Table 2: Flowchart of the data collection and analysis

Data and Preprocessing: TCGA database (Totally 182 patients’ data)

- Labeled with Ensemble Genes ID
- Identification of normal or tumor tissue
- Constructed IncRNA expression matrix (14086)
- Screened the patients with paired clinical information

- Extracted the m5C related IncRNAs expression (242)
- Filtered the prognostic m5C related IncRNA in PDAC patients (17)
- Construct a prognostic risk model for PDAC with LASSO regression method

- Depend on the co-expression relationship between m5C related genes (13) and IncRNAs
- Univariate Cox analysis (p < 0.001) and detecting the expression level

- Patients were divided into high or low risk group based on the risk scores and survival analysis

- Relationship with clinical pathological parameters
- Independent prognostic factor analysis
- Validation in vitro and functional analysis
- Tumor immune microenvironment analysis