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Genetic Check-Up
Health & Reproduction

Animal : **Coco Chanel von Kopfrein**

Identification No. :	**756 097 201 020 808**	Owner :	**Monika RINDISBACHER**
Breed :	**Bernese Mountain Dog**	Sample No. :	**E00889555** (sampled on 04/10/2023)
Gender :	**Female**	Result code :	**A00051459**
Birth date:	**26/02/2022**	Sampler :	Daniela GERBER-MATTLI
Pedigree :			Sample **authenticated**
Result validated on :	20/10/2023	Document issued on :	20/10/2023

DISEASES	GENE Mutation	Expression mode	RESULT	EXPRESSION	TRANSMISSION
Degenerative Myelopathy					
DM	SOD1 c.118G>A	Autosomal recessive	**Normal homozygous**	✓	✓
DM-sod1B	SOD1 c.52A>T	Autosomal recessive	**Normal homozygous**	✓	✓
von Willebrand Disease (vWD1)	VWF c.7142C>T	Autosomal recessive	**Normal homozygous**	✓	✓
Multidrug Sensitivity (MDR1)	MDR1 c.227_230delATAG	Autosomal codominant	**Normal homozygous**	✓	✓

INTERPRETATION OF THE RESULT
Normal homozygous : the animal carries 2 normal copies of the gene.
Heterozygous : the animal carries a normal copy and a defective copy of the gene.
Mutated homozygous : the animal carries 2 defective copies of the gene.

	EXPRESSION	TRANSMISSION
✓	The animal will not develop the form of the disease associated to the tested mutation.	The animal does not transmit the tested mutation.
!	The animal will develop the disease without being able to predict the age of onset or severity of symptoms.	The animal will transmit the tested mutation to all or part of its offspring. Reproduction is to be avoided or adapted according to the disease and the associated frequency.

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The results of morphological traits do not allow you to determine the animal's appearance precisely, but inform you about their transmission to offspring.

MORPHOLOGICAL TRAITS

	GENE Mutation	Expression mode	RESULT
Curly or Wavy Coat (c^1)	KRT71 c.451C>T	Autosomal dominant	**Non-carrier (C/C)**
Polydactyly	LMBR1 DC-2	Autosomal dominant	**Homozygous polydactyl**
Shedding	MC5R g.24430748C>T	Autosomal codominant	**High shedding**

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RISK FACTORS

	Expression mode	RESULT
Histiocytic Sarcoma	Polygenic and multifactorial	**Index A**

Index A: The tested dog has a four times lower risk of developing Histiocytic Sarcoma.
Index B : Neutral index - No higher or lower risk of developing Histiocytic Sarcoma.
Index C : The tested dog has a four times higher risk of developing Histiocytic Sarcoma. The risk of the markers associated with the disease being transmitted to offspring is greatly increased. An Index C dog with a number of other positive qualities should not be removed from the breeding programme, rather it is necessary to adapt its matings. It is recommended to use the HSIMS tools to assess the best partners.

Explanation
This genetic test should be just one of the many selection criteria. It is important within a breeding population to give priority to individuals with the best index but is also of the utmost importance when selecting breeding pairs that sufficient genetic diversity is maintained in the breed.

This genetic test for Histiocytic Sarcoma is based on 9 genetic markers (Panel SH0912) identified from scientific research on Histiocytic Sarcoma on Bernese Mountain Dogs carried out by the Canine Genetics Team of the CNRS of Rennes, France. The methods used to calculate the genetic index were based on a population of 1081 European dogs, mainly from France. The test for Histiocytic Sarcoma has three possible results expressed as an index: index A, the individual tested has a four times lower risk of developing Histiocytic Sarcoma ; index B means neutral index ; index C, the individual tested has a four times higher risk of developing Histiocytic Sarcoma. This genetic test is simply a probability test, and this must be clearly accepted by the user.

This genetic test is designed solely to be a tool to help breeders in their breeding decisions. As a probability test, the test SH is subject to error and should not therefore be used, under no circumstances, as a commercial or advertising point by breeders.

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