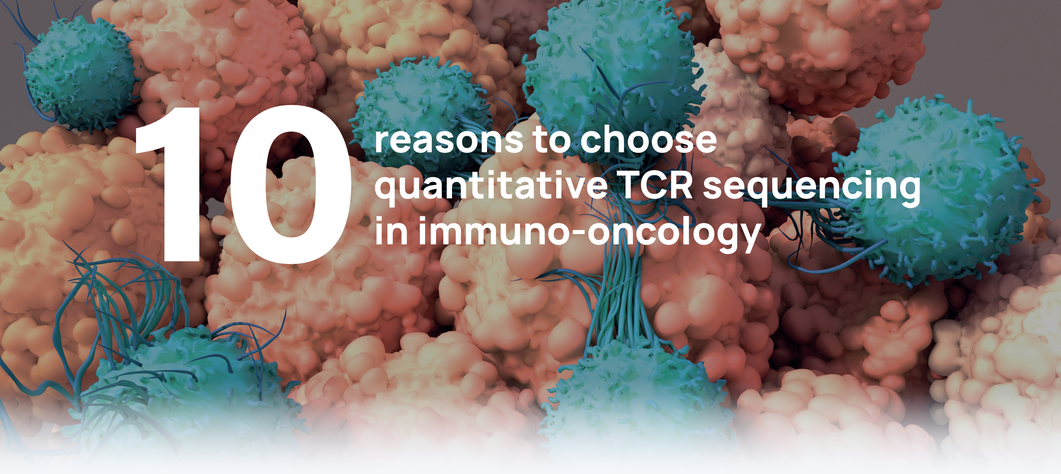

10 reasons to choose quantitative TCR sequencing in immuno-oncology

01

Delivery of **accurate absolute quantifications** of the T-lymphocyte receptor repertoires (technology based on RNA sequencing)

02

Seamless TCR-sequencing analysis platform, from extraction of the genetic material, library preparation, sequencing and bio-IT analysis, to the (optional) interpretation by specialised clinical immuno-oncologists

03

Platform **developed** and implemented **by clinical oncologists** from the Laboratory of Translational Oncology IPG / GHdC in Charleroi (Belgium) **to answer research and clinical questions from medical end-users**

04

Flexibility to use starting material from multiple sample types (PBMC blood samples, frozen tissue samples, cultured cells, sorted cells...)

05

Technical approach (using unique molecular indexes) to overcome the well-known pitfalls of other types of TCR-sequencing analyses, such as library amplification bias and polymerase errors

06

Sensitivity of the analysis down to a few cells in case of solid tumours

07

Possibility to **combine quantitative TCR-sequencing analysis with anatomo-pathology, immuno-histochemistry analysis** (e.g. routine PDL-1 staining, CD8 & PD-1) and **spatial biology**

08

Comparable quality in benchmarking against other marketed solutions for TCR-sequencing analyses

09

On-demand **delivery of more comprehensive in-depth reports** with additional tailor-made scientific analysis, such as T-cell clonotype tracking, multiple samples and time-points comparisons and the corresponding medical interpretation

10

Ideal support of quantitative TCR sequencing for target discovery, pre-clinical and clinical projects (uncovering predictive and companion biomarkers) in immuno-oncology

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