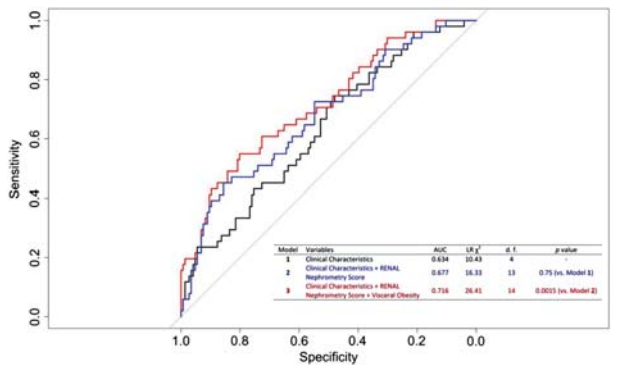

P1.29 Fig. 2: Receiver operating characteristic curves for high grade disease in clinical T1a renal cell carcinoma. The curves represent 3 multivariate models.

P1.29 VISCERAL OBESITY IS ASSOCIATED WITH INCREASED RISK OF HIGH-GRADE DISEASE IN CLINICAL T1A RENAL CELL CARCINOMA

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Objective: Accurate assessment of disease characteristics is a prerequisite for treatment decision making in small renal mass. Recent evidence suggests visceral adipose tissue is an important metabolic tissue and secretes factors that systemically alter the metabolic, endocrine and immunological milieu. The aim of the current study was to evaluate the association between visceral obesity and Fuhrman grade (FG) in a cohort of cT1a renal cell carcinoma (RCC).

Material and Methods: We retrospectively collected 197 patients with surgically treated cT1a RCC from January 2008 to January 2012. In each subject, a single sliced computed tomography image was used to measure the area of visceral and subcutaneous adipose tissue (Figure 1). The percentage of visceral adipose tissue (VAT%) was calculated as the area of visceral adipose tissue divided by the area of total adipose tissue. Other analyzed factors included clinical characteristics (age, gender, body mass index and tumor size) and tumor's anatomic features defined by RENAL nephrometry score. High grade tumor was defined as FG III or IV.

Results: Fifty-one (25.9%) tumors were classified as high grade. VAT% was increased in male participants, but didn't correlate with body mass index, age and tumor size. Multivariate analysis showed that tumor size (odds ratio = 1.82, $p = 0.046$) and VAT% (odds ratio = 1.05, $p = 0.0026$) were significant predictors of high grade cancer. Addition of VAT% to the model included clinical characteristics and tumor's anatomic features remarkably improved the discrimination ability ($p = 0.0015$) (Figure 2).

Conclusions: Increased visceral obesity was found to strongly associate with higher FG in cT1a RCC. The new prognostic factor provided a distinctive value other than clinical characteristics and tumor's anatomic features. Further studies are needed to confirm these findings and discover the underlying biological mechanism.
Funds: Supported by National Natural Science Foundation of China (Project 81001131).

P1.30 INTRATUMORAL HETEROGENEITY IN EXPRESSION OF CHEMOTHERAPY RESPONSE MARKERS IN INVASIVE DUCTAL BREAST CARCINOMA NOS

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Background: Chemotherapy response is composed of drug resistance and sensitivity. Previously, we found that intratumoral heterogeneity of invasive ductal breast carcinoma not otherwise specified (IDBC NOS), presented by the different types of morphological structures (tubular, trabecular, solid, alveolar structures, and discrete groups of tumor cells) displaying architectural arrangements of tumor cells may influence on chemotherapy response (Zavyalova et al., 2008); however, the mechanism of this effect is unknown.

Aim: We aimed to analyze expression of the multidrug resistance (MDR) and chemosensitivity genes in the different types of morphological structures and their microenvironment of tumor in IDBC NOS.

Materials and methods: Tubular, trabecular, alveolar structures, and their microenvironment (local and distant) were isolated by laser microdissection PALM (Carl Zeiss, Gemany) from 10 um sections of FFPE breast tumor. The isolated and whole amplified cDNA (RNA) was used for analysis of the MDR (*ABCB1*, *ABCC1*, *ABCC2*, *ABCC5*, *ABCG2*, *GSTP1*, and *MVP*) and chemosensitivity *(TOP1*, *TUBB3*, and *TYMS)* genes by the real-time TaqMan PCR.

Results: As seen in Table 1, expression of the MDR and chemosensitivity genes was significantly different between both the studied types of morphological structures and their microenvironment. Moreover, we observed the interesting phenomenon consisting in the fact that different types of morphological structures and their local microenvironments are supplemented each other in expression of the MDR and chemosensitivity genes. Tubular structures had a significantly higher activity of the MDR and chemosensitivity genes in comparison with other types of morphological structures, whereas their microenvironment was fully inactive in respect of the expressing genes. In contrast, a low expression level of the MDR and chemosensitivity genes in alveolar structures was compensated by high activity of these genes in the surrounding microenvironment. Interestingly that trabecular structures displaying moderate expression of the analyzed genes had microenvironment with a similar level of activity of these genes.

Conclusion: Together, the data obtained demonstrates that within IDBC NOS tumor there are subclones of tumor cells and their specific microenvironment with different expression of chemotherapy response markers.
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P1.31 SNP Q787Q OF EGFR GENE AND EFFICACY OF EGFR-TKI IN PATIENTS WITH NON-SMALL CELL LUNG CANCER

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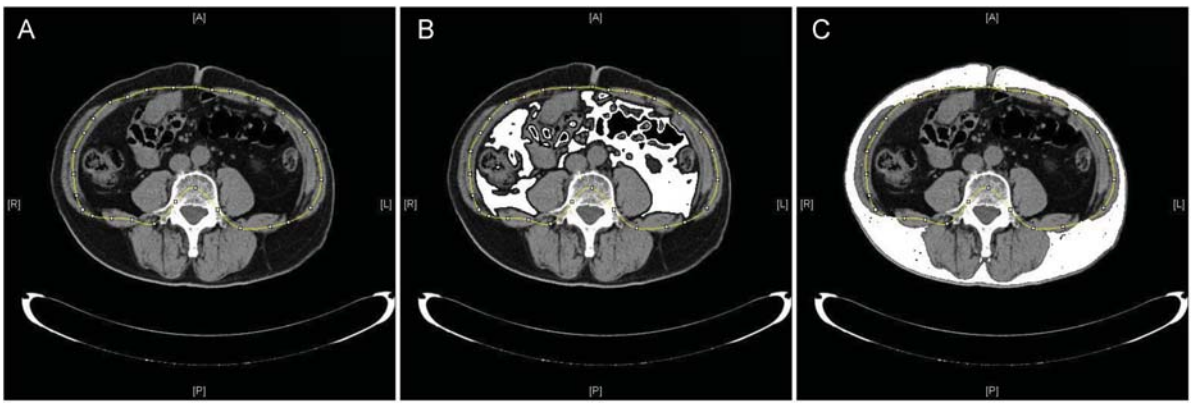
Background: Many activating mutations in epidermal growth factor receptor (EGFR) gene have been correlated with sensitivity to EGFR tyrosine kinase inhibitors (TKIs). Single nucleotide polymorphism (SNP) in exon 20 of EGFR



P1.29 Fig. 1: Representative examples of the measurement of visceral adipose tissue and subcutaneous adipose tissue in computed tomography images.