Domino

WISDOM PANEL™

Kit type: Essential

ID kit: ESTDXJG
Test date: 2024-06-19

Domino's Profile

Pet information

Registered name
Domino

Date of birth
2023-04

Sex
F

Spayed
No

Top breeds

71% Australian Shepherd
29% Miniature American Shepherd

Predicted ideal adult weight

20-33 lbs

Health summary

At Risk 0 conditions
Carrier 0 conditions
Clear 30 conditions

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Breed ancestry

We detected 2 breeds in Domino's DNA.

Herding

71 % Australian Shepherd

29 % Miniature American Shepherd

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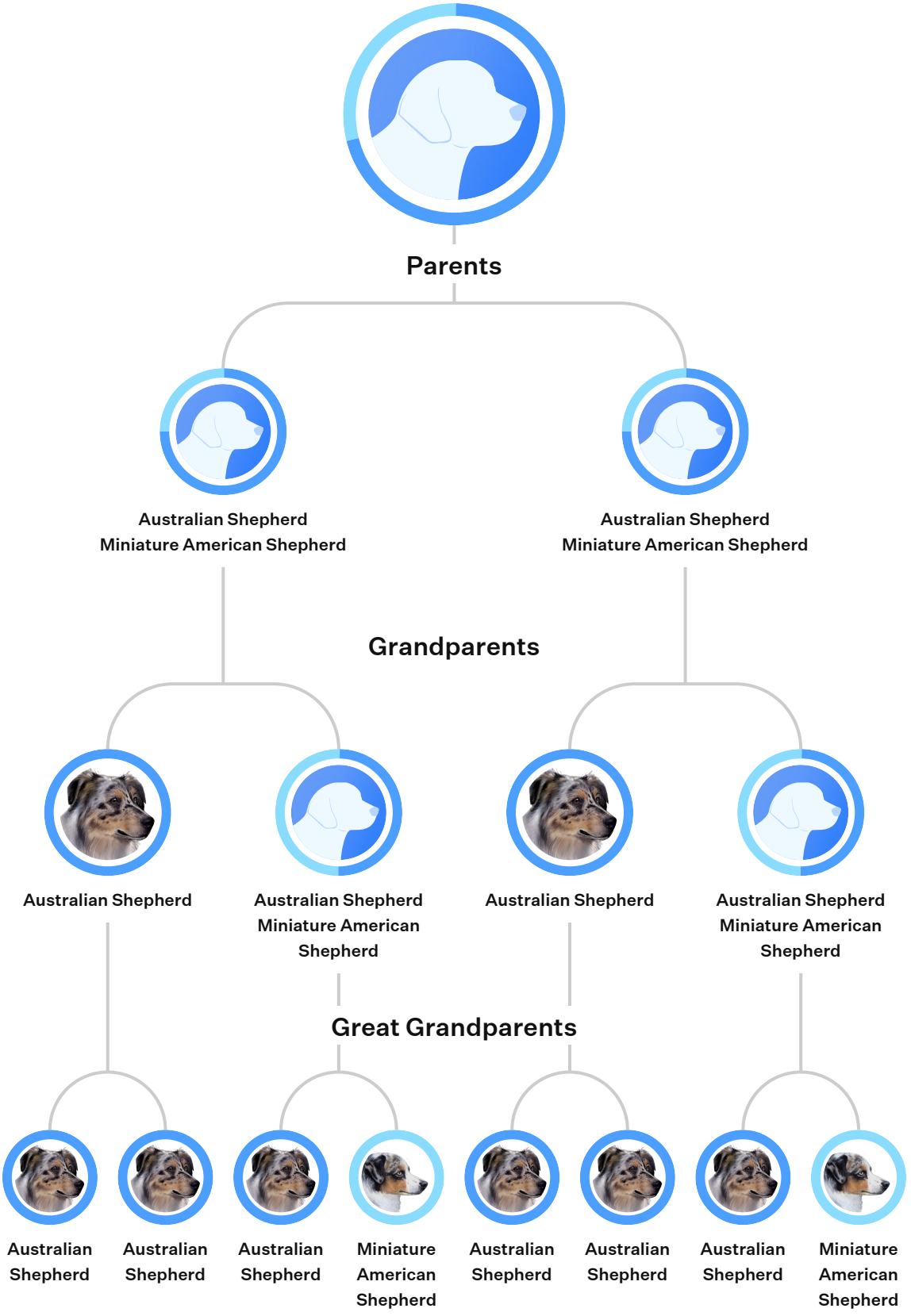
Family Tree



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Summary of health conditions

Key Findings

We detected 0 genetic conditions in Domino's DNA.

0	0	30
At Risk	Carrier	Clear

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Health conditions tested

Genetic Condition	Gene	Risk Variant	Copies	Inheritance	Result
Canine Leukocyte Adhesion Deficiency (CLAD), type III	FERMT3	Insertion	0	AR	Clear
Canine Scott Syndrome	ANO6	G>A	0	AR	Clear
Chondrodystrophy (CDDY) and Intervertebral Disc Disease (IVDD) Risk	FGF4 retrogene	Insertion	0	AD	Clear
Complement 3 Deficiency	C3	Deletion	0	AR	Clear
Factor VII Deficiency	F7	G>A	0	AR	Clear
Factor XI Deficiency	FXI	Insertion	0	AD	Clear
Glanzmann Thrombasthenia Type I (Discovered in Great Pyrenees)	ITGA2B	C>G	0	AR	Clear
Glanzmann Thrombasthenia Type I (Discovered in mixed breed dogs)	ITGA2B	C>T	0	AR	Clear
Hemophilia A (Discovered in Old English Sheepdog)	FVIII	C>T	0	XR	Clear
Hemophilia A (Discovered in the Boxer)	FVIII	C>G	0	XR	Clear
Hemophilia A (Discovered in the German Shepherd Dog - Variant 1)	FVIII	G>A	0	XR	Clear
Hemophilia A (Discovered in the German Shepherd Dog - Variant 2)	FVIII	G>A	0	XR	Clear
Hemophilia A (Discovered in the Havanese)	FVIII	Insertion	0	XR	Clear
Hemophilia B	FIX	G>A	0	XR	Clear
Hemophilia B (Discovered in the Airedale Terrier)	FIX	Insertion	0	XR	Clear
Hemophilia B (Discovered in the Lhasa Apso)	FIX	Deletion	0	XR	Clear
May-Hegglin Anomaly	MYH9	G>A	0	AD	Clear
MDR1 Medication Sensitivity	MDR1/ABCB1	Deletion	0	AD	Clear
P2RY12-associated Bleeding Disorder	P2RY12	Deletion	0	AR	Clear
Prekallikrein Deficiency	KLKB1	T>A	0	AR	Clear

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Health conditions tested

Genetic Condition	Gene	Risk Variant	Copies	Inheritance	Result
Severe Combined Immunodeficiency (Discovered in Frisian Water Dogs)	RAG1	G>T	0	AR	Clear
Severe Combined Immunodeficiency (Discovered in Russell Terriers)	PRKDC	G>T	0	AR	Clear
Trapped Neutrophil Syndrome	VPS13B	Deletion	0	AR	Clear
von Willebrand's Disease, type 1	VWF	G>A	0	AD	Clear
von Willebrand's Disease, type 2	VWF	T>G	0	AR	Clear
von Willebrand's Disease, type 3 (Discovered in the Kooiker Hound)	VWF	G>A	0	AR	Clear
von Willebrand's Disease, type 3 (Discovered in the Scottish Terrier)	VWF	Deletion	0	AR	Clear
von Willebrand's Disease, type 3 (Discovered in the Shetland Sheepdog)	VWF	Deletion	0	AR	Clear
X-Linked Severe Combined Immunodeficiency (Discovered in the Basset Hound)	IL2RG	Deletion	0	XR	Clear
X-Linked Severe Combined Immunodeficiency (Discovered in the Cardigan Welsh Corgi)	IL2RG	Insertion	0	XR	Clear

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Traits

Coat Color

	Gene	Variant	Copies	Result
Fawn	ASIP	a^y	0	No effect
Recessive Black	ASIP	a	0	No effect
Tan Points Two copies, or occasionally one copy, of this variant may result in a black and tan coat color pattern.	ASIP	a^t	2	Tan points possible
Dominant Black	CBD103	K^B	0	No effect
Mask	MC1R	E^m	0	No effect
Recessive Red (e1)	MC1R	e^1	0	No effect
Recessive Red (e2)	MC1R	e^2	0	No effect
Recessive Red (e3)	MC1R	e^3	0	No effect
Sable (Discovered in the Cocker Spaniel)	MC1R	e^H	0	No effect
Widow's Peak (Discovered in Ancient dogs)	MC1R	e^A	0	No effect
Widow's Peak (Discovered in the Afghan Hound and Saluki)	MC1R	E^G	0	No effect

Color Modification

	Gene	Variant	Copies	Result
Cocoa (Discovered in the French Bulldog)	HPS3	co	0	No effect
Red Intensity Dogs with two copies of the Red Intensity variant are more likely to show yellow, cream or white coat shades instead of deeper red shades. If the dog does not display solid red or red coat patterns, there will be no visible effect. Other genes, notably variants in the KITLG gene, are also thought to contribute to red pigment intensity variation, so some dogs may have yellow or buff colored coats.	MFSD12	i	2	White to yellow coat shades likely
Dilution (d1) Linkage test	MLPH	d^1	0	No effect

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Color Modification

	Gene	Variant	Copies	Result
Dilution (d2)	MLPH	d^2	0	No effect
Dilution (d3)	MLPH	d^3	0	No effect
Chocolate (basd)	TYRP1	b^{asd}	0	No effect
Chocolate (bc) To show chocolate coloration a dog must inherit two chocolate variants, one from each parent. This can either be two copies of a particular variant, such as this one ("bc"), or two of any combination of chocolate variants.	TYRP1	b^c	1	Black features likely, chocolate possible
Chocolate (bd) To show chocolate coloration a dog must inherit two chocolate variants, one from each parent. This can either be two copies of a particular variant, such as this one ("bd"), or two of any combination of chocolate variants. This variant is unique in that it can occur on the same chromosome as another chocolate variant, where both variants are donated from one parent. If the other parent does not also donate a chocolate variant, the dog will still express black pigment, not chocolate.	TYRP1	b^d	1	Black features likely, chocolate possible
Chocolate (be)	TYRP1	b^e	0	No effect
Chocolate (bh)	TYRP1	b^h	0	No effect
Chocolate (bs)	TYRP1	b^s	0	No effect

Coat Patterns

	Gene	Variant	Copies	Result
Piebald	MITF	s^p	0	No effect
Merle Most dogs with one copy of the Merle variant will show Merle patterning. Most dogs with two copies will be mostly white, but in some cases will show Merle patterning. Some dogs with this variant will not show the Merle pattern. This is because the Merle variant can sometimes be shortened (known as cryptic or atypical Merle), and these forms do not have an effect on appearance.	PMEL	M	1	Merle possible

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Coat Patterns

	Gene	Variant	Copies	Result
Harlequin	PSMB7	H	0	No effect
Saddle Tan	RALY	-	0	No effect
Roan (Linkage test)	USH2A	T^r	0	No effect

Coat Length and Curl

	Gene	Variant	Copies	Result
Long Hair (lh1) To show a long coat, a dog must inherit two copies of a Long Hair variant, one from each parent. This can either be two copies of a particular variant, such as this one (lh1) or two of any combination of long hair variants. However, there are other variants suspected to influence coat length.	FGF5	lh^1	2	Long coat
Long Hair (lh2)	FGF5	lh^2	0	No effect
Long Hair (lh3)	FGF5	lh^3	0	No effect
Long Hair (lh4)	FGF5	lh^4	0	No effect
Long Hair (lh5)	FGF5	lh^5	0	No effect
Curly Coat	KRT71	C	0	No effect

Hairlessness

	Gene	Variant	Copies	Result
Hairlessness (Discovered in the Chinese Crested Dog) Linkage test	FOXI3	Hr^{cc}	0	No effect
Hairlessness (Discovered in the American Hairless Terrier)	SGK3	hr^{aht}	0	No effect
Hairlessness (Discovered in the Scottish Deerhound)	SKG3	hr^{sd}	0	No effect

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Shedding

	Gene	Variant	Copies	Result
Reduced Shedding	MC5R	sd	0	Seasonal shedder

More Coat Traits

	Gene	Variant	Copies	Result
Hair Ridge	FGF3, FGF4, FGF19, ORAOV1	R	0	No effect
Furnishings	RSPO2	F	0	No effect
Albino	SLC45A2	c^{al}	0	No effect

Head Shape

	Gene	Variant	Copies	Result
Short Snout (BMP3 variant)	BMP3	-	0	No effect
Short Snout (SMOC2 variant) Copies of this skull shape variant usually results in a shorter snout, whereas dogs with no copies of this variant tend to have a longer snout.	SMOC2	-	1	Shortened snout likely

Eye Color

	Gene	Variant	Copies	Result
Blue Eyes (Discovered in the Siberian Husky)	ALX4	-	—	Inconclusive

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Ears

	Gene	Variant	Copies	Result
Floppy Ears Dogs with zero copies of this variant are more likely to have permanently upright or prick ears, and fully folded ears are more likely with two copies inherited. Please note however that many genetic variants influence ear carriage. Dogs with some cartilage stiffness to their ears can sometimes raise their ears upright when 'at alert' but will flop down when relaxed.	MSRB3	-	1	Partially floppy ears more likely

Extra Toes

	Gene	Variant	Copies	Result
Hind Dewclaws (Discovered in Asian breeds)	LMBR1	DC-1	0	No effect
Hind Dewclaws (Discovered in Western breeds)	LMBR1	DC-2	0	No effect

More Body Features

	Gene	Variant	Copies	Result
Back Muscle and Bulk	ACSL4	-	0	No effect
High Altitude Adaptation	EPAS1	-	0	No effect
Short Legs (Chondrodysplasia, CDPA)	FGF4	-	0	No effect
Short Legs (Chondrodystrophy, CDDY)	FGF4	-	0	No effect
Short Tail	T-box	T	0	Full tail length likely

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Glossary of genetic terms

Test result definitions

At Risk: Based on the disorder's mode of inheritance, the dog inherited a number of genetic variant(s) which increases the dog's risk of being diagnosed with the associated disorder.

Carrier: The dog inherited one copy of a genetic variant when two copies are usually necessary to increase the dog's risk of being diagnosed with the associated disorder. While carriers are usually not at risk of clinical expression of the disorder, carriers of some complex variants may be associated with a low risk of developing the disorder.

Clear: The dog did not inherit the genetic variant(s) associated with the disorder and will not be at elevated risk of being diagnosed with the disorder due to this genotype. However, similar clinical signs could develop from different genetic or clinical causes.

Inconclusive: An inconclusive result indicates a confident call could not be made based on the data for that genetic variant. Health testing is performed in replicates, and on occasion the outcomes do not agree. This may occur due to an unusual sequence of DNA in the region tested, multiple cell genotypes present due to chimerism or acquired mutations, or due to quality of the DNA sample.

Inheritance mode definitions

Autosomal Recessive (AR): For autosomal recessive disorders, dogs with two copies of the genetic variant are at risk of developing the associated disorder. Dogs with one copy of the variant are considered carriers and are usually not at risk of developing the disorder. However, carriers of some complex variants grouped in this category may be associated with a low risk of developing the disorder. Dogs with one or two copies may pass the disorder-associated variant to their puppies if bred.

Autosomal Dominant (AD): For autosomal dominant disorders, dogs with one or two copies of the genetic variant are at risk of developing the associated disorder. Inheriting two copies of the variant may increase the risk of development of the disorder or cause the condition to be more severe. These dogs may pass the disorder-associated variant to their puppies if bred.

X-linked Recessive (XR): For X-linked recessive disorders, the genetic variant is found on the X chromosome. Female dogs must inherit two copies of the variant to be at risk of developing the condition, whereas male dogs only need one copy to be at risk. Males and females with any copies of the variant may pass the disorder-associated variant to their puppies if bred.

X-linked Dominant (XD): For X-linked dominant disorders, the genetic variant is found on the X chromosome. Both male and female dogs with one copy of the variant are at risk of developing the disorder. Females inheriting two copies of the variant may be at higher risk or show a more severe form of the disorder than with one copy. Males and females with any copies of the variant may pass the disorder-associated variant to their puppies if bred.

Mitochondrial (MT): Unlike the two copies of genomic DNA held in the nucleus, there are thousands of mitochondria in each cell of the body, and each holds its own mitochondrial DNA (mtDNA). Mitochondria are called the "powerhouses" of the cell. For a dog to be at risk for a mitochondrial disorder, it must inherit a certain ratio of mtDNA with the associated variant compared to normal mtDNA. mtDNA is inherited only from the mother.