Stellingen behorende bij het proefschrift

"Foregut development: an act of balance"
Next generation sequencing and copy number variation profiling in esophageal atresia

1 The presence of a genetic syndrome is a risk factor for *esophageal atresia. This thesis*

2 Inherited rare and private mutations and copy number variations can shift the balance from normal to abnormal development. *This thesis*

3 Genome sequencing and high resolution copy number variation profiling will identify previously known and new genetic syndromes in many previously "VACTERL association" diagnosed patients. *This thesis*

4 Comparison of monozygous twin DNA is an excellent method to optimize next generation sequencing. *This thesis*

5 In view of the genetically heterogeneous etiology of EA/TEF, only worldwide collaboration will permit us to identify patients who share the same causal factor. *This thesis*

6 Genomic data matures like fine wine, it is best to wait a few years before reanalysis.

7 We can only speculate on our future knowledge on what is or isn't "pathogenic" variation. Therefore, true "*informed* consent" of parents is impossible.

8 At first sight, only failure to close the bow doors triggered the capsizing of the "Herald of free Enterprise". However, closer examination revealed that many cumulative acts resulted in this catastrophe.

9 If you torture the data long enough, it will confess.
(Ronald Coase, economics Nobel Prize laureate 1991)

10 The larger part of research budgets is spent on investigating what causes a disease, more budget should be allocated to disease prevention and dissemination of what is already known.

11 A PhD trajectory is like a long distance race, you start optimistically, halfway you wonder if you are going to make it to the finish and in the end you get a sense of accomplishment.