	2	<i>MRC1</i>	missense_	Misse	XM_011283	XM_011283622.3:c.	p.Asp63Gly	1	0,17		17		51
D1:																				
106																				
982		VQSRTrancheSNP99.00to99.90		0.003	82															
531	G/A		3	62319	8	1	1	2	<i>MS4A15</i>	missense_	Misse	XM_003993	XM_003993487.4:c.	p.Ala49Thr	1	0,15		15		45
C1:																				
113																				
590		VQSRTrancheSNP99.00to99.90		0.002	82															
948	C/T		2	41546	8	0	1	1	<i>MYO7B</i>	missense_	Misse	XM_019837	XM_019837914.2:c.	p.Val1691Met	0,928571	1,13		14		32
A1:																				
210																				
532				0.003	82															
841	C/T	PASS	3	62319	8	1	1	2	<i>OSMR</i>	missense_	Misse	XM_023238	XM_023238963.1:c.	p.Val697Met	1	0,21		21		63
E1:																				
181																				
026				0.002	82															
61	A/G	PASS	2	41546	8	0	1	1	<i>PROCA1</i>	missense_	Misse	XM_006940	XM_006940026.4:c.	p.Glu198Gly	1	0,14		14		42
C2:																				
426																				
893		VQSRTrancheSNP99.00to99.90		0.002	82															
2	C/T		2	41546	8	0	1	1	<i>RIPK4</i>	missense_	Misse	XM_023238	XM_023238708.1:c.	p.Ala699Val	1	0,18		18		53
D3:																				
834																				
279		VQSRTrancheSNP99.00to99.90		0.003	82															
65	C/G		3	62319	8	1	1	2	<i>SERP1NB5</i>	missense_	Misse	XM_003995	XM_003995237.4:c.	p.Gln71Glu	1	0,17		17		51
A2:																				
129																				
435		VQSRTrancheSNP99.00to99.90		0.002	82															
80	G/A		2	41546	8	0	1	1	<i>SLC27A1</i>	missense_	Misse	XM_011290	XM_011290625.2:c.	p.Gly561Ser	1	0,23		23		69
E1:																				
579																				
367		VQSRTrancheSNP99.00to99.90		0.002	82															
61	C/A		2	41546	8	0	1	1	<i>SRP68</i>	missense_	Misse	XM_003997	XM_003997170.4:c.	p.Val224Leu	1	0,26		26		78
A2:																				
113																				
332		VQSRTrancheSNP99.00to99.90		0.003	82															
17	C/G		3	62319	8	1	1	2	<i>SYDE1</i>	missense_	Misse	XM_023241	XM_023241193.1:c.	p.Pro184Ala	1	0,21		21		63
B4:																				
415																				
675				0.002	82															
58	T/A	PASS	2	41546	8	0	1	1	<i>TAPBP L</i>	missense_	Misse	XM_023256	XM_023256705.1:c.	p.Val131Glu	1	0,20		20		60
B3:																				
124																				
328				0.002	82															
158	G/A	PASS	2	41546	8	0	1	1	<i>TMEM63C</i>	missense_	Misse	XR_440592.3	XR_440592.3:n.1465G>A		1	0,25		25		75
B4:																				
166																				
627				0.003	82															
34	A/T	PASS	3	62319	8	1	1	2	<i>TMEM236</i>	missense_	Misse	XM_019834	XM_019834003.2:c.	p.Thr34Ser	1	0,26		26		78
C2:																				
160		PASS,VQSRTrancheSNP99.00to99.90		0.003	82															
653																				
073	A/G		3	62319	8	1	1	2	<i>TOPAZ1</i>	missense_	Misse	XM_023260	XM_023260821.1:c.	p.Asn149Ser	1	0,26		26		78
C1:																				
381																				
515				0.002	82															
02	C/T	PASS	2	41546	8	0	1	1	<i>TRABD2B</i>	missense_	Misse	XR_0021608	XR_002160835.2:n.1574G>A		1	0,13		13		39

920		NP99.00to9																	
4		9.90																	
A3:																			
189				0.003	82					splice_regi		XM_019826							
658	A/G	PASS	3	62319	8	1	1	2	<i>CHD6</i>	on_variant	Other	498.2	XM_019826498.2:c.975-4A>G		1	0,20		20	60
E1:																			
426																			
715				0.002	82					3_prime_U		XM_003996							
62	T/G	PASS	2	41546	8	0	1	1	<i>CNP</i>	TR_variant	Other	870.5	XM_003996870.5:c.*745T>G		1	0,19		19	57
C2:																			
744		VQSRTran																	
671		cheSNP99.		0.003	82					synonymo		XM_003991	XM_003991783.3:c.	p.Leu452					
64	T/C	00to99.90	3	62319	8	1	1	2	<i>CPN2</i>	us_variant	Other	783.3	1354T>C	=	1	0,39		39	99
E1:																			
598																			
468				0.003	82					3_prime_U		XM_023244							
20	C/T	PASS	3	62319	8	1	1	2	<i>CYTH1</i>	TR_variant	Other	156.1	XM_023244156.1:c.*96G>A		1	0,20		20	59
C1:																			
447		VQSRTran																	
230		cheSNP99.		0.002	82					3_prime_U		XM_023258							
94	C/T	00to99.90	2	41546	8	0	1	1	<i>DHCR2</i>	TR_variant	Other	735.1	XM_023258735.1:c.*912G>A		1	0,19		19	56
C2:																			
226																			
189				0.003	82					3_prime_U		XM_023260							
0	G/C	PASS	3	62319	8	1	1	2	<i>DNMT</i>	TR_variant	Other	865.1	XM_023260865.1:c.*575G>C		1	0,22		22	66
D3:																			
583		VQSRTran																	
900		cheINDEL9		0.002	82					splice_regi		XR_0021476	XR_002147625.2:n.986+6_986+8d						
10	GGT/-	9.00to99.90	2	41546	8	0	1	1	<i>DTNA</i>	on_variant	Other	25.2	eITGG		1	0,3		3	9
D3:																			
584		PASS,VQS																	
506		RTrancheS																	
64	C/A	NP99.00to9	3	62319	8	1	1	2	<i>DTNA</i>	us_variant	Other	XR_0021476	XR_002147625.2:n.2226C>A		1	0,21		21	63
C1:																			
154		VQSRTran																	
016		cheSNP99.		0.002	82					synonymo		XM_011285	XM_011285347.2:c.	p.Thr229=					
015	G/T	00to99.90	2	41546	8	0	1	1	<i>FAP</i>	us_variant	Other	347.2	687C>A		1	0,23		23	69
C1:																			
154		VQSRTran																	
016		cheSNP99.		0.002	82					synonymo		XM_011285	XM_011285347.2:c.	p.Phe226=					
024	A/G	00to99.90	2	41546	8	0	1	1	<i>FAP</i>	us_variant	Other	347.2	678T>C		1	0,22		22	66
B4:																			
416		VQSRTran																	
330		cheSNP99.		0.003	82					synonymo		NM_001009	NM_001009307.1:c.	p.Gly171=					
60	A/G	00to99.90	3	62319	8	1	1	2	<i>GAPD</i>	us_variant	Other	307.1	513A>G		1	0,20		20	60
A3:																			
174		VQSRTran																	
768		cheINDEL9		0.002	82					splice_regi		XR_0027408							
6	C/-	9.00to99.90	2	41546	8	0	1	1	<i>GATA5</i>	on_variant	Other	78.1	XR_002740878.1:n.919-3delC		1	0,21		21	63
X:1																			
122																			
459				0.002	82					3_prime_U		XM_004000							
52	A/G	PASS	2	41546	8	0	1	1	<i>GPC4</i>	TR_variant	Other	909.5	XM_004000909.5:c.*945T>C		1	0,11		11	33
C1:																			
113																			
570				0.003	82					synonymo		XM_006935	XM_006935193.3:c.						
748	G/A	PASS	3	62319	8	1	1	2	<i>GPR17,</i>	us_variant	Other	193.3, XM_0	9205.1:c.434+4155	p.Asn289					
C1:																			
112																			
980		VQSRTran		0.003	82					synonymo		XM_023259	XM_023259197.1:c.						
091	G/A	00to99.90	3	62319	8	1	1	2	<i>HS6ST</i>	us_variant	Other	197.1	849G>A	p.Lys283=	1	0,21		21	63

E1: 431 199 46 C1: 154 070 791 E2: 714 340 7 C1: 100 108 969 C1: 113 705 553 C1: 113 705 781 E1: 584 615 21 E1: 584 621 22 E1: 584 623 51 E1: 584 626 77 E1: 584 640 96 E1: 584 642 75 E1: 584 643 67 E1: 584 646 49 C2: 771 606 9	C/T	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>HSD17 BI</i>	synonymo us_variant	Other	XM_006940 403.4	XM_006940403.4:c. 291C>T	p.Leu97=	1	0,18	18	52
	TA/-	PASS	2	0.002 41546	82 8	0	1	1	<i>IFIH1</i>	3_prime_U TR_variant	Other	XM_006935 321.4	XM_006935321.4:c.*133_*134del TA		1	0,25	25	75
	G/A	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>IGLON 5</i>	synonymo us_variant	Other	XM_023245 114.1	XM_023245114.1:c. 600C>T	p.Gly200=	1	0,30	30	88
	GTCT/-	PASS	3	0.003 62319	82 8	1	1	2	<i>IGSF3</i>	3_prime_U TR_variant	Other	XM_019837 688.2	XM_019837688.2:c.*168_*171del AGAC		1	0,20	20	60
	C/T	PASS	3	0.003 62319	82 8	1	1	2	<i>IWS1</i>	synonymo us_variant	Other	XR_0021613 35.2	XR_002161335.2:n.825C>T		1	0,22	22	66
	C/T	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>IWS1</i>	synonymo us_variant	Other	XR_0021613 35.2	XR_002161335.2:n.1053C>T		1	0,17	17	51
	C/T	PASS	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*3168G>A		1	0,21	21	63
	C/G	PASS	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*2567G>C		1	0,24	24	72
	A/G	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*2338T>C		1	0,19	19	57
	C/T	PASS	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*2012G>A		1	0,21	21	63
	C/T	PASS	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*593G>A		1	0,10	10	29
	C/T	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*414G>A		1	0,14	14	42
	C/T	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*322G>A		1	0,18	18	54
	C/T	PASS	2	0.002 41546	82 8	0	1	1	<i>JMJD6</i>	3_prime_U TR_variant	Other	XM_003997 181.5	XM_003997181.5:c.*40G>A		1	0,24	24	72
	G/A	VQSRTran cheSNP99. 00to99.90	2	0.002 41546	82 8	0	1	1	<i>KCNJ6</i>	5_prime_U TR_variant	Other	XM_003991 434.5	XM_003991434.5:c.-327G>A		1	0,19	19	57

C2: 803 338 10 C2: 804 143 97 C2: 211 073 9 C2: 211 120 6 D3: 930 049 57 C1: 113 033 585 C1: 113 510 845 A1: 186 050 8 B2: 221 705 2 B2: 211 569 3	G/- G/A C/A G/A C/T G/A TC/- A/T G/A A/G	PASS VQSRTrancheSNP99.00to99.90 PASS VQSRTrancheSNP99.00to99.90 PASS PASS PASS PASS VQSRTrancheSNP99.00to99.90	2 2 3 3 2 2 2 2	0.002 0.002 0.003 0.003 0.002 0.002 0.002 0.002	82 82 82 82 82 82 82 82 82	0 0 1 1 0 0 1 0 0 1 0	1 1 1 1 1 1 1 1 1 1	1 1 2 2 1 1 2 1 1 1 1	<i>TP63</i> <i>TP63</i> <i>TRPM2</i> <i>TRPM2</i> <i>TSHZ1</i> <i>UGGT1</i> <i>WDR33</i> <i>XPO4</i> <i>ZSCAN9</i> <i>ZSCAN31</i>	3_prime_UTR_variant synonymous_variant 3_prime_UTR_variant 3_prime_UTR_variant synonymous_variant 3_prime_UTR_variant synonymous_variant synonymous_variant synonymous_variant	Other Other Other Other Other Other Other Other Other	XM_003991796.5 XM_003991796.5 XM_011285792.3 XM_011285792.3 XM_023242110.1 XM_023259198.1 XM_003990676.4 XM_003980253.5 XM_019831673.2 XM_006931335.3	XM_003991796.5:c.*93delC XM_003991796.5:c.570C>T XM_011285792.3:c.*749G>T XM_011285792.3:c.*282C>T XM_023242110.1:c.2136C>T XM_023259198.1:c.*108C>T XM_003990676.4:c.*250_*251delCT XM_003980253.5:c.747T>A XM_019831673.2:c.399C>T XM_006931335.3:c.1134A>G	p.Gly190= p.Thr712= p.Leu133= p.Pro378=	1 1 1 1 1 1 1 1 1 1 1	0.17 0.25 0.18 0.12 0.24 0.18 0.13 0.35 0.14 0.30	17 25 18 12 24 18 13 35 14 30	51 74 53 36 72 54 38 99 42 90
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Table S2. Private heterozygous genetic variants identified uniquely in the case of 414 cats of the 99 Lives Cat Genome Sequencing Consortium dataset including WGS data from 362 cats and whole exome sequencing data from 52 cats. Variant calling was performed with respect to the *Felis_catus_9.0* reference genome assembly. Presented are variants affecting the coding sequence of genes or existing in 10 bp regions flanking exons.

Chr:POS	Ref/Alt	Filter	Allele Count	Allele Frequency	# Homozygotes	# Heterozygotes	# Homozygotes	# Heterozygotes	Gene Names	Sequence Ontology (Combined)	Effect (Combined)	Transcript Name (Clinically Relevant)	HGVS c. (Clinically Relevant)	HGVS p. (Clinically Relevant)	Variant Allele Freq of the Case	Allelic Depths (AD) of the Case	Read Depths (DP) of the Case	Genotype Qualities (GQ) of the Case	
X:1758	GCGTGCT/-	PASS	1	0.0073	8	2	1	0	1	ARSD	frameshift_variant	XM_023249531.1	XM_023249531.1:c.1398_1404delAGCACGC	p.Ala67Glyfs*15	0.61538	5	10,16	26	99
A2:129	TTTTC/-	PASS	1	0.0073	8	2	1	0	1	DNAJB9	frameshift_variant	XM_003982962.5	XM_003982962.5:c.530_534delCTTTT	p.Ser177Tyrfs*4	0.52941	2	8,9	17	99
A2:120	-TTTTTTA	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	EVXI	frameshift_variant	XM_023250457.1	XM_023250457.1:c.726_727insTTTTTTA	p.Thr243Phefs	0.22222	2	14,4	18	99
A2:120	CG/-	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	EVXI	frameshift_variant	XM_023250457.1	XM_023250457.1:c.728_729delCG	p.Thr243Metfs	0.21052	6	15,4	19	99
A2:120	GCCGC/-	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	EVXI	frameshift_variant	XM_023250457.1	XM_023250457.1:c.732_736delGCCGC	p.Trp244Ter	0.21052	6	15,4	19	99
A2:120	C/-	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	EVXI	frameshift_variant	XM_023250457.1	XM_023250457.1:c.744delC	p.Asp249Thrfs*8	0.23529	4	13,4	17	99
A2:120	-A	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	EVXI	frameshift_variant	XM_023250457.1	XM_023250457.1:c.748_749insA	p.Pro250Hisfs	0.23529	4	13,4	17	99
A3:185	-TTTTTTAA	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	LAMA5	frameshift_variant	XM_023251034.1	XM_023251034.1:c.1033_1034insTTTTTTAA	p.Trp345Phefs*64	0.21428	6	11,3	14	90
A3:185	-T	VQSRTTrancheINDEL99.9	1	0.0073	8	2	1	0	1	LAMA5	frameshift_variant	XM_023251034.1	XM_023251034.1:c.1036_1037insT	p.Lys346Ilefs*61	0.23076	9	10,3	13	93

		0to100.0	0															
A3:		VQSRTr																
185		ancheIN																
202		DEL99.9	0.00	8														
5	GC/-	0to100.0	1207	2	1	0	1	LAMA5	frameshift_v	LoF	XM_0232	XM_023251034.1:c.1038_1	p.Lys34	0.23076				
D1:		0	73	8	1	0	1		ariant		51034.1	039delG	6Asnfs*	9	10,3		13	93
875		VQSRTr																
737		ancheSN	0.00	8														
30	G/A	P99.0to	1207	2	1	0	1	LOC10			XM_0198	XM_019812218.2:c.661C>	p.Arg22	0.60869				
E1:		99.90	73	8	1	0	1	108600	stop_gained	LoF	12218.2	T	1Ter	6	9,14		23	99
306		VQSRTr																
563		ancheIN	0.00	8														
35	-/CCGT	DEL99.9	1207	2	1	0	1	LOC10	frameshift_v	LoF	XM_0039	XM_003996638.3:c.845_84	p.Asn28	0.15789				
603		0to100.0	1207	2	1	0	1	109817	ariant		96638.3	6insACGG	3Argfs*	5	16,3		19	76
175		0	73	8	1	0	1	7					28					
74	-/T	PASS	0.00	8	1	0	1	LOC11	frameshift_v	LoF	XM_0232	XM_023254723.1:c.565_56	p.Ala18	0.55	9,11		20	99
E1:		VQSRTr	1207	2				156058	ariant		54723.1	6insA	9Aspfs*					
113		ancheSN	0.00	8														
295		P99.0to	1207	2	1	0	1				XR_00273			0.58823				
12	C/A	99.90	73	8	1	0	1	MIEF2	stop_gained	LoF	8041.1	XR_002738041.1:n.2301G>T		5	7,10		17	99
216		VQSRTr																
815		ancheIN	0.00	8														
13	CA/-	DEL99.9	1207	2	1	0	1	RREB1	frameshift_v	LoF	XM_0112	XM_011282167.3:c.5210_5	p.Val17	0.52173				
B2:		0to100.0	73	8	1	0	1		ariant		82167.3	211delTG	37Alafs	9	11,12		23	99
216		0	73	8	1	0	1											
815	-/TCTT	PASS	0.00	8	1	0	1	RREB1	frameshift_v	LoF	XM_0112	XM_011282167.3:c.5205_5	p.Leu17	0.52173				
19		VQSRTr	1207	2					ariant		82167.3	206insAAGA	36Lysfs	9	11,12		23	99
E1:		ancheSN	0.00	8														
621		P99.0to	1207	2	1	0	1	SLC25A	frameshift_v	LoF	XM_0232	XM_023244311.1:c.140_14	p.Leu49					
728	-/TGGC	100.00	73	8	1	0	1	10	ariant	LoF	44311.1	3dupTGGC	Glyfs*3	0.5	9,9		18	99
52		0	73	8	1	0	1						6					
C2:		VQSRTr																
160		ancheIN	0.00	8														
701		DEL99.9	1207	2	1	0	1	TOPAZ	frameshift_v	LoF	XM_0232	XM_023260821.1:c.3585_3	p.Val11					
824	-/TTTTTTTTTT	0to100.0	73	8	1	0	1	1	ariant	LoF	60821.1	586insTTTTTTTTTT	*5	0.25	6,2		8	66
C1:		0	73	8	1	0	1											
200		VQSRTr																
587		ancheSN	0.00	8														
034	T/C	P99.90to	1207	2	1	0	1	ABCA1	missense_va	Miss	XM_0198	XM_019838638.1:c.6110A>	p.Asn20	0.26315				
E2:		100.00	73	8	1	0	1	2	ariant	ense	38638.1	G	37Ser	8	14,5		19	99
367		VQSRTr																
535		ancheIN	0.00	8														
39	G/A	DEL99.9	1207	2	1	0	1	ADGR	missense_va	Miss	XM_0198	XM_019819797.2:c.1006G>	p.Glu33	0.5	6,6		12	99
E2:		0to100.0	73	8	1	0	1	G3	ariant	ense	19797.2	A	6Lys					
366		0	73	8	1	0	1											
431	G/A	PASS	0.00	8	1	0	1	ADGR	missense_va	Miss	XR_00273	XR_002738471.1:n.537G>A		0.57142				
76		VQSRTr	1207	2				G5	ariant	ense	8471.1			9	9,12		21	99
C1:		ancheSN	0.00	8														
204		P99.90to	1207	2	1	0	1	ANKZF	missense_va	Miss	XM_0198	XM_019838707.1:c.1883G>	p.Arg62	0.63636				
228	G/A	100.00	73	8	1	0	1	1	ariant	ense	38707.1	A	8Gln	4	8,14		22	99
319		0	73	8	1	0	1											
B2:		VQSRTr																
421		ancheIN	0.00	8														
077		DEL99.9	1207	2	1	0	1	APOBE	inframe_dele	Miss	XM_0039	XM_003986124.5:c.30_38d	p.Ala13	0.69230				
35	GGCCGCTGC/-	100.00	73	8	1	0	1	C2	tion	ense	86124.5	eICGCTGCGGC	_Ala15d	8	4,9		13	99

232																				
351																				
B1:		VQSRTr																		
130		ancheSN		0.00	8															
318		P99.00to		1207	2															
500	G/A	99.90	1	73	8	1	0	1	GRID2	missense_v	Miss	XM_0198	XM_019829242.1:c.337C>	p.His11						
D1:																				
893				0.00	8															
512				1207	2															
89	C/T	PASS	1	73	8	1	0	1	HIPK3	missense_v	Miss	XM_0198	XM_019812241.2:c.266C>	p.Ala89	0.41666		7	14,10	24	99
D2:																				
323				0.00	8															
449				1207	2															
06	C/A	PASS	1	73	8	1	0	1	HKDC1	missense_v	Miss	XM_0039	XM_003994002.4:c.638C>	p.Thr21						
E2:		VQSRTr																		
339		ancheSN		0.00	8															
642		P99.00to		1207	2															
43	C/T	99.90	1	73	8	1	0	1	IRX3	missense_v	Miss	XM_0232	XM_023245118.1:c.475G>	p.Gly15	0.625		6,10	16	99	
A2:		VQSRTr																		
850		ancheSN		0.00	8															
158		P99.00to		1207	2															
8	C/T	99.90	1	73	8	1	0	1	KANK2	missense_v	Miss	XM_0069	XM_006928415.4:c.1229G>	p.Arg41	0.46428		6	15,13	28	99
E3:																				
225				0.00	8															
590				1207	2				KIAA05	missense_v	Miss	XM_0069	XM_006942221.3:c.4609G>	p.Asp15						
85	C/T	PASS	1	73	8	1	0	1	56	riant	ense	XM_0069	XM_006942221.3:c.4609G>	37Asn	0.4		9,6	15	99	
E2:																				
368				0.00	8															
478				1207	2															
00	C/T	PASS	1	73	8	1	0	1	KIFC3	missense_v	Miss	XM_0232	XM_023245836.1:c.484G>	p.Ala16						
A3:		VQSRTr																		
185		ancheIN		0.00	8															
201		DEL99.9		1207	2															
3	GCAGCC/-	0to100.0	1	73	8	1	0	1	LAMA5	inframe_de	Miss	XM_0232	XM_023251034.1:c.1027_1	p.Gln34						
A3:		VQSRTr																		
185		ancheSN		0.00	8															
202		P99.90to		1207	2															
1	G/T	100.00	1	73	8	1	0	1	LAMA5	missense_v	Miss	XM_0232	XM_023251034.1:c.1034G>	p.Trp34	0.21428					
D1:																				
108				0.00	8															
925				1207	2															
605	G/A	PASS	1	73	8	1	0	1	LGALS12	missense_v	Miss	XR_00273	XR_002736394.1:n.1113G>A		0.6		10,15	25	99	
D1:																				
871				0.00	8															
529				1207	2				LOC10	missense_v	Miss	XM_0198	XM_019812218.2:c.5329C>	p.Arg17	0.57142					
35	G/A	PASS	1	73	8	1	0	1	1086002	riant	ense	XM_0198	XM_019812218.2:c.5329C>	77Cys	9		6,8	14	99	
D1:																				
102				0.00	8															
461				1207	2				LOC10	missense_v	Miss	XM_0039	XM_003993298.4:c.398T>	p.Ile133	0.55555					
643	T/C	PASS	1	73	8	1	0	1	1089895	riant	ense	XM_0039	XM_003993298.4:c.398T>	Thr	6		8,10	18	99	
C1:																				
194				0.00	8															
526				1207	2				LOC10	missense_v	Miss	XM_0039	XM_003991080.3:c.50A>G	p.Tyr17						
654	T/C	PASS	1	73	8	1	0	1	1093129	riant	ense	XM_0039	XM_003991080.3:c.50A>G	Cys	0.75		4,12	16	90	
B2:																				
108				0.00	8															
948				1207	2				LOC10	missense_v	Miss	XM_0232	XM_023254289.1:c.433C>	p.Leu14						
452	C/T	PASS	1	73	8	1	0	1	1093938	riant	ense	XM_0232	XM_023254289.1:c.433C>	5Phe	0.6		6,9	15	99	
E1:		VQSRTr																		
306	G/T	ancheSN	1	73	8	1	0	1	LOC101098177	missense_v	Miss	XM_0039	XM_003996638.3:c.844C>	p.Leu28	0.11111		1	16,2	18	76

563		P99.90to																	
36		100.00																	
B2:																			
571			0.00	8															
894			1207	2															
12	G/A	PASS	1	73	8	1	0	1	4	LOC10109996	missense_variant	Missense	XM_023254076.1	XM_023254076.1:c.816G>A	p.Met272Ile	0.527778	17,19	36	99
E2:																			
358			0.00	8															
853			1207	2															
72	G/C	PASS	1	73	8	1	0	1	41	LOC109494886,LOC111558141	missense_variant	Missense	XM_023246150.1XR_002738727.1	XM_023246150.1:c.17G>C, XR_002738727.1:n.39C>G	p.Arg6Pro,	0.555556	12,15	27	99
A2:		VQSRTrancheSN																	
368		P99.90to	0.00	8															
902		100.00	1207	2															
23	A/C	PASS	1	73	8	1	0	1	5	LOC111556285	missense_variant	Missense	XR_002740338.1	XR_002740338.1:n.766A>C		0.119658	206,28	234	99
B2:																			
603			0.00	8															
175			1207	2															
74	C/A	PASS	1	73	8	1	0	1	9	LOC111560589	missense_variant	Missense	XM_023254723.1	XM_023254723.1:c.565G>T	p.Ala189Ser	0.526316	9,10	19	99
E3:																			
319			0.00	8															
114			1207	2															
69	G/A	PASS	1	73	8	1	0	1		MARF1	missense_variant	Missense	XM_023247059.1	XM_023247059.1:c.2803G>A	p.Gly935Arg	0.466667	8,7	15	99
C1:																			
186			0.00	8															
523			1207	2															
332	C/G	PASS	1	73	8	1	0	1		MARS2, RFTN2	missense_variant	Missense	XM_003990998.5XM_003990998.5:c.617C>G, XM_019838417.2:c.-9+2600G>C	p.Thr206Ser,	0.666667	9,18	27	99	
A3:		VQSRTrancheSN																	
103		P99.00to	0.00	8															
281		99.90	1207	2															
004	T/C	PASS	1	73	8	1	0	1	5	MRPL35	missense_variant	Missense	XR_439970.4	XR_439970.4:n.332T>C		0.454545	6,5	11	99
B1:		VQSRTrancheSN																	
124		P99.00to	0.00	8															
459		99.90	1207	2															
394	C/T	PASS	1	73	8	1	0	1		MTTP	missense_variant	Missense	XM_019829170.2	XM_019829170.2:c.625G>A	p.Gly209Ser	0.551724	13,16	29	99
B1:																			
174			0.00	8															
314			1207	2															
632	T/C	PASS	1	73	8	1	0	1		N4BP2	missense_variant	Missense	XR_002156413.2	XR_002156413.2:n.2445A>G		0.45	11,9	20	99
B3:																			
767			0.00	8															
766			1207	2															
86	G/A	PASS	1	73	8	1	0	1		NOP9	missense_variant	Missense	XM_003987519.4	XM_003987519.4:c.452G>A	p.Arg151Gln	0.40625	19,13	32	99
B2:																			
142			0.00	8															
818			1207	2															
834	C/T	PASS	1	73	8	1	0	1		NOX3	missense_variant	Missense	XM_023254521.1	XM_023254521.1:c.964G>A	p.Val322Ile	0.434783	13,10	23	99
A3:		VQSRTrancheSN																	
278		P99.00to	0.00	8															
838		99.90	1207	2															
64	C/T	PASS	1	73	8	1	0	1		NRSN2	missense_variant	Missense	XM_003983669.3	XM_003983669.3:c.233C>T	p.Ala78Val	0.736842	5,14	19	99
A3:																			
128			0.00	8															
790			1207	2															
460	G/A	PASS	1	73	8	1	0	1		NT5C1B	missense_variant	Missense	XM_003984482.5	XM_003984482.5:c.872G>A	p.Arg291Gln	0.294118	12,5	17	99
A1:																			
120			0.00	8															
031			1207	2															
912	C/G	PASS	1	73	8	1	0	1		PCDH12	missense_variant	Missense	XM_003980868.4	XM_003980868.4:c.154G>C	p.Glu52Gln	0.461538	14,12	26	99
B4:																			
536	A/C	PASS	1	73	8	1	0	1		PIK3C2G	missense_variant	Missense	XM_006933551.3	XM_006933551.3:c.590A>C	p.Asn197Thr	0.333333	12,6	18	99

936																				
30																				
B4:		VQSRTr																		
144		ancheSN	0.00	8																
058		P99.00to	1207	2																
679	C/T	99.90	1	73	8	1	0	1	<i>PLXNB</i>	missense_v	Miss	XM_0198			p.Val14	0.5625	7,9	16	99	
A2:		VQSRTr																		
763		ancheSN	0.00	8																
141		P99.90to	1207	2																
50	G/A	100.00	1	73	8	1	0	1	<i>POU6F</i>	missense_v	Miss	XM_0232	XM_023250204.1:c.646C>		p.Pro21	0.44444	4	5,4	9	99
A2:		VQSRTr																		
555		ancheSN	0.00	8																
733		P99.00to	1207	2																
8	C/A	99.90	1	73	8	1	0	1	<i>PRAMI</i>	missense_v	Miss	XR_00214	XR_002148534.2:n.4808C>A			0.5	10,10	20	99	
D1:																				
107			0.00	8																
960			1207	2																
526	G/A	PASS	1	73	8	1	0	1	<i>RAB31L</i>	missense_v	Miss	XM_0069	XM_006937395.3:c.632C>		p.Thr21	0.59259	3	11,16	27	99
D4:																				
915			0.00	8																
651			1207	2																
48	C/T	PASS	1	73	8	1	0	1	<i>RAPGE</i>	missense_v	Miss	XM_0112	XM_011288359.3:c.2515G>		p.Gly83	0.56	11,14	25	99	
B1:		VQSRTr																		
165		ancheSN	0.00	8																
621		P99.00to	1207	2																
779	C/A	99.90	1	73	8	1	0	1	<i>RASL11</i>	missense_v	Miss	XM_0039	XM_003985387.5:c.439G>		p.Val14	0.42105	3	22,16	38	99
B2:																				
216			0.00	8																
815			1207	2																
11	T/G	PASS	1	73	8	1	0	1	<i>RREB1</i>	missense_v	Miss	XM_0112	XM_011282167.3:c.5213A>		p.Gln17	0.57142	9	9,12	21	99
B2:																				
216			0.00	8																
815			1207	2																
17	A/G	PASS	1	73	8	1	0	1	<i>RREB1</i>	missense_v	Miss	XM_0112	XM_011282167.3:c.5207T>		p.Leu17	0.52173	9	11,12	23	99
A1:																				
247			0.00	8																
427			1207	2																
15	G/A	PASS	1	73	8	1	0	1	<i>RUBCN</i>	missense_v	Miss	XM_0069	XM_006927291.4:c.529G>		p.Gly17	0.57142	9	9,12	21	99
B3:		VQSRTr																		
712		ancheSN	0.00	8																
907		P99.00to	1207	2																
62	G/A	99.90	1	73	8	1	0	1	<i>RYR3</i>	missense_v	Miss	XR_00274	XR_002742989.1:n.5150G>A			0.36	16,9	25	99	
D4:		VQSRTr																		
940		ancheSN	0.00	8																
244		P99.00to	1207	2																
70	G/A	99.90	1	73	8	1	0	1	<i>SARDH</i>	missense_v	Miss	XM_0198	XM_019816743.2:c.2359G>		p.Gly78	0.39130	4	14,9	23	99
B3:																				
139			0.00	8																
663			1207	2																
555	C/T	PASS	1	73	8	1	0	1	<i>SERPIN</i>	missense_v	Miss	XM_0069	XM_006933077.2:c.-		p.Met1e	0.57142	9	9,12	21	99
B2:		VQSRTr																		
147		ancheSN	0.00	8																
049		P99.00to	1207	2																
241	C/T	99.90	1	73	8	1	0	1	<i>SLC22A</i>	missense_v	Miss	XM_0039	XM_003986693.5:c.872C>		p.Ser29	0.41666	7	14,10	24	99
D1:																				
110			0.00	8																
406			1207	2																
583	A/G	PASS	1	73	8	1	0	1	<i>SLC22A</i>	missense_v	Miss	XM_0039	XM_003993589.3:c.1580A>		p.Gln52	0.38095	2	13,8	21	99
E1:																				
591			0.00	8																
718	CCCCGGCA/-	PASS	1	73	8	1	0	1	<i>SPNS2</i>	inframe_de	Miss	XR_00273	XR_002738273.1:n.313_321delACCCC			0.33333	3	6,3	9	99

A2: 648		VQSRT ancheSN	0.00	8														
381		P99.00to	1207	2														
86	C/A	99.90	1	73	8	1	0	1	<i>ABCA1</i>	synonymous	Othe	XM_0232	XM_023241981.1:c.14145C	p.Ile471	0.44444			
E2: 366		VQSRT ancheSN	0.00	8					<i>ADGR</i>	_variant	r	41981.1	>A	5=	4	10,8	18	99
542		P99.00to	1207	2					<i>G5,LO</i>			XM_0069	XM_006941542.2:c.1461C>					
10	C/T	99.90	1	73	8	1	0	1	<i>C11155</i>	synonymous	Othe	R_002738	T,XR_002738472.1:n.107+1	p.Tyr48	0.5	13,13	26	99
D4: 878		VQSRT ancheSN	0.00	8					<i>ANGPT</i>			472.1	XM_006939476.4:c.339C>					
479		P99.00to	1207	2					<i>L2,RAL</i>	synonymous	Othe	M_019816	T,XM_019816547.2:c.610+	p.Thr11	0.5	10,10	20	99
77	G/A	99.90	1	73	8	1	0	1	<i>GPS1</i>	_variant	r	547.2	37902G>A	3=,				
A1: 806		VQSRT ancheSN	0.00	8														
990		P99.00to	1207	2					<i>ANKRD</i>	synonymous	Othe	XM_0232	XM_023253212.1:c.1152C>	p.Ala38	0.76470			
88	G/A	99.90	1	73	8	1	0	1	<i>10</i>	_variant	r	53212.1	T	4=	6	4,13	17	73
D4: 119		VQSRT ancheSN	0.00	8														
998		P99.00to	1207	2						3_prime_UT	Othe	XM_0232			0.55555			
85	A/T	99.90	1	73	8	1	0	1	<i>APBA1</i>	R_variant	r	43333.1	XM_023243333.1:c.*183T>A		6	8,10	18	99
F2: 197			0.00	8														
313			1207	2					<i>ARFGE</i>	synonymous	Othe	XM_0112	XM_011291364.3:c.4752A>	p.Arg15	0.41176			
39	T/C	PASS	1	73	8	1	0	1	<i>F1</i>	_variant	r	91364.3	G	84=	5	10,7	17	99
D2: 176		VQSRT ancheSN	0.00	8														
397		P99.90to	1207	2						3_prime_UT	Othe	XM_0232			0.16363			
09	G/C	100.00	1	73	8	1	0	1	<i>ARV1</i>	R_variant	r	40424.1	XM_023240424.1:c.*835C>G		6	46,9	55	91
D2: 176			0.00	8														
398			1207	2						3_prime_UT	Othe	XM_0232			0.19642			
91	G/A	PASS	1	73	8	1	0	1	<i>ARV1</i>	R_variant	r	40424.1	XM_023240424.1:c.*653C>T		9	45,11	56	99
D2: 176		VQSRT ancheSN	0.00	8														
402		P99.90to	1207	2						3_prime_UT	Othe	XM_0232			0.16666			
52	C/T	100.00	1	73	8	1	0	1	<i>ARV1</i>	R_variant	r	40424.1	XM_023240424.1:c.*292G>A		7	30,6	36	74
C1: 220		VQSRT ancheSN	0.00	8														
138		P99.00to	1207	2						5_prime_UT	Othe	XM_0232						
332	T/A	99.90	1	73	8	1	0	1	<i>ASB1</i>	R_variant	r	59934.1	XM_023259934.1:c.244+66T>A		0.5	7,7	14	99
C1: 999		VQSRT ancheIN	0.00	8														
207		DEL99.0	1207	2					<i>ATP1A</i>	splice_regio	Othe	XM_0112	XM_011285086.3:c.1216+3_1216+4del					
69	AG/-	0to99.90	1	73	8	1	0	1	<i>1</i>	n_variant	r	85086.3	AG		0.4375	9,7	16	99
A2: 515			0.00	8														
086			1207	2					<i>ATP2B</i>	synonymous	Othe	XM_0232	XM_023250008.1:c.2820C>	p.Tyr94	0.33333			
13	G/A	PASS	1	73	8	1	0	1	<i>2</i>	_variant	r	50008.1	T	0=	3	8,4	12	99
B3: 249			0.00	8														
966			1207	2					<i>ATP10</i>	synonymous	Othe	XM_0232	XM_023255028.1:c.3438G>	p.Gln11	0.36363			
86	C/T	PASS	1	73	8	1	0	1	<i>A</i>	_variant	r	55028.1	A	46=	6	14,8	22	99
B3: 250			0.00	8														
111			1207	2					<i>ATP10</i>	synonymous	Othe	XM_0232	XM_023255028.1:c.2485C>	p.Leu82				
30	G/A	PASS	1	73	8	1	0	1	<i>A</i>	_variant	r	55028.1	T	9=	0.6	8,12	20	99
B3: 250			0.00	8														
195			1207	2					<i>ATP10</i>	synonymous	Othe	XM_0232	XM_023255028.1:c.1920C>	p.Thr64	0.48148			
21	G/A	PASS	1	73	8	1	0	1	<i>A</i>	_variant	r	55028.1	T	0=	1	14,13	27	99

B1: 610			0.00	8															
093			1207	2															
46	A/G	PASS	1	73	8	1	0	1	<i>CLCN3</i>	synonymous _variant	Othe r	XM_0039 84867.5	XM_003984867.5:c.159T>	p.Val53 =	0.5	13,13	26	99	
D2: 590		VQSRTr ancheSN		0.00	8														
369	C/T	P99.00to 99.90	1	1207	2	1	0	1	<i>CRTAC1</i>	synonymous _variant	Othe r	XM_0198 13654.2	XM_019813654.2:c.864G>	p.Pro28 8=	0.46153 8	7,6	13	99	
11				0.00	8														
C2: 117				1207	2				<i>CRYZL1</i>	3_prime_UT R_variant	Othe r	XM_0039 91454.5	XM_003991454.5:c.*26G>C		0.66666 7	10,20	30	99	
712	G/C	PASS	1	73	8	1	0	1											
32				0.00	8														
B1: 141				1207	2				<i>DCTD</i>	3_prime_UT R_variant	Othe r	XM_0232 52314.1	XM_023252314.1:c.*268T>G		0.61904 8	8,13	21	99	
593	A/C	PASS	1	73	8	1	0	1											
53				0.00	8														
B3: 767				1207	2				<i>DHRS1</i>	synonymous _variant	Othe r	XM_0039 87518.5	XM_003987518.5:c.885G>	p.Leu29 5=	0.34782 6	15,8	23	99	
703	C/T	PASS	1	73	8	1	0	1											
D3: 13		VQSRTr ancheSN		0.00	8														
537	G/A	P99.00to 99.90	1	1207	2	1	0	1	<i>DHX37</i>	synonymous _variant	Othe r	XM_0232 41282.1	XM_023241282.1:c.1170G>	p.Ala39 0=	0.75	2,6	8	40	
244				0.00	8														
7				1207	2														
A2: 851				0.00	8														
587	G/A	PASS	1	73	8	1	0	1	<i>DOCK6</i>	synonymous _variant	Othe r	XM_0232 45498.1	XM_023245498.1:c.4626C>	p.Thr15 42=	0.42857 1	8,6	14	99	
7		VQSRTr ancheSN		0.00	8														
B1: 115		P99.00to 99.90	1	1207	2	1	0	1	<i>EGF</i>	synonymous _variant	Othe r	NM_0010 09381.1	NM_001009381.1:c.423A>	p.Thr14 1=	0.24	19,6	25	99	
461	T/C			0.00	8														
553		VQSRTr ancheSN		1207	2														
A3: 760		P99.00to 99.90	1	73	8	1	0	1	<i>EML6</i>	synonymous _variant	Othe r	XR_00274 1131.1	XR_002741131.1:n.4908C>T		0.5	13,13	26	99	
888	C/T			0.00	8														
30				1207	2														
A2: 862				0.00	8														
320	C/A	PASS	1	73	8	1	0	1	<i>EPOR</i>	synonymous _variant	Othe r	XM_0232 45578.1	XM_023245578.1:c.63G>T	p.Gly21 =	0.46153 8	7,6	13	99	
8				0.00	8														
A1: 178				1207	2				<i>ERGIC1</i>	synonymous _variant	Othe r	XM_0232 59579.1	XM_023259579.1:c.111C>	p.Leu37 =	0.55555 6	8,10	18	99	
981	G/A	PASS	1	73	8	1	0	1											
295				0.00	8														
A2: 120				1207	2														
655	C/T	PASS	1	73	8	1	0	1	<i>EVX1</i>	synonymous _variant	Othe r	XM_0232 50457.1	XM_023250457.1:c.738C>	p.His24 6=	0.23529 4	13,4	17	99	
693				0.00	8														
A2: 120				1207	2														
655	C/G	PASS	1	73	8	1	0	1	<i>EVX1</i>	synonymous _variant	Othe r	XM_0232 50457.1	XM_023250457.1:c.753C>	p.Ala25 1=	0.26666 7	11,4	15	99	
708				0.00	8														
D2: 176				1207	2				<i>FAM89A</i>	3_prime_UT R_variant	Othe r	XM_0232 40417.1	XM_023240417.1:c.*281G>A		0.2	52,13	65	99	
276	G/A	PASS	1	73	8	1	0	1											
08		VQSRTr ancheSN		0.00	8														
D2: 176		P99.90to 100.00	1	1207	2	1	0	1	<i>FAM89A</i>	3_prime_UT R_variant	Othe r	XM_0232 40417.1	XM_023240417.1:c.*368C>T		0.14814 8	46,8	54	99	
276	C/T			0.00	8														
95				1207	2														

B3: 334				0.00	8														
052				1207	2														
92	TTC/-	PASS	1	73	8	1	0	1	<i>FAM21 9B</i>	3_prime_UT R_variant	Othe r	XM_0039 86942.5	XM_003986942.5:c.*1291_*1294delCT TT		0.54166 7	11,13	24	99	
D4: 946				0.00	8														
542	G/A	PASS	1	73	8	1	0	1	<i>FGD3</i>	3_prime_UT R_variant	Othe r	XM_0039 95335.5	XM_003995335.5:c.*537G>A		0.69565 2	7,16	23	99	
C2: 118				0.00	8														
445				1207	2														
74	C/T	PASS	1	73	8	1	0	1	<i>GART</i>	3_prime_UT R_variant	Othe r	XM_0039 91457.5	XM_003991457.5:c.*13C>T		0.47368 4	10,9	19	99	
E1: 635				0.00	8														
181	T/C	PASS	1	73	8	1	0	1	<i>GGT6</i>	3_prime_UT R_variant	Othe r	XM_0198 17018.2	XM_019817018.2:c.*238A>G		0.64	9,16	25	99	
B1: 433				0.00	8														
469				1207	2														
61	A/G	PASS	1	73	8	1	0	1	<i>GPAT4</i>	5_prime_UT R_variant	Othe r	XM_0039 84761.5	XM_003984761.5:c.*60T>C		0.55	9,11	20	99	
E2: 200				0.00	8														
324				1207	2				<i>GPATC</i>	synonymous	Othe	XM_0039	XM_003997950.5:c.1218A>	p.Pro40 6=	0.60869 6	9,14	23	99	
78	T/A	PASS	1	73	8	1	0	1	<i>H1</i>	_variant	r	XM_0039 97950.5	T						
D2: 754		VQSRTr ancheSN		0.00	8														
626		P99.00to		1207	2				<i>HSPA1</i>	3_prime_UT	Othe	XM_0232	XM_023240980.1:c.*14C>T		0.64705 9	6,11	17	99	
50	G/A	99.90	1	73	8	1	0	1	<i>2A</i>	R_variant	r	XM_0232 40980.1							
B3: 173		VQSRTr ancheSN		0.00	8														
017		P99.00to		1207	2				<i>IGF1R</i>	synonymous	Othe	XM_0232	XM_023254966.1:c.3453C>	p.Ile115 1=	0.5	13,13	26	99	
78	G/A	99.90	1	73	8	1	0	1	<i>IGF1R</i>	_variant	r	XM_0232 54966.1	T						
B3: 173		VQSRTr ancheSN		0.00	8														
063		P99.00to		1207	2				<i>IGF1R</i>	synonymous	Othe	XM_0232	XM_023254966.1:c.3114C>	p.Ala10 38=	0.38095 2	13,8	21	99	
66	G/A	99.90	1	73	8	1	0	1	<i>IGF1R</i>	_variant	r	XM_0232 54966.1	T						
C1: 201		VQSRTr ancheSN		0.00	8														
986		P99.00to		1207	2				<i>IGFBP</i>	5_prime_UT	Othe	XM_0112	XM_011285583.3:c.*41C>G		0.55	9,11	20	99	
084	C/G	99.90	1	73	8	1	0	1	<i>2</i>	R_variant	r	XM_0112 85583.3							
A2: 633		VQSRTr ancheSN		0.00	8														
333		P99.00to		1207	2				<i>IGFBP</i>	synonymous	Othe	XM_0232	XM_023250143.1:c.33G>A	p.Ala11 =	0.375	10,6	16	99	
84	C/T	99.90	1	73	8	1	0	1	<i>3</i>	_variant	r	XM_0232 50143.1							
B2: 526				0.00	8														
611				1207	2														
45	C/A	PASS	1	73	8	1	0	1	<i>IL17F</i>	3_prime_UT R_variant	Othe r	XM_0232 54749.1	XM_023254749.1:c.*245G>T		0.5625	7,9	16	99	
D1: 877				0.00	8														
236				1207	2				<i>IMMP1</i>	5_prime_UT	Othe	XM_0069	XM_006937165.3:c.*29-23901G>T		0.48	13,12	25	99	
29	C/A	PASS	1	73	8	1	0	1	<i>L</i>	R_variant	r	XM_0069 37165.3							
D1: 158				0.00	8														
312				1207	2														
73	C/T	PASS	1	73	8	1	0	1	<i>JAML</i>	synonymous	Othe	XM_0198 11359.2	XM_019811359.2:c.711G> A	p.Ala23 7=	0.44444 4	10,8	18	99	
D1: 158				0.00	8														
481				1207	2														
86	G/A	PASS	1	73	8	1	0	1	<i>JAML</i>	5_prime_UT R_variant	Othe r	XM_0069 36675.4	XM_006936675.4:c.*35C>T		0.5	7,7	14	99	
E2: 368				0.00	8														
095				1207	2				<i>KATNB</i>	synonymous	Othe	XM_0039	XM_003998077.5:c.1758G>	p.Leu58 6=	0.72	7,18	25	99	
16	G/A	PASS	1	73	8	1	0	1	<i>1</i>	_variant	r	XM_0039 98077.5	A						

E2: 189				0.00	8														
839				1207	2														
81	T/C	PASS	1	73	8	1	0	1	<i>KIAA0355</i>	5_prime_UTR_variant	Othe	XM_003997945.5	XM_003997945.5:c.-189A>G		0.391304	14,9	23	99	
A1: 451				0.00	8														
083				1207	2														
45	G/A	PASS	1	73	8	1	0	1	<i>KLHL1</i>	synonymous_variant	Othe	XM_011288605.3	XM_011288605.3:c.363C>T	p.Leu121=	0.583333	10,14	24	99	
B4: 806				0.00	8														
918				1207	2														
22	G/A	PASS	1	73	8	1	0	1	<i>KRT80</i>	3_prime_UTR_variant	Othe	XM_003988729.5	XM_003988729.5:c.*1510C>T		0.571429	12,16	28	99	
A3: 185				0.00	8														
203				1207	2														
1	A/G	PASS	1	73	8	1	0	1	<i>LAMA5</i>	synonymous_variant	Othe	XM_023251034.1	XM_023251034.1:c.1044A>G	p.Ala348=	0.230769	10,3	13	96	
A3: 185		VQSRTrancheSN P99.90to		0.00	8														
204				1207	2														
0	A/G	100.00	1	73	8	1	0	1	<i>LAMA5</i>	synonymous_variant	Othe	XM_023251034.1	XM_023251034.1:c.1053A>G	p.Glu351=	0.214286	11,3	14	93	
B3: 147		VQSRTrancheSN P99.00to		0.00	8														
345				1207	2														
192	G/A	99.90	1	73	8	1	0	1	<i>LBHD2</i>	3_prime_UTR_variant	Othe	XM_019833830.1	XM_019833830.1:c.*106G>A		0.473684	10,9	19	99	
C1: 191				0.00	8														
673				1207	2														
54	C/T	PASS	1	73	8	1	0	1	<i>LDLRA1</i>	synonymous_variant	Othe	XM_006934412.4	XM_006934412.4:c.738C>T	p.Ser246=	0.521739	11,12	23	99	
E2: 359		VQSRTrancheSN P99.00to		0.00	8														
050				1207	2														
05	T/G	99.90	1	73	8	1	0	1	<i>LOC101081428</i>	3_prime_UTR_variant	Othe	XM_003998055.5	XM_003998055.5:c.*70T>G		0.473684	10,9	19	99	
A2: 692		VQSRTrancheSN P99.00to		0.00	8														
512				1207	2														
9	C/T	99.90	1	73	8	1	0	1	<i>LOC101083065</i>	synonymous_variant	Othe	XM_003981831.5	XM_003981831.5:c.738C>T	p.Ser246=	0.56	11,14	25	99	
D1: 871				0.00	8														
758				1207	2														
21	T/C	PASS	1	73	8	1	0	1	<i>LOC101086002</i>	synonymous_variant	Othe	XM_019812218.2	XM_019812218.2:c.4314A>G	p.Val1438=	0.454545	12,10	22	99	
D1: 872				0.00	8														
172				1207	2														
59	C/T	PASS	1	73	8	1	0	1	<i>LOC101086002</i>	synonymous_variant	Othe	XM_019812218.2	XM_019812218.2:c.2841G>A	p.Leu947=	0.481481	14,13	27	99	
D1: 102				0.00	8														
155				1207	2														
345	C/T	PASS	1	73	8	1	0	1	<i>LOC101087098</i>	synonymous_variant	Othe	XM_003993290.2	XM_003993290.2:c.537C>T	p.Leu179=	0.55	9,11	20	99	
A3: 970		VQSRTrancheSN P99.00to		0.00	8														
709				1207	2														
28	T/G	99.90	1	73	8	1	0	1	<i>LOC102899911</i>	non_coding_exon_variant	Othe	XR_439962.4	XR_439962.4:n.383A>C		0.611111	7,11	18	99	
A3: 970		VQSRTrancheSN P99.00to		0.00	8														
715				1207	2														
95	A/T	99.90	1	73	8	1	0	1	<i>LOC102899911</i>	non_coding_exon_variant	Othe	XR_439962.4	XR_439962.4:n.305T>A		0.375	15,9	24	99	
F1: 261		VQSRTrancheSN P99.90to		0.00	8														
079				1207	2														
56	A/G	100.00	1	73	8	1	0	1	<i>LOC102900733</i>	non_coding_exon_variant	Othe	XR_002739136.1	XR_002739136.1:n.1367T>C		0.4375	9,7	16	96	

B1: 124 409 361 B1: 124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	C/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 290224 1	3_prime_UT R_variant	Othe r	XM_0069 30945.4	XM_006930945.4:c.*1595C>T	0.4	15,10	25	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 290224 1	3_prime_UT R_variant	Othe r	XM_0069 30945.4	XM_006930945.4:c.*2514G>T	0.44444 4	10,8	18	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 525965 5	synonymous _variant	Othe r	XM_0232 45891.1	XM_023245891.1:c.268C>T	p.Leu90 =	0.25714 3	78,27	105	99
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	C/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 525972 2	3_prime_UT R_variant	Othe r	XM_0232 41195.1	XM_023241195.1:c.*158C>T	0.23529 4	91,28	119	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 526134 7	non_coding_ exon_variant	Othe r	XR_00273 9338.1	XR_002739338.1:n.1894C>G	0.65517 2	10,19	29	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	T/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949242 8	non_coding_ exon_variant	Othe r	XR_00214 6284.2	XR_002146284.2:n.1929_1964del	0.57142 9	12,16	28	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	T/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949293 1	non_coding_ exon_variant	Othe r	XR_00273 6633.1	XR_002736633.1:n.480A>G	0.57894 7	8,11	19	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	A/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949488 6,LOC1 115581 41	synonymous _variant	Othe r	XM_0232 46150.1,X R_002738 727.1	XM_023246150.1:c.25A>C, XR_002738727.1:n.31T>G	p.Arg9= ,	0.56	11,14	25	99
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	A/G	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949863 5	non_coding_ exon_variant	Othe r	XR_00215 5471.2	XR_002155471.2:n.961T>C	0.56521 7	10,13	23	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949927 6	non_coding_ exon_variant	Othe r	XR_00274 1540.1	XR_002741540.1:n.148C>T	0.45454 5	12,10	22	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	T/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949934 1	non_coding_ exon_variant	Othe r	XR_00274 1469.1	XR_002741469.1:n.256T>A	0.52631 6	9,10	19	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 949968 8	non_coding_ exon_variant	Othe r	XR_00274 2293.1	XR_002742293.1:n.847G>A	0.73913	6,17	23	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	CTTC/-	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 950101 4	non_coding_ exon_variant	Othe r	XR_00274 3257.1	XR_002743257.1:n.883_886delTCCT	0.66666 7	6,12	18	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 950116 2	non_coding_ exon_variant	Othe r	XR_00215 9119.2	XR_002159119.2:n.181C>T	0.57142 9	9,12	21	99	
124 410 280 E2: 569 822 5 A2: 117 037 24 A2: 159 585 30 D2: 177 438 66 D2: 136 842 0	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	1	LOC10 950280 0	non_coding_ exon_variant	Othe r	XR_00216 1645.2	XR_002161645.2:n.3C>T	0.60869 6	9,14	23	99	

D2: 696 784 20	C/T	VQSRTr ancheSN P99.90to 100.00 VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>MXII</i>	5_prime_UT R_variant	Othe r	XM_0039 94402.5	XM_003994402.5:c.263-1490C>T	0.29411 8	12,5	17	99	
X:2 001 064 A1: 513 582 48 A1: 513 844 78 A1: 514 901 60 A1: 515 251 60 B4: 132 656 315 D2: 130 335 76 D2: 130 389 91 A2: 778 888 89 E1: 450 227 41 B3: 767 759 51 B3: 767 764 64 E2: 360 463 41 B3: 425 292 52	G/A	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>MXRA5</i>	synonymous _variant	Othe r	XM_0040 00245.5	XM_004000245.5:c.4284C>T	p.Ser14 28=	0.57142 9	9,12	21	99
	A/G	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>MYCBP 2</i>	synonymous _variant	Othe r	XM_0112 80436.3	XM_011280436.3:c.8004T>C	p.Leu26 68=	0.475	21,19	40	99
	G/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>MYCBP 2</i>	synonymous _variant	Othe r	XM_0112 80436.3	XM_011280436.3:c.7105C>A	p.Arg23 69=	0.5	17,17	34	99
	C/T	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>MYCBP 2</i>	synonymous _variant	Othe r	XM_0112 80436.3	XM_011280436.3:c.2544G>A	p.Gly84 8=	0.46153 8	14,12	26	99
	C/T	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>MYCBP 2</i>	synonymous _variant	Othe r	XM_0112 80436.3	XM_011280436.3:c.642G>A	p.Thr21 4=	0.72727 3	6,16	22	99
	G/A	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>MYH9</i>	synonymous _variant	Othe r	XM_0232 57448.1	XM_023257448.1:c.4875C>T	p.His16 25=	0.61111 1	7,11	18	99
	C/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>NID1</i>	synonymous _variant	Othe r	XM_0039 93899.5	XM_003993899.5:c.843C>T	p.Leu28 1=	0.56521 7	10,13	23	99
	C/T	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>NID1</i>	synonymous _variant	Othe r	XM_0039 93899.5	XM_003993899.5:c.1305C>T	p.Asn43 5=	0.5	14,14	28	99
	G/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>NME8</i>	3_prime_UT R_variant	Othe r	XM_0198 25295.2	XM_019825295.2:c.*690C>G	0.55555 6	8,10	18	99	
	-/TA	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>NMT1</i>	3_prime_UT R_variant	Othe r	XM_0039 96998.5	XM_003996998.5:c.*340_*341dupAT	0.46666 7	8,7	15	99	
	A/G	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>NOP9</i>	5_prime_UT R_variant	Othe r	XM_0039 87519.4	XM_003987519.4:c.-71A>G	0.59090 9	9,13	22	99	
	G/C	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>NOP9</i>	splice_regio n_variant	Othe r	XM_0039 87519.4	XM_003987519.4:c.236-6G>C	0.4	15,10	25	99	
	A/G	VQSRTr ancheSN P99.00to 99.90	1	0.00 1207 73	8 2 8	1	0	1	<i>NUP93</i>	synonymous _variant	Othe r	XM_0069 41526.4	XM_006941526.4:c.1728A>G	p.Glu57 6=	0.4	18,12	30	99
	G/A	PASS	1	0.00 1207 73	8 2 8	1	0	1	<i>OAZ2</i>	3_prime_UT R_variant	Othe r	NM_0012 90005.1	NM_001290005.1:c.*54G>A	0.5	10,10	20	99	

A3: 128				0.00	8															
812				1207	2															
051	AA/-	PASS	1	73	8	1	0	1	<i>RDH14</i>	3_prime_UT R_variant	Othe r	XM_0039 84483.4	XM_003984483.4:c.*185_*186delAA	0.57894 7	8,11		19		99	
A3: 103		VQSRTr ancheSN		0.00	8															
292		P99.00to		1207	2															
529	A/C	99.90	1	73	8	1	0	1	<i>REEP1</i>	3_prime_UT R_variant	Othe r	XM_0232 51848.1	XM_023251848.1:c.*162T>G	0.33333 3	18,9		27		99	
D4: 757		VQSRTr ancheSN		0.00	8															
003		P99.00to		1207	2															
56	G/A	99.90	1	73	8	1	0	1	<i>RGS3</i>	3_prime_UT R_variant	Othe r	XM_0198 16366.2	XM_019816366.2:c.*622G>A	0.60869 6	9,14		23		99	
A1: 120				0.00	8															
047				1207	2															
366	C/T	PASS	1	73	8	1	0	1	<i>RNF14</i>	5_prime_UT R_variant	Othe r	XM_0039 80869.5	XM_003980869.5:c.-11C>T	0.41379 3	17,12		29		99	
A1: 120		VQSRTr ancheSN		0.00	8															
059		P99.00to		1207	2															
545	G/A	99.90	1	73	8	1	0	1	<i>RNF14</i>	3_prime_UT R_variant	Othe r	XM_0039 80869.5	XM_003980869.5:c.*176G>A	0.44444 4	10,8		18		99	
A1: 120				0.00	8															
059				1207	2															
695	AGTTAA/-	PASS	1	73	8	1	0	1	<i>RNF14</i>	3_prime_UT R_variant	Othe r	XM_0039 80869.5	XM_003980869.5:c.*331_*336delAAGT TA	0.59375	13,19		32		99	
B3: 478		VQSRTr ancheSN		0.00	8															
280		P99.00to		1207	2															
31	C/G	99.90	1	73	8	1	0	1	<i>RNF11 1</i>	synonymous _variant	Othe r	XM_0039 87100.5	XM_003987100.5:c.48G>C	p.Val16 =	0.5	10,10		20		99
742				0.00	8															
823				1207	2															
50	C/T	PASS	1	73	8	1	0	1	<i>RPGRI P1</i>	synonymous _variant	Othe r	XM_0198 32776.2	XM_019832776.2:c.1626C> T	p.Tyr54 2=	0.38888 9	11,7		18		99
B3: 713		VQSRTr ancheSN		0.00	8															
392		P99.00to		1207	2															
26	A/G	99.90	1	73	8	1	0	1	<i>RYR3</i>	synonymous _variant	Othe r	XR_00274 2989.1	XR_002742989.1:n.6879A>G		0.45	11,9		20		99
B3: 334		VQSRTr ancheSN		0.00	8															
363		P99.90to		1207	2															
59	C/T	100.00	1	73	8	1	0	1	<i>SCAMP 2</i>	synonymous _variant	Othe r	XM_0198 32043.2	XM_019832043.2:c.381C> T	p.Ser12 7=	0.2	24,6		30		92
D1: 101				0.00	8															
390				1207	2															
191	G/A	PASS	1	73	8	1	0	1	<i>SLC39A 13</i>	3_prime_UT R_variant	Othe r	XM_0232 39820.1	XM_023239820.1:c.*9G>A	0.33333 3	14,7		21		99	
E1: 661		VQSRTr ancheSN		0.00	8															
491	C/T	P99.00to	1	73	8	1	0	1	<i>SMTNL 2</i>	5_prime_UT R_variant	Othe r	XM_0232 43730.1	XM_023243730.1:c.-26C>T	0.33333 3	8,4		12		99	
E1: 669		VQSRTr ancheSN		0.00	8															
606	C/T	P99.00to	1	73	8	1	0	1	<i>SMTNL 2</i>	synonymous _variant	Othe r	XM_0232 43730.1	XM_023243730.1:c.756C> T	p.Ser25 2=	0.69230 8	4,9		13		83
E1: 669		VQSRTr ancheSN		0.00	8															
654	C/T	P99.00to	1	73	8	1	0	1	<i>SMTNL 2</i>	synonymous _variant	Othe r	XM_0232 43730.1	XM_023243730.1:c.804C> T	p.Ser26 8=	0.58333 3	5,7		12		99
C2: 117				0.00	8															
995				1207	2															
51	C/A	PASS	1	73	8	1	0	1	<i>SON</i>	3_prime_UT R_variant	Othe r	XM_0232 38789.1	XM_023238789.1:c.6933+431G>T	0.47619	11,10		21		99	

Table S3. Numbers of variants identified by whole genome sequencing in the feline case.

Filter / Variant type	Case genotype	
	Homozygous*	Heterozygous
Pass	101	169
3' UTR	34	36
5' UTR	5	11
Frameshift	2	6
In-frame deletion	1	2
In-frame insertion	0	1
Missense	18	60
Non-coding exon	9	7
Splice donor	0	0
Splice acceptor	2	0
Splice region	3	3
Synonymous	22	43
PASS,VQSRTrancheSNP99.00to99.90	5	0
VQSRTrancheINDEL99.00to99.90	3	3
VQSRTrancheINDEL99.90to100.00	2	11
VQSRTrancheSNP99.00to99.90	61	85
VQSRTrancheSNP99.90to100.00	5	18
Total variants	172	286

*One additional cat in the dataset could also be carriers for any variant.

Table S4. A list of candidate genes evaluated in this study.

Ehlers-Danlos syndromes in humans		Congenital scoliosis in humans		Hereditary connective tissue disorders overlapping phenotype genes in addition to genes associated with Ehlers-Danlos syndromes in humans		Kinked tail in cats	
<i>COL5A1</i>	XM_023242950.1	<i>DLL3</i>	XM_003997806.5	<i>ADAMTS2</i>	XM_023254116.1	<i>HES7</i>	XM_003996191.5
<i>COL5A2</i>	XM_003990962.4	<i>MESP2</i>	XM_019833746.2	<i>B3GALT6</i>	XM_011279777.2	<i>T</i>	XM_003986708.3
<i>COL1A1</i>	XM_003996699.4	<i>LFNG</i>	XM_023246563.1	<i>CHST14</i>	XM_003987275.4		
<i>COL3A1</i>	XM_003990961.3	<i>HES7</i>	XM_003996191.4	<i>COL1A1</i>	XM_003996699.4		
<i>COL1A2</i>	XM_003982764.5	<i>NOTCH2</i>	XM_011285094.3	<i>COL1A2</i>	XM_003982764.5		
<i>ADAMTS2</i>	XM_023254116.1	<i>NOTCH3</i>	XM_023246608.1	<i>COL3A1</i>	XM_003990961.3		
<i>PLOD1</i>	XM_003989499.3	<i>SLC35A3</i>	XM_003990360.4	<i>COL5A1</i>	XM_023242950.1		
<i>FKBP14</i>	XM_003982902.4	<i>T (TBXT)</i>	XM_003986708.3	<i>COL5A2</i>	XM_003990962.4		
<i>TNXB</i>	XM_023254711.1	<i>TBX6</i>	XM_011290514.3	<i>DSE</i>	XM_019831105.2		
<i>COL12A1</i>	XM_019830870.1	<i>FBN1</i>	XM_023255387.1	<i>FKBP14</i>	XM_003982902.4		
<i>CHST14</i>	XM_003987275.4	<i>SHH</i>	XM_023242357.1	<i>PLOD1</i>	XM_003989499.3		
<i>DSE</i>	XM_019831105.2	<i>SOX9</i>	XM_023243815.1	<i>TNXB</i>	XM_023254711.1		
<i>B4GALT7</i>	XM_023254211.1	<i>FLNB</i>	XM_019823423.2	<i>COL12A1</i>	XM_019830870.1		
<i>B3GALT6</i>	XM_011279777.2	<i>PTK7</i>	XM_003986191.4	<i>C1R</i>	XM_019834454.2		
<i>SLC39A13 (ZIP13)</i>	XM_023239820.1	<i>HSPG2</i>	XM_023258277.1	<i>C1S</i>	XM_006933467.4		
<i>ZNF469</i>	XM_023245050.1	<i>KIAA1217</i>	XM_023256446.1	<i>SLC39A13</i>	XM_023239820.1		
<i>PRDM5</i>	XM_023252840.1	<i>DCC</i>	XM_019815281.2	<i>ZNF469</i>	XM_023245050.1		
<i>C1R</i>	XM_019834454.2	<i>DVL3</i>	XM_023260347.1	<i>PRDM5</i>	XM_023252840.1		
<i>C1S</i>	XM_006933467.4	<i>FGFR3</i>	XM_023253489.1	<i>LZTS1</i>	XM_003984723.4		
<i>AEBP1 (ACLP)</i>	XM_023250110.1	<i>RECQL4</i>	XM_019823278.2	<i>FLNA</i>	XM_023249411.1		
		<i>ROBO3</i>	XM_019811488.2	<i>COL4A1</i>	XM_023253172.1		
		<i>WNT7A</i>	XM_011280231.3	<i>COL6A1</i>	XM_011285711.3		
		<i>CHRNA3</i>	XM_003991260.4	<i>COL6A2</i>	XM_023238595.1		
		<i>FGFR1</i>	XM_011281522.3	<i>COL6A6</i>	XM_011286221.3		
				<i>ELN</i>	XM_019820582.2		
				<i>FBLN5</i>	XM_019833518.1		
				<i>FBN1</i>	XM_023255387.1		
				<i>LOX</i>	XM_023254614.1		
				<i>MYH11</i>	XM_023246707.1		
				<i>RYR1</i>	XM_023245508.1		
				<i>SELENON (SEPN1)</i>	XM_023258321.1		
				<i>SGCB</i>	XM_023253126.1		
				<i>myosin-7 (MYH7)</i>	XM_006932746.4		
				<i>TTN</i>	XM_023259509.1		
				<i>SMAD2</i>	XM_023241966.1		
				<i>SMAD3</i>	XM_023255153.1		

<i>COL2A1</i>	XM_023256993.1
<i>COL11A1</i>	XM_023258940.1
<i>COL11A2</i>	XM_003985999.5
<i>COL9A1</i>	XM_003986294.4
<i>COL9A2</i>	XM_023258522.1
<i>COL9A3</i>	XM_023251026.1
<i>MED12</i>	XM_004000604.5
<i>FLNB</i>	XM_019823423.2
<i>LOC105261197 (CANT1)</i>	XM_019818343.2
<i>SLC2A10</i>	XM_006929697.2
<i>ABCC6</i>	XM_011290585.3
<i>GGCX</i>	XM_011281186.3
<i>ENPP1</i>	XM_023254376.1
<i>AEBP1</i>	XM_023250110.1
<i>SKI</i>	XM_023257965.1
<i>TGFB2</i>	XM_003999507.5
<i>TGFB3</i>	XM_003987851.3
<i>TGFBR1</i>	XM_023242499.1
<i>TGFBR2</i>	XM_023260647.1

Table S5. Primer sequences used for amplifying cDNA of the feline *COL6A1* gene.

Primer Name	Primer sequence (5'-3')	Product size (bp)	Annealing temperature (°C)
COL6A1-1F	CCTTCGAGAGCAGAGACAGC	580	58
COL6A1-1R	GGGTGCCCATCAGTCACTAC		
COL6A1-2F	CCCTGGTGGACAAGGTCAAG	657	58
COL6A1-2R	GACCTGGCTTCCCACGTTC		
COL6A1-3F	GCCAGACCATTGACACCATC	688	60
COL6A1-3R	CCTTCTCGTCCCTGGTCAC		
COL6A1-4F	GCCCTGGGGAAAGAGGAC	741	60
COL6A1-4R	GCTCCTGCATCTGGTTGTG		
COL6A1-5F	CATCGACAGGCTGAGCAGAG	682	60
COL6A1-5R	GTGGGAGGGGTTCGTCTTG		
COL6A1-6F	ATCAAGGACATGTTTGGCTTC	905	58
COL6A1-6R	TAGAAACATCCAGCTCATCAGG		
COL6A1-6F-internal*	CTGCAGAACTACACCGTGCTG		
COL6A1-6R-internal*	AGAGCAGCAGCCTCTTCTTG		

*These were used as internal sequencing primers.