Paw Print Genetics
A division of Genetic Veterinary Sciences, Inc.

Coat Color and Trait Certificate

Call Name:	Charlie	**Laboratory #:**	182420
Registered Name:	Not Yet Registered	**Registration #:**	-
Breed:	Australian Shepherd	**Certificate Date:**	July 8, 2020
Sex:	Female		
DOB:	June 2020		

This canine's DNA showed the following genotype(s):

Coat Color/Trait Test	Gene	Genotype	Interpretation
B Locus (Brown)	*TYRP1*	B/b	Black coat, nose and foot pads (carries brown)
D Locus (Dilute)	*MLPH*	D/D	Non dilute
M Locus (Merle)	*PMEL*	M/M	*See detailed interpretation

Interpretation:

This dog carries one copy of **B** and at least one copy of **b** at the b^c, b^d or b^s locus making the overall B locus genotype of this dog **B/b**. The overall B locus genotype for a dog is determined by the combination of the genotypes at the b^c, b^d, and b^s loci. The b^c, b^d, and b^s variants confer brown coat, nose, and foot pads when at least one of these DNA changes is present on both genes of the dog at the B locus. If the dog has one or no copies of **b** then the dog will have a black coat, nose, and foot pads. However, this dog's coat color is also dependent on the E, K, and A genes. This dog will pass on **B** to 50% of its offspring and **b** to 50% of its offspring.

This dog carries two copies of **D** which does not result in the "dilution" or lightening of the black and yellow/red pigments that produce the dog's coat color. The base coat color of this dog will be primarily determined by the E, K, A, and B genes. This dog will pass on **D** to 100% of its offspring.

M Locus Genotype: M^{223}/M^{255}

This dog carries two copies of the **M** (merle insertion variant) allele. The approximate sizes of the M alleles of this dog (+/- 1 base pair) are listed in superscript in the genotype. This dog will pass on one copy of the **M** (merle insertion variant) allele to all of its offspring with 50% of its offspring receiving one of the two versions of the M allele present in this dog and 50% of its offspring receiving the other version of the M allele. Merle is inherited in a dominant fashion, meaning that only one copy of an M allele is necessary for a dog to display some variation of the merle coat color/pattern, which is marked by random dilution of eumelanin (black pigment) leaving patches of normal coat color within areas of diluted pigmentation. The impact of the M alleles on this dog and its offspring will be determined by the approximate size of each M allele found in this dog (see detailed interpretation below). Depending on the sizes of the M alleles present, this dog may be an affected, "double merle". Dogs that inherit two copies of the M allele insertion variant of a certain size are at an increased risk of being mostly white with hearing and/or vision deficits.

Specific sizes of the M allele have been associated with the potential to produce "classic" merle patterning or other M-associated coat color variations. Merle is most appropriately viewed as a spectrum of coat colors/patterns and the size of the variant M allele is associated with a coat color/pattern somewhere within that spectrum. Although some coat color/pattern variations have been associated with specific sizes of the M allele in certain breeds, referred to here as a 'bin', the size of the M allele does not guarantee a specific outcome. In general, dogs with M allele sizes between 200 – 246 base pairs (bp) have been associated with non-merle or

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Call Name:	Charlie	**Laboratory #:**	230551
Registered Name:	MMA It's Classified	**Registration #:**	ASDS-TX-2105472
Breed:	Australian Shepherd	**Microchip #:**	956000012480262
Sex:	Female	**Certificate Date:**	May 11, 2021
DOB:	June 2020		

This canine's DNA showed the following genotype(s):

Coat Color/Trait Test	Gene	Genotype	Interpretation
Chondrodysplasia (CDPA)	*CFA18 FGF4*	cd/cd	No Leg Shortening Associated with CDPA

Interpretation:

Two genetic mutations are associated with shortened legs in dogs. Both mutations consist of copied sections (duplication) of the canine *FGF4* gene (called an *FGF4*-retrogene) that have been inserted into two aberrant locations in the genome; one in chromosome 12 (*CFA12 FGF4*; associated with CDDY and IVDD risk) and one in chromosome 18 (*CFA18 FGF4*; associated with chondrodysplasia [CDPA], but not associated with IVDD). Appropriate breeding decisions regarding dogs which have inherited the *CFA12 FGF4* mutation (WT/M or M/M) need to address both the potential loss of genetic diversity in a population which would occur if dogs with this mutation were prohibited from breeding as well as the loss of the short-legged appearance that is a defining physical characteristic for some breeds. In breeds which inherit both mutations, breeders may use genetic testing results to selectively breed for the CDPA (*CFA18 FGF4*) mutation while breeding away from the CDDY and IVDD risk (*CFA12 FGF4*) mutation to reduce IVDD risk and retain the short-legged appearance. However, the frequency of each mutation varies between breeds and, in some cases, may not be conducive to such a breeding strategy. For example, breeds with extreme limb shortening (e.g. Basset hound, Dachshund, Corgi) typically develop their appearance due to inheritance of both the *CFA12 FGF4* and *CFA18 FGF4* mutations. In addition, depending on the breed, offspring born without either the *CFA12 FGF4* or *CFA18 FGF4* mutations may display longer limbs than cohorts and, therefore, not meet specific breed standards.

This dog carries two copies of the **cd** allele which does not result in leg shortening. However, the actual leg length of the dog is a result of a combination of factors including the mutation associated with CDDY and IVDD risk (*CFA12 FGF4*) as well as variants in other genes. This dog will pass one copy of **cd** to 100% of its offspring.

Paw Print Genetics® has genetic counseling available to you at no additional charge to answer any questions about these test results, their implications and potential outcomes in breeding this dog.

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