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

Dierenkliniek
Ridderkerk
Jacob Catsstraat 3
2985 BE Ridderkerk
Nederland

Report
No.: 2109-N-17370
Date of arrival: 17-09-2021
Date of report: 27-09-2021

Patient identification:	Dog male	* 14.06.20
	Labrador Retriever	
Owner / Animal-ID:	Nugteren, S.	
Type of sample:	EDTA	
Date sample was taken:	28-12-2020	

Additional Order of 17.09.2021 to Report-No. 2012-N-15709
Original Sample received on: 28.12.2020

Name:	**Cedarwood Choc'n Chuckle**
Stud book no.:	**SS20205204**
Chip no.:	**956000004566822**
Tattoo no.:	**---**

D-locus D1 (dilution)

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

Interpretation: No d1-allele was found for this sample.

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

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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

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Report
No.: 2012-N-15709
Date of arrival: 29-12-2020
Date of report: 12-01-2021

Patient identification:	Dog male	* 14.06.20
	Labrador Retriever	
Owner / Animal-ID:	Nugteren, S.	
Type of sample:	EDTA	
Date sample was taken:	28-12-2020	

Name: **Cedarwood Choc'n Chuckle**
Stud book no.: **SS20205204**
Chip no.: **956000004566822**
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.

Exercise Induced Collapse (EIC) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for EIC in the DNM1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Boykin Spaniel, Chesepeake Bay Retriever, Clumber Spaniel, Curly Coated Retriever, Labrador Retriever, Old English Sheepdog, Pembroke Welsh Corgi and Wirehairede Pointer

Hereditary nasal parakeratosis (HNPK) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for HNPK in the SUV39H2-gene.

Trait of inheritance: autosomal-recessive

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

Dwarfism (Skeletal Dysplasia 2) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for SD2 in the COL11A2-gene.

Trait of inheritance: autosomal-recessive

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

Hereditary myopathy (CNM) - PCR

Result: Genotype N/N

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

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and

symptoms of the disease in the following breeds: Labrador Retriever
Other forms of myopathy cannot be excluded by this test.

*__prcd-PRA (partner lab) - PCR__

Result: Genotype N/N (A)

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

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian cattle dog, American Cocker Spaniel, American Eskimo Dog, Australian Shepherd, Australian Stumpy Tail Cattle Dog, Barbet, Bearded Collie, Bolognese, Bolonka Zwetna, Chesapeake Bay Retriever, Chihuahua, Chinese Crested, English Cocker Spaniel, English Shepherd, Entlebucher Mountain Dog, Finnish Lapphund, German Spitz, Giant Schnauzer, Golden Retriever, Jack Russell Terrier, Karelian Beardog, Kuvasz, Lagotto Romagnolo, Lapponian Herder, Labrador Retriever, Markiesje, Norwegian Elkhound, Nova Scotia Duck Tolling Retriever, Parson Russell Terrier, Portugese Water Dog, Poodle, Schipperke, Swedish Lapphound, Silky Terrier, Spanish Water Dog, Swedish Lapphund, Wäller, Yorkshire Terrier.

*__Retinal dysplasia (OSD) - PCR__
Result: Genotype N/N
Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for OSD.
Trait of inheritance: autosomal-dominant Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Labrador Retriever

__E-locus e1 (apricot, cream, lemon, red, yellow) - PCR__

Result for e1: Genotype N/N (before E/E)

Interpretation: No e1-allele was found for this sample.

The overall genotype for the E-locus-complex can only be deduced

if all known variants on the E-locus (e1, e2, e3, eA, eg, eh and EM) 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.

Coat length I (long or short hair) - PCR

HlHd1 SNP G284T: **L/L**

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 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.

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There is a possibility that other mutations may have caused the

sample ID: 2012-N-15709

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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

*: test performed by partnerlaboratory