Detection of EGFR Mutations in Quantity Insufficient Tissue Slides by High Sensitivity Assay Target Selector[™] in Patients with Non-Small Cell Lung Cancer

Vassilios Alexiadis, PhD¹., Jason Poole, PhD²., Veena Singh, MD¹., Barbara Blouw, PhD¹., Michael Dugan, MD¹., Lawrence Weiss, MD³.

¹Biocept, Inc ²Active Motif, Inc ³Neogenomics Laboratories, Inc.



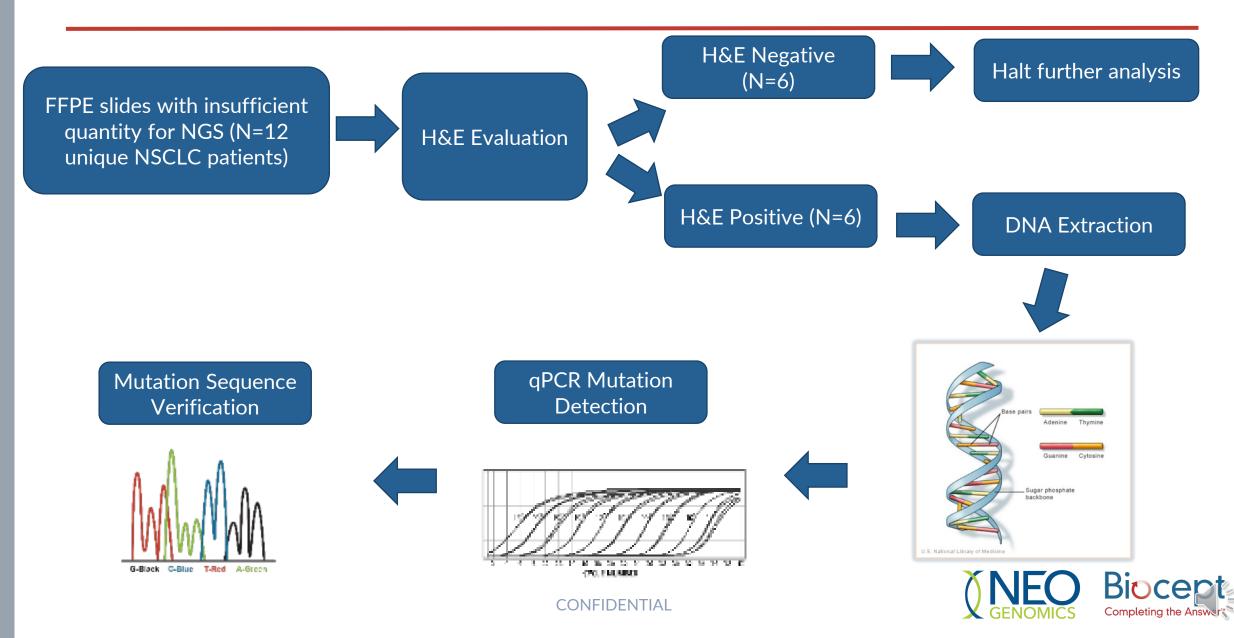
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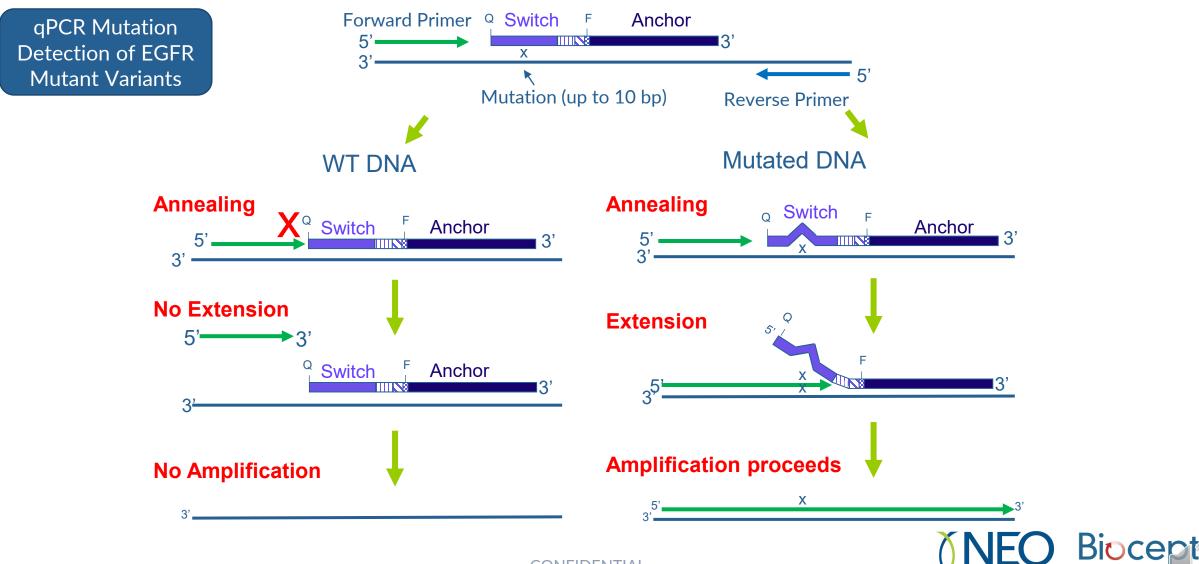
- Lung cancer is the leading cause of cancer-related death worldwide
- The discovery of EGFR mutations and development of Tyrosine Kinase Inhibitors (TKIs) has a major improved clinical benefit over platinum-based therapies.
- Historically, tissue biopsies are used for assessing the biomarker status of solid tumor type.
- Analysis on tissue biopsies has challenges that impede accurate biomarker evaluation including intra-and inter tumor heterogeneity, or insufficient amounts of tissue.
- Biocept's Target Selector[™] contains a highly sensitive technology to detect single gene mutations (Switch Blocker[™]) with a lower limit of detection between 0.01 and 0.03% without the need for tissue micro-dissection.
- Using the Switch Blocker[™] technology, we evaluated the presence of L858R, Del19 and T790M mutations in EGFR as well as G12/G13 mutations in KRAS, of Formalin-Fixed Paraformaldehyde Embedded (FFPE) tissue slides that were deemed 'quantity insufficient' (QNS) for Next Gen Sequencing (NGS) analysis.



Switch Blocker TM Workflow



Switch BlockerTM Technology¹



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Switch Blocker [™] Technology Identifies DNA in FFPE sections deemed QNS for Next-Gen Sequencing

Table 1. H&E Evaluation Results

Patient Number	H&E Result
1	Positive
2	Positive
3	Positive
4	Positive
5	Positive
6	Positive
7	Negative
8	Negative
9	Negative
10	Negative
11	Negative
12	Negative

Table 2. EGFR WT Ct and Copy number Results

Patient Number	EGFR WT Ct Value	Total EGFR copies
1	30.3	3184
2	30.2	3312
3	30.1	3638
4	28.9	7773
5	29.8	4500
6	NA	<1400



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Switch Blocker [™] Technology Identifies Actionable Mutations in samples with insufficient amounts for NGS

Table 3. Results on EGFR and KRAS mutation detection in samples positive for H&E

Patient Number	Mutation Detected
1	None
2	Del19
3	L858R
4	None
5	KRAS G12V and L858R



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- The Switch Blocker[™] technology is a highly sensitive method that allows for the detection of mutations in specimens which are deemed QNS for NGS based assays.
- This could lead to the ability to detect mutational changes in actionable biomarkers in patients that would otherwise not be considered for evaluation.

