dr. van haeringen laboratorium b.v.

a VHLGenetics company

VAN ROOIJ
Rue des Combattants d'Havinnes
7531 Havinnes
BELGIUM
Customer number 127764

Through: Zoolyx NV
Groene Weg 17 17
BE-9320 EREMBODEGEM
BELGIUM

Analysis Certificate

Animal data

Name:	SILKE DU CHEMIN DES CAVALIERS
Date of birth:	21.04.2020
Sexe:	Female
Reg. nr.:	250269500825397
Breed:	Beagle

Sample data

VHL_ID:	H592194
Test ID-nr:	580323 1
Material:	Swab

H364 - Hypocatalasia - Date of test: 19.06.2023
Testresult: NORMAL

H366 - IGS (Selective Cobalamin Malabsorption) 1 - Date of test: 19.06.2023
Testresult: NORMAL

H413 - Cerebellar abiotrophy - Date of test: 19.06.2023
Testresult: NORMAL

H424 - Musladin-Lueke syndrome - Date of test: 19.06.2023
Testresult: NORMAL

H430 - Osteogenesis imperfect Beagle - Date of test: 19.06.2023
Testresult: NORMAL

H435 - Factor VII deficiency - Date of test: 19.06.2023
Testresult: NORMAL

H455 - Pyruvate Kinase Deficiency (PKDef) - Beagle - Date of test: 19.06.2023
Testresult: NORMAL

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H496 - Glaucoma (POAG) - Date of test: 19.06.2023
Testresult: NORMAL

H811 - Hyperuricemia (HUU) - Date of test: 19.06.2023
Testresult: NORMAL

H919 - Hiplaxity 1 - Date of test: 19.06.2023
Testresult: HL/HL

H421 - Hiplaxity 2 - Date of test: 19.06.2023
Testresult: HL/HL

H346 - Chondrodystrophy and Intervertebral Disc Disease - Date of test: 19.06.2023
Testresult: AFFECTED

H468 - Lafora Disease - Date of test: 23.06.2023
Testresult: NORMAL

D. Mioch, MSc Veterinary Medicine
CEO

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H364 - Hypocatalasia
Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H366 - IGS (Selective Cobalamin Malabsorption) 1
Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H413 - Cerebellar abiotrophy
Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H424 - Musladin-Lueke syndrome
Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H430 - Osteogenesis imperfect Beagle
This genetic factor was detected as a heterozygous mutation in a severely affected proband which indicates a dominant mode of inheritance. This is in agreement with the homozygous human variant of Osteogenesis imperfecta, where in the vast majority of instances, the phenotype results from heterozygousity for mutations in one of the genes that encode chains of type I collagen. However, as the number of cases analysed in dogs is currently low, this conclusion contains a certain degree of uncertainty.

H435 - Factor VII deficiency
Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop

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the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H455 - Pyruvate Kinase Deficiency (PKDef) - Beagle

Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H496 - Glaucoma (POAG)

Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H811 - Hyperuricemia (HUU)

Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H919 - Hiplaxity 1

The disease is of multifactorial origin, which means that the symptoms are a combination of genetic factors as well as the environment.
This marker is part of a panel of genetic factors influencing hip laxity. For each genetic factor of a multifactorial disease, the desirable genetic variant is indicated as 'N/N'. Animals carrying one copy of the undesirable genetic variant are indicated as 'N/HL', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'HL/HL'.

H421 - Hiplaxity 2

The disease is of multifactorial origin, which means that the symptoms are a combination of genetic factors as well as the environment.
This marker is part of a panel of genetic factors influencing hip laxity. For each genetic factor of a multifactorial disease, the desirable genetic variant is indicated as 'N/N'. Animals carrying one copy of the undesirable genetic variant are indicated as 'N/HL', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'HL/HL'.

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H346 - Chondrodystrophy and Intervertebral Disc Disease

Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will most likely develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that is will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the decribed clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

H468 - Lafora Disease

Explanation about the result:
NORMAL: The animal has two normal alleles and is therefore not affected by this specific variant. The animal will not develop the described clinical features due to this variant. When used in breeding, a healthy allele will be passed to all offspring.
CARRIER: The animal is a carrier; it has one normal and one affected allele. The animal will not develop the described clinical features due to this variant. In breeding, there is a 50% chance for each offspring that it will receive an affected allele.
AFFECTED: The animal is affected; it has two affected alleles. The animal will most likely develop the described clinical features due to this variant. When used in breeding, all offspring will receive an affected allele.

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