Whole mitochondrial genome sequencing analysis of canine testicular tumours

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Supporting Information

Supplementary items:

Table S1. List of polymorphisms detected in blood, tumour, and healthy tissue collected from dogs with testicular tumours generated using Unipro uGene.

Table S2. Heteroplasmy and polymorphisms found in the VNTR region of the D-loop between 16,130 and 16,430 nucleotides.

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Table S8. Detailed information about sequencing data generated using the Illumina MiSeq sequencer.

Table S1. List of polymorphisms detected in blood, tumour, and healthy tissue collected from dogs with testicular tumours generated using Unipro uGene.

Positon	GENE/ REGI0N	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195	Position	GENE/ REGION	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195
16	*tRNA Phe*	T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.	3106	*ND1*	A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.
165	*12s rRNA*	T	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	3196		T	C	C	C	C	C	C	.	C	C	C	C	C	.	C	C
381		T	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.	3406		C	T	T	.	.	.	.	.	T	T	T	.	.	.	.	.
445		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.	3469		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
463		T	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	3494		T	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.
557		A	G	.	.	.	.	.	.	.	G	.	.	.	.	.	.	3598		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
571		T	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	4135	*ND2*	C	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.
947		C	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	4169		A	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.
1046	*tRNA Val*	G	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	4204		G	.	A	.	.	.	.	.	.	.	A	.	.	.	.	.
1204	*16s rRNA*	T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	4234		C	T	.	.	.	.	.	.	.	T	.	.	.	.	.	.
1351		A	.	.	.	G	G	G	.	.	.	.	.	.	.	G	G	4277		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
1454		G	A	A	.	.	.	.	.	A	A	A	.	.	.	.	.	4303		A	.	.	.	G	G	G	.	.	.	.	.	.	.	G	.
1493		-	.	A	.	.	.	.	.	.	A	A	.	.	.	.	.	4390		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
1662		C	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	4503		A	G	.	.	.	.	.	.	.	G	.	.	.	.	.	.
1709		G	A	.	.	.	.	.	.	.	A	.	.	.	.	.	.	4517		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
1748		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	4572		T	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.
1756		C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.	4646		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
2185		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.	4940		T	.	.	.	C	C	C	.	.	.	.	.	.	.	C	C
2232		A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.	5009	*tRNA Trp*	C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.
2678	*tRNALeu (UUR)*	-	insG															5126	*tRNA Asn*	C	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.
2683		G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	5367	*COX1*	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
2800	*ND1*	C	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	5444		T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
2812		C	.	T	.	.	.	.	.	.	.	T	.	.	.	.	.	5624		G	A	.	.	.	.	.	.	.	A	.	.	.	.	.	.
2833		C	.	.	C	.	.	.	.	.	.	.	C	.	.	.	.	5855		C	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.
2962		C	T	T	T	T	T	T	.	T	T	T	T	T	.	T	T	5906		A	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.
3028		A	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.	6065		A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G

Position	GENE/ REGION	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195
6236	*COX1*	A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.
6257		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
6302		A	.	.	G	.	.	.	.	.	.	.	G	.	.	.	.
6401		C	.	.	.	T	T	T	.	.	.	.	.	.	.	T	T
6407		A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.
6470		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
6518		G	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.
6554		T	.	.	.	C	C	C	.	.	.	.	.	.	.	C	C
6683		T	.	.	C	.	.	.	.	.	.	.	C	.	.	.	.
6711		T	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.
6740		G	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.
6764		C	.	T	.	.	.	.	.	.	.	T	.	.	.	.	.
6836		T	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.
6863		C	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.
6967	*tRNA Asp*	A	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.
7014		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
7058	*COX2*	T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.
7112		A	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.
7186		C	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.
7363		T	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.
7383		A	.	.	G	.	.	.	.	.	.	.	G	.	.	.	.
7426		A	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.
7593		T	.	.	.	C	C	C	.	.	.	.	.	.	.	C	C
7914	*ATP8*	A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.
7923		T	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.
8048	*ATP6*	A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.
8101	*ATP6*	G	.	A	.	.	.	.	.	.		A	.	.	.	.	.
8221		A	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.
8225		T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.
8242		G	.	.	A	.	.	.	.	.	.	.	A	.	.	.	.
8281		T	C	C	C	C	C	C	.	C	C	C	C	C	.	C	C
8323		A	G	G	.	.	.	.	.	G	G	G	.	.	.	.	.
8368		C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
8411		T	.	.	.	.	.	.	.	C		.	.	.	.	.	.
8425		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
8536		C	.	.	.	.	.	.	T	.	.	.	.	.	T	.	.
8569		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
8703	*COX3*	G	A	A	.	.	.	.	.	A	A	A	.	.	.	.	.
8736		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
8760		A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.
8764		G	T	T	.	.	.	.	.	T	T	T	.	.	.	.	.
8807		G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
8817		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
8877		A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.
8991		A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.
9219		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
9222		C	T	.	.	.	.	.	.	.	T	.	.	.	.	.	.
9708	*ND3*	C	T		.	.	.	.	.	.	T	.	.	.	.	.	.
9825		G	.	A	.	.	.	.	.	.	.	A	.	.	.	.	.
9838		G	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.
9865	*tRNA Arg*	-	A	.	.	.	.	.	.	.	A	.	.	.	.	.	.
9896		T	.	.	C	.	.	.	.	.	.	.	C	.	.	.	.

Position	GENE/ REGION	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195	Position	GENE/ REGION	S_REF	T010	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195
9911	*ND4L*	-	insTG															11657	*tRNA Ser (AGY)*	C	.	.	A	.	.	.	.	.	.	.	A	.	.	.	.
9988		A	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.	11728	*tRNA Leu (CUN)*	A	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.
10165		C	.	.	.	.	.	.	T	.	.	.	.	.	T	.	.	11813	*ND5*	A	.	.	G	.	.	.	.	.	.	.	G	.	.	.	.
10257	*ND4*	G	.	A	.	.	.	.	.	.	.	A	.	.	.	.	.	11839		T	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.
10346		C	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	11948		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
10354		T	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	11959		C	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.
10404		C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.	11963		C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.
10440		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.	12063		G	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.
10533		A	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.	12122		C	T	.	.	.	.	.	.	.	T	.	.	.	.	.	.
10542		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.	12200		C	.	.	.	.	T	.	.	.	.	.	.	.	.	T	.
10611		A	.	.	.	T	T	T	.	.	.	.	.	.		T	T	12272		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.
10613		A	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	12330		A	G	.	.	.	.	.	.	.	G	.	.	.	.	.	.
10776		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	12346		T	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.
10785		A	G	.	.	.	.	.	.	.	G	.	.	.	.	.	.	12401		T	.	.	.	.	.	.	.	.		.	.	C	.	.	.
10863		A	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12636		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.
10917		G	A	A	.	.	.	.	.	A	A	A	.	.	.	.	.	12665		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
10992		G	A	A	A	A	A	A	.	A	A	A	A	.	A	A	A	12788		T	C	C	.	.	.	.	.	C	C	C	.	.	.	.	.
11100		G	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12813		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.
11172		A	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	13112		G	A	.	.	.	.	.	.	.	.		.	.	.	.	.
11176		C	.	T	.	.	.	.	.	.	.	T	.	.	.	.	.	13202		T	.	.	.	.	.	.	.	C	.		.	.	.	.	.
11247		A	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	13261		C	T	T	.	.	.	.	.		T	T	.	.	.	.	.
11250		T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.	13299		T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A
11322		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	13427		T	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.
11400		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	13459		T	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.
11402		T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.	13594	*ND5/ND6***	G	.	A	.	.	.	.	.	.		A	.	.	.	.	.
11572		A	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	13618	*ND6*	A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.

Position	GENE/ REGION	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195	Position	GENE/ REGION	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195
13660	*ND6*	C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.	15526	D-LOOP HVI	C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.
13708		C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.	15553		A	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.
13777		G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.	15595		C	.	T	.	.	.	.	.	.	.	T	.	.	.	.	.
13791		T	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	15611		T	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.
13802		G	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	15612		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
13864		C	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	15620		T	.	.	.	C	C	C	.	.	.	.	.	.	.	C	C
14329	*CYTB*	A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	15621		C	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
14383		C	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	15627		A	.	.	G	G	G	G	.	.	G	.	G	G		G	G
14425		T	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	15632		C	.	T	T	.	.	.	.	.	.	T	T	.	.	.	.
14467		C	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	15639		T	G	G	A	A	A	A	A	A	G	G	A	A	A	A	A
14474		G	.	.	.	.	.	.	A	.	.	.	.	.	A	.	.	15643		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
14534		G	.	.	A	.	.	.	.	.	.	.	A	.	.	.	.	15650		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.
14608		A	G	.	.	.	.	.	.	.	G	.	.	.	.	.	.	15652		G	.	A	.	.	.	.	.	A	.	A	.	.	.	.	.
14647		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	15710		C	.	.	.	.	.	.	.	.	T		.	.	.	.	.
14671		G	.	A	.	.	.	.	.	.	.	A	.	.	.	.	.	15750		C	.	.	T	.	.	.	.	.	.	.	T	.	.	.	.
14692		G	A	.	.	.	.	.	.	.	A	.	.	.	.	.	.	15800		T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.
14930		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.	15814		C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T
14977		T	.	.	.	C	C	C	.	.	.	.	.	.	.	C	C	15815		T	.	C	.	.	.	.	.	.	.	C	.	.	.	.	.
14998		A	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	15912		C	T	T	.	.	.	.	.	.	T	T	.	.	.	.	.
15185		T	C	.	.	.	.	.	.	.	C	.	.	.	.	.	.	15938		G	-	.	.	.	.	.	.	.	-	.	.	.	.	.	.
15213		G	A	A	A	A	A	A	.	A	A	A	A	A	.	A	A	15955		C	T	T	.	T	T	T	.	.	T	T	.	.	.	T	.
15220		T	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	16003		A	G	G	.	.	.	.	.	.	G	G	.	.	.	.	.
15372	*tRNA Thr*	G	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	16025		T	.	.	C	.	.	.	C	.	.	.	C	.	C	.	.
15435	*tRNA Pro*	G	A	A	.	.	.	.	.	.	A	A	.	.	.	.	.	16083		A	.	G	.	.	.	.	.	.	.	G	.	.	.	.	.
15475	D-LOOP HVI	T	.	.	C	.	.	.	.	.	.	.	C	.	.	.	.	16128		G	.	A	.	.	.	.	.	.	.	A	.	.	.	.	.
15483		C	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	16148	*D-loop (VNTR)*	A	.	.	G	.	G	.	.	.	.	.	.	G		G	G
15508		C	T	.	.	.	.	.	.	.	T	.	.	.	.	.	.	16158		A	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.

Position	*GENE/ REGION*	S_REF	T015	T066	T087	T104	T105	T121	T137	T138	T139	T141	T149	T153	T156	T163	T195
16168	*D-loop (VNTR)*	A	.	.	G	.	.	.	.	.	.	.	.	.	.	G	G
16198		G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A
16248		A	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.
16258		G	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.
16268		A	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.
16288		A	.	.	.	G	.	G	.	.	.	.	.	.	.	.	.
16298		A	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.
16318		A	.	.	.	G	.	G	.	.	.	.	.	.	.	.	G
16358		A	.	.	.	.	.	.	-[1]	.	.	.	.	.	.	G	.
16368		G	A	A	.	.	.	.	.	.	.	.	.	.	.	A	.
16378		G	A	.	.	.	A	.	.	.	.	.	.	.	.	.	.
16388		A	.	.	G	G	G	.	.	.	.	.	.	.	.	.	G
16398		A	G	G	G	G	.	G	.	.	.	G	.	G	.	G	G
16408		G	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.
16408		.	.	.	.	.	.	.	.	.	.	.	- 2	.	.	.	.
16418		A	G	G	G	G	G	G	.	- 3	G	.	.	G	.	G	G
16421		.	.	.	.	.	.	.	.	- 3	.	.	.	.	.	.	.
16431	D-LOOP HVII	C	T	T	.	.	.	.	.	.	T	.	.	.	.	.	.
16439		T	C	C	.	.	.	.	.	.	C	C	.	.	.	.	.
16663		-	.	.	.	insCC			.	.	.	.	.	.	.	insCC	
16671		T	C	.	.	.	.	.	.	.	C		.	.		.	.
16672		C	.	T	.	T	.	T	.	.	.	T	.	.	T	.	.
16705		C	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.

- deletion; - [1] – m.16358delGTACACGTGC; - [2] – m.16408delGTACACGTAC; - [3] – m.16418del GTACACGTAC; ** - the polymorphisms occurred in a region spanning ND5 and ND6 genes; . .– the variant is the same as in the reference sequence.

Table S2. Heteroplasmy and polymorphisms found in the VNTR region of the D-loop between 16,130 and 16,430 nucleotides.

Sample/ Position	16138	16148	16158	16168	16178	16188	16198	16208	16218	16228	16238	16248	16258	16268	16278	16288	16298	16308	16318	16326	16328	16338	16348	16356	16358	16368	16378	16388	16398	16408	16418
S_REF	A	A	A	A	A	G	G	A	G	G	G	A	G	A	G	A	A	G	A	G	G	G	G	G	A	G	G	A	A	G	A
T015B*	.	.	.	R	.	R	R	.	.	A	.	R	.	R	.	R	.	R	R	.	.	.	.	.	.	A	A	.	.	.	G
T015T*	.	.	.	R	R	R	R	.	.	A	.	R	.	R	.	R	.	R	R	.	.	.	.	.	.	A	A	.	.	.	G
T015H*	.	.	.	R	R	R	R	.	.	R	.	R	.	R	.	R	.	R	R	.	.	.	.	.	.	A	A	.	.	.	G
T066B	.	.	.	R	R	R	R	.	.	.	R	.	A	.	R	.	.	.	R	.	R	R	A	.	.	A	A	G	G	.	G
T066T	.	.	.	.	R	R	R	.	R	.	R	.	A	.	R	.	.	R	R	.	R	R	R	.	.	A	R	R	G	.	G
T066H	.	.	.	R	R	R	R	.	R	.	R	.	A	.	R	.	.	R	R	.	R	R	R	.	.	A	A	R	G	.	G
T087B	.	G	.	G	.	R	R	.	.	A	.	.	.	.	.	R	R	.	R	.	.	.	.	.	R	R	.	G	G	A	G
T087T	.	G	.	G	.	.	A	.	.	A	.	.	.	R	.	R	R	.	R	.	.	.	.	.	R	R	.	G	G	A	G
T087H	.	G	.	G	.	R	R	.	.	R	.	.	.	.	.	.	R	.	R	.	.	.	.	.	R	R	.	G	G	A	G
T104B	.	.	R	R	.	R	R	R	.	.	.	G	.	G	.	G	G	.	G	.	.	.	.	.	R	R	.	G	G	.	G
T104T	.	.	G	R	.	R	R	R	.	.	.	G	.	G	.	G	G	.	G	.	.	.	.	.	G	R	.	G	G	.	G
T104H	.	.	R	R	.	R	R	R	.	.	.	G	.	G	.	G	G	.	G	.	.	.	.	.	R	R	.	G	G	.	G
T105B	.	G	.	R	R	R	.	G	.	.	.	.	.	.	.	R	R	.	.	.	.	.	.	R	.	.	A	G	.	.	G
T105T	.	G	.	R	R	R	.	R	.	.	.	.	.	.	.	R	R	.	.	.	.	R	.	R	.	.	A	G	.	.	G
T105H	.	G	.	R	R	R	.	G	.	.	.	.	.	.	.	R	R	.	.	.	.	R	.	R	.	.	A	G	.	.	G
T121B	.	.	.	.	R	R	.	R	.	.	.	R	.	R	.	G	R	.	G	.	.	R	.	.	R	R	.	G	G	.	G
T121T	.	.	.	.	R	R	.	R	.	.	.	R	.	R	.	G	R	.	G	.	.	.	.	.	R	R	.	-	G	.	G
T121H	.	.	.	.	R	R	.	R	.	.	.	R	.	R	.	G	R	.	G	.	.	.	.	.	R	R	.	G	G	.	G
T137B	.	G	.	G	.	R	.	.	R	R	.	.	.	.	.	R	R	.	.	.	.	R	.	.	-[1]	.	.	.	.	.	.
T137T	.	.	G	.	R	A	.	.	R	R	R	.	.	.	R	.	.	.	.	.	.	R	R	.	-[1]	.	.	.	.	.	.
T137H	.	G	.	G	.	R	.	.	.	R	R	.	.	.	.	R	.	.	.	.	.	A	.	.	-[1]	.	.	.	.	.	.
T138B	.	R	R	.	R	.	.	R	R	R	R	R	R	R	.	R	R	.	.	.	.	R	.	.	.	.	.	.	.	.	-[3]

Sample/ Position	16138	16148	16158	16168	16178	16188	16198	16208	16218	16228	16238	16248	16258	16268	16278	16288	16298	16308	16318	16326	16328	16338	16348	16356	16358	16368	16378	16388	16398	16408	16418
T138T	.	.	R	.	R	R	R	.	R	R	R	R	R	R	.	.	R	.	.	.	.	A	.	.	.	.	.	.	.	.	-[3]
T138H	.	.	R	R	R	R	R	R	R	R	R	R	R	R	.	R	R	.	.	.	.	R	.	.	.	.	.	.	.	.	-[3]
T139B	.	.	R	.	R	.	.	R	.	.	.	R	.	R	.	.	.	R	R	.	.	.	.	.	R	.	.	R	R	.	G
T139T	R	.	.	R	R	.	.	R	.	.	R	R	.	R	.	.	.	R	R	.	.	.	.	.	R	.	.	R	G	.	G
T139H	R	R	R	.	R	R	R	R	R	R	R	R	R	R	R	.	R	R	R	.	.	.	R	.	R	.	.	G	G	.	G
T141B	.	.	.	R	R	R	R	.	R	R	.	R	.	.	.	R	R	.	R	.	.	.	R	.	R	R	R	R	G	.	G
T141T	.	.	.	R	R	R	R	.	R	R	.	R	.	.	.	R	R	.	R	.	.	.	R	.	R	R	.	R	G	.	-[3]
T141H	.	.	.	R	R	R	R	.	R	R	.	R	.	.	.	R	R	.	R	.	.	.	R	.	R	R	R	R	G	.	G
T149B	.	R	.	R	R	R	R	.	R	R	R	.	.	.	.	.	.	.	.	.	.	R	.	.	R	.	.	R	R	-[2]	G
T149T	.	R	.	R	.	R	R	R	R	R	R	R	.	R	.	.	.	.	.	.	.	R	.	.	R	.	.	R	R	-[2]	G
T149H	.	R	.	R	R	R	R	.	R	R	R	.	.	.	.	.	R	.	R	.	.	R	.	.	R	.	.	R	R	-[2]	G
T153B	.	G	G	.	.	.	.	R	R	R	R	.	.	.	.	.	.	R	R	.	R	R	R	.	R	R	R	R	G	.	G
T153T	.	G	G	.	.	.	.	R	R	R	R	.	.	R	.	R	.	R	.	.	R	R	R	.	R	R	R	-	G	.	G
T153H	.	G	G	.	.	.	.	R	R	R	R	.	.	R	.	R	.	R	.	.	R	R	R	.		R	R	R	G	.	G
T156B	G	G	G	G	.	.	R	.	.	R	R	.	.	.	.	.	.	.	.	.	R	R	R	.	.	.	.	.	.	.	.
T156T	.	.	R	R	R	R	R	.	R	R	R	.	.	.	.	.	.	.	.	.	R	R	R	.	.	.	.	.	.	.	.
T156H	G	G	G	G	.	.	R	.	.	R	R	.	.	.	.	.	.	.	R	.	R	R	R	.	.	.	.	.	.	.	.
T163B	.	G	.	G	.	.	R	R	R	R	.	.	.	.	.	.	R	R	.	.	.	.	.	.	G	A	.	.	G	.	G
T163T	.	G	.	G	.	.	R	R	R	R	.	R	R	.	.	R	.	.	R	.	.	.	R	.	G	A	.	.	G	.	G
T163H	.	G	.	G	.	R	R	R	R	R	.	.	.	.	.	.	R	R	.	.	.	.	.	.	G	A	.	.	G	.	G
T195B	.	G	R	G	R	R	A	R	.	.	.	.	R	R	.	R	R	.	G	.	R	R	R	.	.	R	.	G	G	.	G
T195T	.	G	.	G	G	.	A		.	.	.	.	R	R	.	R	R	.	G	R	R	R	R	.	.	R	.	G	G	.	G
T195H	.	G	R	G	R	R	A	R	.	.	.	.	R	R	.	R	R	.	G	R	R	R	R	.	.	R	.	G	G	.	G

*B-blood; T-tumour; H- healthy tissue; - – deletion; -[1] – m.16358delGTACACGTGC; -[2] – m.16408delGTACACGTAC; -[3] – m.16418del GTACACGTAC; . .– the variant is the same as in the reference sequence.

Table S3. Total number of polymorphisms, mutations, heteroplasmy, and indels found in the analysed samples.

Gene/ Region	SNP		Indel	
	Polymorphisms (*)	Mutations (*)	Polymorphisms	Mutations
12s rRNA	12			
16s rRNA	27	1	3	1
tRNA ^{Phe}	4			
tRNA ^{Val}	1			
tRNA $^{Leu\ (UUR)}$	15		15	
tRNA ^{Trp}	4			
tRNA ^{Asn}	1			
tRNA ^{Asp}	3			
tRNA ^{Arg}	2		2	
tRNA $^{Ser\ (AGY)}$	2			
tRNA $^{Leu\ (CUN)}$	1			
tRNA ^{Thr}	1			
tRNA ^{Pro}	4			
ND1	48			
ND2	28	1		
ND3	5			
ND4L	3		30	
ND4	64	(*1)		
ND5	57			
ND5/6*	2			
ND6	19	(*1)		
COX1	80			
COX2	13			
COX3	45	(*2)		
ATP8	2			
ATP6	55			
CYB	40			
D-loop, HVI	104		2	1
D-loop, VNTR	61 (*31)	10		2
D-loop, HVII	19		10	1
Sum	722 (*31)	12 (4)	62	5
Total	801 (*35)			

*heteroplasmic site; **the polymorphisms occurred in a region spanning *ND5* and *ND6* genes.

Table S4. Number and percentage of polymorphisms identified in malignant and benign testicular tumours.

Gene/ Region	Total	SNP polymorphisms		Total	Indel polymorphisms	
		Malignant [%]	Bening [%]		Malignant [%]	Bening [%]
12s rRNA	12	9 (75,0%)	3 (25,0%)			
16s rRNA	27	21 (77,7%)	6 (22,3%)	3	2 (66,6%)	1 (33,4%)
tRNA ^{Phe}	4	3 (75,0%)	1 (25,0%)			
tRNA ^{Val}	1	1 (100,0%)				
tRNA $^{Leu\ (UUR)}$	15	10 (66,6%)	5 (33,4%)	15	10 (66,6%)	5 (33,4%)
tRNA ^{Trp}	4	3 (75,0%)	1 (25,0%)			
tRNA ^{Asn}	1	1 (100,0%)				
tRNA ^{Asp}	3	2 (66,6%)	1 (33,4%)			
tRNA ^{Arg}	2		2 (100,0%)	2	2 (100,0%)	
tRNA $^{Ser\ (AGY)}$	2		2(100,0%)			
tRNA $^{Leu\ (CUN)}$	1		1 (100,0%)			
tRNA ^{Thr}	1	1 (100,0%)				
tRNA ^{Pro}	4	3 (75,0%)	1 (25,0%)			
ND1	48	31 (64,6%)	17 (35,4%)			
ND2	28	20 (71,4%)	8 (28,6%)			
ND3	5	4 (80,0%)	1 (20,0%)			
ND4L	3	3 (100,0%)		30	20 (66,6%)	10 (33,4%)
ND4	64	48 (75,0%)	16 (25,0%)			
ND5	57	44 (77,2%)	13 (22,8%)			
ND5/6*	2	1 (50,0%)	1 (50,0%)			
ND6	19	15 (79,0%)	4 (21,0%)			
COX1	80	54 (67,5%)	26 (32,5%)			
COX2	13	8 (61,5%)	5 (38,5%)			
COX3	45	32 (71,1%)	13 (28,9%)			
ATP8	2	2 (100,0%)				
ATP6	55	37 (67,3%)	18 (32,7%)			
CYB	40	29 (72,5%)	11 (27,5%)			
D-loop, HVI	104	66 (63,5%)	38 (36,5%)	2	2 (100,0%)	
D-loop, VNTR	61	40 (65,6)	21 (34,4%)			
D-loop, HVII	19	14 (73,7%)	5 (26,3%)	10	6 (60,0%)	4 (40,0%)
Sum	722	502 (69,5%)	220 (30,5%)	62	42 (67,7%)	20 (32,3%)

Table S5. List of mutations and heteroplasmy found in genes and mutations in the non-coding D-loop region present in dogs with TTs.

Gene/ Region	Reference sequence	Sequence variant	Codon change	Amino acid changes
12s rRNA	m.634C	m.634C/T*[1]	-	-
16s rRNA	m.1486A	m.1486delAA		
ND2	m.4303A	m.4303A>G	CTA→CTG	p.Leu159=
COX3	m.9041A	m.9041A/G*	AAC→AGC	p.Asn133Ser
ND4	m.11003G	m.11003G/A*	GGC→GAC	p.Gly268Asp
ND6	m.13995T	m.13995T/C*	TTA→TCA	p.Leu52Ser
D-loop, HVI	m.15938G	m.15938delG	-	-
D-loop, VNTR	m.16158A	m.16158A>G		
	m.16178A	m.16178A>G		
	m.16188G	m.16188G>A		
	m.16198G	m.16198G>A		
	m.16338G	m.16338G>A		
	m.16348G	m.16348G>A		
	m.16358A	m.16358A>G		
	m.16388A	m.16388A>G		
		m.16388delA		

* - heteroplasmy.

Table S6. List of polymorphisms identified in tRNA genes in samples collected from dogs with TTs. Localisation of tRNA variants were determined using the Canis mitoSNP tool (Kowal et al. 2023).

Gene	Reference sequence	Sequence variant	Codon change/ position in tRNA	Amino acid change/ tRNA region	Sample number	Types of testicular tumours*
tRNA ^{Phe}	m.16T	m.16T>C	16	DHU loop	T15, T66, T139, T141	LCT, SEM, SCT
tRNA $^{Leu\ (UUR)}$	m.2678	m.2678_2679insG	8_9	DHU arm	all samples	LCT, SEM, SCT
	m.2683G	m.2683G>A	13			
tRNA ^{Trp}	m.5009C	m.5009C>T	54	TΨC loop	T15, T66, T139, T141	LCT, SEM, SCT
tRNA ^{Asn}	m.5126C	m.5126C>T	53		T138	SEM
tRNA ^{Asp}	m.6967A	m.6967A>G	2	Acceptor arm	T153	
	m.7014T	m.7014T>C	49	TΨC arm	T66, T141	SEM, SCT
tRNA ^{Arg}	m.9865	m. 9865_9866insA	24	DHU arm	T15, T139	LCT, SCT
	m.9896T	m.9896T>C	55	TΨC loop	T87, T149	
tRNA $^{Ser\ (AGY)}$	m.11657C	m.11657C>A	10	Central loop		
tRNA $^{Leu\ (CUN)}$	m.11728A	m.11728A>G	21	DHU arm	T121	LCT
tRNA ^{Thr}	m.15372G	m.15372G>A	50	TΨC loop	T139	SCT
tRNA ^{Pro}	m.15435G	m.15435G>A	23	Central loop	T15, T66, T139, T141	LCT, SEM, SCT

* Types of testicular tumours: LCT - Leydig cell tumour, SCT – Sertoli cell tumour, SEM – seminoma.

Table S7. List of non-synonymous changes identified in protein-coding genes and their protein data from SIFT and SOPMA.

Gene	Sequence variant	Codon change	Amino acid change	SIFT*	Alpha helix	Extended strand	Beta turn	Random coil
ND2			**Normal**		67,46%	8,28%	1,48%	22,78%
	m.4169A>G	ATC→GTC	p.Ile86Val	tolerant	67,46%	9,76%	1,78%	21,01%
	m.4277A>G	ATT→GTT	p.Ile122Val		68,64%	8,58%	2,07%	20,71%
	m.4503A>G	AAC→AGC	p.Asn197Ser		66,86%	10,65%	1,78%	20,71%
	m.4517G>A	GTT→ATT	p.Val202Ile		68,64%	8,58%	2,07%	20,71%
	m.4572T>C	ATA→ACA	p.Met220Thr		67,46%	9,76%	1,78%	21,01%
COX1			**Normal**		51,61%	13,65%	3,41%	31,33%
	m.6711T>A	TCT→ACT	p.Ser455Thr	intolerant	52,41%	12,25%	3,41%	31,93%
COX2			**Normal**		27,48%	23,42%	4,05%	45,05%
	m.7112A>G	ACA→GCA	p.Thr27Ala	tolerant	29,28%	22,06%	4,06%	44,59%
	m.7383A>G	AAC→AGC	p.Asn117Ser		28,83%	22,07%	4,05%	45,05%
	m.7593T>C	ATA→ACA	p.Met187Thr		29,28%	22,07%	4,05%	44,59%
ATP8			**Normal**		21,88%	25,00%	4,69%	48,44%
	m.7914A>G	ATA→GTA	p.Met38Val	tolerant	21,88%	25,00%	4,69%	48,44%
	m.7923T>C	TCT→CCT	p.Ser41Pro		17,19%	26,56%	1,56%	54,69%
ATP6			**Normal**		63,68%	9,42%	4,48%	22,42%
	m.8048A>G	ATT→GTT	p.Ile28Val	tolerant	61,43%	8,97%	4,48%	25,11%
	m.8411T>C	TTT→CTT	p.Phe150Leu		61,43%	8,97%	4,48%	25,11%
COX3			**Normal**		56,00%	12,00%	3,20%	28,80%
	m.8764G>T	GCC→TCC	p.Ala41Ser	tolerant	58,40%	11,20%	2,40%	28,00%
	m.8807G>A	TGC→TAC	p.Cys55Tyr		58,00%	11,60%	2,80%	27,60%
ND3			**Normal**		54,87%	6,19%	3,54%	35,40%
	m.9838G>A	GAA→AAA	p.Glu115Lys	intolerant	61,06%	6,19%	3,54%	29,20%
ND4L			**Normal**		75,51%	9,18%	2,04%	13,27%
	m.10165C>T	GCT→ GTT	p.Ala67Val	intolerant	75,51%	9,18%	2,04%	13,27%
ND4			**Normal**		59,64%	9,64%	3,14%	27,58%
	m.10346C>T	ACA→ATA	p.Thr49Met	tolerant	60,31%	9,19%	3,81%	26,68%
	m.10354T>C	TCC→CCC	p.Ser52Pro		60,31%	10,54%	3,59%	25,56%
	m.10613A>G	AAT→AGT	p.Asn138Ser	intolerant	60,31%	9,19%	3,81%	26,68%
	m.10917G>A	GGC→GAC	p.Gly240Asp		62,33%	9,64%	3,36%	24,66%
	m.11402T>C	ATC→ACC	p.Ile401Thr	tolerant	61,21%	9,19%	3,14%	26,46%
	m.11572A>C	ATC→CTC	p.Ile458Leu		62,33%	9,64%	3,36%	24,66%

Gene	Sequence variant	Codon change	Amino acid change	SIFT	Alpha helix	Extended strand	Beta turn	Random coil
ND5			**Normal**		60,80%	11,56%	3,35%	24,29%
	m.12063G>A	GTC→ATC	p.Val96Ile	tolerant	59,13%	12,56%	3,35%	24,96%
	m.12330A>G	ACC→GCC	p.Thr185Ala		58,53%	12,88%	3,68%	24,92%
	m.12346T>A	CTA→CAA	p.Leu190Gln		58,53%	12,88%	3,68%	24,92%
	m.12401T>A	AAT→AAA	p.Asn208Lys		59,13%	12,56%	3,35%	24,96%
	m.12636T>C	TTT→CTT	p.Phe287Leu	intolerant	58,53%	12,88%	3,68%	24,92%
	m.12813G>A	GTT→ATT	p.Val346Ile	tolerant	60,13%	12,40%	3,69%	23,79%
	m.13261C>T	ACC→ATC	p.Thr495Ile		60,13%	12,40%	3,69%	23,79%
	m.13299T>A	TCA→ACA	p.Ser508Thr		61,47%	11,89%	3,69%	22,95%
	m.13459T>C	ATC→ACC	p.Ile561Thr		60,97%	11,89%	3,69%	23,45%
ND5/ND6*			**Normal**		24,59%	24,59%	14,75%	36,07%
	m.13594G>A	GGG→GAG ACC→ACA	p.Gly606Glu p.Thr172=	tolerant	26,23%	24,59%	11,48%	37,70%
ND6			**Normal**		42,77%	24,28%	8,09%	24,86%
	m.13791T>C	ATT→GTT	p.Ile107Val	tolerant	41,62%	26,01%	8,09%	24,28%
	m.13802G>A	ACT→ATT	p.Thr103Ile		43,35%	23,70%	8,09%	24,86%
CYB			**Normal**		54,45%	8,63%	2,70%	34,23%
	m.14474G>A	GTA→ATA	p.Val98Met	intolerant	53,10%	9,70%	3,23%	33,96%
	m.14534G>A		p.Val118Met		56,72%	7,26%	3,23%	32,80%

*SIFT - sorting intolerant from tolerant ; **The effect of the polymorphism was non-synonymous for ND5 protein, but synonymous for ND6 protein.

Table S8. Detailed information about sequencing data generated using the Illumina MiSeq sequencer.

File name	Format	Num_seqs	Sum_len	Min_len	Avg_len	Max_len	Sequence_ cover
T015K_R1.fastq.gz	FASTQ	72,851	18,068,771	35	248,0	301	1,901
T015K_R2.fastq.gz		72,851	18,217,335		250,1		1,858
T015G_R1.fastq.gz		167,953	39,665,804		236,2		4,175
T015G_R2.fastq.gz		167,953	39,960,576		237,9		4,077
T015TZ_R1.fastq.gz		116,961	27,365,128		234,0		2,880
T015TZ_R2.fastq.gz		116,961	27,585,636		235,9		2,814
T066K_R1.fastq.gz		117,081	27,805,504		239,2		2,926
T066K_R2.fastq.gz		117,081	28,010,317		241,1		2,858
T066G_R1.fastq.gz		71,870	18,012,125		250,6		1,896
T066G_R2.fastq.gz		71,870	18,136,049		252,3		1,850
T066TZ_R1.fastq.gz		136,624	33,222,812		243,2		3,497
T066TZ_R2.fastq.gz		136,624	33,501,479		245,2		3,418
T087K_R1.fastq.gz		88,789	22,140,986		250,7		2,330
T087K_R2.fastq.gz		88,789	22,260,461		247,5		2,271
T087G_R1.fastq.gz		96,235	23,822,852		248,7		2,507
T087G_R2.fastq.gz		96,235	23,937,486		228,3		2,442
T087TZ_R1.fastq.gz		157,059	35,856,066		228,3		3,774
T087TZ_R2.fastq.gz		157,059	36,152,257		230,2		3,689
T0104K_R1.fastq.gz		168,095	41,604,329		247,5		4,379
T0104K_R2.fastq.gz		168,095	41,899,462		249,3		4,275
T0104G_R1.fastq.gz		88,584	21,666,783		244,6		2,280
T0104G_R2.fastq.gz		88,584	21,819,602		246,3		2,226
T0104TZ_R1.fastq.gz		188,001	42,231,935		224,6		4,445
T0104TZ_R2.fastq.gz		188,001	42,530,109		226,2		4,339
T0105K_R1.fastq.gz		92,453	21,984,016		237,8		2,314
T0105K_R2.fastq.gz		92,453	22,139,645		239,5		2,259
T0105G_R1.fastq.gz		128,447	31,821,228		247,7		3,349
T0105G_R2.fastq.gz		128,447	32,004,665		249,2		3,265
T0105TZ_R1.fastq.gz		66,382	16,902,298		255,9		1,779
T0105TZ_R2.fastq.gz		66,382	16,988,422		235,3		1,788
T0121K_R1.fastq.gz		101,587	23,907,238		235,3		2,516

File name	Format	Num_seqs	Sum_len	Min_len	Avg_len	Max_len	Sequence_ cover
T0121K_R2.fastq.gz		101,587	24,065,145		236,9		2,455
T0121G_R1.fastq.gz		91,531	22,733,289		248,4		2,392
T0121G_R2.fastq.gz		91,531	22,896,309		250,1		2,336
T0121TZ_R1.fastq.gz		79,573	18,946,244		238,1		1,994
T0121TZ_R2.fastq.gz		79,573	19,097,059		240,0		1,948
T0137K_R1.fastq.gz		106,514	25,792,408		242,2		2,714
T0137K_R2.fastq.gz		106,514	25,925,719		243,4		2,645
T0137G_R1.fastq.gz		139,654	33,203,549		237,8		3,495
T0137G_R2.fastq.gz		139,654	33,484,318		239,8		3,416
T0137TZ_R1.fastq.gz		62,560	15,693,972		250,9		1,651
T0137TZ_R2.fastq.gz		62,560	15,829,088		253,0		1,615
T0138K_R1.fastq.gz		166,909	40,600,295		243,2		4,273
T0138K_R2.fastq.gz	FASTQ	166,909	40,970,517	35	245,5	301	4,180
T0138G_R1.fastq.gz		124,812	30,090,057		241,1		3,167
T0138G_R2.fastq.gz		124,812	30,383,163		243,4		3,100
T0138TZ_R1.fastq.gz		114,191	28,382,249		248,6		2,987
T0138TZ_R2.fastq.gz		114,191	28,583,244		250,3		2,916
T0139K_R1.fastq.gz		642 422	90 200 064		642,4		9,494
T0139K_R2.fastq.gz		642 422	90 212 785		642,4		9,205
T0139G_R1.fastq.gz		615 566	87 026 295		615, 5		9,160
T0139G_R2.fastq.gz		615 566	87 030 463		615, 5		8,880
T0139TZ_R1.fastq.gz		111,545	25,702,131		232,7		2,705
T0139TZ_R2.fastq.gz		111,545	25,956,174		245,0		2,648
T0141K_R1.fastq.gz		128,048	31,721,383		249,7		3,339
T0141K_R2.fastq.gz		128,048	31,975,247		245,1		3,262
T0141G_R1.fastq.gz		108,327	26,549,659		247,0		2,794
T0141G_R2.fastq.gz		108,327	26,757,200		251,5		2,730
T0141TZ_R1.fastq.gz		83,358	20,967,542		253,5		2,207
T0141TZ_R2.fastq.gz		83,358	21,133,470		237,3		2,156
T0153K_R1.fastq.gz		122,476	28,920,728		236,1		3,044
T0153K_R2.fastq.gz		122,476	29,124,058		237,8		2,971
T0153G_R1.fastq.gz		126,706	30,898,776		243,9		3,252
T0153G_R2.fastq.gz		126,706	31,122,536		245,6		3,175

File name	Format	Num_seqs	Sum_len	Min_len	Avg_len	Max_len	Sequence_ cover
T0153TZ_R1.fastq.gz	FASTQ	52,392	13,555,452	35	260,3	301	1,426
T0153TZ_R2.fastq.gz		52,392	13,639,239		240,0		1,391
T0156K_R1.fastq.gz		128,413	30,819,426		240,0		3,244
T0156K_R2.fastq.gz		128,413	31,142,673		242,5		3,177
T0156G_R1.fastq.gz		81,346	20,099,655		247,1		2,115
T0156G_R2.fastq.gz		81,346	20,238,395		248,8		2,065
T0156TZ_R1.fastq.gz		150,344	35,071,028		233,3		3,691
T0156TZ_R2.fastq.gz		150,344	35,404,302		235,5		3,612
T0163K_R1.fastq.gz		81,931	19,994,696		244,0		2,104
T0163K_R2.fastq.gz		81,931	20,191,809		246,4		2,060
T0163G_R1.fastq.gz		89,750	22,427,998		249,9		2,360
T0163G_R2.fastq.gz		89,750	22,632,832		252,2		2,309
T0163TZ_R1.fastq.gz		23,944	6,273,850		262,0		660,0
T0163TZ_R2.fastq.gz		23,944	6,354,941		265,4		648,0
T0195K_R1.fastq.gz		85,201	21,963,184		257,8		2,311
T0195K_R2.fastq.gz		85,201	22,111,182		259,5		2,256
T0195G_R1.fastq.gz		98,225	24,078,586		245,1		2,534
T0195G_R2.fastq.gz		98,225	24,308,623		247,5		2,480
T0195TZ_R1.fastq.gz		108,187	26,680,851		246,6		2,808
T0195TZ_R2.fastq.gz		108,187	26,879,961		248,5		2,742