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CLASSIFICATION OF TYPE 1 DIABETES SUSCEPTIBILITY REGIONS AND THE EFFECT OF REGULATORY SINGLE NUCLEOTIDE POLYMORPHISM SENSITIVITY

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ABSTRACT

This study shows that associated and non-associated SNPs can be characterised and distinguished by their genomic location within Type 1 Diabetes (T1D) susceptibility regions. It was also established that disease associated single nucleotide polymorphism sensitivity (SNPs) occur quiet frequently in non-coding parts. To do this, the genomic composition of the susceptibility regions and other associated genetic features were identified and analysed. It was found that the T1D susceptibility regions can be grouped into three clusters reflecting genomic content. The clusters are mainly separated by differences in intronic content and gene density. Furthermore, there are twenty-five T1D regions carry markers for fourteen other autoimmune diseases. The study revealed that the cluster of regions characterised by the most relative gene density and counts of non-coding transcript nucleotides than others, also had the strongest degree of susceptibility region sharing with other diseases.

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INTRODUCTION