AI-based detection of *ALK* & *ROS1* fusions in NSCLC directly from H&E scanned slides

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Background

Lung cancer is the leading cause of cancer-related mortality and accounts for approximately 1.76 million deaths per year worldwide.

Anaplastic lymphoma kinase (*ALK*) and *c-ROS* oncogene 1 (*ROS1*) gene fusions are well-established key players in non-small cell lung cancer (NSCLC). Although their frequency is relatively low, their detection is critical for treatment decisions and the implementation of targeted therapy. The accepted methods used for their detection are immunohistochemistry (IHC) and Fluorescent in-situ hybridization (FISH) assay, as well as DNA and RNA-based sequencing assays.

Here, we present an image-based solution for molecular profiling directly from Hematoxylin and Eosin (H&E) stained pathology slide images.

Results

				ALK/ROS1 AI classifier						
	Tot	**# P**	**# N**	**TP**	**TN**	**FP**	**FN**	**Sensitivity**	**Specificity**	**Concordance**
ALK	72	6	66	6	66	0	0	**100%**	**100%**	**100%**
ROS1	72	2	70	2	69	1	0	**100%**	**98.57%**	**98.61%**

Table 1. *Summary of ALK/ROS1 detection*

#P- number of positive; #N- number of negative; TP- True positive; TN- true negative; FP- false positive; FN- false negative; concordance – as compared to IHC/FISH/NGS reporting

Experimental design

Archival H&E whole slide images from NSCLC tumors of patients who underwent *ALK* and *ROS1*-fusions testing were collected. The dataset was split into a training set and a testing set.

(A) Advanced Convolutional Neural Network (CNN) was used to generate *ALK/ROS1* classifier models.

(B) a double-blinded test set, detecting tumors harboring *ALK* and *ROS* rearrangements using only the scanned H&E whole slide images.

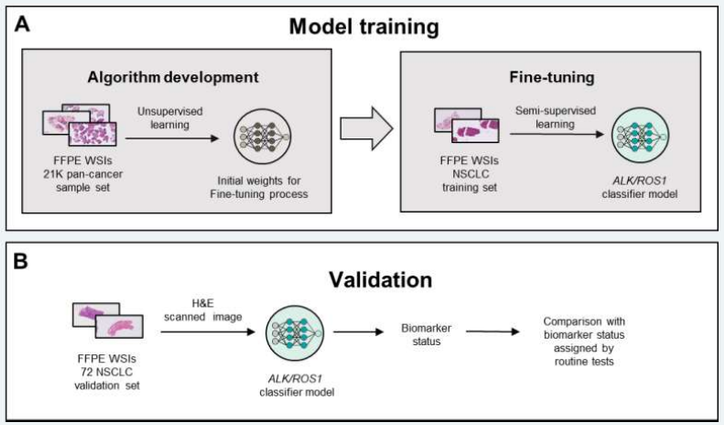

Figure 1. AI-algorithm development and validation

Conclusions

Herein, we demonstrate a real-time AI-based genomic testing solution for *ALK* and *ROS1*-fusions detection in lung cancer, using advanced neural networks directly from an H&E stained slide image.

These results highlight the advantage that machine learning solutions have in the molecular pathology domain, allowing fast, standardized, accurate, and robust biomarker detection.

These results highlight the potential of AI solution implemented within the pathology routine pipeline, in parallel to the traditional methodologies as illustrated in Fig 2.

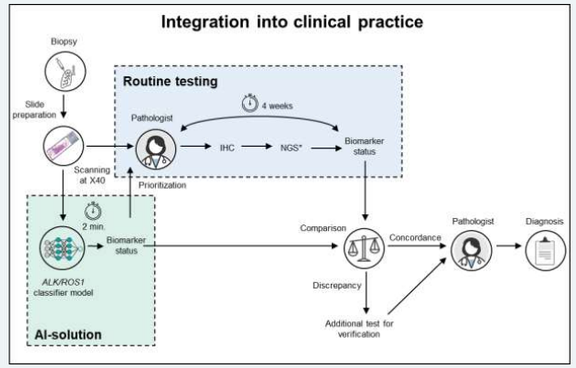

Figure 2. Integration of AI-based solutions in clinical practice.