1. **No.**

   FP01801006

2. **Title**

   Association between germline SNPs and Japanese non-smoker lung adenocarcinoma risk

3. **Period**

   2017-2018

4. **Summary**

   This study was conducted to investigate genetic risk factors of never-smoker's lung adenocarcinoma in Japanese with a genome-wide analysis. A total of 656 never-smoker's lung adenocarcinoma cases and 496 healthy controls with advanced age and without cancer event throughout the lifespan were collected. All samples were genotyped with Japonica Array, which was made on the genetic background of Japanese by Tohoku University. After quality check steps, genome-wide association study (GWAS) was performed in the first year. The results showed some target regions with potential association with lung adenocarcinoma risk but with no genome-wide significance. In the second year, we reconsidered our data and reanalyzed by adding more data of 415 controls to get a total of 911 controls. This time some target regions were found to be associated with lung adenocarcinoma risk with genome-wide significance and some other regions with suggestive significance. Furthermore, the 656 never-smoker's lung adenocarcinoma cases were divided into two subgroups by two most frequently detected EGFR mutations, namely exon19del, 300 cases and exon21L858R, 356 cases. The GWAS results of the two subgroups were distinct and some SNPs were observed potential association with the subgroups of lung adenocarcinoma risk. Our observations may be helpful in early diagnosis and prevention of non-smoker lung adenocarcinoma in Japanese.