Title: -Multi-Omics analysis for understanding the molecular basis of Lung Adenocarcinoma.

Presented by: Agilent Technologies and Strand Life Sciences

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Abstract:

High throughput data from large cohorts of cancer patients is being generated by various consortia and is also being made accessible for use by other researchers. These data sources span multiple platforms and are a valuable resource for understanding the molecular basis of cancer. Key oncogenic and tumor suppressor players have been shown to undergo genomic copy number changes in lung adenocarcinoma patients [Nature 2014, 511:543-550]. In an effort to identify the oncogenes which are triggered by amplifications, we examined the expression levels of these genes in the context of their genomic aberrations (i.e. amplifications and deletions) and regulation by miRNA. Expression patterns of genes differentially expressed in tumors were further correlated with clinical and pathological metadata, as well as with mutational profiles of critical and known drivers of oncogenesis. An independent cohort of lung adenocarcinoma patients were evaluated for de-regulated pathways in the light of the mutational and genomic copy number findings from the TCGA cohort.