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Transforming Precision Diagnostics in Switzerland

Applying Whole Genome and Whole Transcriptome Sequencing for Improved Patient Outcomes in Cancer Care

Clinical solid tumor oncology

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Complex biomarkers
(Molecular pathology & molecular hematology)
MSI
TMB
HRD

Pattern & signature recognition

Somatic alterations
(Molecular pathology & molecular hematology)
SNV
FUSION
CNV

Metagenomics
(Microbiology)

WGS

Germline alterations
(Medical genetics)

Blood & HLA typing
(Immunology)
HLA-A, -B, ...
A, B, 0
+/-

Pharmacogenomics
(Toxicology)

CYP2D6*4

Whole genome sequencing (WGS) has been validated technically and clinically by comparing its performance to established pan-cancer (Foundation One CDx, 324 genes) and melanoma-specific (190 genes) panels[4]. WGS demonstrated analytical validity, by detecting up to 98% of classic mutations and markers. In addition, WGS also identified complex biomarkers such as UV-associated mutational signatures, HLA types, and genome-wide copy number alterations, broadening its clinical utility. The completeness of WGS data further enables its use in reporting pharmacogenomic mutations[5], chimerism, and tissue typing, offering long-term utility as compared to gene panels.

Additionally, metagenomic WGS pipelines have been established for analysis of FFPE samples[6]. In 2022, Swiss pathologists developed a metagenomics-based pipeline that successfully identified an infectious pathogen as the underlying cause of a suspected lung tumor.

WGS is improving patient care by delivering an interdisciplinary wholistic molecular view on the patient with a single analysis. If properly set up, this one-stop-shop type of analysis will save time and may dramatically alter the frequency of unexpected, but actionable feedback.

[4]Litchfield, C. & Nienhold, R et al, Integrating FFPE derived Whole Genome Sequencing into Routine Molecular Pathology. unpublished
[5]Swen J.J. et al, A 12-gene pharmacogenetic panel to prevent adverse drug reactions. The Lancet 2023
[6]Nienhold, R. et al, Unbiased screen for pathogens in human FFPE samples by WGS and metagenomics. Front Cell Infect Microbiol 2022

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