The Tempus Immune Profile Score (IPS) is a multimodal biomarker that can be used as a prognostic indicator for adult patients with advanced pan-solid tumor disease who are already considered candidates for immune checkpoint inhibitor (ICI) based therapy. The IPS test is offered as a laboratory-developed test.

The test uses DNA and RNA sequencing data from the Tempus xT and xR tests to calculate an **IPS**, which ranges from 0 to 100, and classifies patients as either **IPS-Low** (scores 0-44) or **IPS-High** (scores 48-100). Scores between 45-47 are classified as Indeterminate.

The IPS test was developed utilizing a machine learning framework and records from 1,707 patients from the Tempus real-world database. The model includes tumor mutational burden (TMB), 8 single-gene RNA features*, and 3 RNA signatures*.

STUDY DESIGN

Clinical validation of the Tempus IPS test in Chicago, Illinois and Durham, North Carolina was performed in Tempus' CLIA-certified, CAPaccredited labs. The clinical validation cohort was evaluated in a prospective-retrospective analysis involving metastatic and/or stage IV pansolid tumor adult patients from Tempus' real-world database. The evaluated patient population included 1,600 individuals in cancer types with ICI approvals, who were treated with ICI-containing regimens in the first line (1L) or second line (2L) of treatment. Appendix Tables 1-3 provide the full inclusion and exclusion criteria.

The primary objective of the study was to demonstrate that patients classified as IPS-High had a higher real world overall survival (rwOS) compared to those with an IPS-Low result.

RESULTS

To determine the prognostic utility of IPS pan-cancer, the study used a multivariate CoxPH model fit on IPS, controlling for treatment group, and stratified by line of therapy. rwOS was significantly higher in IPS-High patients in the study compared to IPS-Low patients in the study (HR = 0.45 [0.40, 0.52]; p < 0.01).

IPS also demonstrated prognostic utility independent of TMB, PD-L1 IHC, and MSI status. IPS-High patients had longer OS than IPS-Low patients with HR \leq 0.50 in subgroups of patients that were TMB-high, TMB-low, PDL1-positive, PDL1-negative, and MSS (Figure 1). IPS remained significant for OS in separate multivariable models controlling for TMB, MSI, and PD-L1, with HRs of 0.49 ([0.42-0.56]; p<0.001), 0.47 ([0.41-0.53]; p<0.001), and 0.45 ([0.38-0.53]; p<0.001), respectively.

Additional subgroup analyses showed that IPS-High vs. IPS-Low hazard ratios were consistently <1 across demographics, clinically relevant subgroups, and important confounders (Figure 1).

Subgroup	No. of Patients			
All Patients	1519	0.45 (0.40, 0.52)	-	
PD-L1				
Positive	603	0.45 (0.37, 0.56)		
Negative	470	0.43 (0.33, 0.56)		
тмв				1
High	410	0.50 (0.38, 0.65)		
Low	1109	0.48 (0.41, 0.57)		
MSI				
High	76	0.58 (0.29, 1.18)		
Stable	1440	0.46 (0.40, 0.53)	-	
Age				
>=65	708	0.45 (0.37, 0.55)		
<65	811	0.46 (0.38, 0.56)		1
Sex				
Male	907	0.45 (0.37, 0.53)		
Female	612	0.47 (0.38, 0.59)		
Regimen				
IO Only	507	0.42 (0.33, 0.53)		
IO + Other	1012	0.48 (0.41, 0.57)		
Brain Metastases				
Not documented	1269	0.44 (0.37, 0.51)		
Documented	250	0.53 (0.39, 0.73)		
Liver Metastases				
Not documented	1173	0.49 (0.42, 0.57)		
Documented	346	0.41 (0.30, 0.56)		
Additional		(, , ,		
TMB-Low, ICI Only	323	0.41 (0.30, 0.57)		
MSS, ICI Only, LOT1	309	0.33 (0.24, 0.45)		
Cancer Type				
RCC	118	0.34 (0.20, 0.59)	_ 	
HNSCC	121	0.38 (0.22, 0.67)	_ - _	
NSCLC	615	0.42 (0.34, 0.52)		
Melanoma	98	0.47 (0.27, 0.82)		
Urothelial	131	0.55 (0.32, 0.92)		
Hepatocellular	38	0.70 (0.36, 1.36)		
Breast	81	0.75 (0.42, 1.33)		
Gastroesophageal	160	0.86 (0.54, 1.38)		
CRC	45	0.92 (0.32, 2.68)		
-		· · · · · · ·	0.5	4.5
		0	0.5	1.5

Figure 1: Forest plot showing IPS-High vs. IPS-Low hazard ratios and confidence intervals across demographics, clinically relevant subgroups, and important confounders.

*RNA-based features: CD274, SPP1, CXCL9, CD74, CD40, CD276, ID01, PDCD1LG2, a 43-gene gMDSC signature, an 768-gene Tempus immune resistance signature developed from scRNAseq data, and a 105-gene Tempus literature-based meta-analysis signature

INCLUDED CANCER TYPES

breast carcinoma	gastroesophageal squamous cell carcinoma	renal clear cell carcinoma
cervical carcinoma	head and neck squamous cell carcinoma	skin squamous and basal cell carcinoma
cholangiocarcinoma	hepatocellular carcinoma	small cell lung carcinoma
colorectal adenocarcinoma	lung adenocarcinoma	urothelial carcinoma
endometrial serous carcinoma	lung squamous cell carcinoma	urothelial neuroendocrine carcinoma
endometrioid carcinoma	melanoma	
gastroesophageal adenocarcinoma	non small cell lung cancer	

INCLUSION CRITERIA

- Age ≥18 at metastatic dx

De novo Stage IV or metastatic at sample collection

·	IO treatment in 1L or 2L				
	IO in 1L:	IO in 2L:			
	Metastatic dx < 7/1/2023	2L initiation < 1/1/2024			
	Sample date ≤ 90d of 1L initiation, and ≤ 240d for HNSCC , RCC and Cervical	If 1L initiation date < sample date < 2L initiation date: 2L initiation ≤ 90d of sample date			
	Metastatic dx ≤ 90d of 1L initiation, and ≤ 240d for HNSCC, RCC and Cervical	If sample date < 1L initiation date: 2L initiation ≤ 545d of sample date for all cancers			

• IO start ≤ 60d of line of treatment start, and ≤ 180d for maintenance therapy indications (Urothelial cancers)

EXCLUSION CRITERIA

- Prior IO treatment
- Unknown TMB
- ECOG score ≥ 3
- Tumor purity < 30%
- Samples collected from lymph node
- Received an investigational new drug
- Delayed entry >1 year from IO initiation
- Primary dx > 60d of metastatic dx
- Samples collected by 'bone marrow core biopsy', 'venipuncture', 'fine needle aspirate', 'fluid aspirate'