Table S1. The numbers of variants identified in 414 cats of the 99 Lives Cat Genome Sequencing Consortium dataset, including 362 cats' whole genome sequencing and 52 cats' whole exome sequencing data, and unique variants identified in this case

Variant	414 cats' variants*	Case – unique variants[†] Hemi-/homozygous	Heterozygous
3' UTR	779,313	9	158
5' UTR premature start codon gain	14,709	0	1
5' UTR	253,248	8	47
Disruptive inframe deletion	3,232	0	0
Disruptive inframe insertion	7,348	0	0
Downstream gene	11,812	0	0
Frameshift	122,878	3	22
Inframe deletion	12,416	2	5
Inframe insertion	17,437	0	2
Initiator codon	1,320	0	0
Intergenic	24	0	0
Intron	312,834	0	0
Missense	404,240	15	244
Non-coding exon	363,539	5	38
Splice acceptor	6,348	0	3
Splice donor	5,763	0	5
Splice region	99,728	2	59
Stop gained	12,325	1	4
Stop lost	1,019	0	0
Stop retained	444	0	0
Synonymous	692,633	16	236
Upstream gene variant	11,315	0	0
Total variants	**3,133,925**	**61**	**824**

*Variants with lower tranche scores were included. [†]Exon with flanking 10 bp and passing tranche scores.