1. No.
   2017G005

2. Title
   Establishment of biomarker date base for personalized medicine in thoracic malignancies-
   Clinicopathological Features of PD-L1 or PD-L2-Positive Lung Squamous Cell Carcinoma-

3. Period
   2017-2021

4. Summary
   (1) Comprehensive analysis for immune profiles of tumor microenvironment in non-small cell lung cancers
   Gene expressions of PD-L1, PD-L2, co-inhibitory molecules (CTLA-4, PD-1, TIM-3, BTLA, VISTA, and LAG-3), co-stimulatory molecules (CD28, OX40, GITR, CD317, CD27, and HVEM), and markers of immune cells (CD4, CD8, CD25, Foxp3, CD68, and CD204) were quantified for 100 surgically resected non-small cell lung cancers (NSCLCs) by the cap analysis of gene expression (CAGE) analysis. As a result, the immune profiles of tumor microenvironment in NSCLCs were clarified.
   (2) PD-L1 and PD-L2 expression in surgically resected non-small cell lung cancers: Its correlations with the prognosis, driver oncogene alterations and clinicopathological features
   PD-L1 and PD-L2 expression in 980 surgically resected lung adenocarcinoma (LAD) and squamous cell carcinoma (LSCC) specimens were evaluated by immunohistochemistry. Both PD-L1 and PD-L2 positivity
   were defined based on the proportion of stained tumor cells on the tissue microarray. As a result, the relationships between PD-L1 and PD-L2 expression and the prognosis, driver oncogene alterations and clinicopathological features in LAD and LSCC were clarified.