

LABOKLIN NV · Verlengde Klinkertstraat 6 · NL-6433PL Hoensbroek

Dierenarts  
Bart de Winter  
Herentalsesteenweg 57  
2230 Herselt  
Belgien

## Report

No.: 2102-N-02363  
Date of arrival: 22-02-2021  
Date of report: 03-03-2021

Patient identification:	Dog	female	* 13.08.20
	Rottweiler		
Owner / Animal-ID:	Brullemans, Nancy		
Type of sample:	EDTA		
Date sample was taken:	12-02-2021		

Name: **Tequila Rebbels Dream**  
Stud book no.: **LOSH 1314474**  
Chip no.: **981100004779268**  
Tattoo no.: **---**

### Degenerative Myelopathy - PCR

Result: Genotype N/N (exon 2)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the high-risk factor for DM in exon 2 of the SOD1-gene.

Trait of inheritance: autosomal-recessive

Please note: In the Bernese Mountain Dog breed the mutation in exon 1 of the SOD1-gene also occurs in correlation with DM.

### Leukoencephalomyelopathy (LEMP) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for LEMP in the NAPEPLD-gene.

sample ID: 2102-N-02363

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Great Dane, Rottweiler

**Juvenile Laryngeal Paralysis & Polyneuropathy (JLPP) - PCR**

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for JLPP in the RAB3GAP1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Black Russian Terrier, Rottweiler

**Coat length I (long or short hair) - PCR**

HlHd1 SNP G284T: L/1

**Interpretation:**

The test detects the alleles L (shorthair) and l (longhair) in the FGF5 gene.

Allelic series: L dominant over l  
solely genotype L/L: The analysed sample is homozygous for the L-allele for short-haired.

exactly one genotype L/l: The analysed sample is heterozygous for the L-allele and the l-allele. The l-allele for long-haired is forwarded to 50% of the dogs offspring.

multiple Genotypes L/l: The analysed sample is heterozygous for the L-allele and the l-allele on more than one gene-locus. The dog inherits the l-allele for long-haired to it's offspring.

at least one genotype l/l: The analysed sample is homozygous for the l-allele for long-haired.

**Please note:**

Further causative mutations for longhaired have been found in the

sample ID: 2102-N-02363



following breeds:

Afghan Hound, Akita Inu, Alaskan Malamute, Chow Chow, Eurasian, French Bulldog, Husky, Prague Rattler, Shar Pei, Samoyed  
The additional mutations might be responsible for longhair in further breeds.

**X-linked Myopathy (XL-MTM) - PCR**

Result: Genotype female X(N)/X(N), male X(N)/Y

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for XL-MTM in the MTM1-gene.

Trait of inheritance: X chromosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Rottweiler

The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material. The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

\*\*\* END of report \*\*\*

Drs. J.Vis