

DOG COAT COLOR / NATURAL BOBTAIL TEST REPORT

<p><i>Provided Information:</i></p> <p>Name: WOODLANDS TOMMY</p> <p>Registration:</p>	<p>Case: NCD249984</p> <p>Date Received: 06-Feb-2025</p> <p>Report Issue Date: 12-Feb-2025</p> <p>Report ID: 8498-0817-1727-0148</p> <p style="text-align: center; font-size: small;">Verify report at vgl.ucdavis.edu/verify</p>
<p>DOB: 05/09/2024 Sex: Male Breed: French Bulldog</p>	
<p>Sire: PREFERRED HANSOME HANS</p> <p>Reg:</p> <p>Microchip:</p>	<p>Dam: PREFERRED CASEY</p> <p>Reg:</p> <p>Microchip:</p>

RESULT

INTERPRETATION

Locus	Genotype	Interpretation
MC1R (E LOCUS)	E^m/E^m	2 copies of mask.
BROWN (B LOCUS)	B/B	Does not carry brown - cannot have brown offspring.
DILUTE (D LOCUS)	d^l/d^l	Dilute, 2 copies of the dilution variants.
DOMINANT BLACK (K LOCUS)	N/N	Dog does not have the dominant black mutation.
LEGACY AGOUTI	a^l/a	Dog has black-and-tan and carries recessive black.
AGOUTI (A LOCUS)	ASIP^{BB1}/ASIP^a	One copy of black back 1 and one copy of recessive black.
MERLE	N/266	One copy of the merle associated SINE insertion. See attachment (last page) for additional information.
PIEBALD (S LOCUS)	N/N	Dog has no copies of piebald.
INTENSITY DILUTION	In/In	2 copies of intensity dilution. Red pigment is likely to be diluted to cream or white.
ALBINISM (LHASA APSO TYPE)	N/N	No copies of the variant associated with the albinism first identified in the Lhasa Apso.
COCOA	co/co	2 copies of the cocoa variant.

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<p><i>Name:</i> WOODLANDS TOMMY</p>	

Additional Information

If testing for a disease or a disorder was performed and results indicate the animal is affected or at risk, we recommend contacting your veterinarian for further clinical evaluation and for additional information on disease and management.

For more detailed information on Dog Coat Color test results, please visit our website at:
vgl.ucdavis.edu/resources/dog-coat-color

Agouti research is ongoing, and additional variation beyond the resolution of this test may exist.

For terms and conditions of testing, please see vgl.ucdavis.edu/about/terms-and-conditions

Results are determined using PCR-based methods. The results relate only to the sample tested as identified by the submitter (for example, identity and/or breed).

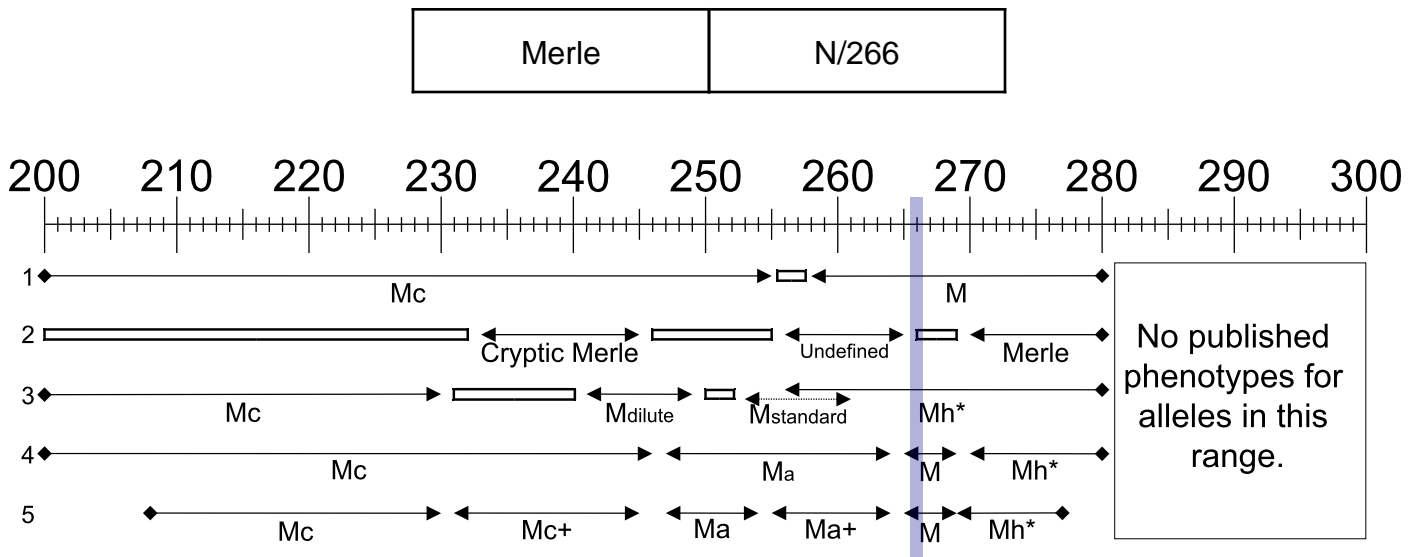
Report authorized by Dr. Rebecca Bellone, VGL Director



**ADDITIONAL INFORMATION FOR
MERLE RESULTS**

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Several interpretations and nomenclatures for the Merle variant have been proposed. Below is a graphical display of the merle alleles detected and the publications that define these nomenclatures.



Open boxes represent unassigned size variants within a specific naming system.

¹Previous merle pattern result reported by the VGL.

Mc=200-255, M=258-280

²Merle pattern nomenclature defined by Clark et al. 2006.

³Merle pattern nomenclature defined by Murphy et al. 2018.

Mc=200-230, Mdilute=241-249, Mstandard=253-261, Mh=256-280

⁴Merle pattern nomenclature defined by Ballif et al. 2018.

Mc=200-246, Ma=247-264, M=265-269, Mh=270-280

⁵Merle pattern nomenclature defined by Langevin et al. 2018.

Mc=208-230, Mc+=231-245, Ma=247-254, Ma+=255-264, M=265-269, Mh=269-277

* Mh “harlequin” is not the true Great Dane Harlequin (H) identified by Clark et al. 2008.

FRENCH BULLDOG GENETIC HEALTH PANEL TEST REPORT

<p><i>Provided Information:</i></p> <p><i>Name:</i> WOODLANDS TOMMY</p> <p><i>Registration:</i></p>	<p><i>Case:</i> NCD249984</p> <p><i>Date Received:</i> 06-Feb-2025</p> <p><i>Report Issue Date:</i> 13-Feb-2025</p> <p><i>Report ID:</i> 9005-4771-0602-1135</p> <p style="text-align: center; font-size: small;">Verify report at vgl.ucdavis.edu/verify</p>
<p><i>DOB:</i> 05/09/2024 <i>Sex:</i> Male <i>Breed:</i> French Bulldog</p>	
<p><i>Sire:</i> PREFERRED HANSOME HANS</p> <p><i>Reg:</i></p> <p><i>Microchip:</i></p>	<p><i>Dam:</i> PREFERRED CASEY</p> <p><i>Reg:</i></p> <p><i>Microchip:</i></p>

RESULT

INTERPRETATION

Canine Multifocal Retinopathy (CMR1)	N/N	Normal - no copies of the CMR1 mutation.
Degenerative Myelopathy (DM)	N/N	No copies of the DM mutation.
Juvenile Hereditary Cataract (JHC)	N/N	No copies of JHC mutation. Cataracts may however develop because of other genetic and environmental factors.
Hyperuricosuria (HUU)	N/N	No copies of the hyperuricosuria mutation detected. Dog is normal.

FRENCH BULLDOG GENETIC HEALTH PANEL TEST REPORT

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For more detailed information on French Bulldog Genetic test results, please visit our website at: vgl.ucdavis.edu/panel/french-bulldog-health-panel-1

For terms and conditions of testing, please see vgl.ucdavis.edu/about/terms-and-conditions

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Veterinary Genetics Laboratory · University of California Davis · One Shields Ave · Davis, CA 95616
vgl.ucdavis.edu · (530) 752-2211

Degenerative Myelopathy is associated with a genetic variant in the *SOD1* gene (c.118G>A). We therefore denote this associated allele as DM on our reports.

Many dog breeds carry the *SOD1* allele associated with Degenerative Myelopathy. The following breeds have been reported as having **clinically-affected** individuals with two copies of the *SOD1* associated variant (denoted on our report as **DM/DM**): American Eskimo Dog, Australian Shepherd, Bernese Mountain Dog, Bloodhound, Borzoi, Boxer, Cardigan Welsh Corgi, Cavalier King Charles Spaniel, Chesapeake Bay Retriever, Czech Wolfhound, English Springer Spaniel, German Shepherd, Golden Retriever, Hovawart, Kerry Blue Terrier, Labrador Retriever, Pembroke Welsh Corgi, Pug, Rhodesian Ridgeback, Rough Collie, Soft Coated Wheaten Terrier, Standard Poodle, and Wire Fox Terrier. Testing is advisable for these breeds.

There have also been reports of crossbred dogs with two copies of the *SOD1* allele that were clinically affected by degenerative myelopathy.

What do the results mean for my dog?

Within clinically-affected breeds, dogs with two copies of DM (**DM/DM**) are considered at higher risk for developing clinical signs of DM. However, not all dogs that are DM/DM will develop clinical signs of disease, and not all cases of degenerative myelopathy are explained by the DM/DM result.

Why some DM/DM dogs display symptoms of disease and others do not, is not yet known, but one hypothesis is that there are other genetic modifiers that contribute to risk. This is still under investigation.

Dogs with one copy of DM (**N/DM**) are not expected to develop clinical signs of degenerative myelopathy. They are considered carriers, because they carry the allele associated with disease.

Dogs with **N/N** genotype do not have this *SOD1* variant associated with degenerative myelopathy.

Please note that there may be other causes for degenerative myelopathy in the dog that are not explained by the *SOD1* variant (c.118G>A) tested by the VGL.

What about breeding my dog?

Dogs with a DM/DM genotype will pass on the DM allele to all of their offspring.

Dogs with an N/DM genotype may pass on the DM allele to ~50% of their offspring. If bred to another N/DM dog, 25% of puppies will be expected to have a DM/DM genotype and be at increased risk for developing DM.

For more detailed information about DM, visit <https://vgl.ucdavis.edu/test/degenerative-myelopathy>

COAT LENGTH TEST REPORT

<p><i>Provided Information:</i></p> <p><i>Name:</i> WOODLANDS TOMMY</p> <p><i>Registration:</i></p>	<p><i>Case:</i> NCD249984</p> <p><i>Date Received:</i> 06-Feb-2025</p> <p><i>Report Issue Date:</i> 13-Feb-2025</p> <p><i>Report ID:</i> 9781-9265-8894-6133</p> <p style="text-align: right; font-size: small;">Verify report at vgl.ucdavis.edu/verify</p>
<p><i>DOB:</i> 05/09/2024 <i>Sex:</i> Male <i>Breed:</i> French Bulldog</p>	
<p><i>Sire:</i> PREFERRED HANSOME HANS</p> <p><i>Reg:</i></p> <p><i>Microchip:</i></p>	<p><i>Dam:</i> PREFERRED CASEY</p> <p><i>Reg:</i></p> <p><i>Microchip:</i></p>

RESULT

INTERPRETATION

COAT LENGTH	S/L
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Carrier of an allele associated with long hair detected.

COAT LENGTH TEST REPORT

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For more detailed information on Dog Coat Type test results, please visit our website at: vgl.ucdavis.edu/services/dog/coat-length-curl-furnishings

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