Exploring the world of non-coding genes in stem cells and autoimmunity.

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Stellingen/propositions bijhorende bij het proefschrift

Exploring the world of non-coding genes in stem cells and autoimmunity

1. The choice of cell type defines the outcome of results, especially for studying non-coding RNAs that are considered more tissue-specific compared to protein coding genes. (*this thesis*)

2. *C5T1lncRNA* is one of the causative candidate genes in the *C5-TRAF1* risk locus, a locus associated with Rheumatoid arthritis. (*this thesis*)

3. Deregulated coding genes with nearby-located deregulated non-coding genes may together contribute to disease pathogenesis. (*this thesis*)

4. Investigating epigenetics in disease-specific manners will aid in understanding disease pathogenesis even if the results are 'negative'. *(this thesis)*

5. The enhancer region of *Sox2ot* plays an important role in influencing Sox2 transcription and may be more important than the Sox2ot transcripts itself. (*this thesis*)

6. Non-coding should not be interpreted as non-important. (*field*)

7. Genetic risk loci can pinpoint genes and pathways involved in disease. (*field*)

8. Genetic variation can be predictive of the risk to acquire a disease but does guarantee its development. (*field*)

9. Long non-coding RNAs are promising novel therapeutic candidates due to their high tissue specificity. (*field*)

10. Titles of scientific articles should be more carefully selected and should address the content of the article.

11. Publicly available datasets are of high value to the scientific society.