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Autor(en) des Beitrags:
Warth, Arne; Endris, Volker; Stenzinger, Albrecht; Penzel, Roland; Harms, Alexander; Duell, Thomas; Abdollahi, Amir; Lindner, Michael; Schirmacher, Peter; Muley, Thomas; Dienemann, Hendrik; Fink, Ludger; Morresi-Hauf, Alicia; Pfarr, Nicole; Weichert, Wilko

Titel des Beitrags:
Genetic changes of non-small cell lung cancer under neoadjuvant therapy.

Abstract:
Large scale sequencing efforts defined common molecular alterations in non-small cell lung cancer (NSCLC) and revealed potentially druggable mutations. Yet, systematic data on the changes of the respective molecular profiles under standard therapy in NSCLC are limited. 14 out of 68 observed coding mutations (21%) and 6 out of 33 (18%) copy number variations (CNV) were lost or gained during therapy. Mutational and CNV changes clustered in 6/37 (16%) and 3/37 (8%) patients. Changes in clinically relevant mutations were rare but present in single cases for genes such as BRAF and PIK3CA. The type of radiochemotherapy but not the duration of therapy impacted on the frequency of mutational changes. We established a lung cancer specific next-generation sequencing panel covering ~7500 hotspots of 41 genes frequently mutated in NSCLC and performed ultradeep multigene sequencing of 37 corresponding pre- and post-therapeutic formalin fixed paraffin-embedded specimens to discover mutational changes and copy number variations under neo-adjuvant radio- (RTX) and/or chemotherapy (CTX). We unraveled changes in common driver gene candidates in NSCLC under neo-adjuvant therapy. Our data shed first light on the genetic...
changes of NSCLC under conventional therapy and might be taken into account when the relevance of sequential biopsy approaches is discussed.

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