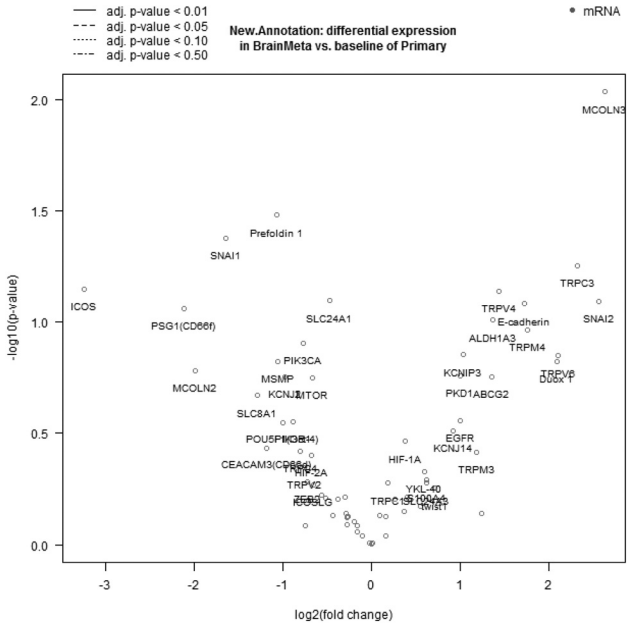
custom-made KMU IonChannel Panel that covered selected 100 genes. Detected data was analyzed by nCounter Advanced Analysis (version 2.0.115). Factors with unadjusted P-value < 0.01 were regarded as candidates for further investigation. **Result:** Brain metastasis showed upregulations of MCOLN3 and YTHDF2 (unadjusted P-value= 0.0093 and 0.0063, respectively) compared to the primary site. Conversely, primary site showed upregulations of IFNAR1, TNFRSF4, CXCL11, CT45A1, MAP3K5, TAL1, LAG3 and MARCO. In LATE-BREAKING ABSTRACT, we will report following data: 1) Immunohistochemistry results of the candidate proteins in resected brain metastasis and primary sites of NSCLC from larger population. In situ hybridization is also planned. 2) Additional data of expression profiles of the candidate genes in sphere cell line from brain metastasis and primary site of NSCLC. **Conclusion:** Biologic profilings of brain metastasis from NSCLC may subsequently help to understand underlying mechanism and ultimately lead to novel targeted therapy. Further details will be added in LATE-BREAKING ABSTRACT. **Keywords:** Brain metastasis, ion channel, nCounter



P2.03-06
Serum Syndechan-1 Levels in Patients with Nonsmall Cell Lung Cancer

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Background: Cytokines as polypeptide or glycopeptide molecules are the essential mediators of immune response and the inflammatory reactions in addition to numerous biological reaction they are involved in. Syndecans have an important role in a variety of cellular functions including cell proliferation and migration, and cell- /cell and cell-/ matrix interactions. Syndechan-1 is a transmembrane heparan sulphate proteoglycans that is present on most cell types. In this study we aimed to evaluate the levels of syndecan-1, levels in non-small cell lung cancer (NSCLC), and to evaluate their relationship with tumor progression. **Method:** Sixtysix patients (F=3, M=63) with non-small cell lung cancer and 22 healthy (F=3, M=19) subject were enrolled this study. Patients with infections or other systemic disease were not included in the study. Serum levels of syndecan-1 was measured by ELISA system. Serum samples were obtained from each patient before the initiation of any type cancer treatment. They were centrifuged at 3000 rpm for 10min, and then stored at -70°C. Unpaired t-test was used to compare continuous variables between the patient group and control group and within the patient group according to TNM classification. Correlation analysis between cytokines and tumor stage was performed using the Pearson correlation coefficient. Sensitivity, specificity, positive predictive value and negative predictive values for syndecan-1 were determined using receiver operator characteristic analysis (ROC). These analyses were done to define clinically valid cutoff points to predict distant metastasis. A two-sided p values less than 0.05 was considered to be statistically significant. **Result:** Serum levels of syndecan-1 in patients with NSCLC were significantly higher than those of controls ($p<0.001$). In addition, mean levels of synde- can-1 in stage IV disease were significantly higher than non-metastatic NSCLC ($p<0.001$). In the patients with only one distant metastasis, levels of syndecan- 1 were found to be lower than those of the patients with multiple distant metastases. Syndecan-1 has high sensitivity (78%), specificity (91%), positive (88%) and negative predictive (80%) values for prediction of metastasis. **Conclusion:** In conclusion, we found that syndecan-1 changes significantly in serum of patients with NSCLC. In our study, these changes correlated well with the stage of lung cancer. Syndecan-1 with a high sensitivity, specificity and positive predictive value may be used in predicting the presence and nature (single or multiple) of metastasis. The authors believe that the current findings will provide clinicians with new insights, allowing them to implement more individualized treatment strategies in patients with lung cancer. **Keywords:** nonsmall lung cancer, syndecan-1, metastasis

P2.03-07
Radiomic Signatures Linked to Genetic Alterations as Detected by Next-Generation Sequencing: A Radiogenomics Analysis of Early-Stage NSCLC

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Background: Radiomics uses large-scale quantitative analysis of extracted image-based features to identify tumor phenotypes. Such frameworks based on computed tomography (CT) have identified informative features in lung cancer related to treatment response and prognosis. Molecular profiles have been increasingly recognized in non-small cell lung carcinoma (NSCLC) as predictors of clinical outcomes. The aim of this study is to isolate radiomic signatures which are associated with genomic alterations discoverable by extended panel testing. **Method:** Patients with early-stage NSCLC who received definitive local treatment and underwent next-generation sequencing were included for this analysis. 35 genomic alterations representing 32 genes were evaluated using SNaPshot (Life Technologies), TruSight (Illumina Inc), Guardant360 (Guardant Health) or a FISH panel of ALK, MET, ROS1 and RET. Regions of interest including each primary tumor volume were delineated on diagnostic CTs datasets; they were defined as either tumor only (TO), or tumor with a 1cm anatomically-modified anisotropic margin (TM). Measures describing delineation and tumor appearance within each volume were extracted using in-house software, recording HU characteristics, inhomogeneity, and first and second-degree texture statistics. 91 structural, textural, and intensity features were extracted. Univariate logistic regression was performed to test the performance between each extracted feature and the presence of genomic alterations. **Result:** 40 patients with diagnostic CTs available for feature extraction were included for analysis. The rate of mutation prevalence in the most commonly altered genes were: TP53 (52.1%), cMET (34.5%), KRAS (27%), PTEN (13.8%), EGFR (13.2%), and