Supplementary Material

Defects in the mitochondrial genome of dogs with recurrent tumours

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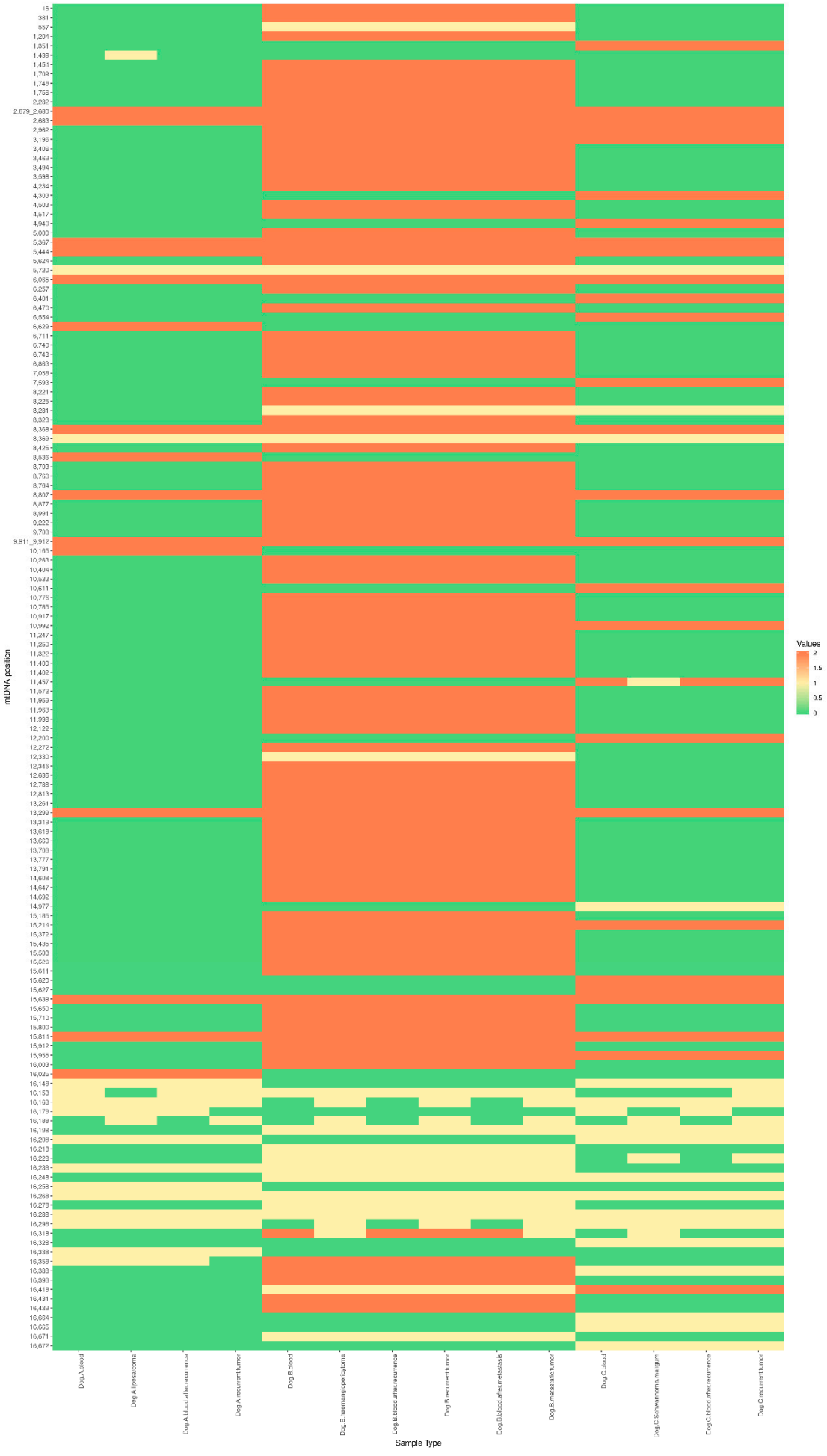
Supplementary table S1. List of all changes detected in analysed sequences obtained from dogs with recurrent tumours generated using Unipro uGene.

DOG		A				B						C				N. of variants observed in each position
POSITION	SEQ. REF.	B25K	B25G	B40K	B40G	B47K	B47G	B111K	B111G	B180K	B180G	B162K	B162G	B169K	B169G	
16	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
381	T	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
557	A	.	.	.	.	R	R	R	R	R	R	.	.	.	.	**6**
1204	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
1351	A	.	.	.	.	.	.	.	.	.	.	G	G	G	G	**4**
1439	A	.	R	.	.	.	.	.	.	.	.	.	.	.	.	**1**
1454	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
1709	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
1748	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
1756	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
2232	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
2679_2680	-	G	G	G	G	G	G	G	G	G	G	G	G	G	G	**14**
2683	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	**14**
2962	C	.	.	.	.	T	T	T	T	T	T	T	T	T	T	**10**
3196	T	.	.	.	.	C	C	C	C	C	C	C	C	C	C	**10**
3406	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
3469	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
3494	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
3598	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
4234	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
4303	A	.	.	.	.	.	.	.	.	.	.	G	G	G	G	**4**
4503	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
4517	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
4940	T	.	.	.	.	.	.	.	.	.	.	C	C	C	C	**4**
5009	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
5367	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	**14**
5444	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	**14**
5624	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
5720	G	R	R	R	R	R	R	R	R	R	R	R	R	R	R	**14**
6065	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	**14**
6257	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
6401	C	.	.	.	.	.	.	.	.	.	.	T	T	T	T	**4**
6470	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
6554	T	.	.	.	.	.	.	.	.	.	.	C	C	C	C	**4**
6629	T	C	C	C	C	.	.	.	.	.	.	.	.	.	.	**4**
6711	T	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
6740	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
6743	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
6863	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
7058	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
7593	T	.	.	.	.	.	.	.	.	.	.	C	C	C	C	**4**
8221	A	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
8225	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
8281	T	.	.	.	.	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	**10**
8323	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
8368	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	**14**
8369	C	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	**14**
8425	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
8536	C	T	T	T	T	.	.	.	.	.	.	.	.	.	.	**4**
8703	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
8760	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
8764	G	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
8807	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	**14**

cont.																
8877	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
8991	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
9222	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
9708	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
9911_9912	-	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	**14**
10165	C	T	T	T	T	.	.	.	.	.	.	.	.	.	.	**4**
10263	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
10404	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
10533	A	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
10611	A	.	.	.	.	.	.	.	.	.	.	T	T	T	T	**4**
10776	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
10785	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
10917	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
10992	G	.	.	.	.	A	A	A	A	A	A	A	A	A	A	**10**
11247	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
11250	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
11322	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
11400	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
11402	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
11457	T	.	.	.	.	.	.	.	.	.	.	C	Y	C	C	**4**
11572	A	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
11959	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
11963	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
11998	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
12122	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
12200	C	.	.	.	.	.	.	.	.	.	.	T	T	T	T	**4**
12272	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
12330	A	.	.	.	.	R	R	R	R	R	R	.	.	.	.	**6**
12346	T	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
12636	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
12788	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
12813	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
13261	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
13299	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	**14**
13319	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
13618	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
13660	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
13708	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
13777	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
13791	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
14608	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
14647	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
14692	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
14977	T	.	.	.	.	.	.	.	.	.	.	Y	Y	Y	Y	**4**
15185	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
15214	G	.	.	.	.	A	A	A	A	A	A	A	A	A	A	**10**
15372	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
15435	G	.	.	.	.	A	A	A	A	A	A	.	.	.	.	**6**
15508	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
15526	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
15611	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
15620	T	.	.	.	.	.	.	.	.	.	.	C	C	C	C	**4**
15627	A	.	.	.	.	.	.	.	.	.	.	G	G	G	G	**4**
15639	T	A	A	A	A	G	G	G	G	G	G	A	A	A	A	**14**
15650	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
15710	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
15800	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
15814	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	**14**
15912	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**

cont.																
15955	C	.	.	.	.	T	T	T	T	T	T	T	T	T	T	**10**
16003	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
16025	T	C	C	C	C	.	.	.	.	.	.	.	.	.	.	**4**
16148	A	R	R	R	R	.	.	.	.	.	.	R	R	R	R	**8**
16158	A	R	.	R	R	R	R	R	R	R	R	.	.	.	R	**10**
16168	A	R	R	R	R	.	R	.	R	.	R	R	R	R	R	**11**
16178	A	R	R	R	.	.	.	.	.	.	.	R	.	R	.	**5**
16188	G	.	R	.	R	.	R	.	R	.	R	.	R	.	R	**7**
16198	G	.	.	.	.	R	R	R	R	R	R	R	R	R	R	**10**
16208	A	R	R	R	R	.	.	.	.	.	.	R	R	R	R	**8**
16218	G	.	.	.	.	R	R	R	R	R	R	.	.	.	.	**6**
16228	G	.	.	.	.	R	R	R	R	R	R	.	R	.	R	**8**
16238	G	R	R	R	R	R	R	R	R	R	R	.	.	.	.	**10**
16248	A	.	.	.	.	R	R	R	R	R	R	R	R	R	R	**10**
16258	G	R	R	R	R	.	.	.	.	.	.	.	.	.	.	**4**
16268	A	R	R	R	R	R	R	R	R	R	R	R	R	R	R	**14**
16278	G	.	.	.	.	R	R	R	R	R	R	.	.	.	.	**6**
16288	A	R	R	R	R	R	R	R	R	R	R	R	R	R	R	**14**
16298	A	R	R	R	R	.	R	.	R	.	R	R	R	R	R	**11**
16318	A	.	.	.	.	G	R	G	G	G	R	.	R	.	.	**7**
16328	G	.	.	.	.	.	.	.	.	.	.	R	R	R	R	**4**
16338	G	R	R	R	R	.	.	.	.	.	.	.	.	.	.	**4**
16358	A	R	R	R	.	G	G	G	G	G	G	.	.	.	.	**9**
16388	A	.	.	.	.	G	G	G	G	G	G	R	R	R	R	**10**
16398	A	.	.	.	.	G	G	G	G	G	G	.	.	.	.	**6**
16418	A	.	.	.	.	R	R	R	R	R	R	G	G	G	G	**10**
16431	C	.	.	.	.	T	T	T	T	T	T	.	.	.	.	**6**
16439	T	.	.	.	.	C	C	C	C	C	C	.	.	.	.	**6**
16664	T	.	.	.	.	.	.	.	.	.	.	Y	Y	Y	Y	**4**
16665	T	.	.	.	.	.	.	.	.	.	.	Y	Y	Y	Y	**4**
16671	T	.	.	.	.	Y	Y	Y	Y	Y	Y	.	.	.	.	**6**
16672	C	.	.	.	.	.	.	.	.	.	.	Y	Y	Y	Y	**4**
N. of changes observed in each sample		**90**	**91**	**90**	**89**	**176**	**179**	**176**	**179**	**176**	**179**	**107**	**109**	**107**	**109**	

Supplementary figure S1. Heatmap of mtDNA variations in the whole mitogenome across different analysed tissues. 0—no changes observed, 1—heteroplasmy transformation from the wild to mutant type, 2—mutation.



Supplementary table S2. Protein profiles based on data from Prot Param.

Protein	Dogs	Amino acid change	Number of amino acids	Weight	Theoretical pI (Isoelectric point)	Instability index above >40 - unstable	Aliphatic index	Grand average of hydropathicity (GRAVY)
ND1	**A, C**	**No changes**	318	35892,30	7,77	**46,15**	126,45	0,859
	B	p.Phe250Leu	318	35858,28	7,77	**45,55**	127,67	0,862
ND2	**A, C**	**No changes**	347	39101,88	9,86	29,67	120,61	0,762
	B	p.Asn197Ser p.Val202Ile	347	39088,89	9,86	31,58	120,89	0,77
COX1	**A, C**	**No changes**	514	57039,28	6,10	27,96	101,89	0,687
	B	p.Ser455Thr	514	57053,31	6,10	27,59	101,89	0,678
COX2	**A, B**	**No changes**	227	26061,55	4,62	36,64	109,91	0,296
	C	p.Met187Thr	227	26031,46	4,62	36,97	109,91	0,285
ATP8	**A, B, C**	**No changes**	67	7978,38	9,16	36,04	84,48	-0,1
ATP6	**—**	**No changes**	226	24789,02	10,11	32,34	140,75	0,977
	A, B, C	p.Pro136=/Ser †	226	24778,98	10,11	31,49	140,75	0,981
COX3	**—**	**No changes**	261	29874,66	6,44	19,67	93,37	0,459
	B	p.Ala41Ser p.Cys55Tyr	261	29950,7	6,44	22,08	92,99	0,434
	A, C	p.Cys55Tyr	261	29934,7	6,44	20,87	93,37	0,444
ND3	**A, B, C**	**No changes**	115	13009,62	4,44	30,24	127,3	0,798
ND4L	**—**	**No changes**	98	10862,32	5,27	**43,22**	140,2	1,302
	A, B, C	p.Met1Val	98	10830,26	5,27	38,74	143,16	1,326
ND4	**A, C**	**No changes**	459	52095,21	9,58	37,22	131,37	0,801
	B	p.Ile401Thr p.Ile458Leu	459	52083,15	9,58	37,22	130,52	0,788
ND5	**—**	**No changes**	606	68361,4	9,28	31,51	109,95	0,591
	A, C	p.Ser508Thr	606	68375,43	9,28	31,07	109,95	0,591
	B	p.Thr61Met p.Met74Thr p.Thr185=/Ala † p.Leu190Gln p.Phe287Leu p.Val346Ile p.Thr495Ile p.Ser508Thr	606	68352,44	9,28	31,64	110,92	0,594
ND6	**A, C**	**No changes**	175	18825,27	4,11	21,49	122,97	1,054
	B	p.Ile106Val	175	18811,24	4,11	20,39	122,4	1,052
CYTB	**A, B, C**	**No changes**	379	42593,51	6,85	38,39	120,95	0,715

† Heteroplasmy, no changes means that the samples were identical to the reference sequence or identified variants did not change the amino acid sequence.

Supplementary table S3. Protein profiles based on data from SOPMA.

Protein	Dogs	Amino acid change	Alpha helix	Extended strand	Beta turn	Random coil
ND1	**A,C**	**No changes**	**56,29%**	**14,47%**	**3,46%**	**25,79%**
	B	p.Phe250Leu	56,29%	12,26%	1,57%	29,87%
ND2	**A,C**	**No changes**	**53,60%**	**15,27%**	**3,46%**	**27,67%**
	B	p.Asn197Ser p.Val202Ile	53,31%	15,56%	3,75%	27,38%
COX1	**A,C**	**No changes**	**51,95%**	**14,98%**	**6,03%**	**27,04%**
	B	p.Ser455Thr	49,22%	15,56%	6,81%	28,40%
COX2	**A,B**	**No changes**	**31,72%**	**24,23%**	**3,08%**	**40,97%**
	C	p.Met187Thr	29,07%	23,35%	3,96%	43,61%
ATP8	**A,B,C**	**No changes**	**19,40%**	**11,94%**		**68,66%**
ATP6	**—**	**No changes**	**65,04%**	**6,19%**	**1,33%**	**27,43%**
	A,B,C	p.Pro136=/Ser †	66,37%	6,64%	0,44%	26,55%
COX3	**—**	**No changes**	**53,26%**	**14,18%**	**4,60%**	**27,97%**
	B	p.Ala41Ser p.Cys55Tyr	50,57%	13,79%	5,36%	30,27%
	A, C	p.Cys55Tyr	53,64%	14,18%	4,98%	27,20%
ND3	**A, B**	**No changes**	**60,87%**	**3,48%**	**2,61%**	**33,04%**
	C	p.Glu115Lys	66,09%	2,61%	0,87%	30,43%
ND4L	**—**	**No changes**	**83,67%**	**6,12%**	**2,04%**	**8,16%**
	A,B,C	p.Met1Val	72,45%	8,16%	2,04%	17,35%
ND4	**A,C**	**No changes**	**50,98%**	**15,90%**	**3,49%**	**29,63%**
	B	p.Ile401Thr p.Ile458Leu	50,11%	16,34%	4,14%	29,41%
ND5	**—**	**No changes**	**55,61%**	**12,87%**	**2,31%**	**29,21%**
	A,C	p.Ser508Thr	56,27%	13,20%	2,31%	28,22%
	B	p.Thr61Met p.Met74Thr p.Thr185=/Ala † p.Leu190Gln p.Phe287Leu p.Val346Ile p.Thr495Ile p.Ser508Thr	58,25%	11,55%	1,65%	28,55%
ND6	**A,C**	**No changes**	**40,00%**	**29,14%**	**7,43%**	**23,43%**
	B	p.Ile106Val	41,71%	29,71%	6,86%	21,71%
CYTB	**A,B,C**	**No changes**	53,03%	9,23%	3,17%	34,56%

† Heteroplasmy, no changes means that the samples were identical to the reference sequence or identified variants did not change the amino acid sequence.

Supplementary table S4. Differences in variants in the VNTR region of the tested dogs.

DOG	A				B						C			
SEQ. REF.	B25	B25	B40	B40	B47	B47	B111	B111	B180	B180	B162	B162	B169	B169
VARIANT	K	G	K	G	K	G	K	G	K	G	K	G	K	G
m.16138A	Identical with the reference sequence in all analysed samples													
m.16148A*	m.16148A/G				Identical with the ref. seq.						m.16148A/G			
m.16158A*	R	A	R	R	m.16158A/G						A	A	A	R
m.16168A*	m.16168A/G				A	R	A	R	A	R	m.16168A/G			
m.16178A*	R	R	R	A	m.16178A/G						R	A	R	A
m.16188G*	G	R	G	R	G	R	G	R	G	R	G	R	G	R
m.16198G*	Identical with the ref. seq.				m.16198G/A									
m.16208A*	m.16208A/G				Identical with the ref. seq.						m.16208A/G			
m.16218G*	Identical with the ref. seq.				m.16218G/A						Identical with the ref. seq.			
m.16228G*	Identical with the ref. seq.				m.16228G/A						G	R	G	R
m.16238G*	m.16238G/A										Identical with the ref. seq.			
m.16248A*	Identical with the ref. seq.				m.16248A/G									
m.16258G*	m.16258G/A				Identical with the ref. seq.									
m.16268A*	Heteroplasmy m.16268A/G in all analysed samples													
m.16278G*	Identical with the ref. seq.				m.16278G/A						Identical with the ref. seq.			
m.16288A*	Heteroplasmy m.16288A/G in all analysed samples													
m.16298A*	m.16298A/G				A	R	A	R	A	R	m.16298A/G			
m.16308G	Identical with the reference sequence in all analysed samples													
m.16318A*	Identical with the ref. seq.				G	R	G	G	G	R	A	R	A	A
m.16328G*	Identical with the ref. seq.										m.16328G/A			
m.16338G*	m.16338G/A				Identical with the ref. seq.									
m.16348G	Identical with the reference sequence in all analysed samples													
m.16358A*	R	R	R	A	m.16358A>G						Identical with the ref. seq.			
m.16368G	Identical with the reference sequence in all analysed samples													
m.16378G	Identical with the reference sequence in all analysed samples													
m.16388A*	Identical with the ref. seq.				m.16388A>G						m.16388A/G			
m.16398A	Identical with the ref. seq.				m.16389A>G						Identical with the ref. seq.			
m.16408G	Identical with the reference sequence in all analysed samples													
m.16418A*	Identical with the ref. seq.				m.16418A/G						m.16418A>G			
m.16428A	Identical with the reference sequence in all analysed samples													

R – heteroplasmy A/G, * - positions with heteroplasmic variants not previously described in the European Variation Archive (EVA) database

Supplementary table S5. Detailed information about the length and quality of PCR generated in Oxford Nanopore Technologies.

Dog	Sample	Mean read length	Mean read quality	Median read length	Median read quality	Number of reads	Read length N50	Total bases
A	**B25G**	9 764,5	11,9	9 862,0	12,1	2 391	9 867	23 346 953
	B25K	9 613,8	11,8	9 753,0	12,0	4 238	9 777	40 743 271
	B40G	9 655,0	11,9	9 830,0	12,0	5 464	9 837	52 754 837
	B40K	9 631,9	11,9	9 733,0	12,0	6 107	9 751	58 821 941
B	**B47K**	9 677,7	11,9	9 808,0	12,0	5 074	9 821	49 104 728
	B47G	9 599,5	11,9	9 640,0	12,1	7 796	9 643	74 837 685
	B111K	9 611,1	11,9	9 632,0	12,0	13 236	9 634	127 213 156
	B111G	9 592,2	11,8	9 642,5	12,0	6 110	9 647	58 608 259
	B180K	9 704,2	11,9	9 754,0	12,0	13 716	9 768	133 103 150
	B180G	9 652,4	11,9	9 650,0	12,1	11 236	9 654	108 454 484
C	**B162K**	9 661,8	11,9	9 757,0	12,0	8 417	9 774	81 322 988
	B162G	9 603,1	11,8	9 725,0	11,9	3 419	9 750	32 832 875
	B169K	9 665,2	11,9	9 725,0	12,0	9 909	9 737	95 772 738
	B169G	9 558,8	11,9	9 634,0	12,0	5 270	9 641	50 374 771

Supplementary table S6. List of false positive INDELS excluded from analysis due to low frequency of reads and proximity to homopolymer regions.

GENE/ REGION	**VARIANT**	**N. of samples**
16s rRNA	m.1092_1093insA	**13**
	m.1182_1183insT	**2**
	m.1460_1461insT	**1**
	m.1753_1754insC	**1**
	m.2071_2072insG	**2**
	m.2439_2440insC	**1**
	m.2463_2464insG	**1**
	m.2549_2550insC	**1**
	m.2628_2629insC	**1**
tRNA-Leu (UUR)	m.2743_2744insA	**4**
tRNA-Ile	m.3717_3718insA	**14**
ND2	m.4872_4873insA	**8**
	m.4883_4884insC	**1**
	m.4886delT	**5**
tRNA-Asn	m.5135_5136insT	**2**
rep_origin	m.5196_5197insA	**1**
	m.5215_5216insC	**1**
COX1	m.6023_6024insG	**1**
	m.6068_6069insC	**2**
	m.6625_6626insC	**3**
	m.6753_6754insT	**1**
COX2	m.7073_7074insC	**5**
	m.7760_7761insT	**2**
ATP6	m.7994_7995insC	**1**
COX3	m.8896_8897insT	**13**
	m.8916_8917insT	**10**
	m.9197_9198insT	**4**
	m.9231_9232insT	**6**
	m.9299_9300insC	**1**
ND3	m.9657_9658insT	**3**
ND4L	m.9860_9861insA	**6**

GENE/ REGION	**VARIANT**	**N. of samples**
ND4	m.10421_10422insCGG	**1**
	m.10608_10609insG	**1**
ND5	m.12617_12618insG	**4**
	m.12671_12672insA	**3**
	m.12776_12777insT	**4**
	m.12875_12876insC	**2**
	m.13026_13027insC	**2**
	m.13079_13080insC	**1**
	m.13089_13090insC	**12**
	m.13123_13124insC	**1**
ND6	m.13963_13964insC	**1**
	m.14032_14033insG	**2**
CYTB	m.14293_14294insG	**1**
	m.14868_14869insC	**8**
	m.14875_14876insG	**2**
	m.14876_14877insC	**6**
	m.14877_14878insC	**1**
	m.14951_14952insC	**1**
	m.14972_14973insC	**2**
	m.15099_15100insC	**1**
D-loop	m.15530_15531insC	**3**
	m.15756_15757insG	**1**
	m.15931_15932insG	**1**
	m.15931delG	**3**
	m.16018_16019insC	**2**
	m.16130delT	**1**
	m.16470delT	**8**
	m.16563_16564insG	**4**
	m.16660_16661insC	**1**
	m.16663delT	**5**