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IDENTIFYING HOMOZYGOUS GENOTYPES ASSOCIATED WITH EARLY-ONSET LYMPHOMA IN BULLMASTIFF BY MELTING CURVE ANALYSIS

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Lymphoma is one of the most common hematopoietic malignancies affecting both humans and dogs. In dogs, some breeds are particularly predisposed to lymphoma, and Bullmastiff is one of them. Based on our laboratory's previous research on Bullmastiff dogs affected by lymphoma, a region of the size of 1.2 Mb on CFA13 containing five haplotypes composed of 20 Single-Nucleotide Polymorphisms (SNPs) are highly associated with early-onset lymphoma in the dog. According to the GWAS, a high percentage, (77.8%) of affected Bullmastiff dogs were found homozygous on those SNPs compared to low frequency of the unaffected Bullmastiff dogs or other breeds. On top of that, five SNPs are specified to determine whether the dog is homozygous or heterozygous through the related regions and hereby categorized into risk, carrier, and normal groups. In a

bid to distinguish genotypes of the tested samples quickly and economically, we developed a method combining quantitative real time Polymerase Chain Reaction (qRT-PCR or qPCR) and SYBR Green melting curves. The concordance and accuracy of our results elucidated that melting curve analysis enable the identification of the homozygosity of SNP in a rapid, inexpensive, and reliable way. CFA13 has been reported to be related to several canine hereditary diseases, while it also contains proto-oncogene *c-MYC* and a region that is syntenic with human *PVT1*. In short, our study is expected to be helpful for revising breeding strategies for Bullmastiff population; the long-term objective will be to improve the health of both dogs and humans.

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