

sample ID: 1807-W-52793

LABOKLIN
LABOR FÜR KLINISCHE DIAGNOSTIK GMBH & CO. KG

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Belgian Shepherd

Coat length I (long or short hair) - PCR

HLHd1 SNP G284T: L/l

Interpretation:

The test detects the alleles L (shorthair) and l (longhair) in the FGF5 gene.

Allelic series: L dominant over l
solely genotype L/L: The analysed sample is homozygous for the L-allele for short-haired.

exactly one genotype L/l: The analysed sample is heterozygous for the L-allele and the l-allele. The l-allele for long-haired is forwarded to 50% of the dogs offspring.

multiple Genotypes L/l: The analysed sample is heterozygous for the L-allele and the l-allele on more than one gene-locus.
The dog inherits the l-allele for long-haired to it's offspring.

at least one genotype l/l: The analysed sample is homozygous for the l-allele for long-haired.

Please note:

Further causative mutations for longhaired have been found in the following breeds:

Afghan Hound, Akita Inu, Alaskan Malamute, Chow Chow, Eurasian, Husky, Prague Rattler, Samoyed

The additional mutations might be responsible for longhair in further breeds.

Sampling:

The following impartial person (veterinarian, breed warden, or similar) signed the form for the sampling and identity check of the animal:

DAP Langens BVBA

The current result is only valid for the sample submitted to our