

LABOKLIN GmbH & Co. KG · Steubenstraße 4 · 97688 Bad Kissingen

Mrs.  
Ines Frohn  
Quinta Silfrohn, Vila Amelia LT 513  
3950- 805 Quinta do Anjo  
Portugal

**Report No.:** **2103-W-23355**  
Date of arrival: 24.03.2021  
Date of report: 22.04.2021  
Testing started: 24.03.2021  
Testing completed: 09.04.2021

|                        |   |
|------------------------|---|
| Species:               | Dog                                     |
| Breed:                 | Altdeutscher Schäferhund                |
| Gender:                | Male                                    |
| Name:                  | Aruk de la Legende du Loup Noir         |
| Stud book No.:         | IHR 2190065                             |
| Chip No.:              | 250208501656236                         |
| Date of birth / Age:   | 10.11.2018                              |
| Type of sample:        | Swab                                    |
| Date sample was taken: | 17.03.2021                              |
| Sampler:               | Dra. Eva Joana Costa da Silva (CP 4153) |
| Owner / Animal-ID:     | Frohn, Ines                             |
| IT No. / Report-ID:    | ---                                     |

### **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.

### **Hyperuricosuria - PCR**

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for HUU in the SLC2A9-gene.

Trait of inheritance: autosomal-recessive

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

HIHd1 SNP G284T: **1/1**

#### **Please note:**

Further causative mutations for longhaired have been found in the 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.

**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.

**Dwarfism - PCR**

Unfortunately, there is no valid result from the submitted sample for this genetic test of the combination.

Please send a new EDTA blood sample for a retest.

The test is included in the price of the combination. Therefore, this retest is free of charge when the above mentioned result number is added to the new sample submission as a reference.

**MDR1 genetic test - PCR**

Result: Genotype N/N (+/+)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for MDR in the ABCB1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Border Collie, Elo, German Shepherd, Longhaired Whippet, McNab, Old English Sheepdog, Rough/Smooth Collie, Shetland Sheepdog, Silken Windhound, Wäller, White Shepherd

Please note: in individual cases, heterozygous dogs can show clinical signs!

The DNA-test is run according to the publication of Mealey et al. (2001) "Ivermectin sensitivity in collies is associated with a deletion mutation of the mdr1 gene." and detects the mutation MDR1 nt230 (del4).

MDR1 genetic test carried out according to DIN EN ISO/IEC 17025 in our partnerlaboratory. Liability for specification of samples (e.g. name, identity of animal) lies by the sender.

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).

**Sampling:**

The following impartial person (veterinarian, breed warden, or similar) signed the form for the sampling and identity check of the animal:

**Dra. Eva Joana Costa da Silva (CP 4153)**

**Breeding club discounts were granted for discountable services!**

These results are based on the sample material submitted to our laboratory.

This was suitable if not stated otherwise. The submitter is responsible for the accuracy of the information regarding the sample. This report can only be transmitted in toto and unchanged. Doing otherwise requires written permission from Laboklin GmbH & Co. KG.



Hr. Dr. Beitzinger  
Dipl.-Biol. Molekularbiologie

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

**PCR diagnostics for equine herpes virus**

Due to the currently increased need for PCR tests for EHV1 and EHV4, we are performing this test for you up to 4 times a day. Results are usually available within 1-2 working days after arrival of the sample in the lab.

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Pets Cunsultorio Veterinario  
Dra. Eva Joana Costa da Silva  
Rua Manuel Martins Gomes Junior 42  
2835- 725 Santo Antonio de Charneca  
Portugal

|                    |                     |
|--------------------|---------------------|
| <b>Report No.:</b> | <b>2104-W-28683</b> |
| Date of arrival:   | 14.04.2021          |
| Date of report:    | 23.04.2021          |
| Testing started:   | 14.04.2021          |
| Testing completed: | 23.04.2021          |

|                        |                                 |
|------------------------|---------------------------------|
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| Breed:                 | Altdeutscher Schäferhund        |
| Gender:                | Male                            |
| Name:                  | Aruk de la Legende du Loup Noir |
| Stud book No.:         | IHR 2190065                     |
| Chip No.:              | 250208501656236                 |
| Date of birth / Age:   | 10.11.2018                      |
| Type of sample:        | EDTA-Blood                      |
| Date sample was taken: | 13.04.2021                      |
| Owner / Animal-ID:     | Frohn, Ines                     |
| IT No. / Report-ID:    | ---                             |

## **Dwarfism - PCR**

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for Dwarfism in the LHX3-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: German Shepherd, Saarlooswolfdog, Czechoslovakian Wolfdog

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.

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

These results are based on the sample material submitted to our laboratory.

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**LABOKLIN is an accredited laboratory according to DIN EN ISO/IEC 17025:2018, DAkkS No. D-PL-13186-01-01 and D-PL-13186-1-02. The accreditation applies to all test procedures listed in the accreditation certificate.**



Hr.LM-Chemiker D. Schindelmann  
Abt. Molekularbiologie

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

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