Detection of actionable genome alterations using hybrid capture based next generation sequencing technology- NEOplus and NEOliquid

Introduction:

Advances in the area of molecular cancer genomics has led to the identification of an increasing number of tumor-driven genetic alterations, with many being already candidates for tailor-made targeted therapies. NEO is a comprehensive molecular diagnostics platform capable of detecting genomic alterations including mutations, copy number alterations and translocations in both liquid biopsy (NEOliquid™) and tumor tissue (NEOplus™) samples to support cancer treatment decisions.

Methods:

We have developed a hybrid capture based next generation sequencing assay capable of detecting clinically relevant genomic alterations, such as point mutations, small insertions and deletions, gene fusions and copy number alterations. The NEOliquid™ assay is specifically designed for liquid biopsies and covers a panel of more than 30 genes. The NEOplus™ panel is specifically designed for FFPE tumor tissue covering more than 90 clinically relevant cancer genes.

Results:

Following signed patient consent, a series of lung cancer patient samples were examined using NEOliquid™ or NEOplus™ analysis. The spectrum of actionable genomic alterations that were detected, included oncogenic alterations (e.g. *ARAF p.S214F, MET exon 14 skipping, BRAF p.N486_A489 deletion, microsatellite instability detection*), resistance mutations (e.g. *EGFR p.T790M*), gene fusions (e.g. *ALK-CARS, EML4-ALK, EGFR-KDD*), and copy number alterations (e.g. *ERBB2 amplifications*) These cases are presented in their clinical context and treatment recommendations and outcome are discussed.

Conclusion:

Using the NEOplus™ and NEOliquid™ assays, we have identified a broad spectrum of therapeutically relevant genomic alterations with high sensitivity and specificity that resulted in concrete therapeutic recommendations. In comparison to standard diagnostics that require several methodologies for different types of genomic alterations, such as sequencing and FISH the NEO assays efficiently detect all relevant alterations in a single assay, thereby conserving both tissue and processing time.