compared to those <65 years. Consequently, IT should be a valid treatment option in this population and its management should be optimized, with the aim of offering the best possible quality of care to this subgroup of patients. **Keywords:** Inmunotherapy (IT), advanced age, lung cancer

P67 TUMOR BIOLOGY AND SYSTEMS BIOLOGY - BASIC AND TRANSLATIONAL SCIENCE - PROTEOMICS

P67.01
Differential Proteomics Analysis on Plasma from Anlotinib-Treated Advanced Non-Small Cell Lung Cancer Patients

B. Han,[1] J. Lu,[1] W. Zhang,[1] Y. Lou,[2] H. Zhong,[3] H. Wang[1] *[1]Shanghai Chest Hospital, Shanghai/CN, [2]Department of Pulmonary, Shanghai Chest Hospital, Shanghai Jiao Tong University, Shanghai/CN, [3]Department of Pulmonary, Shanghai Chest Hospital, Shanghai/CN*

Introduction: Anlotinib has been demonstrated to be effective in advanced non-small cell lung cancer (NSCLC) patients. DNA-seq- and RNA-seq-based anlotinib molecular mechanism and biomarker screening have been introduced in previous studies. The underlying value of proteomics for anlotinib study is still unclear. **Methods:** In this study, 70 plasma samples were selected from 28 anlotinib-treated NSCLC patients (including 14 responders and 14 non-responders). LC-MS/MS analysis was performed on those samples with different time points including baseline, best response and progression disease. Bioinformatics analysis was performed to understand the underlying value of those differential proteins. **Results:** Proteomics analysis suggested the differential proteins from responders after anlotinib administration potential play a role in the molecular mechanism characterization and biomarker screening. The differential proteins between responders and non-responders at baseline mainly contribute to biomarker screening. Integrative analysis indicated 43 proteins could be used as underlying biomarkers for clinical practice. Lastly, we selected *ARHGDIB* and demonstrated that it has potential predictive value for anlotinib. **Conclusion:** This study not only offered the first insight that the proteomic technology potentially be used for anlotinib molecular mechanism characterization, but also provided a basis for anlotinb biomarker screening via proteomics in the future. **Keywords:** proteomics, Anlotinib, Liquid biopsy

P68 TUMOR BIOLOGY AND SYSTEMS BIOLOGY - BASIC AND TRANSLATIONAL SCIENCE - RADIOMICS

P68.01
Qualitative Computed Tomographic Features Predict *Epidermal Growth Factor Receptor* Mutations in Advanced Lung Adenocarcinoma

C.K. Liam,[1] C.S. Chai,[2] M.T. Ramli Hamid,[3] N.F. Muhammad Gowdh,[4] W.Y. Chan,[4] K.H. Ng[4] *[1]Department of Medicine, Faculty of Medicine, University of Malaya, Kuala Lumpur/MY, [2]Department of Medicine, Faculty of Medicine and Health Science, University Malaysia Sarawak, Kota Samarahan/MY, [3]Department of Radiology, Faculty of Medicine University Teknologi Mara, Sungai Buloh/MY, [4]Department of Biomedical Imaging, Faculty of Medicine, University of Malaya, Kuala Lumpur/MY*

Introduction: Current guidelines recommend reflex testing for *EGFR* mutations in patients with advanced lung adenocarcinoma. Although tissue biopsy is considered the "gold standard" for *EGFR* mutation testing, it may not always be feasible in a small group of patients.

Table 1. CT- features of patients with sensitising EGFR mutation

CT features	All patients (n = 158)	Patients with *EGFR* mutation (n = 67)	p value*	Multivariate analysis, OR (95% CI), p value
A. Location				
Lobe, No. (%)				
Right upper lobe	58	26 (44.8)	0.643	
Right middle lobe	11	5 (45.5)		
Right lower lobe	37	18 (48.6)		
Left upper lobe	35	11 (31.4)		
Left lower lobe	17	7 (41.2)		
Distribution, No. (%)				
Central	81	36 (44.4)	0.595	
Periphery	77	31 (40.3)		
B. Size of primary tumour				
Long axis diameter, cm				
Mean (± SD)	6.14 ± 7.51	5.08 ± 3.14	0.114	0.9 (0.86 - 1.02), 0.143
Short axis diameter, cm				
Mean (± SD)	4.52 ± 4.65	3.81 ± 2.41	0.112	1.0 (0.70 - 1.44), 0.975
C. Shape				
Contour, No. (%)				
Round	8	7 (87.5)	**0.029**	**13.6 (1.40 - 13.2), 0.024**
Oval	3	1 (33.3)		0.1 (0.01 - 2.46), 0.175
Irregular/lobulation[#]	147	59 (40.1)		
D. Margin				
Border, No. (%)				
Well-defined	23	12 (52.2)	0.566	
Mild-moderate ill-defined	35	15 (42.9)		
Ill-defined	100	40 (40.0)		
Spiculation, No. (%)				
Fine line from margin	46	22 (47.8)	0.556	
Coarse line from margin	89	37 (41.6)		

(continued)