

Feasibility of an explainable AI-based therapeutic recommendation-tool utilizing tumor gene expression profiles for precision medicine in advanced & refractory solid tumors

Ouissam Al Jarroudi^{1,2,3*}, Coralie Williams⁴, Rita Santos², Armelle Dufresne⁵, Valéry Attignon⁶, Anthony Ferrari⁷, Sandrine Boyault⁶, Laurie Tonon⁷, Séverine Tabone-Eglinger⁸, Philippe Cassier⁵, Nadège Corradini⁹, Armelle Vinceneux⁵, Aurélie Swalduz⁵, Alain Viari⁷, Sylvie Chabaud¹⁰, David Pérol¹⁰, Mohammad Afshar^{2,4}, Jean-Yves Blay^{5,11}, Olivier Trédan⁵, Pierre Saintigny^{1,5,11*}

1- Department of translational medicine, Centre Léon Bérard, Lyon, France; 2- OmiCure Inc, Paris, France; 3- Faculty of medicine and pharmacy, Oujda, Morocco; 4- Ariana Pharma, Paris, France; 5- Department of Medical Oncology, Centre Léon Bérard, Lyon, France; 6- Platform of Cancer Genomics, Centre Léon Bérard, Lyon, France; 7- Platform of Bioinformatics Gilles-Thomas, Centre Léon Bérard, Lyon, France; 8- Biobank, Centre Léon Bérard, Lyon, France; 9- Department of Pediatric Oncology, Institute of Pediatric Hematology and Oncology, Centre Léon Bérard, Lyon, France; 10- Department of Clinical Research, Centre Léon Bérard, Lyon, France; 11- Univ Lyon, Claude Bernard Lyon 1 University, INSERM 1052, CNRS 5286, Centre Léon Bérard, Cancer Research Center of Lyon, Lyon, France.



Funding: the work was funded by OmiCure, Ariana Pharma and INCa-DGOS-Inserm_12563 (LYRICAN)

Background

- Precision oncology aims to guide patient treatment decisions by matching biological features with available drugs.
- Extensive genomic analysis allows to identify an actionable alteration in only 40-60% of patients [1].
- Recently, a study of 50 pts with advanced refractory diseases included in PROFILER trial (NCT01774409) [2], whole exome and fusion transcripts had a limited value over a 90-tumor gene panel to increase molecular-based treatment recommendations (MBTR).

Objective

- To evaluate the feasibility of the AI-transcriptional-based therapeutic recommendation-tool Onco KEM[®] to guide treatment recommendations for patients without tractable DNA-alterations.



Methods

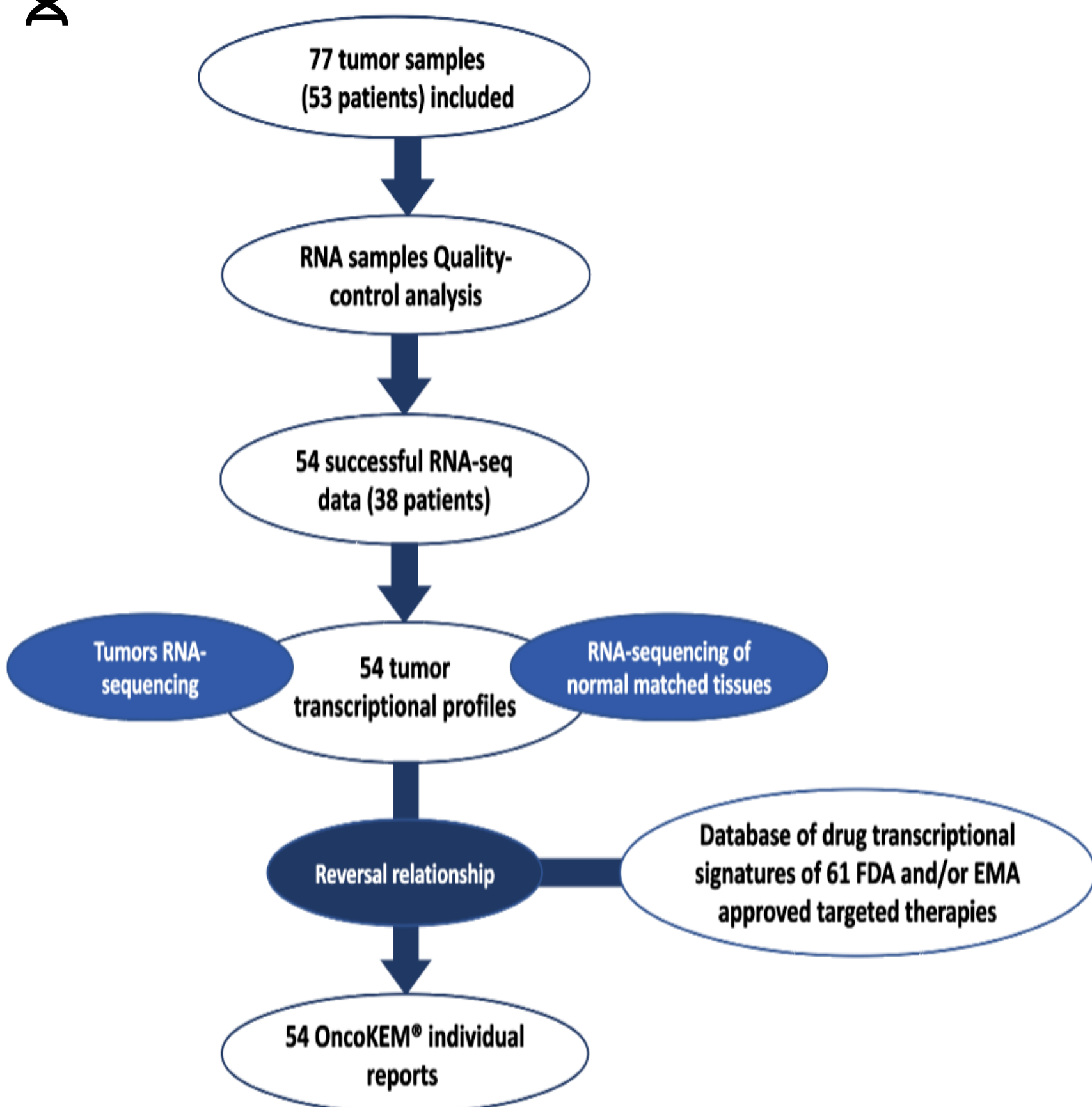


Figure 1: Description of study methodology

Results

- Most common diagnoses were gynecological cancers (23.6% of which 77.8% were ovarian cancers), followed by breast cancers (21% of which 66.7% were triple-negative breast cancer [TNBC]), digestive cancers (18.4% of which 71.4% were colorectal cancers [CRC]), and soft tissue sarcomas [STS] (13.1%) (Table 1).
- Most frequently proposed drugs among the top 10 were **palbociclib, talazoparib, infigratinib** in TNBC; **bosutinib, sapanisertib, SAR125844** in OC; **SAR125844, osimertinib, onartuzumab** in CRC; **ipilimumab, cabozantinib, sapanisertib** in STS (Figure 2).
- Even in the 30 patients cohort (79%) without any MBTR based on TGP/WES/fusion transcript analysis, all had at least 2 proposed targeted therapies in the Onco KEM[®] report (Median: 4) (Figure 3).

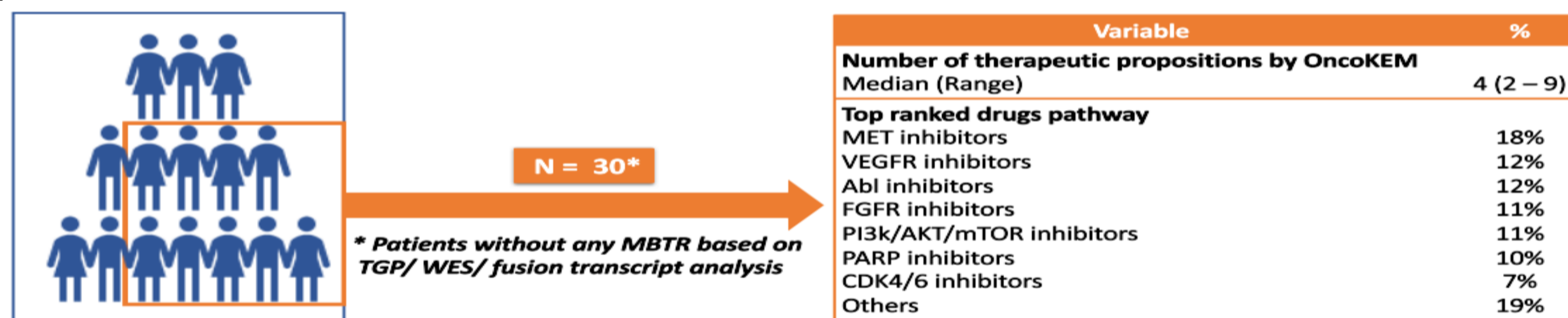


Figure 3: Description of most ranked drugs pathway

Table 1: Baseline characteristics

Characteristics	%
Age: Median (Range)	53 (21 – 70)
Gender	
Female	60.5%
Male	39.5%
Primary tumor site	
<i>Gynecological</i>	23.6%
<i>Breast</i>	21%
<i>Digestive</i>	18.4%
<i>Sarcomas</i>	13.2%
Others	23.8%
Disease stage	
Metastatic	92.1%
Locally advanced	7.9%
Number of metastasis sites: Median (Range)	2 (1 – 5)
Number of previous treatment lines: Median (Range)	4 (1 – 11)

Only **21%** of patients had a recommendation (Molecular Based Treatment Recommendation based on TGP/WES/fusion transcript analysis).

For all patients, at least 2 (median 4) targeted therapies were proposed using the **AI-transcriptional-based therapeutic recommendation-tool OncoKEM[®]**.

This tool has the **potential to expand** personalized cancer treatment in patients with advanced & refractory diseases **without tractable genomic alterations**.

Its **clinical relevance** assessment is planned in an **upcoming clinical trial**.



SCAN ME

Copies of this poster are for personal use only and may not be reproduced without permission from ASCO[®] and the author of this poster

* Corresponding authors email address: rita@omicure.com and Pierre.SAINTIGNY@lyon.unicancer.fr

References: 1. Malone ER, et al. Molecular profiling for precision cancer therapies. *Genome Med* 12, 8 (2020).
2. Trédan O, et al. Molecular screening program to select molecular-based recommended therapies for metastatic cancer patients: analysis from the PROFILER trial. *Annals of Oncology*, 2019

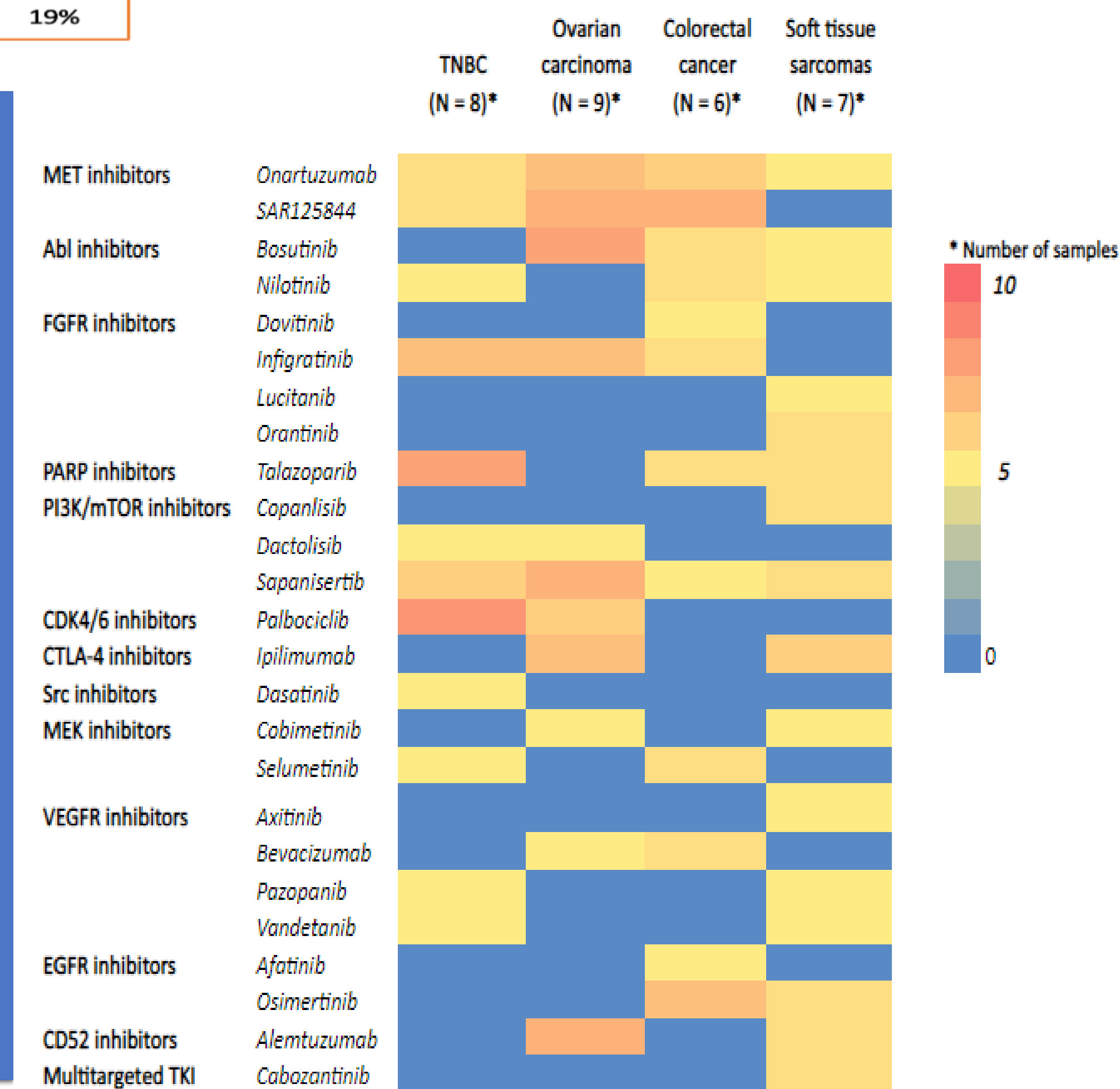


Figure 2: Ranking of targeted therapies in the 4 most frequent types of cancer