Fast TRACKing Precision Oncology for Rare Cancers: A National Decentralized Trial Offering Comprehensive Genomic Profiling and a Molecular Tumor Board

TRACK — TARGET → RARE → CANCER → KNOWLEDGE

TargetCancer Foundation

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TargetCancer Foundation

BACKGROUND

The TCF-001 TRACK study (Target RAre Cancer Knowledge, NCT0404604) initiated on October 1st, 2020, is a fully remote, decentralized precision medicine trial seeking to evaluate the clinical impact of utilizing comprehensive genomic profiling (CGP) reviewed by a molecular tumor board (MTB) for patients with rare cancers.

METHODS

- Patients (pts) were remotely enrolled/consented.
- Blood samples were collected via mobile phlebotomy and tested with FoundationOne Liquid CDx.
- Tissue biopsies (TBx) were tested using FoundationOne CDx ± laboratory developed test (LDT) FoundationOne RNA or LDT FoundationOne Heme.
- Liquid biopsy (LBx) testing included algorithmic predictions for clonal hematopoiesis (CH).
- MTB reviewed the results and provided recomendations.

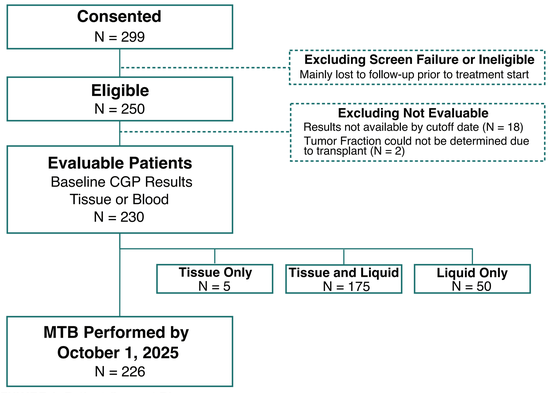

FIGURE 1: Patient Consort Diagram.

AFFILIATIONS

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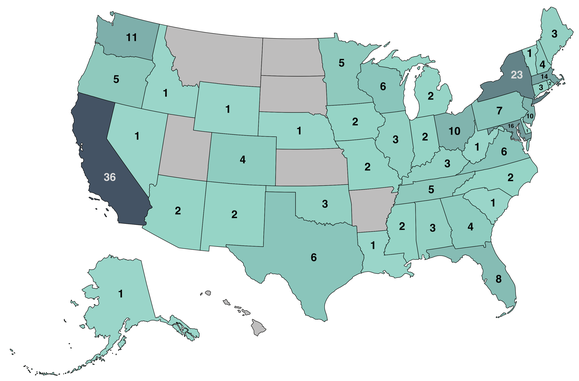
10. Foundation Medicine, Inc. Boston, MA USA
11. Stanford Cancer Institute, Stanford University School of Medicine, Palo Alto, CA USA
12. Medical College of Wisconsin Cancer Center, Milwaukee, WI USA

RESULTS: Geographic Distribution of Patients

FIGURE 2: Geographic distribution of Evaluable Patients



As of Oct 01, 2025, 230 pts from 43 US states and Washington, DC were enrolled with evaluable results; 76% (175/230) had TBx and LBx, 22% LBx, and 2% TBx. MTB review was completed for 226 pts.

RESULTS: Patient Characteristics

Characteristic	N = 230[1]
Age at First Sample Collection	57 (47, 66[1])
Sex at Birth	
Female	126 (55%)
Male	104 (45%)
Tumor Type	
Cholangiocarcinoma	80 (35%)
GI Tumors	43 (19%)
Soft Tissue-related Sarcomas	39 (17%)
Brain Tumors	33 (14%)
Other	35 (15%)
Microsatellite instability (MSI) Status	
Stable (MSS)	135 (78%)
Equivocal (MS-E)	3 (2%)
High (MSI-H)	3 (2%)
Unknown	32 (18%)
First on-study LBx - Not Included	57
Homologous Recombination Deficiency Signature (HRDsig)	
Negative	133 (77%)
Positive	3 (2%)
Unknown	37 (21%)
First on-study LBx - Not Included	57
ctDNA Tumor Fraction (TF)	
<1%	41 (72%)
≥1%	16 (28%)
Tumor Mutational Burden* (muts/Mbp)	1.26 (0.81, 3.62[1])
Blood TMB (bTMB; muts/Mbp)	1.26 (0, 2.53[1])
Number of States with Patients	43

[1]Median (Q1, Q3); N (%)

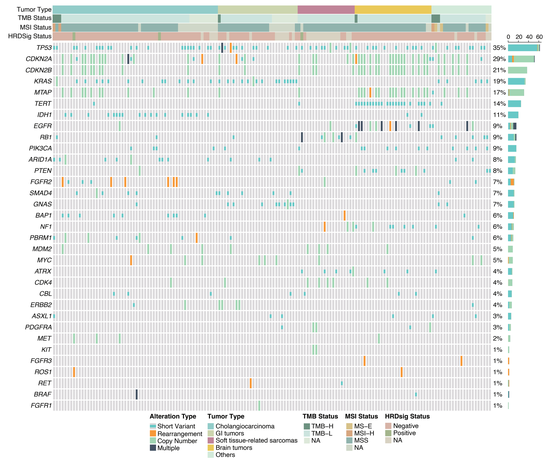
Over 60 tumor types were represented

First on-study TBx CGP (n=173) showed:
- MSI-H in 2% of pts.
- HRDsig in 2% of pts.
- Median TMB of 1.3 mut/Mb (IQR: 0.8,3.6)
- 5 pts with TMB ≥ 10 muts/Mb.

In LBx (n=57):
- ctDNA TF was ≥1% in 28% of pts.
- Median bTMB was 1.3 (IQR: 0,2.5).
- 1 patient with TMB ≥ 10 muts/Mb.

RESULTS: Prevalence of Alterations in TBx

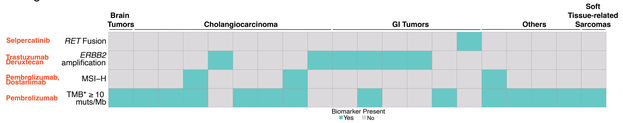
FIGURE 3: Prevalence of alterations in TBx. A total of 179 patients are shown. Each column represents an individual patient, rows represent genes. Patients are grouped by tumor type. TMB, MSI, and HRDsig values are shown at the top of the oncoplot.



TBx CGP detected alterations in 96% (172/179) pts:
- Most frequent: *TP53* (35%), *CDKN2A* (29%), *CDKN2B* (21%), *KRAS* (19%), *MTAP* (17%), and *TERT* (14%).

RESULTS: Biomarkers for tissue-agnostic therapies

FIGURE 5: Detection of eligibility biomarkers for FDA-approved tissue-agnostic therapies. Each column represents an individual patient, grouped by tumor type. FDA-approved tissue-agnostic therapies are listed in orange.



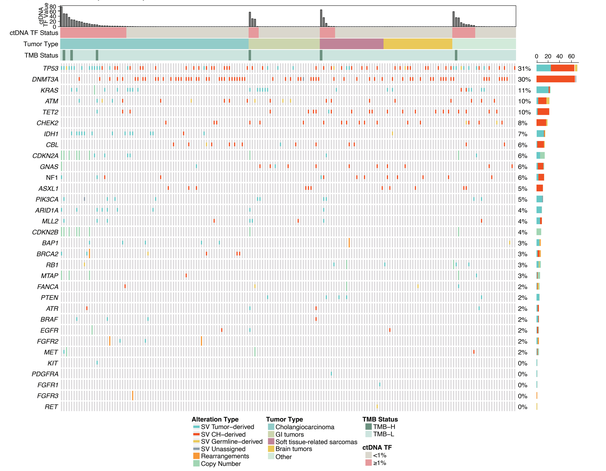
Across all tumor types, 9% (20/230) had biomarkers for FDA-approved tissue-agnostic therapies. This includes *ERBB2* amplification (2% overall) which is correlated with *HER2* immunohistochemistry positivity.

RESULTS: TBx/LBx Concordance and RNA Added Value

- LBx sensitivity for DNA tissue-detected clonal SVs and rearrangements was 85% (95% CI: 0.74,0.92) when ctDNA TF≥1% and 24% (95% CI: 0.19,0.29) when TF <1%.
- Pathogenic fusions detected by RNA sequencing were not detected by DNA in 33% of cases (9/27).

RESULTS: Prevalence of Alterations in LBx

FIGURE 4: Prevalence of alterations in LBx. A total of 225 patients are shown. Each column represents an individual patient, rows represent genes. Patients are grouped by tumor type. bTMB, ctDNA TF estimate and status are denoted at the top of the plot.



LBx CGP detected alterations in 85% (192/225) of pts, 25% had TF ≥1%:
- Predominantly tumor-derived (TD) included *KRAS* (11% of pts; 88% TD), *IDH1* (7%; 87% TD), and *CDKN2A* (6%; 100% TD).
- *TP53* alterations were common (31%) and mixed, with 57% CH and 38% TD.
- Predominantly CH included *DNMT3A* (30%; 98% CH), *TET2* (10%; 92% CH), *CHEK2* (8%; 90% CH), and *ATM* (10%; 64% CH).
- In brain tumors LBx (N = 28), 87% of detected variants were CH.

CONCLUSIONS

- TRACK, a first-of-its-kind national decentralized trial, demonstrates precision oncology can be democratized.
- CGP identified pathogenic alterations in nearly all rare cancer patients, with tissue-agnostic biomarkers in 9%.
- RNA sequencing adds diagnostic yield.
- CH in liquid biopsies underscores the need for expert MTB interpretation.
- This model provides a scalable framework for equitable access for patients with rare cancers.

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