

Coat Color in dogs

VetGen DNA CHROMAGENE Coat Color Testing

For many years geneticists and breeders have been aware of several "loci" that are responsible for the color patterns we see in dogs and other mammals. Each of these loci are known to be responsible for one or more traits either independently, or in conjunction with another locus. All of them act on the pathways that produce the two major pigments, phaeomelanin and eumelanin, or affect the distribution of those pigments. The familiar examples are B (brown), E (extension), D (dilution), A (agouti), M (merle), C (chinchilla) and so on. Over the past several years, scientists at VetGen and elsewhere have determined the actual genes associated with many of these loci, and identified the mutations responsible for the different versions (alleles) of these genes. Due to the complex interactions of these genes, it is possible for dogs to carry hidden colors. The fruit of this work are the tests available for many of the common coat colors and traits.

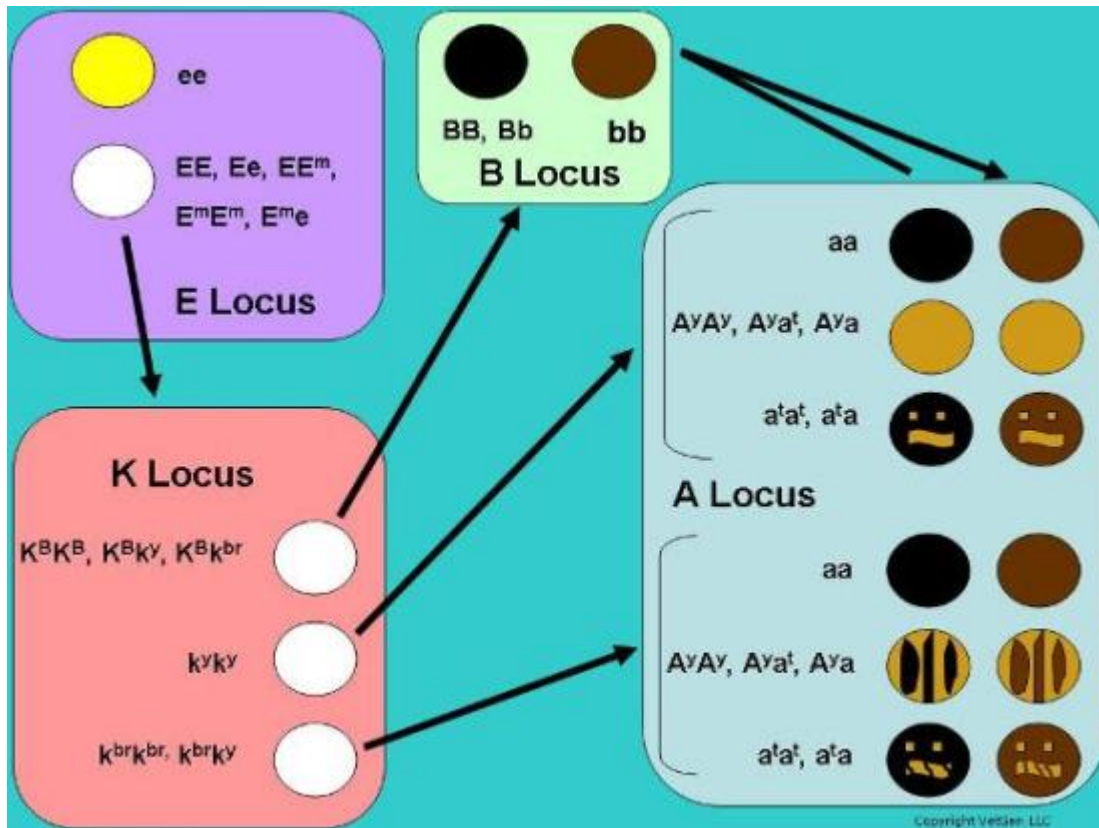
Descriptions of each locus and each of the coat color tests that VetGen offers can be found by scrolling down this page. We suggest stopping first at the diagram below which illustrates the relationships between the major loci involved in determining coat color.

How do the A, B, E, and K loci affect each other in determining coat color?

The cartoon below illustrates the interactions of the genes at these four loci in a hierarchy in terms of their role in coat color. If a circle is filled with color, it means the color of the dog has been determined at that point. If a circle is still white, it means information about an additional gene is required.

The first locus to look at is the **E locus**. The gene at this locus is responsible for black masks when present as well as most shades of yellow and red. Any dog that is "ee" will be some shade of yellow to red, and everything happening at the A, B, and K loci will be hidden until the next generation. If the dog has any E or E^m alleles, then it will not be yellow and we must look next at the K locus.

There are three versions, or alleles, of the **K locus**: K^B, k^{br}, and k^y. If a dog has even a single copy of K^B (K^BK^B, K^Bk^y, K^Bk^{br}) it will be solid colored in the pigmented areas, and we go directly to the B locus to determine color. Everything happening at the A locus in these dogs is hidden until the next generation. If a dog is k^yk^y, it will not be brindled, and we go next to the A locus to see which alleles are expressed. If a dog is k^{br}k^{br}, or k^{br}k^y, it will nearly always be brindled and we look next at the A locus to see the background color and pattern of that brindling.



The **A locus** has at least four alleles. There are direct tests available for A^y (fawn or sable) and "a" (recessive black), and in many breeds these two tests can be used to yield information about a^t (tan points). There is no direct test for the Wild type (think wolf pattern) allele which is designated a^w . Any dog which has at least one copy of A^y (and no K^B) will be fawn or sable, either with or without brindling. Any dog that is "a" (and no K^B) will be black. Any dog that is $a^t a^t$ or $a^t a$ (and no K^B) will have tan points, either with or without brindling.

The next step is the **B locus**. Any dog which is "bb" will be have brown fur in those areas that would otherwise be black. This holds true for both solid colored and agouti-patterned animals.

The **D locus** (not shown in the diagram) can alter the intensity of pigment. Animals which are "dd" exhibit grey or blue fur in place of black, and light tan or "Isabella" in place of brown. This tan is similar to some A^y shades but lacking any banding or black tips on individual hairs.



E locus

The E locus is responsible for the black mask seen in many breeds, and more significantly, for the presence of the yellow to red coats of many dogs. The gene involved is known as MC1-R, which has at least three versions affecting the appearance of the dog, E, E^m, and e. Dogs with two copies of e will be yellow, orange or red in their pigmented coat regardless of their genotype at all the other loci.

Test for "e"

Analysis proves absence or presence of the mutation typically responsible for yellow, lemon, red, cream, apricot and some white in at least the following breeds and all dogs with these breeds in their lineage:

Afghan, Australian Cattle Dog, Australian Shepherd, Border Collie, Beagle, Brittany Spaniel, Cardigan Welsh Corgi, Chinese Shar-pei, Chow Chow, Cocker Spaniel, Dachshund, Dalmatian, Doberman Pinscher, English Cocker Spaniel, English Setter, English Springer Spaniel, Field Spaniel, Flat-Coated Retriever, Foxhound, French Bulldog, German Longhaired Pointer, German Shepherd, German Shorthaired Pointer, German Wirehaired Pointer, Irish Setter, Labrador Retriever, Lowchen, Pointer, Pomeranian, Poodle, Pudelpointer.

Test for E^m

Analysis reveals whether a dog with a mask has one or two copies of this version of the extension locus. Animals with a single copy can produce offspring with or without a mask, while those with two copies will only produce masked offspring. The test may also be applied to black dogs where it may not be possible to tell if there is a mask. It may be present in the following breeds and all dogs with them in their lineage:

Afghan, Belgian Shepherd, Boxer, Bull Mastiff, Cairn Terrier, Cardigan Welsh Corgi, Chihuahua, Chinese Shar-pei, English Bulldog, German Shepherd, Great Dane, Greyhound, Lakemois, Pekinese, Pug, Saint Bernard, Saluki, Staffordshire Bull Terrier, Whippet.

B Locus

The B locus is responsible for the presence of brown, chocolate, or liver animals. It is also responsible for nose color. The gene associated with this locus is known as TYRP1. In breeds where the A locus does not come into play, any animal that has at least one B allele (and is not "ee"), will be black in



pigmented coat. Those dogs, which have two copies of any of several *b* alleles will be brown. There are at least three such *b* alleles. Regardless of other loci, any animal with at least one *B* allele will have a black nose and pads, while those with any two *b* alleles will have a liver nose and pads.

Test for *b*

This test analyzes whether an animal has 0, 1 or 2 copies of the mutations typically responsible for brown, which is also known in some breeds as liver, chocolate, sedge, and less frequently, red.

It can be present at least, but not exclusively, in the following breeds:

Australian Cattle Dog, Australian Shepherd
Bedlington Terrier, Border Collie, Brittany Spaniel
Cardigan Welsh Corgi, Chihuahua, Chinese Shar-pei, Cocker Spaniel, Curly Coated Retriever
Dachshund, Dalmatian, Doberman Pinscher
English Cocker Spaniel, English Setter, English Springer Spaniel
Field Spaniel, Flat-Coated Retriever, Fox Terrier, French Bulldog
German Longhaired Pointer, German Shorthaired Pointer, German Wirehaired Pointer
Labrador Retriever, Lowchen
Miniature Pinscher
Newfoundland
Pointer, Pomeranian, Poodle, Portuguese Water Dog, Pudelpointer
Scottish Terrier, Skye Terrier
Weimaraner, Wirehaired Pointing Griffon
Also:
Any dogs that contain these breeds in their lineage.

K Locus

The *K* locus plays a pivotal role in coat color. This locus is a relative newcomer in our understanding of canine color, and includes traits formerly attributed by some to other genes.

The dominant allele in the series is K^B , which is responsible for self-coloring, or solid colored fur in pigmented areas. This trait was formerly attributed to the Agouti (*A*) locus as A^S , but recent breeding studies had shown this not to be the case.

There are two other alleles, k^{br} , and k^y . K^B is dominant to both k^{br} and k^y , while k^{br} is dominant only to k^y . k^{br} is responsible for the brindle trait and for a long time had been considered to belong in the *E*

locus. Recent breeding studies had also shown this to be incorrect. The recessive allele, k^y , allows the basic patterns of the A locus to be expressed. So too does the k^{br} allele, but with brindling of any tan, fawn, or tawny areas.

Any animal with at least one K^B allele will be self-colored.

Any animal with at least one k^{br} allele, and no K^B allele will be brindled on agouti background (see A locus).

Any animal with two k^y alleles will show agouti patterns (see A locus).

The mutations responsible for these alleles were identified and described primarily by Sophie Candille in the laboratory of Dr. Greg Barsh at Stanford University.

Test for K^B and k^y

Vetgen can presently test for these two alleles. In some breeds, where no brindle is present, this represents a complete analysis of the locus. An example would be the Pug. In breeds where the breed standard disqualifies all but self-colored dogs, testing for these two alleles is once again all that is needed. Any animal with two K^B alleles cannot produce anything except self-colored offspring. A prime example here is the Labrador retriever. In breeds where many variations are allowed, these tests can help predict the probability of potential litters to include fawn, sable, tawny, tan point, tricolor or recessive black puppies.

$K^B K^B$	self-colored (solid color in pigmented areas)
$K^B k^{br}$	self-colored (solid color in pigmented areas)
$K^B k^y$	self-colored (solid color in pigmented areas)
$k^{br} k^{br}$	allows A locus to express (tan point, tricolor, fawn, sable, tawny) with brindling
$k^{br} k^y$	allows A locus to express (tan point, tricolor, fawn, sable, tawny) with brindling
$k^y k^y$	allows expression of agouti patterns without brindling

A Locus

The A locus is responsible for a number of common coat patterns in the dog. Expression of all of them requires any combination of two k^y or K^{br} alleles at the K locus, and at least one E or E^m allele at the E locus. The gene involved is the Agouti gene, and variations in it are responsible for fawn and sable dogs (A^y), wild type (A^w), tan points (a^t), and recessive black (a).

A^y analysis proves absence or presence of the mutation typically responsible for fawn or sable. In fawn/ sable dogs this test shows if other agouti alleles are present but hidden (only one copy of A^y). It also demonstrates how many copies of this allele are hidden in dogs, which cannot express agouti types ($K^B K^B$, $K^B k^{br}$, $K^B k^y$, at the k locus and/or "ee" at the E locus).

"a" analysis shows whether a black dog is black due to "recessive black," or the more common black at the K locus. It also reveals whether a non-black animal carries "recessive black." Examples of breeds:

German Shepherd Dog, Shetland Sheepdog, Belgians (Tervuren, Malinois, Lakenois, Groenendael).

a^t allele (tan points, tricolors)

There is no direct test yet for this recessive allele, but in some breeds, carriers may be deduced by use of the other two agouti tests.

In breeds where only the A^y , a^t and "a" alleles are present, the A^y test can be used to see if the fawn/sable dog is A^y/A^y (homozygous) or only has one A^y (heterozygous). If it only has one, the other allele must be a^t . Examples of breeds:

Afghans, Collies, Cardigan Welsh Corgi, Dachshund, Norwich Terrier, Staffordshire Terrier.

In breeds where only A^y , a^t and "a" alleles are present, both the A^y test and the "a" test need to be performed. Any alleles unaccounted for by these two tests will be a^t . For example, if a dog is A^y/A^y both alleles are accounted for. If a fawn/sable dog only has a single A^y , then the other allele must either be an "a" or an a^t , and this can be determined by running the recessive black ("a") test. Examples of breeds:

Shetland Sheepdog, Belgians (Tervuren, Malinois, Lakenois, Groenendael).



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D Locus

The D locus is the primary locus associated with diluted pigment, which results in coats that would otherwise be black or brown instead showing up as gray, or blue in the case of black, and pale brown or Isabella in the case of brown. The melanophilin gene has recently been shown to be responsible, but not all of the dilute causing mutations have been identified yet.

We now offer this test for Newfoundland, Doberman Pinscher and Great Dane.

M Locus

The M locus is responsible for the merle and double merle color patterns seen in some breeds. The gene associated with this locus has recently been shown by Dr Keith Murphy and researchers at Texas A & M to be the pmel gene.

VetGen does not currently offer a test for merle.

Coat Length

While it is not a color trait, the length of a dog's coat is of interest to many. It has recently been demonstrated that in many breeds, the gene FGF5 is responsible for whether a dog has a long coat (rough or fluffy), or a short (smooth) coat. The test Vetgen offers detects the presence or absence of the recessive allele that results in long coats when present in two copies, and as such allows dogs with short coats that carry a hidden "long coat" allele to be detected.