

Figure 2.1: Representation of a normal healthy heart beat as seen on an electrocardiogram (Goldberger *et al.*, 2018).

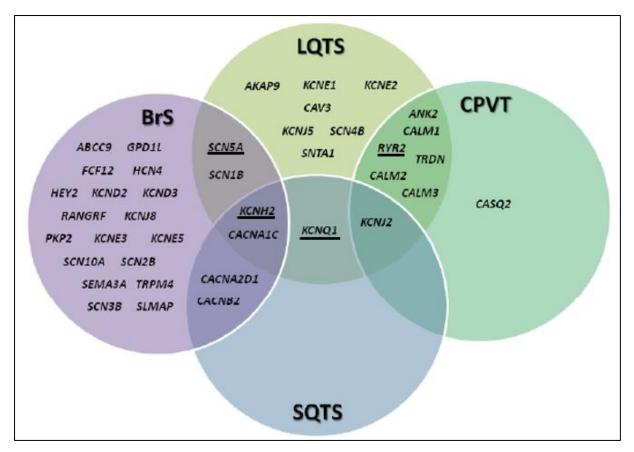


Figure 2.2: Genes associated with the relevant channelopathies: Brugada syndrome (BrS), long QT syndrome (LQTS), short QT syndrome (SQTS) and catecholaminergic polymorphic ventricular tachycardia (CPVT) (Fernández-Falgueras *et al.*, 2017). The underlined genes are the genes that are most predominantly linked to channelopathies (Anderson *et al.*, 2016).

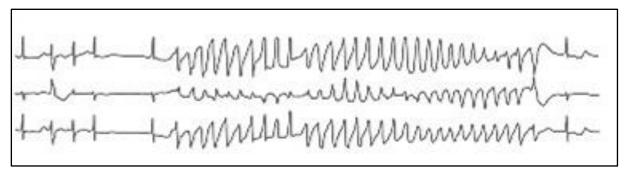


Figure 2.3: An electrocardiogram recording of a patient with prolonged QT interval and occurrences of variable torsade de pointes (Nussbaum *et al.*, 2015).

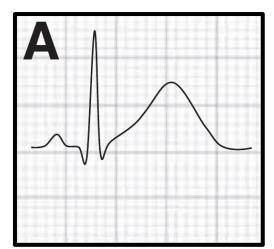


Figure 2.4: An electrocardiogram example of long QT syndrome one (Asatryan & Medeiros-Domingo, 2019).

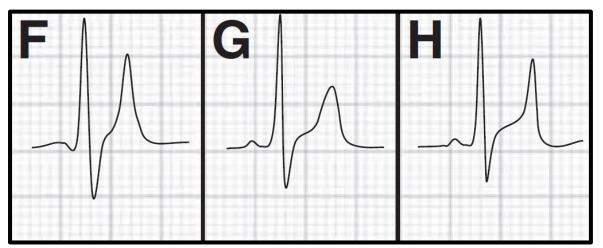


Figure 2.5: An electrocardiogram example of short QT syndrome one to three (Asatryan & Medeiros-Domingo, 2019).

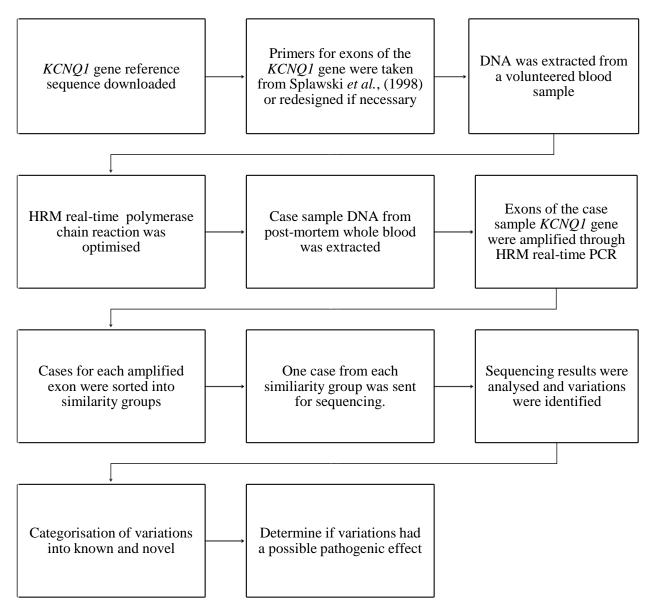


Figure 3.1: A step-by-step representation of the procedure that was followed for this research study.

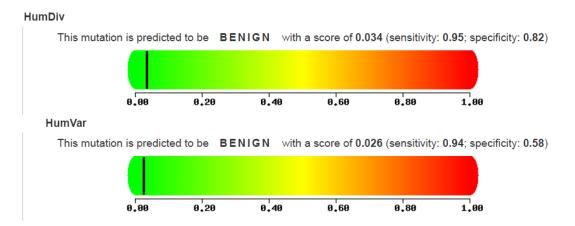


Figure 4.31: The results from PolyPhen-2 program on the significance of the VUS c.1007 G>C. HumDiv is the preferred model for rare alleles and HumVar is the preferred model for Mendelian diseases (Adzhubei *et al.*, 2013).

References:

Adzhubei, I., Jordan, D.M. and Sunyaev, S.R. 2013. A method and server for predicting damaging missense mutations. *Nature Methods*, 7 (4), pp.248-249.doi:10.1038/nmeth0410–248.

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Nussbaum, R., McInnes, R. and Willard, H. 2015. *Thompson & Thompson Genetics in Medicine*. 8th ed. Tennessee, USA: Elsevier.