dr. van haeringen laboratorium b.v.

a VHLGenetics company

"YESSI"
YESSI DE LA SERROTA
28.09.2014 - LOE 2229161

LABORATORIOS LABOCOR S.L.

CombiGen® GENETICS IN PRACTICE for vets

NOMBRE	**YESSI DE LA SERROTA**
Nº DE REGISTRO	LOE 2229161
CHIP	941000017340688
DÍA DE NACIMIENTO	28/09/2014
SEXO	HEMBRA
RAZA	BRACO HÚNGARO DE PELO CORTO
NOMBRE DEL PADRE	LUXATORI ORJA
Nº REGISTRO DEL PADRE	LOE 2149464 - Export Pedigre 19652 - Mv.5276/07
NOMBRE DE LA MADRE	LUXATORI FAMA
Nº REGISTRO DE LA MADRE	LOE 2176820 Mv. 9787/13

H480 CombiBreed FCI Grupo 07

H699 CombiGen Perro

H765 CombiGen Longitud Pelo

BRACOS HUNGAROS
MAGYAR VIZSLA

CanBrúguera

dr. van haeringen laboratorium b.v.
a VHLGenetics company

dr. van haeringen laboratorium b.v.
a VHLGenetics company

LABOCOR, S.L.
Alamillo 41
ES-28770 COLMENAR VIEJO (MADRI
SPAIN
Customer number 23465

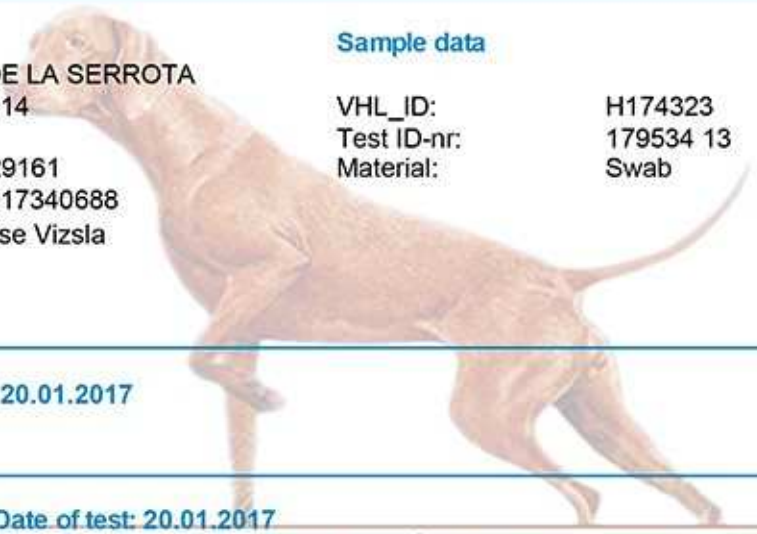
Analysis Certificate

Animal data

Name:	YESSI DE LA SERROTA
Date of birth:	28.09.2014
Sexe:	Female
Reg. nr.:	LOE 2229161
Chip number:	941000017340688
Breed:	Hongaarse Vizsla

Sample data

VHL_ID:	H174323
Test ID-nr:	179534 13
Material:	Swab



H717 - PFK Test - Date of test: 20.01.2017
Testresult: NORMAL

H811 - Hyperuricemia (HUU) - Date of test: 20.01.2017
Testresult: NORMAL

H770 - rcd3-PRA - Date of test: 20.01.2017
Testresult: NORMAL

H728 - CSNB Test - Date of test: 20.01.2017
Testresult: NORMAL

H871 - CMR1 - Date of test: 20.01.2017
Testresult: NORMAL

H724 - L2-HGA - Date of test: 20.01.2017
Testresult: NORMAL

H787 - TNS - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H456 - SCID 2 - Date of test: 20.01.2017
Testresult: NORMAL

H450 - Bleeding disorder P2RY12 def. - Date of test: 20.01.2017
Testresult: NORMAL

H493 - Muscular hypertrophy (double muscling) - Date of test: 20.01.2017
Testresult: NORMAL

H873 - Ichthyosis 2 - GR - Date of test: 20.01.2017
Testresult: NORMAL

H703 - Cystinuria, type I - A - 1 - Date of test: 20.01.2017
Testresult: NO RESULT

H868 - GR-PRA1 - Date of test: 20.01.2017
Testresult: NORMAL

H804 - Cerebellar Ataxia / NCL-A - Date of test: 20.01.2017
Testresult: NO RESULT

H849 - PLL - Date of test: 20.01.2017
Testresult: NORMAL

H730 - CMR2 Test - Date of test: 20.01.2017
Testresult: NORMAL

H919 - Hiplaxity 1 - Date of test: 20.01.2017
Testresult: AFFECTED

H421 - Hiplaxity 2 - Date of test: 20.01.2017
Testresult: AFFECTED

H748 - Mucopolysacc. Type 7 - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H414 - Ciliary dyskinesia primary - Date of test: 20.01.2017
Testresult: NORMAL

H812 - Neonatal Encephalopathy - Date of test: 20.01.2017
Testresult: NORMAL

H424 - Musladin-Lueke syndrome - Date of test: 20.01.2017
Testresult: NORMAL

H427 - Myotubular myopathy 1 - Date of test: 20.01.2017
Testresult: NORMAL

H740 - PDP1 Deficiency - Date of test: 20.01.2017
Testresult: NORMAL

H435 - Factor VII deficiency - Date of test: 20.01.2017
Testresult: NORMAL

H741 - Piruvatekinase Def. - Date of test: 20.01.2017
Testresult: NORMAL

H510 - Skeletal Dysplasia 2 (SD2) - Date of test: 20.01.2017
Testresult: NORMAL

H487 - Brachyury (Bobtail) - Date of test: 20.01.2017
Testresult: NORMAL

H709 - CLAD, type I - Date of test: 20.01.2017
Testresult: NORMAL

H913 - Dry Eye Curly Coat - Date of test: 20.01.2017
Testresult: NORMAL

H768 - rcd1-PRA - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H733 - B-locus (CC Brown) - Date of test: 26.01.2017
Testresult: >2 b

H734 - E-locus (CC Yellow) - Date of test: 20.01.2017
Testresult: e/e

H765 - Hair Length - Date of test: 20.01.2017
Testresult: S/S

H818 - Em locus - Date of test: 20.01.2017
Testresult: N/N

H351 - Amelogenesis Imperfecta - Date of test: 20.01.2017
Testresult: NORMAL

H355 - Cerebellar Hypoplasia Resembling - Date of test: 20.01.2017
Testresult: NORMAL

H356 - Chondrodysplasia, Disproportionate Short-Limbed - Date of test: 20.01.2017
Testresult: NORMAL

H357 - Cone Rod Dystrophy 1 (crd1) - Date of test: 20.01.2017
Testresult: NORMAL

H358 - Cone Rod Dystrophy 2 (crd2) - Date of test: 20.01.2017
Testresult: NORMAL

H359 - Muscular Dystrofie, Duchenne type (MDM) 2 - Date of test: 20.01.2017
Testresult: NORMAL

H360 - Gallbladder Mucocele - Date of test: 20.01.2017
Testresult: NORMAL

H361 - Gangliosidosis, GM2, Type I (B variant) - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H363 - Hyperkeratosis, epidermolytic - Date of test: 20.01.2017
Testresult: NORMAL

H364 - Hypocatalasia - Date of test: 20.01.2017
Testresult: NORMAL

H365 - Hypomyelination - Date of test: 20.01.2017
Testresult: NORMAL

H366 - IGS (Selective Cobalamin Malabsorption) 1 - Date of test: 20.01.2017
Testresult: NORMAL

H367 - IGS (Selective Cobalamin Malabsorption) 2 - Date of test: 20.01.2017
Testresult: NORMAL

H368 - Myopathy - Date of test: 20.01.2017
Testresult: NORMAL

H370 - Nephritis, X-linked - Date of test: 20.01.2017
Testresult: NORMAL

H371 - PRA - Date of test: 20.01.2017
Testresult: NORMAL

H372 - PRA crdPRA - Date of test: 20.01.2017
Testresult: NO RESULT

H373 - PRA type 3 - Date of test: 20.01.2017
Testresult: NO RESULT

H374 - Primary Hyperoxaluria - Date of test: 20.01.2017
Testresult: NORMAL

H375 - Dog_Skin Fragility - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H377 - Dog_Spinal Dysraphism - Date of test: 20.01.2017
Testresult: NO RESULT

H473 - GR-PRA2 - Date of test: 20.01.2017
Testresult: NORMAL

H511 - rcd4-PRA - Date of test: 20.01.2017
Testresult: NORMAL

H697 - Narcolepsie Doberman Pinscher - Date of test: 20.01.2017
Testresult: NO RESULT

H698 - Narcolepsy Labrador Retriever - Date of test: 20.01.2017
Testresult: NORMAL

H699 - Hereditary Cataract 2 (HC) -HSF4 - Date of test: 20.01.2017
Testresult: NORMAL

H701 - Coppertoxicosis Test - Date of test: 20.01.2017
Testresult: NORMAL

H738 - Myotonia Congenita - Date of test: 20.01.2017
Testresult: NORMAL

H749 - Centronucleaire Myopatie (CNM) - Date of test: 20.01.2017
Testresult: NORMAL

H766 - crd4-PRA - Date of test: 20.01.2017
Testresult: NORMAL

H809 - Heriditary Cateract (HC) - HSF4 - Date of test: 20.01.2017
Testresult: NORMAL

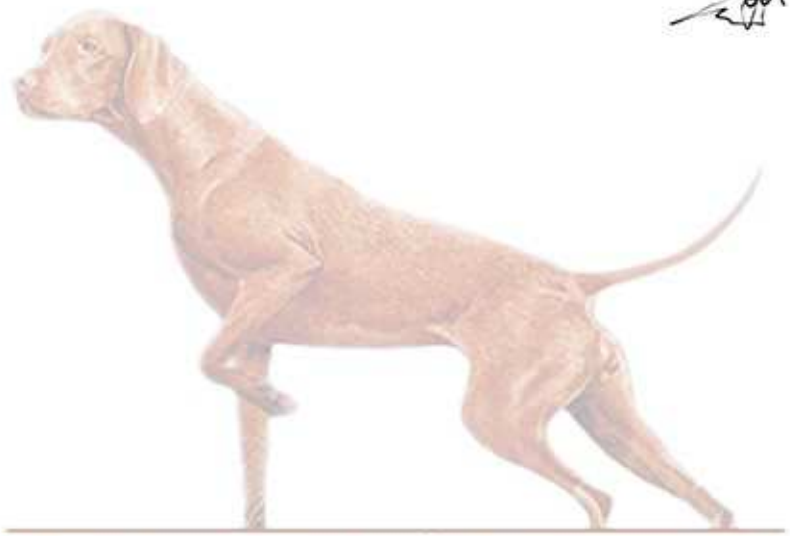
H872 - Pituitary Dwarfism - Date of test: 20.01.2017
Testresult: NORMAL

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

dr. van haeringen laboratorium b.v.
a VHLGenetics company

H847 - Coat Colour D-Locus Improved (MLPH) - Date of test: 20.01.2017
Testresult: D/D

W.A. van Haeringen, PhD
Executive Director



VHL exercises the utmost care in performing each of its engagements. No party other than the principal may derive any rights from the results of these engagements, and the principal expressly indemnifies VHL in respect of any third-party claims. VHL policy provides that any complaints must be received within eight days of the completion of an engagement and imposes restrictions on liability. In that respect, VHL refers to its General Conditions, which are applicable to all engagements VHL performs and which were enclosed with the submission form. These General Conditions can also be reviewed at www.vhlgenetics.com. The work VHL performs is based on the material and/or data it receives from its principal. This report may only be copied in its entirety. The organization is ISO:9001 certified for all her work. This test is based on PCR technology.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H717 - PFK Test

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H811 - Hyperuricemia (HUU)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H770 - rcd3-PRA

Information about the rcd3 PRA test:

Result Normal (N/N): The dog is homozygous normal for the mutation that is responsible for rcd3-type PRA.

Result Carrier (N/n): The dog is carrier of the mutation that is responsible for rcd3-type PRA.

Result Affected (n/n): The dog is homozygous affected for the mutation that is responsible for rcd3-type PRA.

H728 - CSNB Test

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H871 - CMR1

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H724 - L2-HGA

Explanation about the result:

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H787 - TNS

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H456 - SCID 2

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H450 - Bleeding disorder P2RY12 def.

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H493 - Muscular hypertrophy (double muscling)

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H873 - Ichthyosis 2 - GR

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H703 - Cystinuria, type I - A - 1

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H868 - GR-PRA1

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H804 - Cerebellar Ataxia / NCL-A

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H849 - PLL

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H730 - CMR2 Test

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

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 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

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 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

H748 - Mucopolysacc. Type 7

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H414 - Ciliary dyskinesia primary

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H812 - Neonatal Encephalopathy

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H424 - Musladin-Lueke syndrome

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H427 - Myotubular myopathy 1

Explanation about the result for females:
NORMAL: The animal is free and has two healthy alleles. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.
Explanation about the result for males:
NORMAL: The animal is free and has one healthy allele and the sex chromosome Y. It cannot spread the disease in the population.
AFFECTED: The animal is affected and has one mutant (disease) allele and the sex chromosome Y. When used in breeding, all male offspring will receive the sex chromosome Y. All female offspring will receive the mutant (disease) allele.

H740 - PDP1 Deficiency

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H435 - Factor VII deficiency

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H741 - Piruvatekinase Def.

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H510 - Skeletal Dysplasia 2 (SD2)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H487 - Brachyury (Bobtail)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H709 - CLAD, type I

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H913 - Dry Eye Curly Coat

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H768 - rcd1-PRA

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H733 - B-locus (CC Brown)

Information about the brown coat colour (B-locus):
Result B/B: The dog is non-carrier of the mutation that is responsible for the brown coat colour.
Result B/b: The dog is carrier of the mutation that is responsible for the brown coat colour.
Result b/b: The dog is homozygous for the mutation that is responsible for the brown coat colour.
Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.
Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

Explanation about result >2 b:
This dog carries more than two b-alleles. The colour of this dog can be brown or black.
Option 1: The dog is black. In this case it also carries one copy of the B-allele and therefore can pass either B or b to its offspring.
Option 2: The dog is brown. In this case it carries only b-alleles and therefore can only pass b to its offspring.

H734 - E-locus (CC Yellow)

Information about the yellow coat colour (E-locus):
Result E/E: The dog is non-carrier of the mutation that is responsible for the yellow coat colour.
Result E/e: The dog is carrier of the mutation that is responsible for the yellow coat colour.
Result e/e: The dog is homozygous for the mutation that is responsible for the yellow coat colour.
Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.
Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

H765 - Hair Length

Information about the test for hairlength:
- L/L: The test result shows that the animal is homozygous for the mutation which is suggested to cause long-haired coat.
- S/L: The test result shows that the animal is carrier of the mutation for long-haired coat.
- S/S: The test result shows that the animal does not carry the mutation which is suggested to cause long-haired coat.

Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.
Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

H818 - Em locus

Information about the Em coat colour (Em-locus):
Result Em/Em: The dog is homozygous for the mutation that is responsible for a black mask.
Result Em/N: The dog is carrier from the mutation that is responsible for a black mask. Due to the dominant inheritance it has a melanistic mask.
Result N/N: The dog is no carrier from the mutation that is responsible for a black mask.
Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

H351 - Amelogenesis Imperfecta

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H355 - Cerebellar Hypoplasia Resembling

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H356 - Chondrodysplasia, Disproportionate Short-Limbed

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H357 - Cone Rod Dystrophy 1 (crd1)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H358 - Cone Rod Dystrophy 2 (crd2)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H359 - Muscular Dystrofie, Duchenne type (MDM) 2

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H360 - Gallbladder Mucocele

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H361 - Gangliosidosis, GM2, Type I (B variant)

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H363 - Hyperkeratosis, epidermolytic

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H364 - Hypocatalasia

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H365 - Hypomyelination

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H366 - IGS (Selective Cobalamin Malabsorption) 1

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H367 - IGS (Selective Cobalamin Malabsorption) 2

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H368 - Myopathy

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H370 - Nephritis, X-linked

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H371 - PRA

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

will receive the mutant allele from this animal. Affected animals will become ill.

H372 - PRA crdPRA

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H373 - PRA type 3

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H374 - Primary Hyperoxaluria

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H375 - Dog_Skin Fragility

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H377 - Dog_Spinal Dysraphism

Explanation about the result:

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H473 - GR-PRA2

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H511 - rcd4-PRA

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H697 - Narcolepsie Doberman Pinscher

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H698 - Narcolepsy Labrador Retriever

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H699 - Hereditary Cataract 2 (HC) -HSF4

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H701 - Coppertoxicosis Test

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H738 - Myotonia Congenita

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H749 - Centronucleaire Myopatie (CNM)

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H766 - crd4-PRA

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H809 - Heriditary Cateract (HC) - HSF4

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H872 - Pituitary Dwarfism

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT: The genetic test for this mutation is known to exist in a few breeds. This may lead to a situation where the test does not produce a result. In such cases, it is not possible to determine whether an animal is free, carrier or affected for this mutation.

H847 - Coat Colour D-Locus Improved (MLPH)

Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.
Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

dr. van haeringen laboratorium b.v.
a VHLGenetics company

LABOCOR, S.L.
Alamillo 41
ES-28770 COLMENAR VIEJO (MADRI
SPAIN
Customer number 23465

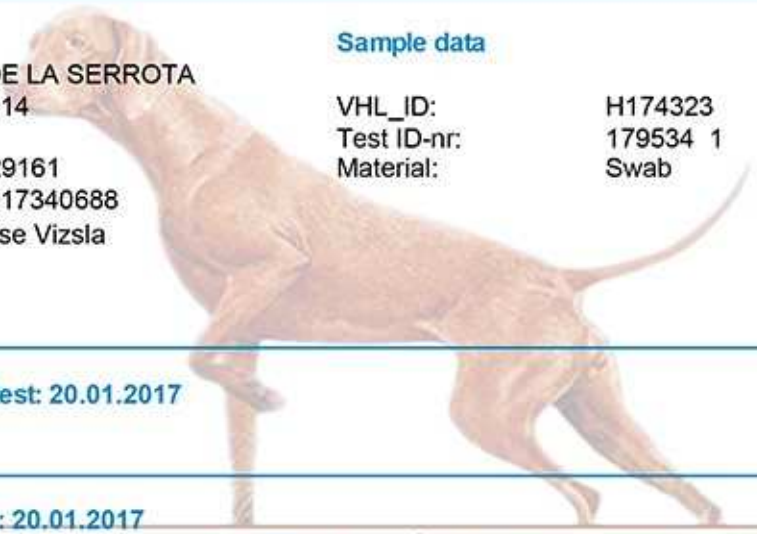
Analysis Certificate

Animal data

Name:	YESSI DE LA SERROTA
Date of birth:	28.09.2014
Sexe:	Female
Reg. nr.:	LOE 2229161
Chip number:	941000017340688
Breed:	Hongaarse Vizsla

Sample data

VHL_ID:	H174323
Test ID-nr:	179534 1
Material:	Swab



H412 - C3 deficiency - Date of test: 20.01.2017
Testresult: NORMAL

H421 - Hiplaxity 2 - Date of test: 20.01.2017
Testresult: AFFECTED

H425 - Myasthenic syndrome congenital - Date of test: 20.01.2017
Testresult: NORMAL

H709 - CLAD, type I - Date of test: 20.01.2017
Testresult: NORMAL

H811 - Hyperuricemia (HUU) - Date of test: 20.01.2017
Testresult: NORMAL

H918 - Cone Degeneration - Date of test: 20.01.2017
Testresult: NORMAL

H919 - Hiplaxity 1 - Date of test: 20.01.2017
Testresult: AFFECTED

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

dr. van haeringen laboratorium b.v.
a VHLGenetics company

H768 - rcd1-PRA - Date of test: 20.01.2017
Testresult: NORMAL

H511 - rcd4-PRA - Date of test: 20.01.2017
Testresult: NORMAL

H377 - Dog_Spinal Dysraphism - Date of test: 20.01.2017
Testresult: NO RESULT

H743 - vWD Type II - Date of test: 20.01.2017
Testresult: NORMAL

W.A. van Haeringen, PhD
Executive Director

VHL exercises the utmost care in performing each of its engagements. No party other than the principal may derive any rights from the results of these engagements, and the principal expressly indemnifies VHL in respect of any third-party claims. VHL policy provides that any complaints must be received within eight days of the completion of an engagement and imposes restrictions on liability. In that respect, VHL refers to its General Conditions, which are applicable to all engagements VHL performs and which were enclosed with the submission form. These General Conditions can also be reviewed at www.vhlgenetics.com. The work VHL performs is based on the material and/or data it receives from its principal. This report may only be copied in its entirety. The organization is ISO:9001 certified for all her work. This test is based on PCR technology.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H412 - C3 deficiency

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

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 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

H425 - Myasthenic syndrome congenital

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H709 - CLAD, type I

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H811 - Hyperuricemia (HUU)

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.

CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.

AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H918 - Cone Degeneration

Explanation about the result:

NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

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 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

H768 - rcd1-PRA

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will also become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H511 - rcd4-PRA

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

H377 - Dog_Spinal Dysraphism

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

NO RESULT. The sample has been tested without a result for this specific test. However, as this sample was submitted for multiple tests, these other results confirm that the sample quality was sufficient and the test protocols have performed well. In order to receive a result for this missing test, a new test should be ordered.

H743 - vWD Type II

Explanation about the result:
NORMAL: The animal is free and has two healthy alleles. When used in breeding, this animal will not become ill

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

due to the disease. It cannot spread the disease in the population.
CARRIER: The animal is carrier and has one healthy and one mutant (disease) allele. When used in breeding, 50 percent of the offspring will receive the disease allele. Carriers will not become ill.
AFFECTED: The animal is affected and has two mutant (disease) alleles. When used in breeding, all offspring will receive the mutant allele from this animal. Affected animals will become ill.

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

dr. van haeringen laboratorium b.v.
a VHLGenetics company

LABOCOR, S.L.
Alamillo 41
ES-28770 COLMENAR VIEJO (MADRI
SPAIN
Customer number 23465

Analysis Certificate

Animal data

Name:	YESSI DE LA SERROTA
Date of birth:	28.09.2014
Sexe:	Female
Reg. nr.:	LOE 2229161
Chip number:	941000017340688
Breed:	Hongaarse Vizsla

Sample data

VHL_ID:	H174323
Test ID-nr:	179534 85
Material:	Swab

H765 - Hair Length - Date of test: 20.01.2017

Testresult: S/S

W.A. van Haeringen, PhD
Executive Director

H765 - Hair Length

Information about the test for hairlength:
- L/L: The test result shows that the animal is homozygous for the mutation which is suggested to cause long-haired coat.
- S/L: The test result shows that the animal is carrier of the mutation for long-haired coat.
- S/S: The test result shows that the animal does not carry the mutation which is suggested to cause long-haired coat.

Detailed information about Coat Colours and Coat Variation is available at www.combibreed.com.
Direct link: http://www.combibreed.com/en-us/customerservice/informationcoatvariation/dog.aspx

(Certificate nr: H26763/Date of issue: 20.01.2017)

 <end of report>

Agro Business Park 100,NL-6708 PW Wageningen - T.+31(0)317416402 - F.+31(0)317426117 - info@vhlgenetics.com - www.vhlgenetics.com
Chamber of commerce Arnhem 09112692 - VAT nr NL8088.07.973.B.01

H919 Hiplaxity 1

Background

Laxity of the hip joint is a frequent disorder in dogs. The disease is of multifactorial origin, which means that the symptoms are a combination of genetic factors as well as the environment.

Hip Laxity has two main characteristics:
• Laxity: This can be defined by 'an abnormal freedom of movement of the bone in the hip joint'. As a result, the hip is less stable compared to healthy dogs.
• Ossification and bone formation. In younger dogs, the normal process of bone formation can be slowed down.

Both Laxity and Ossifcation disorders lead to the development of artrosis when dogs mature. Dogs which are affected most can already express symptoms after a few months. Other affected dogs develop artrosis at later ages.

This marker is part of a panel of genetic factors influencing hip laxity.

Test specific information

Age

The disease may show itself on different ages, in which it cannot be estimated when the first symptoms may show themselves. Differences may exist between littermates, and between breeds.

Throughput

Normally the result can be expected within 10 working days. This turn-around-time starts when both the sample and the fully filled-out and signed submission form have been received.

Location of disease or trait

This disease is located in the hip.

Breed dependence

For this test samples from all breeds are accepted.

Sample type

For this DNA test we accept the following materials: Blood EDTA, Blood Heparin, Tissue, Swab, Semen. Please contact Dr. Van Haeringen Laboratorium if you wish to submit other material as listed.

Result

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 results are inidcated as 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

Inheritance

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.

Treatment

For this disease, treatment is available

H421 Hiplaxity 2

Background

Laxity of the hip joint is a frequent disorder in dogs. The disease is of multifactorial origin, which means that the symptoms are a combination of genetic factors as well as the environment.

Hip Laxity has two main characteristics:
• Laxity: This can be defined by 'an abnormal freedom of movement of the bone in the hip joint'. As a result, the hip is less stable compared to healthy dogs.
• Ossification and bone formation. In younger dogs, the normal process of bone formation can be slowed down.

Both Laxity and Ossifcation disorders lead to the development of artrosis when dogs mature. Dogs which are affected most can already express symptoms after a few months. Other affected dogs develop artrosis at later ages.

This marker is part of a panel of genetic factors influencing hip laxity.

Test specific information

Age

The disease may show itself on different ages, in which it cannot be estimated when the first symptoms may show themselves. Differences may exist between littermates, and between breeds.

Throughput

Normally the result can be expected within 10 working days. This turn-around-time starts when both the sample and the fully filled-out and signed submission form have been received.

Location of disease or trait

This disease is located in the hip.

Breed dependence

For this test samples from all breeds are accepted.

Sample type

For this DNA test we accept the following materials: Blood EDTA, Blood Heparin, Swab, Tissue, Semen. Please contact Dr. Van Haeringen Laboratorium if you wish to submit other material as listed.

Result

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 results are inidcated as 'Normal'. Animals carrying one copy of the undesirable genetic variant are indicated as 'Carrier', whereas animals carrying two copies of the undesirable genetic variant are indicated as 'Affected'.

Inheritance

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.

Treatment

For this disease, treatment is available.

H919 Hiplaxity 1

Fondo

La laxitud de la articulación de la cadera es un trastorno frecuente en los perros. La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente.

La laxitud de cadera tiene dos características principales:

• La laxitud: Esto puede ser definido por "una libertad de movimiento anormal del hueso en la articulación de la cadera '. Como resultado, la cadera es menos estable en comparación con los perros sanos.

• La osificación y la formación de hueso. En los perros más jóvenes, el proceso normal de formación de hueso puede ser frenado.

Tanto laxitud y trastornos Ossifcation conducen al desarrollo de la artrosis perros cuando maduran. Los perros que más se ven afectados ya se pueden expresar los síntomas después de unos pocos meses. Otros perros afectados desarrollan artrosis a edades más tardías.

Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Información específica de prueba

Edad

La enfermedad puede manifestarse en diferentes edades, en la que no se puede estimar cuando los primeros síntomas pueden mostrarse. Pueden existir diferencias entre los hermanos de camada, y entre las razas.

Resultado

Normalmente, el resultado se puede esperar dentro de los 10 días hábiles. Esta-around-time a su vez comienza cuando se han recibido tanto la muestra y el de salida llenado completamente y firmado formulario de envío.

Localización de la enfermedad o rasgo

Esta enfermedad se encuentra en la cadera.

Dependencia de la raza

Para esta prueba se aceptan muestras de todas las razas.

Tipo de test

Para esta prueba de ADN aceptamos los siguientes materiales: Sangre con EDTA, heparina de la sangre, de tejidos, de hisopo, el semen. Por favor, póngase en contacto con el Dr. Van Haeringen Laboratorium si desea presentar otro material que se enumeran.

Resultado

La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente. Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Para cada factor genético de una enfermedad multifactorial, los resultados se inidcated como "Normal". Los animales que tienen una copia de la variante genética indeseable se indican como "portador", mientras que los animales que llevan dos copias de la variante genética indeseable se indican como "afectadas".

Herencia

La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente.

Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Tratamiento

Para esta enfermedad, el tratamiento está disponible

D-Locus: H847 Coat colour D-Locus Improved (MLPH)

The dilute gene (MLPH gene) is responsible for the intensity of the coat colour by affecting the distribution of melanin-containing cells. This gene is also known as the D-Locus and dilutes all colours. Besides the hair colour also the colour of the nose is diluted and the colour of the eyes lightens to amber. The Coat Colour D-Locus Improved (MLPH) test (H847) tests for the genetic status of the D-Locus. The D-Locus has two variants (alleles). The allele D is dominant and does not have an effect on the coat colour. Only when the dog has two copies of the recessive allele d the coat colour is diluted. The dilution of black results in grey, also called blue or charcoal. The coat ranges from silver to almost black, but all have a blue nose. Chocolate/brown/liver dilutes into lilac/light tan/Isabella, their noses vary from pink, liver to isabella. Red/yellow/cream dilutes into champagne. In some breeds another, yet unidentified, mutation is present that causes coat colour dilution. This unidentified mutation is known to occur in Doberman Pinscher, French Bulldog, Italian Greyhound, Chow Chow and Shar-Pei.

The Coat Colour D-Locus Improved (MLPH) test encloses the following results, in this scheme the results of the Coat Colour D-Locus Improved (MLPH) test are shown in combination with the possible results for the E-Locus and B-Locus):

D-Locus	E-Locus	B-Locus	Coat Colour	Nose/foot pads
D/D	Em/Em, Em/E or Em/e	B/B or B/b	Black, melanistic mask is not visible	Black
D/D	Em/Em, Em/E or Em/e	b/b	Brown/chocolate/liver, with melanistic mask	Pink to Brown
D/D	E/E or E/e	B/B,B/b	Black, no melanistic mask	Black
D/D	E/E or E/e	b/b	Brown/chocolate/liver, no melanistic mask	Pink to Brown
D/D	e/e	B/B,B/b	Red/Yellow/Cream	Black
D/D	e/e	b/b	Red/Yellow/Cream	Pink to Brown
D/d	Em/Em, Em/E or Em/e	B/B or B/b	Black, melanistic mask is not visible	Black
D/d	Em/Em, Em/E or Em/e	b/b	Brown/chocolate/liver, with melanistic mask	Pink to Brown
D/d	E/E or E/e	B/B,B/b	Black, no melanistic mask	Black
D/d	E/E or E/e	b/b	Brown/chocolate/liver, no melanistic mask	Pink to Brown
D/d	e/e	B/B,B/b	Red/Yellow/Cream	Black
D/d	e/e	b/b	Red/Yellow/Cream	Pink to Brown
d/d	Em/Em, Em/E or Em/e	B/B or B/b	Blue/Grey/Charcoal, melanistic mask is not visible	Blue to Black
d/d	Em/Em, Em/E or Em/e	b/b	Lilac/Light tan/Isabela, with melanistic mask	Pink to Brown
d/d	E/E or E/e	B/B,B/b	Blue/Grey/Charcoal, no melanistic mask	Blue to Black
d/d	E/E or E/e	b/b	Lilac/Light tan/Isabela, no melanistic mask	Pink to Brown
d/d	e/e	B/B,B/b	Champagne	Blue to Black
d/d	e/e	b/b	Champagne	Pink to Brown

BACK TO TOP

A-Locus: H820 Coat Colour A-Locus

The Agouti gene (ASIP gene) is responsible for the production of a protein that regulates the distribution of black pigment (eumelanin) within the hair shaft. This gene is also known as the A-locus and determines whether an animal expresses an agouti appearance, and if so what type, by controlling the distribution of pigment in individual hairs. The agouti pattern can be seen in both black-based and red-based colours. The coat colour is further complicated by the interaction with the K-locus and the E-locus. The agouti pattern is only expressed if on the K-locus no copy of the KB allele is present in combination with at least one copy of the E or Em allele on the E-locus. The Coat Colour A-Locus test (H820) tests for the genetic status of the A-locus. The A-locus has four variants (alleles). The most dominant allele is Ay, followed by aw, then at, then a. The dominant Ay allele produces a sable or fawn coat colour. The allele aw produces a colour known as wild sable or wild type. With this colouration, the hairs switch pigmentation from black to reddish or fawn. This colour is sometimes seen in German Shepherds and other shepherd breeds. The allele at results in tan points (tan markings on a dark dog) and produces black-and-tan and tricolour dogs. A tricolour dog is black-and-tan plus white. The allele a is also called the recessive black allele and results in a solid black/brown/blue/lilac or bicolour dog. Some breeds are fixed for only one variant. The Norwegian Elkhound is fixed for the aw allele and the Beagle is fixed for the at allele. In many breeds 2 or 3 alleles are present.

The Coat Colour A-Locus test encloses the following results.

Resultado

La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente. Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Para cada factor genético de una enfermedad multifactorial, los resultados se inidcated como "Normal". Los animales que tienen una copia de la variante genética indeseable se indican como "portador", mientras que los animales que llevan dos copias de la variante genética indeseable se indican como "afectadas".

Herencia

La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente.

Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Tratamiento

Para esta enfermedad, el tratamiento está disponible.

Canine Coat Colours

Dogs display a wide variety of coat colours and patterns. Classification of these colours can be confusing sometimes because different registries or associations may use different names for the same colour. In each dog two pigments are the basis for their coat colour: black pigment (eumelanin) and red/yellow/cream pigment (pheomelanin). The production of black and red/yellow/cream pigment is controlled by the Melanocortin 1 Receptor (MC1R) gene, also known as Extension gene or E-Locus. Several other genes are involved that modify the black and red/yellow/cream pigment resulting in a variety of colours and patterns found in the domestic dog. The Tyrosinase-Related Protein 1 (TYRP1) gene, also known as Brown gene or B-Locus dilutes black pigment to brown but does not have an effect on red/yellow/cream pigment. Another gene involved in the coat colour of dogs is the Agouti (ASIP), also known as A-Locus, which controls the distribution of black and red/yellow/cream pigment. The Dilute (MLPH) gene, also known as D-Locus dilutes the black and red/yellow/cream pigment. The Beta-defensin (CBD-103), also known as K-Locus is unique to dogs and is responsible for dominant black. Some other genes that add white patterns and dilute colours are also present but are specific to certain breeds.

Within the above described coat colour genes, three genes explain the major differences; the E-, B-, and D-Locus genes. In the table below the possible combinations of the genes are indicated.

E-Locus	B-Locus	D-Locus	Coat Colour	Nose/foot pads
e/e	B/B	D/D or D/d	Red/Yellow/Cream	Black
e/e	B/B	d/d	Champagne	Blue to Black
e/e	B/b	D/D or D/d	Red/Yellow/Cream (carrierblack/brown/chocolate/liver)	Black
e/e	B/b	d/d	Champagne (carrierblack/brown/chocolate/liver)	Blue to Black
e/e	b/b	D/D or D/d	Red/Yellow/Cream (carrierblack/brown/chocolate/liver)	Pink to Brown
e/e	b/b	d/d	Champagne (carrierblack/brown/chocolate/liver)	Pink to Brown
E/e	B/B	D/D or D/d	Black, no melanistic mask (carrier red/yellow/cream)	Black
E/e	B/B	d/d	Blue/Grey/Charcoal, no melanistic mask (carrier red/yellow/cream)	Blue to Black
E/e	B/b	D/D or D/d	Black, no melanistic mask (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Black
E/e	B/b	d/d	Blue/Grey/Charcoal, no melanistic mask (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Blue to Black
E/e	b/b	D/D or D/d	Brown/chocolate/liver, no melanistic mask (carrier red/yellow/cream)	Pink to Brown
E/e	b/b	d/d	Lilac/Light tan/Isabela, no melanistic mask (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Pink to Brown
Em/e	B/B	D/D or D/d	Black, melanistic mask is not visible (carrier red/yellow/cream)	Black
Em/e	B/B	d/d	Blue/Grey/Charcoal, melanistic mask is not visible (carrier red/yellow/cream)	Blue to Black
Em/e	B/b	D/D or D/d	Black, melanistic mask is not visible (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Black
Em/e	B/b	d/d	Blue/Grey/Charcoal, melanistic mask is not visible (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Blue to Black
Em/e	b/b	D/D or D/d	Brown/chocolate/liver, with melanistic mask (carrier red/yellow/cream)	Pink to Brown
Em/e	b/b	d/d	Lilac/Light tan/Isabela, with melanistic mask (carrierblack/brown/chocolate/liver and carrier red/yellow/cream)	Pink to Brown
E/E	B/B	D/D or D/d	Black, no melanistic mask	Black
E/E	B/B	d/d	Blue/Grey/Charcoal, no melanistic mask	Blue to Black

E/E	B/b	D/D or D/d	Black, no melanistic mask (carrierblack/brown/chocolate/liver)	Black
E/E	B/b	d/d	Blue/Grey/Charcoal, no melanistic mask (carrierblack/brown/chocolate/liver)	Blue to Black
E/E	b/b	D/D or D/d	Brown/chocolate/liver, no melanistic mask	Pink to Brown
E/E	b/b	d/d	Lilac/Light tan/Isabela, no melanistic mask (carrierblack/brown/chocolate/liver)	Pink to Brown
Em/E	B/B	D/D or D/d	Black, melanistic mask is not visible	Black
Em/E	B/B	d/d	Blue/Grey/Charcoal, melanistic mask is not visible	Blue to Black
Em/E	B/b	D/D or D/d	Black, melanistic mask is not visible (carrierblack/brown/chocolate/liver)	Black
Em/E	B/b	d/d	Blue/Grey/Charcoal, melanistic mask is not visible (carrierblack/brown/chocolate/liver)	Blue to Black
Em/E	b/b	D/D or D/d	Brown/chocolate/liver, with melanistic mask	Pink to Brown
Em/E	b/b	d/d	Lilac/Light tan/Isabela, with melanistic mask (carrierblack/brown/chocolate/liver)	Pink to Brown
Em/Em	B/B	D/D or D/d	Black, melanistic mask is not visible	Black
Em/Em	B/B	d/d	Blue/Grey/Charcoal, melanistic mask is not visible	Blue to Black
Em/Em	B/b	D/D or D/d	Black, melanistic mask is not visible (carrierblack/brown/chocolate/liver)	Black
Em/Em	B/b	d/d	Blue/Grey/Charcoal, melanistic mask is not visible (carrierblack/brown/chocolate/liver)	Blue to Black
Em/Em	b/b	D/D or D/d	Brown/chocolate/liver, with melanistic mask	Pink to Brown
Em/Em	b/b	d/d	Lilac/Light tan/Isabela, with melanistic mask (carrierblack/brown/chocolate/liver)	Pink to Brown

* Three variants (bs,bc and bd) of the b-allele are known. Since all three variants result in the same effect, in the above scheme all variants are named b.

BACK TO TOP

COAT COLOURS:

E-Locus: H734 Coat Colour E-Locus and H818 Coat Colour Em-Locus

In each dog two pigments are the basis for their coat colour: black pigment (eumelanin) and red/yellow/cream pigment (pheomelanin). The production of black and red/yellow/cream pigment is controlled by the Melanocortin 1 Receptor (MC1R) gene, also known as Extension gene or E-Locus. The Coat Colour E-Locus (H734) and Coat Colour Em-Locus (H818) combined reveal the genetic status of the E-Locus. The E-Locus has three variants (alleles). The Em allele is dominant over the alleles E and e; allele E is dominant over allele e. The dominant allele Em causes a melanistic face mask. Dogs that are solid black may have the allele Em but the mask is not visible as it is indistinguishable from the body colour. Dogs with white muzzles may have the allele Em but the mask is overridden by white spotting patterns. The Melanistic face mask is present in a variety of breeds (e.g. Afghans, Akitas, Boxers, French Bulldogs, German Shepherds, Great Danes, Greyhounds, Pug Dogs and Whippets). Pug Dogs and Boxers are fixed for the Em allele. The allele E results in a black coat colour and the allele e results in a red coat colour. In Afghan and Saluki hounds a fourth allele has been identified which only is expressed when the dominant black (K-Locus) is not present and the A-Locus is at/at. This fourth allele Eg causes a pattern that is called grizzle or domino. VHLGenetics does not offer a test that detects the Eg allele.

The Coat Colour E-Locus and Coat Colour Em-Locus tests (together E-Locus) enclose the following results, in this scheme the results of the E-Locus are shown in combination with the possible results for the B-Locus:

E-Locus	Em-Locus	E-Locus (complete)	B-Locus*	Coat Colour

E/E	Em/Em	Em/Em	B/B or B/b	Black, melanistic mask is not visible
			b/b	Brown/chocolate/liver, with melanistic mask
E/E	Em/N	Em/E	B/B or B/b	Black, melanistic mask is not visible
			b/b	Brown/chocolate/liver, with melanistic mask
E/e	Em/N	Em/e	B/B or B/b	Black, melanistic mask is not visible
			b/b	Brown/chocolate/liver, with melanistic mask
E/E	N/N	E/E	B/B or B/b	Black, no melanistic mask
			b/b	Brown/chocolate/liver, no melanistic mask
E/e	N/N	E/e	B/B or B/b	Black, no melanistic mask
			b/b	Brown/chocolate/liver, no melanistic mask
e/e	N/N	e/e	B/B, B/b or b/b	Red/Yellow/Cream

* Three variants (bs,bc and bd) of the b-allele are known. Since all three variants result in the same effect, in the above scheme all variants are named b. (B/bc, B/bd and B/bs are in the above scheme B/b. bc/bc, bc/bd/bd/bd, bs/bc, bs/bd and bs/bs are in the above scheme b/b). More explanation about the result > 2b please is available under B-Locus: H733 Coat Colour B-Locus.

BACK TO TOP

B-Locus: H733 Coat Colour B-Locus

The Tyrosinase-Related Protein 1 (TYRP1) gene, also known as Brown gene or B-Locus controls the dilution from black pigment to brown. The TYRP1 gene has no effect on the hair colour of dogs that are homozygous ee for the E-Locus as they do not have black pigment, but does have an effect on the colour of the nose and foot pads of these dogs. The Coat Colour B-Locus (H733) tests for the genetic status of the B-Locus. The B-Locus has four variants (alleles). The B allele is dominant and does not dilute the black pigment. From the recessive b allele three variants exist bs, bd and bc. All three variants of the recessive b allele have the same effect resulting in dilution of the black pigment into brown/chocolate/liver. Only when the dog has two copies of the recessive allele b (homozygous bb) the black pigment will be diluted to brown/chocolate/liver. For dogs that are red/yellow/cream and carry two copies of the recessive allele b the hair colour is not diluted but the colour of the nose and foot pads is changed from black to brown. In some breeds other mutations are present that cause chocolate colour that have not been identified yet. For example, the mutation for chocolate in French Bulldogs has not been found yet and the genetic basis is not known at this time

The Coat Colour B-Locus test encloses the following results, in this scheme the results of the Coat Colour B-Locus test are shown in combination with the possible results for the E-Locus):

B-Locus	E-Locus	Coat Colour	Nose/foot pads
B/B	Em/Em, Em/E or Em/e	Black, melanistic mask is not visible	Black
B/B	E/E or E/e	Black, no melanistic mask	Black
B/B	e/e	Red/Yellow/Cream	Black
B/b*	Em/Em, Em/E or Em/e	Black, melanistic mask is not visible	Black
B/b*	E/E or E/e	Black, no melanistic mask	Black
B/b*	e/e	Red/Yellow/Cream	Black
b/b*	Em/Em, Em/E or Em/e	Brown/chocolate/liver, with melanistic mask	Brown
b/b*	E/E or E/e	Brown/chocolate/liver, no melanistic mask	Brown
b/b*	e/e	Red/Yellow/Cream	Brown
> 2b	This dog carries more than two b-alleles. The colour of this dog can be brown or black. Option 1: The dog is black. In this case it also carries one copy of the B-allele. Option 2: The dog is brown. In this case it carries only b-alleles.		

* Three variants (bs,bc and bd) of the b-allele are known. Since all three variants result in the same effect, in the above scheme all variants are named b. (B/bc, B/bd and B/bs are in the above scheme B/b. bc/bc, bc/bd/bd/bd, bs/bc, bs/bd and bs/bs are in the above scheme b/b).

BACK TO TOP

H421 Hiplaxity 2

Fondo

La laxitud de la articulación de la cadera es un trastorno frecuente en los perros. La enfermedad es de origen multifactorial, lo que significa que los síntomas son una combinación de factores genéticos, así como el medio ambiente.

La laxitud de cadera tiene dos características principales:

• La laxitud: Esto puede ser definido por "una libertad de movimiento anormal del hueso en la articulación de la cadera '. Como resultado, la cadera es menos estable en comparación con los perros sanos.

• La osificación y la formación de hueso. En los perros más jóvenes, el proceso normal de formación de hueso puede ser frenado.

Tanto laxitud y trastornos Ossifcation conducen al desarrollo de la artrosis perros cuando maduran. Los perros que más se ven afectados ya se pueden expresar los síntomas después de unos pocos meses. Otros perros afectados desarrollan artrosis a edades más tardías.

Este marcador es parte de un panel de factores genéticos que influyen en la laxitud de la cadera.

Información específica de prueba

Edad

La enfermedad puede manifestarse en diferentes edades, en la que no se puede estimar cuando los primeros síntomas pueden mostrarse. Pueden existir diferencias entre los hermanos de camada, y entre las razas.

Resultado

Normalmente, el resultado se puede esperar dentro de los 10 días hábiles. Esta-around-time a su vez comienza cuando se han recibido tanto la muestra y el de salida llenado completamente y firmado formulario de envío.

Localización de la enfermedad o rasgo

Esta enfermedad se encuentra en la cadera.

Dependencia de la raza

Para esta prueba se aceptan muestras de todas las razas.

Tipo de test

Para esta prueba de ADN aceptamos los siguientes materiales: Sangre con EDTA, heparina Sangre, Gamuza, Tejido, Semen. Por favor, póngase en contacto con el Dr. Van Haeringen Laboratorium si desea presentar otro material que se enumeran.

A-Locus	Coat Colour
Ay/Ay	Fawn/Sable, only allele Ay will be passed on to an offspring
Ay/aw	Fawn/Sable, either allele Ay or aw will be passed on to anan offspring
Ay/at	Fawn/Sable, either allele Ay or at will be passed on to an offspring
Ay/a	Fawn/Sable, either allele Ay or a will be passed on to an offspring
aw/aw	Wild sable/Wild type, it can only pass on allele aw will be passed on to an offspring
aw/at	Wild sable/Wild type, either allele aw or at will be passed on to an offspring
aw/a	Wild sable/Wild type, either allele aw or a will be passed on to an offspring
at/at	Tan Points/Black-and-tan/Tricolour, it can only pass on allele at will be passed on to an offspring
at/a	Tan Points/Black-and-tan/Tricolour, either allele at or a will be passed on to an offspring
a/a	Solid Black(Brown/Blue/Lilac)/Bicolour, it can only pass on allele a will be passed on to an offspring

BACK TO TOP

K-locus: H819 Coat Colour K-Locus:

The Beta-defensin gene (CBD103 gene) produces dominant black vs. brindle vs. fawn coat colours. This gene is also known as the K-locus or Dominant black gene. The coat colour is further complicated by the interaction with the E-locus and the A-locus (agouti). The Coat Colour K-Locus (H819) tests for the genetic status of the K-Locus. The K-locus has three variants (alleles). The allele KB is dominant over the alleles kbr and ky; allele kbr is dominant over allele ky. The dominant allele KB, also called dominant black allele, does not allow the agouti gene to be expressed. A dog with at least one copy of the KB allele expresses a base colour, which is determined by the B- and E-Locus. The allele kbr results in brindling and allows the agouti to be expressed but causes brindling of the agouti patterns. The A-Locus (agouti) represents several different colours, such as fawn/sable, wild sable, tan points and recessive black. The allele ky allows the agouti to be expressed without brindling. When a dog has two copies of the ky allele (homozygous ky/ky) the agouti locus determines the dog's coat colour. The test does not discriminate between the alleles kbr and ky.

The Coat Colour K-Locus test encloses the following results:

K-Locus	Coat Colour
KB/KB	Self-colored (solid color in pigmented areas), hides expression of the A-locus, basic colour determined by B- and E-locus, only allele KB will be passed on to an offspring
KB/N	Self-colored (solid color in pigmented areas), hides expression of the A-locus, basic colour determined by B- and E-locus. The test does not discriminate between the alleles kbr and ky, N can be allele kbr or ky. The dog is KB/kbr or KB/ky, either allele KB or kbr/ky will be passed on to an offspring
N/N	The test does not discriminate between the alleles kbr and ky, N can be allele kbr or ky. The dog is kbr/kbr, kbr/ky or ky/ky. If the dog is kbr/kbr: Brindling and expression of A-locus, it can only pass on allele kbr to an offspring. If the dog is kbr/ky: Brindling and expression of A-locus, either allele kbr or ky will be passed on to an offspring. If the dog is ky/ky: Expression of A-locus without brindling, only allele ky will be passed on to an offspring.

BACK TO TOP

M-Locus: H930 Coat Colour Merle

The Silver gene (SILV gene), also called premelanosome protein (PMEL17 gene) is responsible for Merle. This gene is also known as M-Locus. Merle only dilutes eumelanin (black) pigment; dogs with two copies of the allele e (homozygous e/e) at E-Locus have no black pigment, thus do not express merle. Merle is an incompletely dominant coat color pattern characterized by irregularly shaped patches of diluted pigment and solid color. Blue and partially blue eyes are typically seen with merle, and merle dogs often have a wide range of auditory and ophthalmologic defects. Breeds with merle coat pattern are Shetland Sheepdog, Collie, Border Collie, Australian Shepherd, Cardigan Welsh Corgi, Catahoula Leopard Dog, Dachshund, Great Dane, Bergamasco Sheepdog and Pyrenean Shepherd. The Coat Colour Merle test (H930) tests for the genetic status of the M-locus. The M-locus has three variants (alleles): M (merle, SINE with longer poly-A tail), Mc (cryptic merle, SINE with shorter poly-A tail) and N (non-merle, no SINE insertion. Dogs with cryptic merle (also called phantom or ghost merle), typically display little to no merling and some may be misclassified as non-merles. Inheritance of merle is genetically unstable for both M and Mc alleles. During DNA replication and cell division, M may occasionally undergo poly-A tail reduction to produce Mc (germline rate of 3-4%) while Mc may undergo expansion and revert to M.

The Coat Colour Merle test encloses the following results.

M-Locus	Coat Colour
M/M	Merle coat colour, two copies of merle are present (double merle). Dog may exhibit auditory and ophthalmologic defects
M/Mc	Merle coat colour, One copy of merle and one copy of cryptic merle are present. Dog may exhibit auditory and ophthalmologic defects
M/N	Merle coat colour, one copy of merle is present. Dog may exhibit auditory and ophthalmologic defects
Mc/Mc	Cryptic-merle, two copies of cryptic merle are present. The dog is genetically healthy with regards to the merle factor
Mc/N	Cryptic-merle, one copy of cryptic merle is present, the dog is genetically healthy with regards to the merle factor
N/N	Non-merle, no copies of merle or cryptic merle are present, the dog is genetically healthy with regards to the merle factor

BACK TO TOP

H353 Coat Colour Saddle tan vs black-and-tan

The hnRNP associated with lethal yellow gene (RALY gene) defines whether tan points or saddle tan is expressed in Basset Hounds and Pembroke Welsh Corgi dogs. Black and tan colour is characterized by light colour on the muzzle, above the eyes (tan points) and on the undersides of the dog on otherwise dark coat. Saddle tan resembles black and tan colour but the lighter areas are expanded leaving usually only the back to have dark patch. Saddled tan dogs are usually born black-and-tan and the black recedes as the dog grows. The coat colour is further complicated by the interaction with the E-locus, K-locus, A-locus and a yet unidentified gene. In order for the saddle tan pattern or tan points to be expressed, the dog needs to have at least one copy of the E or Em allele at the E-locus, two copies of the ky allele at the K-locus and one or two copies of the at allele at the A-locus. The Coat Colour Saddle tan vs black-and-tan test (H353) tests for the genetic status of the RALY gene. The RALY gene has two variants (alleles). The allele WT is dominant and causes the saddle tan coat colour. Only when the dog has two copies of the recessive allele dup the coat colour is black-and-tan. The saddle tan coat colour is present in a limited number of dog breeds including some of the terriers, scent hounds and herding dogs. In breeds that have only tan point dogs and no saddled tan dogs, the tan pointed dogs can have any genotype for the RALY gene. This suggests that more complex interactions are behind tan points in breeds that are not able to express saddle tan.

The Coat Colour Saddle tan vs black-and-tan test encloses the following results:

RALY gene	Coat Colour
WT/WT	Saddle tan, only allele WT will be passed on to an offspring
WT/dup	Saddle tan, either allele WT or dup will be passed on to an offspring
dup/dup	Black-and-tan, only allele dup will be passed on to an offspring

BACK TO TOP

H354 Coat Colour Panda White Spotting

A mutation in the KIT-gene is associated with a white spotting pattern in German Shepherd Dogs, this pattern is also called Panda White Spotting. The mutation is very recent, it appeared spontaneously in a female born in 2000. The gene for white-spotting is known as the S-locus (MITF-Gene), however this mutation in the German Shepherd dogs is in a different gene then the mutation causing white spotting in other dog breeds. The mutation causes white markings on the face, limbs, belly, neck, and tip of the tail, with the white being concentrated toward the front of the dog, similar to the irish spotting pattern. The amount of white can vary from dog to dog. The mutation that causes the Panda White pattern in German Shepherd dogs is in homozygous state (two copies of the mutation) considered embryonic lethal as no live dogs with the pattern and with two copies of the mutation have been observed. This means that pups that are homozygous for the Panda mutation do not develop in the uterus and are reabsorbed very early in the development process. Dogs that are heterozygous (one copy of the mutation) do not have any health defects associated with the Panda pattern. The Coat Colour Panda White Spotting test (H354) tests for the genetic status of the KIT-gene. This gene has two variants (alleles), P and N. The allele P is dominant. One copy of the P allele results in dogs with the Panda white pattern. Two copies of the P allele result in early embryonic death. The allele N does have no effect on the coat colour.

The Coat Colour Panda White Spotting test encloses the following results.

KIT-gene	Coat Colour
N/N	No Panda White spotting unless modified by other colour modifying factors, only allele N will be passed on to an offspring
N/P	Panda White spotting, either allele N or P will be passed on to an offspring

BACK TO TOP

H-Locus: H316 Coat Colour H-locus (Harlequin)

The 20S proteasome β2 subunit (PSMB7) gene is responsible for the Harlequin coat pattern in Great Danes. This gene is also known as H-Locus. Harlequin is a pattern resulting from interaction of the Merle (M-locus) gene and the Harlequin (H-locus) gene on black pigment. The

Harlequin gene can modify the Merle gene. The Harlequin pattern is only expressed if on the M-locus at least one copy of the M allele is present in combination with at least one copy of the E or Em allele on the E-locus. Dogs that are not merle, or only have red pigment, cannot express the Harlequin gene. The dominant Merle gene, by itself produces dark spots on a diluted background. If a Merle dog also inherits one copy of the Harlequin gene, the dark spots increase in size and the background pigment is removed (turns white). The Harlequin mutation in Great Danes is in homozygous state (two copies of the mutation) considered embryonic lethal as no live dogs with two copies of the mutation have been observed. This means that pups that are homozygous for the Harlequin mutation do not develop in the uterus and are reabsorbed very early in the development process. Therefore all Harlequin patterned dogs have only 1 copy of the Harlequin mutation. The Coat colour H-locus (Harlequin) test (H316) tests for the genetic status of the H-locus. This gene has two variants (alleles), H and N. The allele H is dominant. One copy of the H allele, together with at least one copy of both the M allele for the M-locus and the E allele for the E-locus results in dogs with the Harlequin pattern. Two copies of the H allele result in early embryonic death. The allele N does have no effect on the coat colour.

The Coat colour H-locus (Harlequin) test encloses the following results.

H-Locus	Coat Colour
N/N	No Harlequin pattern unless modified by other colour modifying factors, only allele N will be passed on to an offspring
N/H	Harlequin mutation is present. In order to express the Harlequin pattern the dog must carry at least one copy of both the M-allele for the M-locus and the E-allele for the E-locus. Either allele N or P will be passed on to an offspring

BACK TO TOP

S-locus

Unfortunately, for this coat colour no DNA-test is available at VHLGenetics yet. As the mutation causing White Spotting has been described in literature VHLgenetics is currently investigating the possibilities to set-up a DNA test.

C-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour C-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

G-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour G-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

I-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour I-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

P-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour P-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

R-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour R-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

T-Locus

Unfortunately, for this coat colour no DNA-test has been described in the scientific literature yet. As the inheritance of the coat colour may be only partially defined, for a description of coat colour T-Locus we refer to Schmutz SM and Berryere TG., (2007) Genes affecting coat colour and pattern in domestic dogs: a review. Anim Genet 38, 539-549.

BACK TO TOP

COAT VARIATON:

There are three variables involved in canine coat type: hair length, the presence of furnishings, and the presence of curly hair. When genotyping genetic variants on all three genes, there are a few coat patterns that can be discriminated. In the table below the possible combinations of these mutations are indicated.

Hair Lenght (FGF5)	Improper Coat/ Furnishings (RSPO2)	Curly Coat (KRT71)	Coat type
S/L or S/S	IC/IC	N/N	Short (no furnishings, non-curly)
S/L or S/S	IC/IC	N/CC or CC/CC	Short (no furnishings, curly)
S/L or S/S	N/N or N/IC	N/N	Wire (short, furnishings, non-curly)
S/L or S/S	N/N or N/IC	N/CC or CC/CC	Wire and Curly (short, furnishings, curly)
L/L	IC/IC	N/N	Long (no furnishings, non-curly)
L/L	N/N or N/IC	N/N	Long with Furnishings (long, furnishings, non-curly)
L/L	IC/IC	N/CC or CC/CC	Curly (long, no furnishings, curly)
L/L	N/N or N/IC	N/CC or CC/CC	Curly with Furnishings (long, furnishings, curly)

BACK TO TOP

H765 Hair length

The Fibroblast Growth Factor 5 (FGF5) determines the hair length. The Hair Length test (H765) tests for the genetic status of the FGF5-gene and has two variants (alleles). The allele S is dominant and results in short hair. Only when the dog has two copies of the recessive allele L the dog has long hair. Some breeds, such as Labradors, are fixed for the dominant allele S. Other breeds, such as Poodles, are fixed for the recessive allele L and some breeds, such as Dachshund, can have either long or short hair. In some breeds another, yet unidentified, mutation is present that influences hair length. This unidentified mutation is known to occur in Afghan Hounds, Yorkshire Terriers, and Silky Terriers.

The Hair Length test encloses the following results:

Result Hair Length test	Hair Length
L/L	Long Hair, unless modified by another mutation influencing hair length
S/L	Short Hair, unless modified by another mutation influencing hair length
S/S	Short Hair, unless modified by another mutation influencing hair length

BACK TO TOP

H848 Improper Coat /Furnishing

The R-spondin 2 (RSPO2) gene influences both the wiry texture and a growth pattern of the coat. The growth pattern of the coat, also known as "furnishings", increases hair growth on the face and legs and is typified by the canine moustache and eyebrows. The term "furnishings" refers to the longer mustache and eyebrows seen in wire-haired dogs and other breeds. In breeds such as the Portuguese Water Dog, Labradoodle and Goldendoodles furnishings can be variable, but are the breed standard. Portuguese Water Dogs without furnishings are referred to as having an "Improper Coat" which is characterized by short hair on the head, face and legs. The Improper Coat/Furnishings test (H848) tests for the genetic status of the RSPO2 gene. The RSPO2 gene has two variants (alleles). The allele N is dominant and results in "furnishings". Only when the dog has two copies of the recessive allele IC the dog does not have "furnishings". Some breeds, such as the Airedale Terrier, are fixed for the dominant allele N.

The Improper Coat/Furnishings test encloses the following results:

Result Improper Coat/Furnishings test	Coat
N/N	Dog has furnishings in some breeds this means dog has a normal coat with longer hair on the muzzle and eyebrows
N/IC	Dog has furnishings in some breeds this means dog has a normal coat with longer hair on the muzzle and eyebrows
IC/IC	Dog does not have furnishings, in some breeds this means an Improper coat without longer hair on the muzzle and eyebrows

BACK TO TOP

H921 Curly Coat

The Keratin 71 (KRT71) gene influences the hair formation. The Curly Coat test (H921) tests for the genetic status of the KRT71 gene. The KRT71 gene has two variants (alleles). The allele CC is dominant and results in a curly coat. Only when the dog has two copies of the recessive allele N the coat is of a non-curly type. Some breeds, such as the Irish Water Dog, are fixed for the dominant allele CC. Other breeds, such as Kuvasz, can have either curly or non-curly hair.

The Curly Coat test encloses the following results:

Result Curly Coat test	Coat
CC/CC	Curly coat, unless modified by another mutation influencing hair formation
N/CC	Curly coat, unless modified by another mutation influencing hair formation
N/N	Non-curly coat, unless modified by another mutation influencing hair formation

BACK TO TOP