Propositions

1. *DNMT3A*, *TET2* and *ASXL1* mutations persisting in complete hematological remission after induction therapy are not associated with an impending relapse [this thesis].
2. Next-generation sequencing is not only essential at diagnosis for AML risk stratification but also the preferred tool to determine residual disease in heterogeneous malignancies such as AML [this thesis].
3. Molecular minimal residual disease as defined by persisting *TP53* mutations in complete remission is not associated with an increased risk of relapse in *TP53* mutant AML [this thesis].
4. Detailed molecular analysis of a single clinical specimen can reveal common mechanisms of disease pathogenesis [this thesis].
5. Archived bone marrow glass slides are an excellent source to study the genetic evolution of AML during the course of disease [this thesis].
6. Detailed molecular analyses on a single cell level will replace bulk mutation detection in cancer research and diagnostics.
7. Monitoring mutation dynamics and kinetics during treatment of cancer in patients will provide guidance to how this disease can be best treated.
8. Due to the complexity of our cells and the mechanisms involved in cellular functions, the underlying causes leading to malignancy will never be fully elucidated.
9. Global collaborative studies are required to determine the significance of less commonly mutated genes in cancer.
10. Our genetic material doesn't determine our behavior but the environment we live in does.
11. "*Seek knowledge from cradle to the grave.*" Prophet Muhammad (PBUH)

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