1. No.
   2019T012

2. Title
   Genomic and Pathological Analysis of Lung Cancer

3. Period
   2019-2022

4. Summary

In order to perform next generation sequencing (NGS) analysis including cancer panel testing, it is important to extract enough nucleic acids. However, that procedure could be difficult in cases of small formalin-fixed paraffin embedded tissues. In some cases, numerous cut sections are needed. A method to precisely predict minimum number of cut sections are needed. We evaluated the cellularity of a representative cut sections of 42 biopsy samples that were submitted to cancer panel testing in a 5-tier manner. Then, the correlation between the 5-tier grading and the amount of nucleic acid extracted per tissue area was analyzed. Finally, an algorithm was established for the appropriate number of sections made according to the 5-tier grading system. The amount of nuclei acid extracted per tissue area increased as the cellularity grading went higher. When adjusted by square of the grade, the correlation became the strongest. By applying the algorithm for the appropriate number of sections based on the reciprocal of the square of cellularity-score, proved that the nucleic acid extraction would be optimized. Evaluation of cellularity in 5-tier grading could be a useful adjunct tool to predict nuclei acid yield from formalin-fixed paraffin-embedded tissues, and our algorithm can be utilized to avoid sequence failure due to insufficient input.

We then analyzed thymic cysts and found that they can be subclassified into S- and C-types. Mucinous epithelium is extremely rare. The significant difference in the sizes and CT values of S- and C-type cysts suggests these two types to be distinct. Based on the result of genomic profiling, we presume most thymic cysts to be non-neoplastic.