# *Stellingen*

1. Next Generation Sequencing experiments should only be performed after consulting a bioinformatician and a statistician. *This thesis*

2. Nuclear RNA sequencing data are a rich, yet often not fully explored source of information due to limiting bioinformatic analysis tools. *This thesis*

3. Skewing of gene expression towards the same allele in multiple breast cancer patients can be explained by a selective advantage caused by a gain of that allele (or a loss of the other allele). *This thesis*

4. Well-tuned statistical models for assessing age-induced changes in fundamental biological processes still need to be further developed and optimized. *This thesis*

5. The correlation between the stability of intronic secondary structures and the efficiency of intron splicing suggests a functional relationship between pre-mRNA secondary structure and splicing. *S. Rogic et al., BMC Genomics 9, 355 (2008)*

6. Despite the fact that the majority of RNA editing sites are situated in non-coding RNA and non-coding parts of coding transcripts, RNA editing has a potential role in protein sequence and structure diversification. *P. Danecek et al., Genome Biology 13:4, 26 (2012)*

7. Allele-specific expression observed exclusively in certain tumor types is associated with increased expression of specific transcription factors and changes in methylation patterns. *H. Ongen et al., Nature, 512, 7512 (2014*)

8. Substantial age-dependent decoupling of mRNA and protein expression appearing after 20 years of age could be caused by the deregulation of a specific set of RNA binding proteins and microRNAs. *Y.N. Wei et al., Genome Biology, 16, 14 (2015)*

9. I hear and I forget. I see and I remember. I do and I understand. *Confucius*

10. Climate is what we expect, weather is what we get. *Mark Twain*

11. It is too late to save the world, but you can always try to save one man. *Joseph Brodsky*