

### Result certificate #147555

Detection of deletion in RBM20 gene causing DCM in Schnauzers

# Sample

Sample: 20-09208

Name: Hanny Fortuna Moravia

**Breed: Schnauzer** 

Microchip: 203 098 100 387 798 Reg. number: CMKU/KS/8802/15/18

Date of birth: 8.7.2015

Sex: female

Date received: 16.04.2020 Sample type: buccal swab

## Customer

Petra Kříčková Dolní Albeřice 25 54226 Horní Maršov Czech Republic

# Result: Mutation was not detected (N/N)

**Legend:** N/N = wild-type genotype. N/P = carrier of the mutation. P/P = mutated genotype (individual will be most probably affected with the disease). (N = negative, P = positive)

### **Explanation**

Presence or absence of mutation c.2472\_2493delGAAGGTCAAAATCTGCCCAGAA in RBM20 gene causing dilated cardiomyopathy (DCM) in Schnauzer and Giant Schnauzer was tested. The DCM is a condition in which the heart's ventricular walls are stretched and the walls become thinner. Thinning of the walls causes enlargement of the ventricles and in most cases the left heart ventricle is affected first. These changes result in worsened function of the heart, the heart's ability to contract and to pump the required amount of blood. The perfusion of the bodily organs is poor; systemic oedemas and pulmonary oedema occur resulting in dyspnoea and coughing. The symptoms of the disease also include ventricular arrhythmia and myocardial scarring. The first clinical signs occur between the first and the third year of age. At the early stage of DCM, the affected dogs show reduced tolerance to physical stress and overall weakness, fainting and collapse. The prognosis is not good and DCM is the most common cause of invalidity and untimely death of dogs.

Mutation that causes DCM in Schnauzer is inherited autosomally recessively which means that the disease develops only in those dogs who inherit mutated allele from both parents; disease affects dogs with P/P genotype only. The dogs with N/P genotype are considered carriers of the disease (heterozygotes). In offspring of two heterozygous animals following genotype distribution can be expected: 25 % N/N, 25 % P/P and 50 % N/P.

Method: SOP171-DCM, fragment analysis

Report date: 24.04.2020

Responsible person: Mgr. Markéta Dajbychová, Deputy Laboratory Manager

GENOMIA GENERALITY CONTROL OF THE CHARACTER OF THE CHARAC

Genomia s.r.o, Republikánská 6, 31200 Plzeň, Czech Republic www.genomia.cz, laborator@genomia.cz, tel: +420 373 749 999