

Orthopedic Foundation for Animals
Preliminary Elbow Dysplasia Evaluation Report



A Not-for-Profit
Organization

SERENA
registered name

HYBRID
breed

film/testlab #

900219001712741
tattoo/microchip/DNA profile

2619557
application number

04/11/2025
date of report

NOREG2619557
registration no.

F
sex

03/02/2024
date of birth

12
age at evaluation in months

Owner

WAYNE MILLER
3750 TR 124
MILLERSBURG OH 44654

Veterinarian

DANVILLE VETERINARY CLINIC
PO BOX 6200
DANVILLE OH 43014

Preliminary Elbow Dysplasia Evaluation Report

✓ negative for elbow dysplasia

L ✓ R ✓

ELBOW DYSPLASIA

GRADE I
GRADE II
GRADE III

L _____ R _____
L _____ R _____
L _____ R _____

RADIOGRAPHIC FINDINGS

degenerative joint disease (DJD)
united anconeal process (UAP)
fragmented coronoid process (FCP)
osteochondrosis

L _____ R _____
L _____ R _____
L _____ R _____
L _____ R _____

G.G. Keller, DVM

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

Orthopedic Foundation for Animals
Preliminary Hip Dysplasia Evaluation Report



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Preliminary Hip Dysplasia Evaluation Report

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

EXCELLENT HIP JOINT CONFORMATION

superior hip joint conformation as compared with other individuals of the same breed and age

GOOD HIP JOINT CONFORMATION

well formed hip joint conformation as compared with other individuals of the same breed and age

FAIR HIP JOINT CONFORMATION

minor irregularities of the hip joint conformation as compared with other individuals of the same breed and age

BORDERLINE HIP JOINT CONFORMATION

marginal hip joint conformation of indeterminate status with respect to hip dysplasia at this time -- Repeat study in six months

MILD HIP DYSPLASIA

radiographic evidence of minor dysplastic changes of the hip joints

MODERATE HIP DYSPLASIA

well defined radiographic evidence of dysplastic changes of the hip joints

SEVERE HIP DYSPLASIA

radiographic evidence of marked dysplastic changes of the hip joints

RADIOGRAPHIC FINDINGS

_____ subluxation
_____ remodeling of femoral head/neck
_____ osteoarthritis/degenerative joint disease
_____ shallow acetabula
_____ acetabular rim/edge change

_____ unilateral _____ left _____ right
_____ transitional vertebra
_____ spondylolysis
_____ panosteitis

G.G. Keller DVM

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ORTHOPEDIC FOUNDATION FOR ANIMALS, INC.

SERENA
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HYBRID
breed

film/test/lab #

900219001712741
tattoo/microchip/DNA profile

2619557
application number

07/17/2025
date of report

RESULTS:

Based upon the exam dated 05/09/2025, this dog has been found to be free of observable inherited eye disease and has been issued an Eye Certification Registry Number which is valid for one year from the time of the exam.

NOREG2619557
registration no.

F
sex

03/02/2024
date of birth

14
age at evaluation in months



A Not-For-Profit Organization

HY-EYE11613/14F-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

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

www.ofa.org

This electronic OFA certificate was generated on: 07/17/2025

This certification can be verified on the OFA website by entering the dog'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



AKC DNA Profile

DNA Profile#: **V10221822**

Sex: **Female**

Date of Birth: **03/02/2024**

ID #: **900219001712741**

Date of Analysis: **06/29/2026**

AKC #:

Breed: **Bernese Mountain Dog**

AKC Name: **Serena**

Owner(s): **Angela Miller**

AC	AA	AG	AA	GG	AA	AA	AA	AA	AA	AG	AA	GG	GG	AA	AG	AA	AC	AA	CG	GG	AG	AG	AA	GG
AKC001	AKC002	AKC003	AKC004	AKC005	AKC006	AKC007	AKC008	AKC009	AKC010	AKC011	AKC012	AKC013	AKC014	AKC015	AKC016	AKC017	AKC018	AKC019	AKC020	AKC021	AKC022	AKC023	AKC024	AKC025
AG	GG	AA	GG	AA	GG	AA	AG	AG	AA	AG	GG	AA	GG	GG	AG	AA	AG	AA	AG	AA	AG	GG	AA	AG
AKC026	AKC027	AKC028	AKC029	AKC030	AKC031	AKC032	AKC033	AKC034	AKC035	AKC036	AKC037	AKC038	AKC039	AKC040	AKC041	AKC042	AKC043	AKC044	AKC045	AKC046	AKC047	AKC048	AKC049	AKC050
GG	AG	GG	GG	AG	AG	AG	AA	AG		GG	AG	AC	AA	AA	CC	GG	GG	GG	GG	AA	AG	AG	AA	GG
AKC051	AKC052	AKC053	AKC054	AKC055	AKC056	AKC057	AKC058	AKC059	AKC060	AKC061	AKC062	AKC063	AKC064	AKC065	AKC066	AKC067	AKC068	AKC069	AKC070	AKC071	AKC072	AKC073	AKC074	AKC075
AA	AA	AA	AA	AG	AA	GG	AT	AC	AG	AC	CG	GG	CC	AG	AG	AA	AG	GG	AG	AC	GG	CC	AG	AG
AKC076	AKC077	AKC078	AKC079	AKC080	AKC081	AKC082	AKC083	AKC084	AKC085	AKC086	AKC087	AKC088	AKC089	AKC090	AKC091	AKC092	AKC093	AKC094	AKC095	AKC096	AKC097	AKC098	AKC099	AKC100
AA	AG	TT	AA	AG	AG	GG	AG	AA	AG	AG	AC	AG	AA	AA	CC	GG	AG	AA	GG	AG	CC	AG	GG	TT
AKC101	AKC102	AKC103	AKC104	AKC105	AKC106	AKC107	AKC108	AKC109	AKC110	AKC111	AKC112	AKC113	AKC114	AKC115	AKC116	AKC117	AKC118	AKC119	AKC120	AKC121	AKC122	AKC123	AKC124	AKC125
GG	GG	AG	GG	AA	AA	GG	AA	GG	GG	AG	AG	AC	CC	AG	AG	GG	AG	AC	AA	GG	AA	AC	AC	GG
AKC126	AKC127	AKC128	AKC129	AKC130	AKC131	AKC132	AKC133	AKC134	AKC135	AKC136	AKC137	AKC138	AKC139	AKC140	AKC141	AKC142	AKC143	AKC144	AKC145	AKC146	AKC147	AKC148	AKC149	AKC150
AG	GG	AC	AA	AA	AG	AA	AG	AA	AA	AG	CC	GG	AA	GG	AA	AG	GG	AG	AG	AG	AA	AC	GG	GG
AKC151	AKC152	AKC153	AKC154	AKC155	AKC156	AKC157	AKC158	AKC159	AKC160	AKC161	AKC162	AKC163	AKC164	AKC165	AKC166	AKC167	AKC168	AKC169	AKC170	AKC171	AKC172	AKC173	AKC174	AKC175
AG	AG	AG	AC	AG	AA	GG	GG	AG	AA	GG	AA	CC	GG	GG	GG	AA	AG	AG	AA	CC	AA	AG	AG	CC
AKC176	AKC177	AKC178	AKC179	AKC180	AKC181	AKC182	AKC183	AKC184	AKC185	AKC186	AKC187	AKC188	AKC189	AKC190	AKC191	AKC192	AKC193	AKC194	AKC195	AKC196	AKC197	AKC198	AKC199	AKC200

XX

AKC201

Dr. Jerry Klein, DVM, Chief Veterinary Officer
American Kennel Club

Dr. Jiansheng Qiu, Directory of Quality
Neogen Corporation

"SERENA"



SERENA

DNA Test Report

Test Date: December 10th, 2024

embk.me/serena138

BREED ANCESTRY



GENETIC STATS

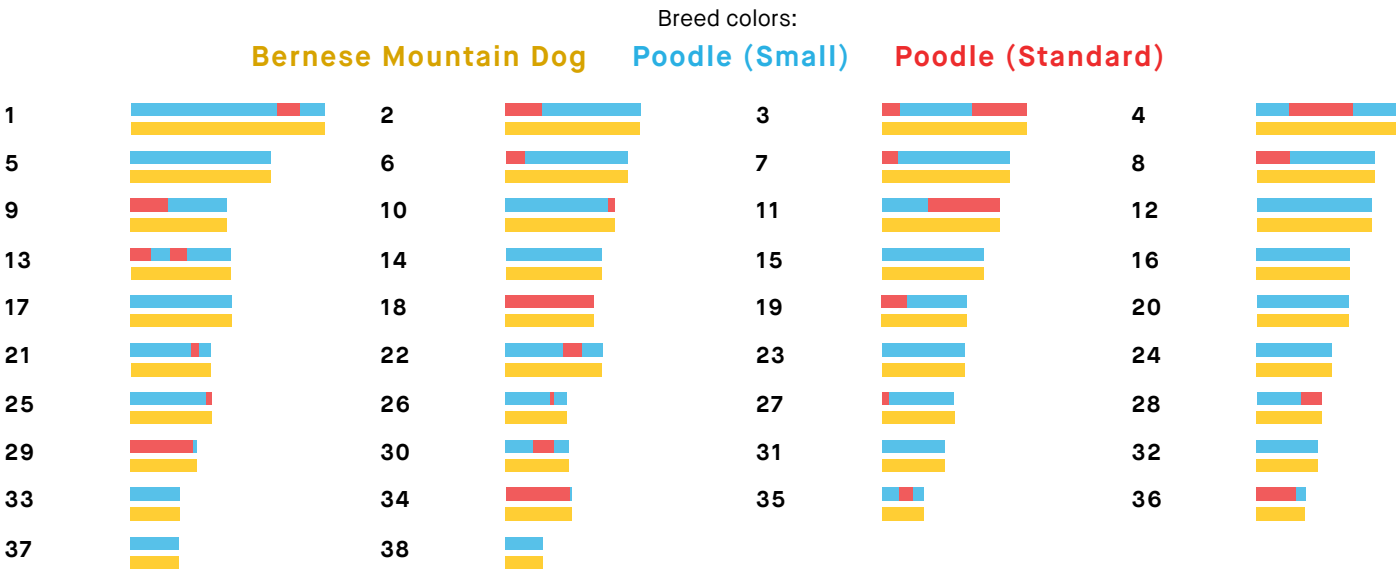
Predicted adult weight: **43 lbs**
Life stage: **Young adult**
Based on your dog's date of birth provided.

TEST DETAILS

Kit number: EM-53824914
Swab number: 31220710609796

BREED ANCESTRY BY CHROMOSOME

Our advanced test identifies from where Serena inherited every part of the chromosome pairs in her genome.



TRAITS: COAT COLOR

TRAIT

RESULT

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.

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.

No dark mask or grizzle (Ee)

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.

More likely to have a patterned haircoat (k^yk^y)

TRAITS: COAT COLOR (CONTINUED)

TRAIT

RESULT

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 light hair likely yellow or tan (Intermediate 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.

Black/Brown and tan coat color pattern (a⁺a⁺)

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.

Dark areas of hair and skin are not lightened (DD)

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".

Black or gray hair and skin (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.

Likely saddle tan patterned (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)

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)

"SERENA"



SERENA

DNA Test Report

Test Date: December 10th, 2024

embk.me/serena138

TRAITS: COAT COLOR (CONTINUED)

TRAIT	RESULT
Panda White Spotting Panda White Spotting originated in a line of German Shepherd Dogs and causes a mostly symmetrical white spotting of the head and/or body. This is a dominant variant of the KIT gene, which has a role in pigmentation. Dogs with one copy of the I allele will exhibit this white spotting. Dogs with two copies of the I allele have never been observed, as two copies of the variant is suspected to be lethal to the developing embryo. Dogs with the NN result will not exhibit white spotting due to this variant.	Not expected to display Panda pattern (NN)

"SERENA"

SERENA



DNA Test Report

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embk.me/serena138

TRAITS: OTHER COAT TRAITS

TRAIT

RESULT

Furnishings (RSP02)

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.

**Likely furnished
(mustache, beard,
and/or eyebrows) (FI)**

TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT

RESULT

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.

TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT

RESULT

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 (CT)

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 wavy coat (CT)

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)

"SERENA"



SERENA

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TRAITS: OTHER COAT TRAITS (CONTINUED)

TRAIT RESULT

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)

TRAITS: OTHER BODY FEATURES

TRAIT

RESULT

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 (CC)

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.

Likely to have hind dew claws (CT)

TRAITS: OTHER BODY FEATURES (CONTINUED)

TRAIT

RESULT

Chondrodysplasia (Chr. 18 FGF4 Retrogene)

Dogs with one or two copies of the **I** allele will exhibit a short-legged trait known as chondrodysplasia (CDPA). CDPA is a breed-defining characteristic of many breeds exhibiting the "short-legged, long-bodied" appearance known as disproportionate dwarfism, including the corgi, dachshund and basset hound. The impact of the **I** allele on leg length is additive. Therefore, dogs with the **II** result display the largest reduction in leg length. Dogs with the **NI** genotype will have an intermediate leg length, while dogs with the **NN** result will not exhibit leg shortening due to this variant. Breeds that display disproportionate dwarfism also frequently inherit a genetic variant known as the chondrodystrophy (CDDY) variant. The CDDY variant also shortens legs (in a less significant amount than CDPA) but, secondarily, increases the risk of Type I Intervertebral Disc Disease (IVDD). Test results for CDDY are listed in this dog's health testing results under "Intervertebral Disc Disease (Type I)". In contrast, the CDPA variant has NOT been shown to increase the risk of IVDD.

Not indicative of chondrodysplasia (normal leg length) (NN)

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)

"SERENA"

SERENA



DNA Test Report

Test Date: December 10th, 2024

embk.me/serena138

TRAITS: BODY SIZE

TRAIT	RESULT
Body Size (IGF1) The I allele is associated with smaller body size.	Intermediate (NI)
Body Size (IGFR1) The A allele is associated with smaller body size.	Intermediate (GA)
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.	Larger (GG)
Body Size (GHR - P177L) The T allele is associated with smaller body size.	Larger (CC)

"SERENA"

SERENA



DNA Test Report

Test Date: December 10th, 2024

embk.me/serena138

TRAITS: PERFORMANCE

TRAIT	RESULT
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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)**

HEALTH REPORT

How to interpret Serena's genetic health results:

If Serena 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 Serena 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 274 genetic health risks we analyzed, we found 3 results that you should learn about.

Notable results (3)

ALT Activity

Copper Toxicosis (Attenuating)

Degenerative Myelopathy, DM

Clear results

Breed-relevant (6)

Other (264)

"SERENA"



SERENA

DNA Test Report

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BREED-RELEVANT RESULTS

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

 Degenerative Myelopathy, DM (SOD1A)	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
 Progressive Retinal Atrophy, prcd (PRCD Exon 1)	Clear
 Von Willebrand Disease Type I, Type I vWD (VWF)	Clear



HEALTH REPORT

Notable result

ALT Activity

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

Why is this important to your vet?

Serena has one copy of a variant associated with reduced ALT activity as measured on veterinary blood chemistry panels. Please inform your veterinarian that Serena has this genotype, as ALT is often used as an indicator of liver health and Serena is likely to have a lower than average resting ALT activity. As such, an increase in Serena'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?

ALT is a liver enzyme that vets measure to monitor liver health. With this result, your dog may naturally have a lower ALT baseline. Knowing this helps your veterinarian interpret future bloodwork results more accurately.

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.

Actions to take if your dog is affected

- Talk to your vet about your dog's ALT result, as it may help them better interpret your dog's blood work.
- Dogs with this result do not exhibit symptoms or develop health issues associated with this variant.

HEALTH REPORT

Notable result

Copper Toxicosis (Attenuating)

Serena inherited one copy of the variant we tested for Copper Toxicosis (Attenuating)

Why is this important to your vet?

Serena has a genotype at the ATP7A gene that modifies and may help mitigate some of the symptoms from dogs with variants at ATP7B (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>). This variant is not associated with an increased risk of any disease. As this variant resides on the X- chromosome, male dogs with one copy of the variant are better protected from copper accumulation due to the ATP7B variant than female dogs with one copy of the variant.

What is Copper Toxicosis (Attenuating)?

This genetic variant may help lessen the effects of copper buildup in dogs that also carry the copper toxicosis risk variant ATP7B (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>). On its own, it is not known to cause health problems.

When signs & symptoms develop in affected dogs

A variant in this gene may delay or have no effect on the onset of clinical signs of copper toxicosis in dogs with the ATP7B (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>) variant. If your dog has the ATP7B variant, please read more about the age of onset on the ATP7B page.

How vets diagnose this condition

No diagnostics are required for this variant. If your dog has the ATP7B (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>) variant, please read what diagnostics may be considered on the ATP7B page.

How this condition is treated

No treatment is required for this variant. If your dog has the ATP7B (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>) variant, please read the available treatment on the ATP7B page.

Actions to take if your dog is affected

- No specific action is needed for dogs with this variant alone.
- If your dog also has the ATP7B variant, please review what actions you can take on the ATP7B page (<https://my.embarkvet.com/members/results/health/condition/140102?i=35>).
- Routine veterinary care and a balanced diet are appropriate for most dogs with this result.

HEALTH REPORT

Notable result

Degenerative Myelopathy, DM

Serena inherited one copy of the variant we tested for Degenerative Myelopathy, DM

What does this result mean?

This variant should not impact Serena'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. Serena is unlikely to develop this condition due to this variant because she only has one copy of the variant.

Impact on Breeding

Your dog carries this variant and will pass it on to ~50% of her 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 Degenerative Myelopathy, DM?

This condition affects the spinal cord nerves involved in movement, most noticeably in the hind limbs. It is progressive, meaning symptoms worsen over time, including weakness, muscle loss, and changes in walking.

When signs & symptoms develop in affected dogs

Affected dogs do not usually show signs of DM until they are at least 8 years old.

How vets diagnose this condition

Definitive diagnosis requires microscopic analysis of the spinal cord after death. However, veterinarians use clues such as genetic testing, breed, age, and other diagnostics to determine if DM is the most likely cause of your dog's clinical signs.

How this condition is treated

As dogs are seniors at the time of onset, the treatment for DM is aimed towards increasing their comfort through a combination of lifestyle changes, medication, and physical therapy.

Actions to take if your dog is affected

- Talk to your vet about your dog's degenerative myelopathy result, as it may influence how they monitor your dog's mobility and overall health, especially in their senior years.
- Keep your dog active with regular, low-impact exercise to help them maintain a healthy weight and support their mobility.
- Watch for changes in movement, such as wobbling, reluctance to jump, or dragging their back paws, and consult your vet if you notice any of these signs.
- Provide good traction in your home with rugs or mats to help prevent slipping as your dog ages. If mobility becomes difficult, ask your vet about supportive devices such as harnesses or wheelchairs.

INBREEDING AND DIVERSITY

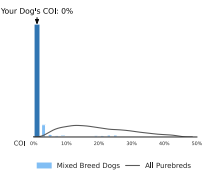
CATEGORY

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.

0%

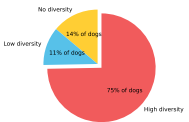


MHC Class II - DLA DRB1

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.

High Diversity

How common is this amount of diversity in mixed breed dogs:



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.

High Diversity

How common is this amount of diversity in mixed breed dogs:

