

Analysis Certificate

H948 CombiBreed Rhodesian Ridgeback + Ridge
Predisposition

Customer Info

Name	:	Arlinde van Leuveren
Adress	:	[REDACTED]
Zip Code / City	:	[REDACTED]
Customer no.	:	[REDACTED]

Animal Info

Name	:	Harmakhis Wisdom Nsoah
Animal ID	:	[REDACTED]
Breed	:	Rhodesian Ridgeback
Sex	:	Male
Date of Birth	:	24.6.2008
VHL ID	:	H703030

Sample Info

Order number	:	EN91641
Sample type	:	Semen
Certificate number	:	[REDACTED]
Test date	:	3.9.2026

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Name : Harmakhis Wisdom Nsoah Test Code : H948
Animal ID : XXXXXXXXXX VHL ID : H703030
Breed : Rhodesian Ridgeback Test Date : 3.9.2026

Health Conditions

An explanation of these results is accessible in our Online Results Portal, which can be found in your account on the CombiBreed Webshop. Within this portal, you will also discover comprehensive details for each test, including the breed relevance associated with each DNA test.

Breed Relevant Test Results

Code	Test Name	Gene	Mode of Inheritance	Result
H673	Degenerative Myelopathy Exon 2 (DM Exon 2)	SOD1	Autosomal Recessive with Incomplete Penetrance	Normal
H756	Early-onset adult deafness (Rhodesian Ridgeback)	EPS8L2	Autosomal Recessive	Normal
H672	Exercise Induced Collapse, EIC	DNM1	Autosomal Recessive	Normal
H931	Haemophilia A – Rhodesian Ridgeback	F8	X-Linked Recessive	Normal
H607	Haemophilia B – Rhodesian Ridgeback	F9	X-Linked Recessive	Normal
H811	Hyperuricemia (HUU, SLC2A9-related)	SLC2A9	Autosomal Recessive	Normal
H335	Juvenile Myoclonic Epilepsy (JME) – Rhodesian Ridgeback	DIRAS1	Autosomal Recessive	Normal
H932	Ventricular Arrhythmias and Sudden Death	QIL1	Unknown	Normal

Other Tests

Genetic traits are often influenced by other genetic traits and environmental factors. For in-depth insight into these genetic traits you can visit the online portal.

Code	Test Name	Gene	Mode of Inheritance	Result	Phenotype
H944	Ridge Predisposition (External Lab)	Large insertion on Chr18	Autosomal Incomplete Dominant	Ridge (R/R)	--

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Trait Characteristics

Coat colour and patterns are caused by the interaction of several genetic traits. For in-depth insights into these genetic traits, you can visit the online portal with test results or access the knowledgebase via the CombiBreed webshop.

Coat Colours

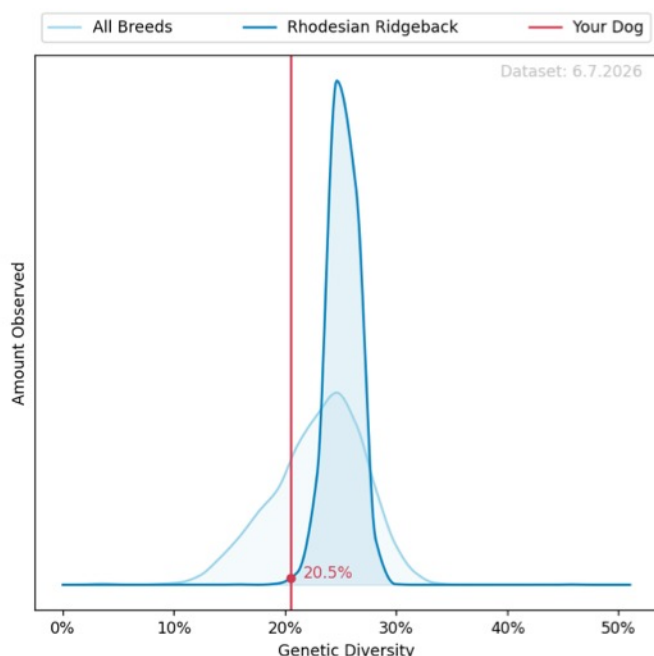
Code	Test Name	Gene	Mode of Inheritance	Result	Phenotype
H733	Coat Colour B-Locus	TYRP1	Autosomal Recessive	B/B	No effect
H764	Coat Colour B-Locus Be	TYRP1	Autosomal Recessive	B/B	No effect
H767	Coat Colour B-Locus Bh	TYRP1	Autosomal Recessive	B/B	No effect
H453	Coat Colour B-Locus – Australian Shepherd	TYRP1	Autosomal Recessive	B/B	No effect
H847	Coat Colour D-Locus 1 - Dog	MLPH	Autosomal Recessive	D/D	No effect

On behalf of VHLGenetics B.V.,
A. de Lange MBA



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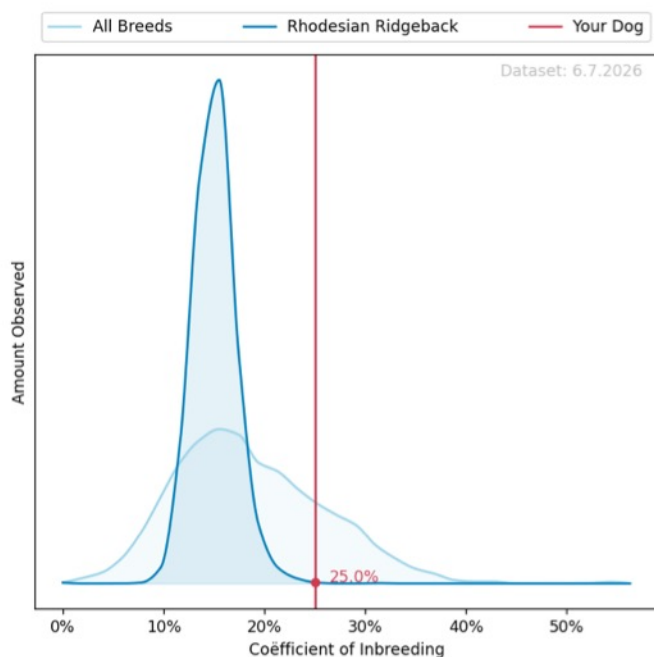
Genetic Information



H917 - Diversity/Heterozygosity

Heterozygosity in dogs refers to the genetic situation where a dog inherits two different alleles (gene variants) for a specific trait or gene locus from its parents. This genetic diversity contributes to the variation seen in physical traits, behaviors, and health among individual dogs and different breeds. Maintaining a certain level of heterozygosity is important in breeding programs to avoid an excessive accumulation of harmful recessive traits and promote overall genetic health within dog populations.

*In case there is an insufficient amount of animals for your specific breed, only a comparison with all breeds will be shown.



H916 - Coefficient of Inbreeding

The Coefficient of Inbreeding (COI) in dogs is a numerical measure that quantifies the probability of two copies of the same gene being inherited from a common ancestor. In simpler terms, it reflects how closely related the parents of a dog are within their family tree. A higher COI indicates a higher likelihood of the dog inheriting identical genes from both parents, which can lead to an increased risk of passing on genetic disorders or health issues.

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Modes of Inheritance

Autosomal Co-Dominant: A mode of inheritance where the affected and normal alleles are expressed equally, leading to an intermediate phenotype when both alleles are present in carriers.

Autosomal Dominant: A single copy of a dominant allele from one parent is sufficient to express the disease/trait. Individuals with at least one dominant allele will exhibit the trait.

Autosomal Dominant with Incomplete Penetrance: A genetic inheritance pattern that functions as normal Autosomal Dominant. However, carriers are not guaranteed to express the trait.

Autosomal Incomplete Dominant: A mode of inheritance where the phenotype is dependent on the number of copies present. Individuals with a single copy of the affected allele express a version of the trait specific to carriers. This is often an intermediate/blended version of the homozygous phenotypes. Individuals with two copies express the version specific to affected. This inheritance pattern is also known as semi-dominant or partial dominant.

Autosomal Recessive: Two copies of a recessive allele must be present for the trait to be expressed. If they have one recessive allele, they are a carrier who do not exhibit the trait, though can pass on the recessive allele.

Autosomal Recessive Lethal: A genetic inheritance pattern where an individual must inherit two copies of the recessive allele to express a lethal trait, typically resulting in spontaneous abortion, stillbirth or early death.

Autosomal Recessive with Incomplete Penetrance: A genetic inheritance pattern that functions as normal Autosomal Recessive. However, affected individuals are not guaranteed to express the disease/trait.

Mitochondrial: Genes located in the mitochondria, outside the cell nucleus, are inherited from the mother. Both sons and daughters can inherit these genes, but only daughters pass them on to their offspring.

Multifactorial: Disease/trait is influenced by multiple genetic and/or environmental factors, and may be difficult to predict.

Resistance/Susceptibility: The genetic predisposition of an individual or organism to either resist or be susceptible to a particular condition, disease, or treatment.

Risk factor: A risk factor in genetics refers to a specific genetic variation, trait, or condition that increases the likelihood of an individual developing a particular disease or health issue.

Unknown: Refers to cases where the mode of inheritance associated with the mutation is not yet (fully) identified or understood.

X-Linked Dominant: Dominant alleles located on the X chromosome result in the expression of the disease or trait. In females, a single copy of the allele is sufficient. In males, who have only one X chromosome, presence of the dominant allele leads to the trait's expression.

X-Linked Incomplete Dominant: A mode of inheritance where the phenotype is dependent on the number of copies present. Females with a single copy of the affected allele express a version of the trait specific to carriers. Females with two copies, and males carrying the allele, express the version specific to affected animals. This pattern of inheritance is also known as X-linked Semi-Dominant.

X-Linked Recessive: Recessive alleles located on the X chromosome result in the expression of the disease or trait. In females, who have two X-chromosomes, two copies of the allele are needed. In males, who have only one X chromosome, presence of the recessive allele already leads to the trait's expression.

Y-Linked: Males have one Y chromosome, females have none. This chromosome will always pass on to male offspring. Genes on the Y chromosome are passed on exclusively and always from father to son. Traits determined by Y-linked genes are therefore inherited down the paternal lineage.