LABOKLIN
LABOR FÜR KLINISCHE DIAGNOSTIK GMBH & CO. KG

HV Atlántico
Paulo Borges
Rua Quintino Antonio Gomes 12
2640- 402 Mafra (Portugal)
Portugal

Eingangsdatum: 18-03-2023

Angaben zum Patienten:	Dog	Male
Rasse:	Pastor alemán	
Probenentnahme:		
Patientenbesitzer:	Quinta Silfrohm, Vila Amelia	
Probenmaterial:	EB(x2)	

Befund-Nummer: 2303-M-05814

Messgrößen	Ist	Normalwert

Classic STR DNA-Profile (ISAG 2006) - PCR

breeder association: ---
name: Drulak
stud book no.: ---
tattoo no.: ---
chip no.: 616093901760422

Name:	Drulak
ZB-Nr.:	---
Tattoo-Nummer:	---
Chip-Nr.:	616093901760422
Amelogenin:	Y/X
AHT 121:	102/104
AHT 137:	133/137
AHTH 130:	-/-
AHTH 171:	225/225
AHTH 260:	242/242
AHTK 211:	89/89
AHTK 253:	288/288
CXX 279:	116/116
FH 2054:	152/168
FH 2848:	232/240
INRA 21:	97/99
INU 005:	110/126
INU 030:	150/150

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INU 055:	218/218
REN 105 L 03:	227/241
REN 162 C 04:	212/212
REN 169 D 01:	212/216
REN 169 O 18:	162/168
REN 247 M 23:	270/270
REN 54 P 11:	226/234
REN 64 E 19:	155/155

Nomenclature is based on ISAG comparison test 2006 standards.

The results are only for the sample material submitted to the laboratory. Responsibility for the accuracy of the information on the sample provided lies with the submitter. No warranty obligation for that information is provided. Damage claim liabilities, if legally permissible, are limited to the invoice value of the testing done. We are also only liable for intentional and gross negligence, if legally possible. Additional genetic modifications which might also influence the development of the disease/trait, cannot be ruled out. Testing was carried out according to current general scientific knowledge.

The laboratory is accredited for the tests listed in this report according to DIN EN ISO 17025:2018.

In the requested DNA profile an issued Certificate is included (not for breed classifications) if the sample has been collected by a veterinarian. Please thoroughly verify the animal and owner data provided to you. Any corrections afterward can only be carried out in accordance with prior written confirmation from the veterinarian.
Please note that an extra charge will be invoiced separately upon changes to an already issued certificate.

Sampling:

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

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Paulo Borges

Stud book no.: ---
Chip no.: 616093901760422
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.

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

HlHd1 SNP G284T: l/l

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.

MDR1 gene variant - 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!

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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).

Pituitary 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, Tibetan Terrier, White Swiss Shepherd Dog

I locus (pheomelanin intensity) - PCR

Result: Genotype I/I

Interpretation: The examined animal is homozygous for the I-allele.

The test detects the alleles I and i.
Allelic series: I dominant over i

Genetic analysis K-Lokus (PCR)
Result: Genotype Kb/ky

Interpretation: The examined animal is heterozygous for the Kb- and ky-allele.

The test detects the alleles Kb and ky.
Allelic series: Kb dominant over ky

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K locus (brindle)

Please note: LABOKLIN offers no longer shipment of samples for the brindle gene test. There is the possibility to test for the K locus at LABOKLIN, but this test only for the alleles KB and ky. From this result, no statement about the presence or absence of kbr (brindle) allele can be made.

D-locus D1 (dilution)

Result for d1: Genotype N/d1 (before D/d1)

Interpretation: One d1-allele was found for this sample. The animal is heterozygous for this variant.

The overall genotype for the D-locus-complex can only be deduced if all known variants on the D-locus (d1, d2 and d3) are analysed. Some of these alleles only exist in specific breeds.

Please note: The nomenclature of the results has been changed due to harmonizing efforts for genetic tests.

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).

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Luisa Murcia Giro - Veterinaria