Stellingen behorende bij het proefschrift

Molecular profiling of non-small cell lung carcinomas
A genome-wide DNA methylation analysis

1. In NSCLC, as in most types of cancer, DNA is aberrantly methylated (this thesis).
2. MethylCap-seq is a reliable and quantitative method to profile the methylation status of NSCLC samples (this thesis).
3. Identification of differentially methylated regions (DMRs) can be used to develop sensitive biological markers for NSCLC (this thesis).
4. DMRs can distinguish between the two major NSCLC histological subtypes (this thesis)
5. The analysis of DMRs in DNA isolated from sputum or serum samples may enable non-invasive diagnosis and early detection of NSCLC (this thesis).
6. The distinctive pattern of CG sequences in the genome is of central importance in determining its biological significance (Brid, A. Nat. Genet., 2011).
7. Aberrant methylation patterns of non-CpG island promoters may also contribute to tumorigenesis and should therefore be included in analyses of cancer epigenetics (Han et al., Hum Mol Genet., 2011).
8. In early embryonic stages, DNA methylation marks are removed to ensure pluripotency of the embryonic stem cells (Gu et al., Stem Cells, 2011).
9. Small elements that reside within promoters are sufficient to precisely recapitulate DNA methylation patterns in stem cells and to replicate the changes that occur during differentiation (Lienert et al., Nat. Genet., 2011).
10. A widely divergent clinical, radiologic, molecular, and pathologic spectrum exists within lung adenocarcinoma. Diagnosis of lung adenocarcinoma therefore requires a multidisciplinary approach. (Travis, et al. J Thorac Oncol., 2011)
11. "Maior que a tristeza de não haver vencido é a vergonha de não ter lutado." - Bigger than the sadness of not having won is the shame of not having fought (Rui Barbosa, Brazilian jurist and writer)

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