

*Genome analysis identifies the mutant genes for common industrial Silverblue and Hedlund white coat colours in American mink*

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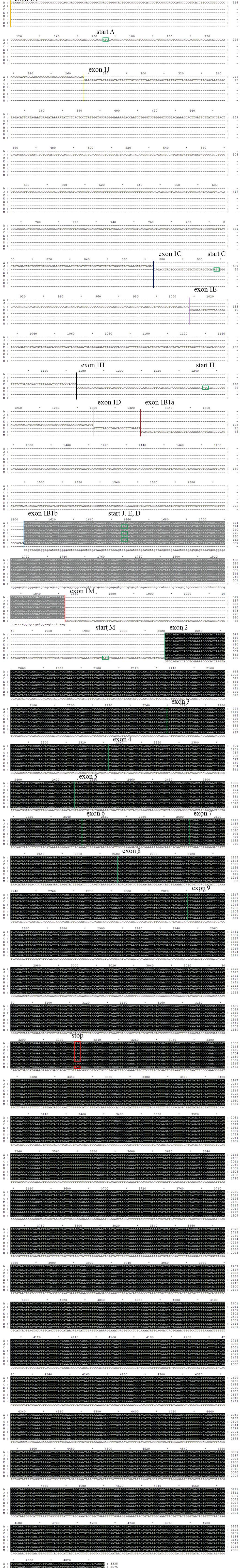
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**Supplementary Table 1.** Results of sequencing American mink genomes. Statistics were calculated with samtools<sup>1</sup>, picard, and GATK<sup>2</sup> software, ferret genome (MusPutFur1.0) was used as reference.

Sample	Colour	N of reads	Mapped %	Duplicates %	Coverage*
mink_3-261	Standard dark brown	266,270,413	96,18	4,41	10,04
mink_3-247	Standard dark brown	257,506,707	97,64	3,06	9,78
mink_3-265	Standard dark brown	235,071,238	96,77	2,56	9,14
mink_1-663	<i>p/p</i>	177,249,440	95,38	11,11	6,63
mink_0-329	<i>p/p</i>	170,946,890	97,18	3,43	6,54
mink_9-431	<i>p/p</i>	151,699,053	95,36	4,27	5,57
mink_1-679	<i>h/h</i>	140,973,939	95,14	4,38	5,29
mink_1-725	<i>h/h</i>	139,370,841	95,82	3,57	5,26
mink_1-681	<i>h/h</i>	136,213,566	94,09	3,27	5,02

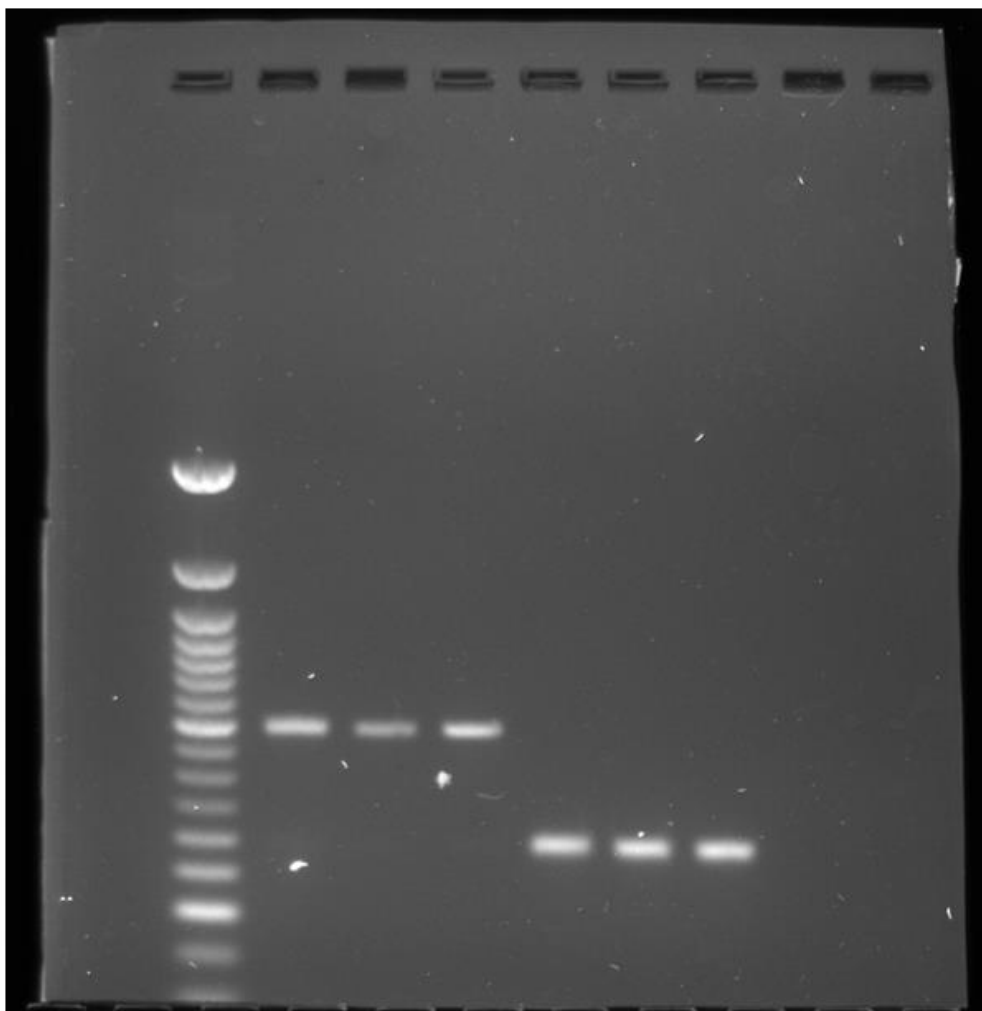
1. Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078–2079 (2009).
2. McKenna, A. *et al.* The genome analysis toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res.* **20**, 1297–1303 (2010).

Supplementary 2. Ferret *MITF* isoforms.



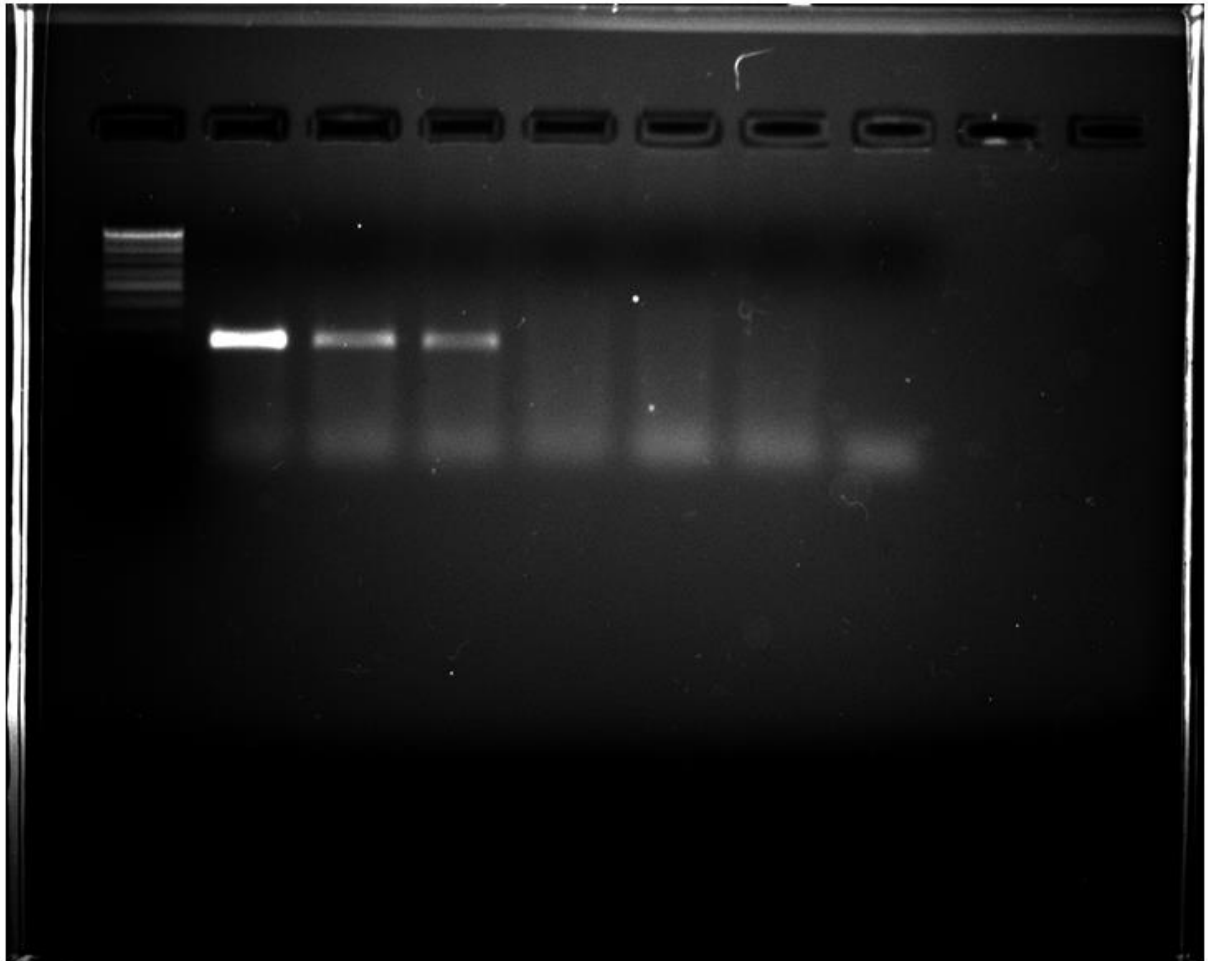
**Supplementary 3.** Original agarose gel electrophoresis of *MLPH* cDNA exons 6–9. M – 50 bp DNA Ladder (NEB, USA). Genotypes for GL896909.1:662639 G/A (*MLPH* C.901+1 G>A) mutation are presented.

M G/G G/G G/G A/A A/A A/A K-



**Supplementary 4.** Original agarose gel electrophoresis of *MITF-M* cDNA 1M-2 exons and *B2M* cDNA 1–2 exons. No *MITF-M* cDNA 1–2 exons were observed in the cortex of Hedlund white (*h/h*) minks, which were homozygous for this mutation. M – DNA ladder 100 bp + 50 bp (SibEnzyme, Russia). Genotypes for GL896899.1:18635719 G/A (*MITF-M* C.33+1 G>A) mutation are presented.

M G/G G/G G/G A/A A/A A/A K-



**Supplementary 5.** Original agarose gel electrophoresis of *B2M* cDNA 1–2 exons. 50 bp DNA Ladder (NEB). Genotypes for GL896899.1:18635719 G/A (MITF-M C.33+1 G>A) mutation are presented.

M G/G G/G G/G A/A A/A A/A K-

