

ORTHOPEDIC FOUNDATION FOR ANIMALS, INC.

PINE CREEK OSCAR
registered name

POODLE, MINIATURE
breed

film/test/lab #

992021000004444
tattoo/microchip/DNA profile

2642029
application number

03/24/2026
date of report

RESULTS:

The elbows are normal. No radiographic evidence of elbow dysplasia is present.

NOREG2642029
registration no.

M
sex

01/13/2023
date of birth

37
age at evaluation in months



A Not-For-Profit Organization

PO-EL10759M37-C-VPI
O.F.A. NUMBER

*This number issued with the right to correct or
revoke by the Orthopedic Foundation for Animals.*

NORMAL

owner WAYNE MILLER
NAOMI MILLER
3750 TR 124
MILLERSBURG OH 44654

OFA eCert



Verify QR scan

G.G. KELLER, DVM, MS, DACVR
CHIEF OF VETERINARY SERVICES

www.ofa.org

This electronic OFA certificate was generated on: 03/24/2026

This certification can be verified on the OFA website by entering the animal's registration number into the orange search box located at the top of the page or by scanning the QR code above.

If there are any errors on this certificate, please email CORRECTIONS@OFA.ORG to request a correction.

Orthopedic Foundation for Animals, Inc.
2300 E. Nifong Blvd.
Columbia, MO 65201-3806

OFA website: www.ofa.org
E-mail address: ofa@ofa.org
Phone number: 573-442-0418
Fax number: 573-875-5073

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film/test/lab #

99202100004444
tattoo/microchip/DNA profile

2642029
application number

03/24/2026
date of report

RESULTS:

No radiographic evidence of hip dysplasia is present. The consensus evaluation is: GOOD

owner
WAYNE MILLER
NAOMI MILLER
3750 TR 124
MILLERSBURG OH 44654

OFA eCert



Verify QR scan

NOREG2642029
registration no.

M
sex

01/13/2023
date of birth

37
age at evaluation in months



A Not-For-Profit Organization

PO-36886G37M-C-VPI
O.F.A. NUMBER

This number issued with the right to correct or revoke by the Orthopedic Foundation for Animals.

G.G. KELLER, DVM, MS, DACVR
CHIEF OF VETERINARY SERVICES

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OFA website: www.ofa.org
E-mail address: ofa@ofa.org
Phone number: 573-442-0418
Fax number: 573-875-5073



"OSCAR"

PINECREEK OSCAR




DNA Test Report

Test Date: October 26th, 2023

embk.me/pinecreekoscar

BREED ANCESTRY

 **Poodle (Small) : 100.0%**

GENETIC STATS

Predicted adult weight: **22 lbs**

Life stage: **Young adult**

Based on your dog's date of birth provided.

TEST DETAILS

Kit number: EM-53833106

Swab number: 31220710600173



"OSCAR"

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DNA Test Report

Test Date: October 26th, 2023

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TRAITS: COAT COLOR

TRAIT	RESULT
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E Locus (MC1R)

The E Locus determines if and where a dog can produce dark (black or brown) hair. Dogs with two copies of the recessive **e** variant do not produce dark hairs and will express a red pigment called pheomelanin over their entire body. The shade of red, which can range from a deep copper to white, depends on other genetic factors, including the Intensity loci. In addition to determining if a dog can develop dark hairs, the E Locus can give a dog a black "mask" or "widow's peak" unless the dog has overriding coat color genetic factors.

No dark hairs anywhere (ee)

Dogs with one or two copies of the **E^m** variant may have a melanistic mask (dark facial hair as commonly seen in the German Shepherd Dog and Pug). In the absence of **E^m**, dogs with the **E^g** variant can have a "grizzle" phenotype (darker color on the head and top with a melanistic "widow's peak" and a lighter underside, commonly seen in the Afghan Hound and Borzoi and also referred to as "domino"). In the absence of both **E^m** and **E** variants, dogs with the **E^a** or **E^h** variants can express the grizzle phenotype. Additionally, a dog with any combination of two of the **E^g**, **E^a**, or **E^h** variants (example: **E^gE^a**) is also expected to express the grizzle phenotype.

K Locus (CBD103)

The K Locus **K^B** allele "overrides" the A Locus, meaning that it prevents the A Locus genotype from affecting coat color. For this reason, the **K^B** allele is referred to as the "dominant black" allele. As a result, dogs with at least one **K^B** allele will usually have solid black or brown coats (or red/cream coats if they are **ee** at the E Locus) regardless of their genotype at the A Locus, although several other genes could impact the dog's coat and cause other patterns, such as white spotting. Dogs with the **k^Yk^Y** genotype will show a coat color pattern based on the genotype they have at the A Locus. Dogs who test as **K^Bk^Y** may be brindle rather than black or brown.

Not expressed (K^Bk^Y)

Registration:





"OSCAR"

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DNA Test Report

Test Date: October 26th, 2023

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TRAITS: COAT COLOR (CONTINUED)

TRAIT	RESULT
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Intensity Loci

Areas of a dog's coat where dark (black or brown) pigment is not expressed either contain red/yellow pigment, or no pigment at all. Five locations across five chromosomes explain approximately 70% of red pigmentation "intensity" variation across all dogs. Dogs with a result of **Intense Red Pigmentation** will likely have deep red hair like an Irish Setter or "apricot" hair like some Poodles, dogs with a result of **Intermediate Red Pigmentation** will likely have tan or yellow hair like a Soft-Coated Wheaten Terrier, and dogs with **Dilute Red Pigmentation** will likely have cream or white hair like a Samoyed. Because the mutations we test may not directly cause differences in red pigmentation intensity, we consider this to be a linkage test.

Any pigmented hair likely apricot or red (Intense Red Pigmentation)

A Locus (ASIP)

The A Locus controls switching between black and red pigment in hair cells, but it will only be expressed in dogs that are not **ee** at the E Locus and are **k^Yk^Y** at the K Locus. Sable (also called "Fawn") dogs have a mostly or entirely red coat with some interspersed black hairs. Agouti (also called "Wolf Sable") dogs have red hairs with black tips, mostly on their head and back. Black and tan dogs are mostly black or brown with lighter patches on their cheeks, eyebrows, chest, and legs. Recessive black dogs have solid-colored black or brown coats.

Not expressed (a¹a)

D Locus (MLPH)

The D locus result that we report is determined by three different genetic variants that can work together to cause diluted pigmentation. These are the common **d** allele, also known as "**d1**", and the less common alleles known as "**d2**" and "**d3**". Dogs with two **d** alleles, regardless of which variant, will have all black pigment lightened ("diluted") to gray, or brown pigment lightened to lighter brown in their hair, skin, and sometimes eyes. There are many breed-specific names for these dilute colors, such as "blue", "charcoal", "fawn", "silver", and "Isabella". Note that in certain breeds, dilute dogs have a higher incidence of Color Dilution Alopecia. Dogs with one **d** allele will not be dilute, but can pass the **d** allele on to their puppies.

Not expressed (DD)



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DNA Test Report

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TRAITS: COAT COLOR (CONTINUED)

TRAIT	RESULT
Cocoa (HPS3) Dogs with the coco genotype will produce dark brown pigment instead of black in both their hair and skin. Dogs with the Nco genotype will produce black pigment, but can pass the co allele on to their puppies. Dogs that have the coco genotype as well as the bb genotype at the B locus are generally a lighter brown than dogs that have the Bb or BB genotypes at the B locus.	No co alleles, not expressed (NN)
B Locus (TYRP1) Dogs with two copies of the b allele produce brown pigment instead of black in both their hair and skin. Dogs with one copy of the b allele will produce black pigment, but can pass the b allele on to their puppies. E Locus ee dogs that carry two b alleles will have red or cream coats, but have brown noses, eye rims, and footpads (sometimes referred to as "Dudley Nose" in Labrador Retrievers). "Liver" or "chocolate" is the preferred color term for brown in most breeds; in the Doberman Pinscher it is referred to as "red".	Likely black colored nose/feet (BB)
Saddle Tan (RALY) The "Saddle Tan" pattern causes the black hairs to recede into a "saddle" shape on the back, leaving a tan face, legs, and belly, as a dog ages. The Saddle Tan pattern is characteristic of breeds like the Corgi, Beagle, and German Shepherd. Dogs that have the ll genotype at this locus are more likely to be mostly black with tan points on the eyebrows, muzzle, and legs as commonly seen in the Doberman Pinscher and the Rottweiler. This gene modifies the A Locus a^t allele, so dogs that do not express a^t are not influenced by this gene.	Not expressed (NI)
S Locus (MITF) The S Locus determines white spotting and pigment distribution. MITF controls where pigment is produced, and an insertion in the MITF gene causes a loss of pigment in the coat and skin, resulting in white hair and/or pink skin. Dogs with two copies of this variant will likely have breed-dependent white patterning, with a nearly white, parti, or piebald coat. Dogs with one copy of this variant will have more limited white spotting and may be considered flash, parti or piebald. This MITF variant does not explain all white spotting patterns in dogs and other variants are currently being researched. Some dogs may have small amounts of white on the paws, chest, face, or tail regardless of their S Locus genotype.	Likely solid colored, but may have small amounts of white (Ssp)

Registration:





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TRAITS: COAT COLOR (CONTINUED)

TRAIT **RESULT**

M Locus (PMEL)

Merle coat patterning is common to several dog breeds including the Australian Shepherd, Catahoula Leopard Dog, and Shetland Sheepdog, among many others. Merle arises from an unstable SINE insertion (which we term the "M*" allele) that disrupts activity of the pigmentary gene PMEL, leading to mottled or patchy coat color. Dogs with an **M*m** result are likely to be phenotypically merle or could be "non-expressing" merle, meaning that the merle pattern is very subtle or not at all evident in their coat. Dogs with an **M*M*** result are likely to be phenotypically merle or double merle. Dogs with an **mm** result have no merle alleles and are unlikely to have a merle coat pattern.

No merle alleles (mm)

Note that Embark does not currently distinguish between the recently described cryptic, atypical, atypical+, classic, and harlequin merle alleles. Our merle test only detects the presence, but not the length of the SINE insertion. We do not recommend making breeding decisions on this result alone. Please pursue further testing for allelic distinction prior to breeding decisions.

R Locus (USH2A)

The R Locus regulates the presence or absence of the roan coat color pattern. Partial duplication of the USH2A gene is strongly associated with this coat pattern. Dogs with at least one **R** allele will likely have roaning on otherwise uniformly unpigmented white areas. Roan appears in white areas controlled by the S Locus but not in other white or cream areas created by other loci, such as the E Locus with **ee** along with Dilute Red Pigmentation by I Locus (for example, in Samoyeds). Mechanisms for controlling the extent of roaning are currently unknown, and roaning can appear in a uniform or non-uniform pattern. Further, non-uniform roaning may appear as ticked, and not obviously roan. The roan pattern can appear with or without ticking.

Likely no impact on coat pattern (rr)

H Locus (Harlequin)

This pattern is recognized in Great Danes and causes dogs to have a white coat with patches of darker pigment. A dog with an **Hh** result will be harlequin if they are also **M*m** or **M*M*** at the M Locus and are not **ee** at the E locus. Dogs with a result of **hh** will not be harlequin. This trait is thought to be homozygous lethal; a living dog with an **HH** genotype has never been found.

No harlequin alleles (hh)



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TRAITS: OTHER COAT TRAITS

TRAIT	RESULT
Furnishings (RSPO2)	
<p>Dogs with one or two copies of the F allele have "furnishings": the mustache, beard, and eyebrows characteristic of breeds like the Schnauzer, Scottish Terrier, and Wire Haired Dachshund. A dog with two I alleles will not have furnishings, which is sometimes called an "improper coat" in breeds where furnishings are part of the breed standard. The mutation is a genetic insertion which we measure indirectly using a linkage test highly correlated with the insertion.</p>	Likely furnished (mustache, beard, and/or eyebrows) (FF)

Registration:





“OSCAR”
PINECREEK OSCAR



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TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT	RESULT
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Coat Length (FGF5)

The FGF5 gene affects hair length in many species, including cats, dogs, mice, and humans. In dogs, an **Lh** allele confers a long, silky hair coat across many breeds, including Yorkshire Terriers, Cocker Spaniels, and Golden Retrievers, while the **Sh** allele causes a shorter coat, as seen in the Boxer or the American Staffordshire Terrier. In certain breeds, such as the Pembroke Welsh Corgi and French Bulldog, the long haircoat is described as “fluffy”. The coat length determined by FGF5, as reported by us, is influenced by four genetic variants that work together to promote long hair.

The most common of these is the **Lh1** variant (G/T, CanFam3.1, chr32, g.4509367) and the less common ones are **Lh2** (C/T, CanFam3.1, chr32, g.4528639), **Lh3** (16bp deletion, CanFam3.1, chr32, g.4528616), and **Lh4** (GG insertion, CanFam3.1, chr32, g.4528621). The FGF5_Lh1 variant is found across many dog breeds. The less common alleles, FGF5_Lh2, have been found in the Akita, Samoyed, and Siberian Husky, FGF5_Lh3 have been found in the Eurasier, and FGF5_Lh4 have been found in the Afghan Hound, Eurasier, and French Bulldog.

Likely long coat (LhLh)

The **Lh** alleles have a recessive mode of inheritance, meaning that two copies of the **Lh** alleles are required to have long hair. The presence of two Lh alleles at any of these FGF5 loci is expected to result in long hair. One copy each of **Lh1** and **Lh2** have been found in Samoyeds, one copy each of **Lh1** and **Lh3** have been found in Eurasiers, and one copy each of **Lh1** and **Lh4** have been found in the Afghan Hounds and Eurasiers.

Interestingly, the Lh3 variant, a 16 base pair deletion, encompasses the Lh4 variant (GG insertion). The presence of one or two copies of Lh3 influences the outcome at the Lh4 locus. When two copies of Lh3 are present, there will be no reportable result for the FGF5_Lh4 locus. With one copy of Lh3, Lh4 can have either one copy of the variant allele or the normal allele. The overall FGF5 result remains unaffected by this.



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TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT	RESULT
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Shedding (MC5R)

Dogs with at least one copy of the ancestral **C** allele, like many Labradors and German Shepherd Dogs, are heavy or seasonal shedders, while those with two copies of the **T** allele, including many Boxers, Shih Tzus and Chihuahuas, tend to be lighter shedders. Dogs with furnished/wire-haired coats caused by RSPO2 (the furnishings gene) tend to be low shedders regardless of their genotype at this gene.

Likely light shedding (TT)

Coat Texture (KRT71)

Dogs with a long coat and at least one copy of the **T** allele have a wavy or curly coat characteristic of Poodles and Bichon Frises. Dogs with two copies of the ancestral **C** allele are likely to have a straight coat, but there are other factors that can cause a curly coat, for example if they at least one **F** allele for the Furnishings (RSPO2) gene then they are likely to have a curly coat. Dogs with short coats may carry one or two copies of the **T** allele but still have straight coats.

Likely curly coat (TT)

Hairlessness (FOXI3)

A duplication in the FOXI3 gene causes hairlessness over most of the body as well as changes in tooth shape and number. This mutation occurs in Peruvian Inca Orchid, Xoloitzcuintli (Mexican Hairless), and Chinese Crested (other hairless breeds have different mutations). Dogs with the **NDup** genotype are likely to be hairless while dogs with the **NN** genotype are likely to have a normal coat. The **DupDup** genotype has never been observed, suggesting that dogs with that genotype cannot survive to birth. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.

Very unlikely to be hairless (NN)

Hairlessness (SGK3)

Hairlessness in the American Hairless Terrier arises from a mutation in the SGK3 gene. Dogs with the **DD** result are likely to be hairless. Dogs with the **ND** genotype will have a normal coat, but can pass the **D** variant on to their offspring.

Very unlikely to be hairless (NN)

Registration:





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TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT	RESULT
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Oculocutaneous Albinism Type 2 (SLC45A2)

Dogs with two copies **DD** of this deletion in the SLC45A2 gene have oculocutaneous albinism (OCA), also known as Doberman Z Factor Albinism, a recessive condition characterized by severely reduced or absent pigment in the eyes, skin, and hair. Affected dogs sometimes suffer from vision problems due to lack of eye pigment (which helps direct and absorb ambient light) and are prone to sunburn. Dogs with a single copy of the deletion **ND** will not be affected but can pass the mutation on to their offspring. This particular mutation can be traced back to a single white Doberman Pinscher born in 1976, and it has only been observed in dogs descended from this individual. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.

Likely not albino (NN)



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TRAITS: OTHER BODY FEATURES

TRAIT	RESULT
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Muzzle Length (BMP3)

Dogs in medium-length muzzle (mesocephalic) breeds like Staffordshire Terriers and Labradors, and long muzzle (dolichocephalic) breeds like Whippet and Collie have one, or more commonly two, copies of the ancestral **C** allele. Dogs in many short-length muzzle (brachycephalic) breeds such as the English Bulldog, Pug, and Pekingese have two copies of the derived **A** allele. At least five different genes affect muzzle length in dogs, with BMP3 being the only one with a known causal mutation. For example, the skull shape of some breeds, including the dolichocephalic Scottish Terrier or the brachycephalic Japanese Chin, appear to be caused by other genes. Thus, dogs may have short or long muzzles due to other genetic factors that are not yet known to science.

Likely medium or long muzzle (AC)

Tail Length (T)

Whereas most dogs have two **C** alleles and a long tail, dogs with one **G** allele are likely to have a bobtail, which is an unusually short or absent tail. This mutation causes natural bobtail in many breeds including the Pembroke Welsh Corgi, the Australian Shepherd, and the Brittany Spaniel. Dogs with **GG** genotypes have not been observed, suggesting that dogs with the **GG** genotype do not survive to birth. Please note that this mutation does not explain every natural bobtail! While certain lineages of Boston Terrier, English Bulldog, Rottweiler, Miniature Schnauzer, Cavalier King Charles Spaniel, and Parson Russell Terrier, and Dobermans are born with a natural bobtail, these breeds do not have this mutation. This suggests that other unknown genetic mutations can also lead to a natural bobtail.

Likely normal-length tail (CC)

Hind Dewclaws (LMBR1)

Common in certain breeds such as the Saint Bernard, hind dewclaws are extra, nonfunctional digits located midway between a dog's paw and hock. Dogs with at least one copy of the **T** allele have about a 50% chance of having hind dewclaws. Note that other (currently unknown to science) mutations can also cause hind dewclaws, so some **CC** or **TC** dogs will have hind dewclaws.

Unlikely to have hind dew claws (CC)



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TRAITS: OTHER BODY FEATURES (CONTINUED)

TRAIT	RESULT
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Blue Eye Color (ALX4)

Embark researchers discovered this large duplication associated with blue eyes in Arctic breeds like Siberian Husky as well as tri-colored (non-merle) Australian Shepherds. Dogs with at least one copy of the duplication (**Dup**) are more likely to have at least one blue eye. Some dogs with the duplication may have only one blue eye (complete heterochromia) or may not have blue eyes at all; nevertheless, they can still pass the duplication and the trait to their offspring. **NN** dogs do not carry this duplication, but may have blue eyes due to other factors, such as merle. Please note that this is a linkage test, so it may not be as predictive as direct tests of the mutation in some lines.

Less likely to have blue eyes (NN)

Back Muscling & Bulk, Large Breed (ACSL4)

The **T** allele is associated with heavy muscling along the back and trunk in characteristically "bulky" large-breed dogs including the Saint Bernard, Bernese Mountain Dog, Greater Swiss Mountain Dog, and Rottweiler. The "bulky" **T** allele is absent from leaner shaped large breed dogs like the Great Dane, Irish Wolfhound, and Scottish Deerhound, which are fixed for the ancestral **C** allele. Note that this mutation does not seem to affect muscling in small or even mid-sized dog breeds with notable back muscling, including the American Staffordshire Terrier, Boston Terrier, and the English Bulldog.

Likely normal muscling (CC)

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TRAITS: BODY SIZE

TRAIT	RESULT
Body Size (IGF1) The I allele is associated with smaller body size.	Smaller (II)
Body Size (IGFR1) The A allele is associated with smaller body size.	Larger (GG)
Body Size (STC2) The A allele is associated with smaller body size.	Intermediate (TA)
Body Size (GHR - E191K) The A allele is associated with smaller body size.	Smaller (AA)
Body Size (GHR - P177L) The T allele is associated with smaller body size.	Larger (CC)

Registration:





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TRAITS: PERFORMANCE

TRAIT **RESULT**

Altitude Adaptation (EPAS1)

This mutation causes dogs to be especially tolerant of low oxygen environments (hypoxia), such as those found at high elevations. Dogs with at least one **A** allele are less susceptible to "altitude sickness." This mutation was originally identified in breeds from high altitude areas such as the Tibetan Mastiff.

Normal altitude tolerance (GG)

Appetite (POMC)

This mutation in the POMC gene is found primarily in Labrador and Flat Coated Retrievers. Compared to dogs with no copies of the mutation (**NN**), dogs with one (**ND**) or two (**DD**) copies of the mutation are more likely to have high food motivation, which can cause them to eat excessively, have higher body fat percentage, and be more prone to obesity. Read more about the genetics of POMC, and learn how you can contribute to research, in our blog post (<https://embarkvet.com/resources/blog/pomc-dogs/>). We measure this result using a linkage test.

Normal food motivation (NN)

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HEALTH REPORT

How to interpret Oscar's genetic health results:

If Oscar inherited any of the variants that we tested, they will be listed at the top of the Health Report section, along with a description of how to interpret this result. We also include all of the variants that we tested Oscar for that we did not detect the risk variant for.

A genetic test is not a diagnosis

This genetic test does not diagnose a disease. Please talk to your vet about your dog's genetic results, or if you think that your pet may have a health condition or disease.

Summary

Of the 256 genetic health risks we analyzed, we found 2 results that you should learn about.

Notable results (2)

ALT Activity

Progressive Retinal Atrophy, prcd

Clear results

Breed-relevant (5)

Other (248)



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BREED-RELEVANT RESULTS

Research studies indicate that these results are more relevant to dogs like Oscar, and may influence his chances of developing certain health conditions.

 Progressive Retinal Atrophy, prcd (PRCD Exon 1)	Notable
 GM2 Gangliosidosis (HEXB, Poodle Variant)	Clear
 Intervertebral Disc Disease (Type I) (FGF4 retrogene - CFA12)	Clear
 Neonatal Encephalopathy with Seizures, NEWS (ATF2)	Clear
 Osteochondrodysplasia (SLC13A1, Poodle Variant)	Clear
 Von Willebrand Disease Type I, Type I vWD (VWF)	Clear

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ABA-2000622-002





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HEALTH REPORT

⊖ Notable result

ALT Activity

Pinecreek Oscar inherited one copy of the variant we tested for Alanine Aminotransferase Activity

Why is this important to your vet?

Oscar has one copy of a variant associated with reduced ALT activity as measured on veterinary blood chemistry panels. Please inform your veterinarian that Oscar has this genotype, as ALT is often used as an indicator of liver health and Oscar is likely to have a lower than average resting ALT activity. As such, an increase in Oscar's ALT activity could be evidence of liver damage, even if it is within normal limits by standard ALT reference ranges.

What is Alanine Aminotransferase Activity?

Alanine aminotransferase (ALT) is a clinical tool that can be used by veterinarians to better monitor liver health. This result is not associated with liver disease. ALT is one of several values veterinarians measure on routine blood work to evaluate the liver. It is a naturally occurring enzyme located in liver cells that helps break down protein. When the liver is damaged or inflamed, ALT is released into the bloodstream.

How vets diagnose this condition

Genetic testing is the only way to provide your veterinarian with this clinical tool.

How this condition is treated

Veterinarians may recommend blood work to establish a baseline ALT value for healthy dogs with one or two copies of this variant.



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HEALTH REPORT

⊖ Notable result

Progressive Retinal Atrophy, prcd

Pinecreek Oscar inherited one copy of the variant we tested for Progressive Retinal Atrophy, prcd

What does this result mean?

This variant should not impact Oscar's health. This variant is inherited in an autosomal recessive manner, meaning that a dog needs two copies of the variant to show signs of this condition. Oscar is unlikely to develop this condition due to this variant because he only has one copy of the variant.

Impact on Breeding

Your dog carries this variant and will pass it on to ~50% of his offspring. You can email breeders@embarkvet.com to discuss with a genetic counselor how the genotype results should be applied to a breeding program.

What is Progressive Retinal Atrophy, prcd?

PRA-prcd is a retinal disease that causes progressive, non-painful vision loss. The retina contains cells, called photoreceptors, that collect information about light and send signals to the brain. There are two types of photoreceptors: rods, for night vision and movement, and cones, for day vision and color. This type of PRA leads to early loss of rod cells, leading to night blindness before day blindness.

When signs & symptoms develop in affected dogs

The age affected dogs will first show signs of visual impairment varies by breed. However, most begin showing clinical signs in early adulthood.

How vets diagnose this condition

Veterinarians use a focused light to examine the pupils. In affected dogs, the pupils will appear more dilated and slower to contract. Your vet may also use a lens to visualize the retina at the back of the eye to look for changes in the optic nerve or blood vessels. You may be referred to a veterinary ophthalmologist for a definitive diagnosis.

How this condition is treated

Currently, there is no definitive treatment for PRA. Supplements, including antioxidants, have been proposed for management of the disease, but have not been scientifically proven effective.

Actions to take if your dog is affected

- Careful monitoring by your veterinarian will be required for the rest of your affected dog's life as secondary complications, including cataracts, can develop.
- With blind dogs, keeping furniture in the same location, making sure they are on a leash in unfamiliar territory, and training them to understand verbal commands are some of the ways to help them at home.

Registration:





"OSCAR"

PINECREEK OSCAR



DNA Test Report

Test Date: October 26th, 2023

embk.me/pinecreekoscar

INBREEDING AND DIVERSITY

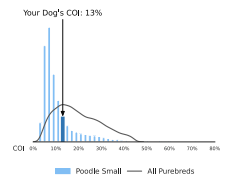
CATEGORY

RESULT

Coefficient Of Inbreeding

Our genetic COI measures the proportion of your dog's genome where the genes on the mother's side are identical by descent to those on the father's side.

13%

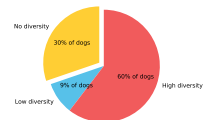


MHC Class II - DLA DRB1

A Dog Leukocyte Antigen (DLA) gene, DRB1 encodes a major histocompatibility complex (MHC) protein involved in the immune response. Some studies have shown associations between certain DRB1 haplotypes and autoimmune diseases such as Addison's disease (hypoadrenocorticism) in certain dog breeds, but these findings have yet to be scientifically validated.

No Diversity

How common is this amount of diversity in purebreds:



MHC Class II - DLA DQA1 and DQB1

DQA1 and DQB1 are two tightly linked DLA genes that code for MHC proteins involved in the immune response. A number of studies have shown correlations of DQA-DQB1 haplotypes and certain autoimmune diseases; however, these have not yet been scientifically validated.

No Diversity

How common is this amount of diversity in purebreds:

