**Background**

Lung cancer and mesothelioma remain a major area of unmet clinical need. While studies in animal models and cell culture are enormously valuable, there is no substitute for studies of primary human tumour tissue. We have therefore established a novel research platform, the Leicester Archival Thoracic Tumour Investigatory Cohort (LATTICe).

**Aims**

Our aim is to establish a multi-dimensional research platform for basic science as well as biomarker discovery, and to exploit this collection with methods for multiplex quantitative *in situ* histopathological assays.

**Methods**

- Pathological and clinical data were collected for a contiguous cohort of 1025 resected primary lung adenocarcinomas from our surgical centre between years 1998-2015.
- Databases of clinicopathological data and digital images of all diagnostic slides completed.
- The entire cohort was sampled into 23 tissue microarrays (TMAs) (3x1mm cores/case).

**Results**

TMA sections undergo wholly automated multiplex staining. Digital images are interrogated using fully automated tissue segmentation/phenotyping and quantification methods to generate tumour, core or single-cell level quantitative data.

**Conclusions**

TMAs in combination with multiplex methods allow quantitation of multiple genes at protein and/or mRNA levels in hundreds of tumours simultaneously, at the level of the tumour, the region, or individual cells. Our cohort is an excellent substrate for biomarker development and to address basic biology questions.