# TargetR: Automated Multi-Omics Report Framework for Target Characterization and Validation of Immunotherapy and Targeted Therapy Candidates Across Cancers

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Abstract #1115

### INTRODUCTION

- Immunotherapy has transformed cancer care, but its effectiveness is often constrained by tumor heterogeneity and immune escape.
- The discovery of novel, robust immunotherapy targets remains a major challenge, limiting the expansion of patient benefit.
- Innovative, scalable strategies are urgently needed to identify and validate new targets that can drive the next generation of immunotherapies.

## METHODS

targetR performs end-to-end analysis on public multi-omics datasets, enabling comprehensive target characterization across diverse data types—including transcriptomics, proteomics, genomics, and cell line data—spanning pan-cancer.

- Input: Gene of Interest (GOI).
- Options: Users can select all analyses or specify particular analyses of interest.
- Output: Detailed HTML reports.

Table 1. Available targetR analyses.

Analysis	Description	<b>Databases Used</b>	Analyses Included
Normal tissue expression	Characterizes normal tissue expression of the GOI across human tissues.	GTEx	Tissue-specificity, expression distribution, context within tissue
Protein abundance	Analyzes protein abundance in tumors and normal-adjacent tissues.	CPTAC	Protein abundance distributions, tumor vs. normal comparison, correlation with gene expression
Gene Expression	Examines gene expression in cancer, both pan-cancer and tumor vs. normal.	TCGA	Pan-cancer expression, tumor vs. normal, stage-specific analysis, survival analysis
Mutational load	Profiles somatic mutations in the GOI across cancer types.	TCGA	Mutation load and variant analysis
Copy Number Variations (CNVs)	Investigates CNVs and their impact on the GOI.	TCGA	CNV class distribution, correlation with expression, CNV concordance analysis with cancer-related genes across the chromosome
Surface scores	Evaluates the surface protein potential of the GOI.	Hu et al. Nature Cancer 2021	Core Genes Encoding Surface Proteins (GESP) score calculation, surface protein annotation
Cell Line Analysis	Analyzes the GOI across cancer cell lines.	DepMap & CCLE	Expression & copy number by cell line lineage or primary disease. CRISPR knock-out gene dependency correlations.

## SUMMARY

- We developed targetR (rebranded as tempustarget), a comprehensive computational framework integrating public and real-world multi-omics datasets to accelerate immunotherapy target discovery and validation.
- Findings generated by targetR can be further validated using real-world data from the Tempus database, which offers a larger patient cohort including extensive clinical features and outcomes.



## targetR EXAMPLE REPORT

Two main GOIs are presented as examples. Only a small subset of analyses from each module is shown.

- CD274 (PD-L1), a key immunotherapy target involved in immune checkpoint regulation.
- EGFR, a well-established target for targeted therapies in oncology.

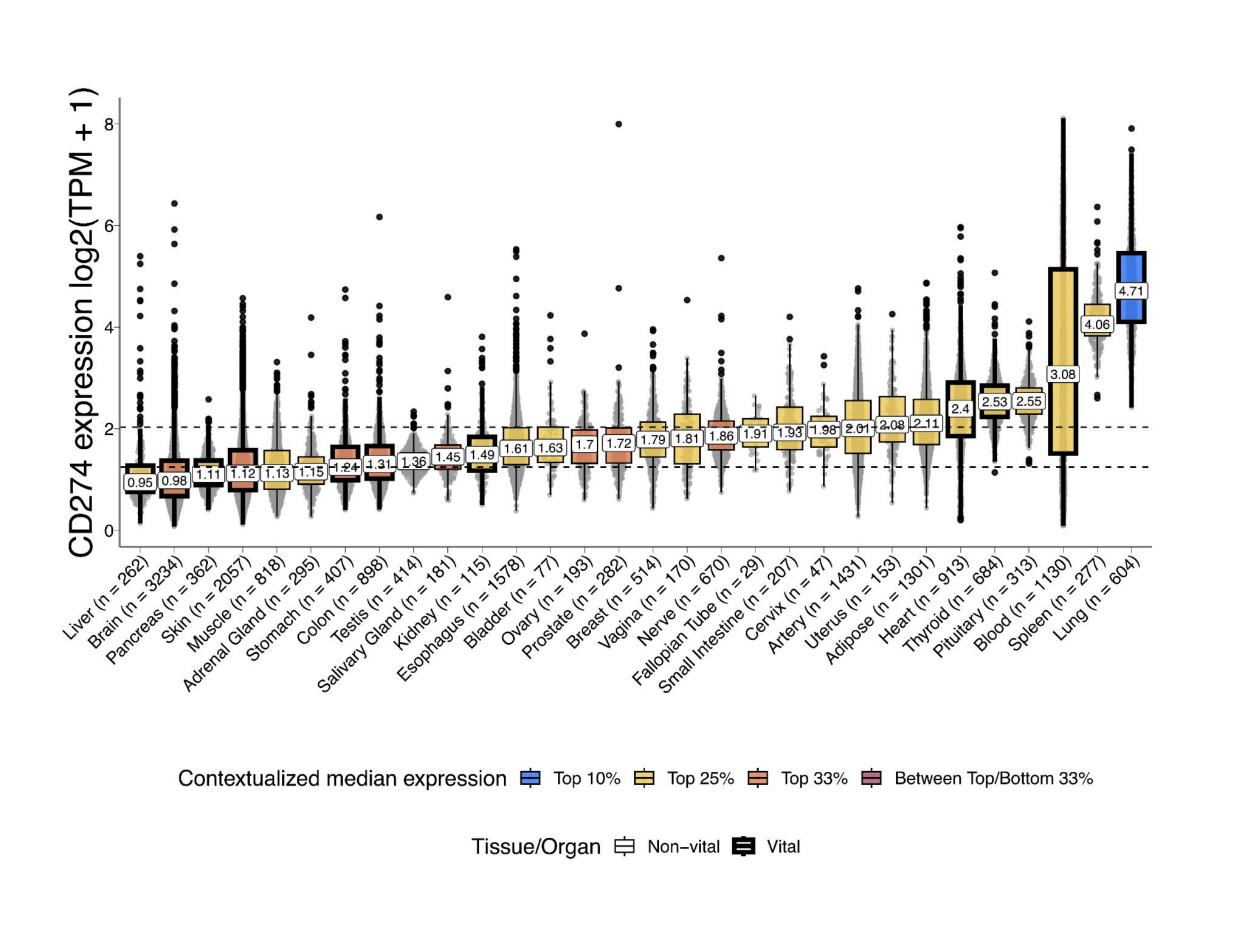


Figure 1. Distribution of normal tissue expression in *CD274*. Vertical lines mark bottom and top 33% median expression. *CD274* expression is shown per tissue, indicating if it falls within the top or bottom 10%, 25%, or 33% of gene expression levels.



Figure 2. Correlation heatmap of protein abundance in *CD274*. The Spearman correlation coefficient (Rho) and the statistical significance (FDR) are annotated with stars (\*). P-value adjustment is done through Bonferroni-Hochberg correction.

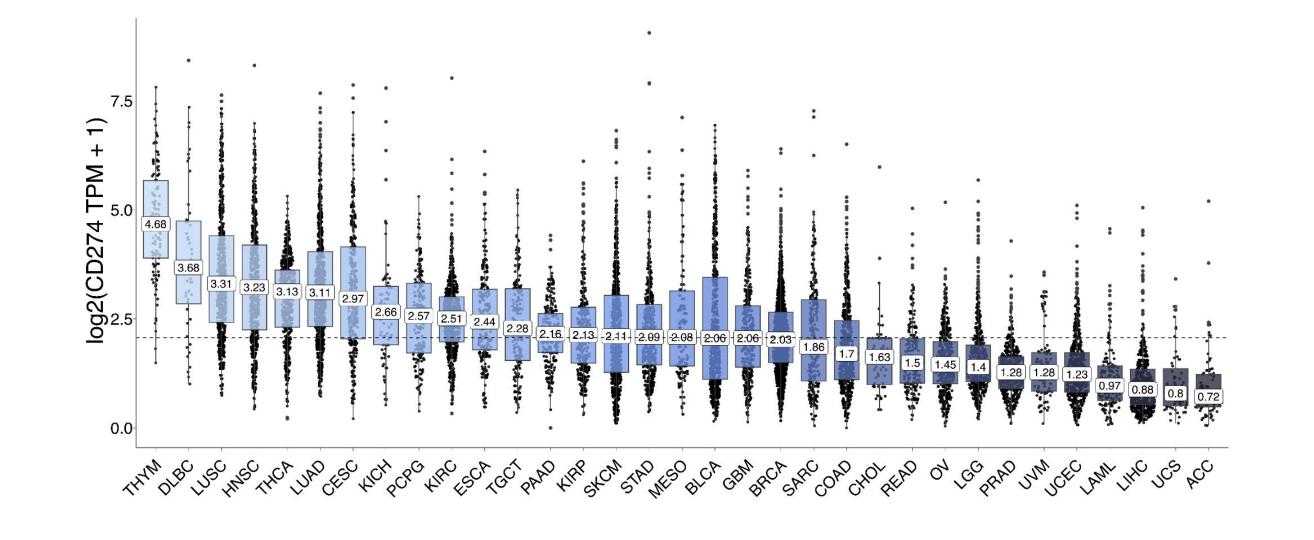


Figure 3. Gene expression across indications in *CD274*. Box plot shows gene expression by cancer stage; vertical line marks *CD274* median.

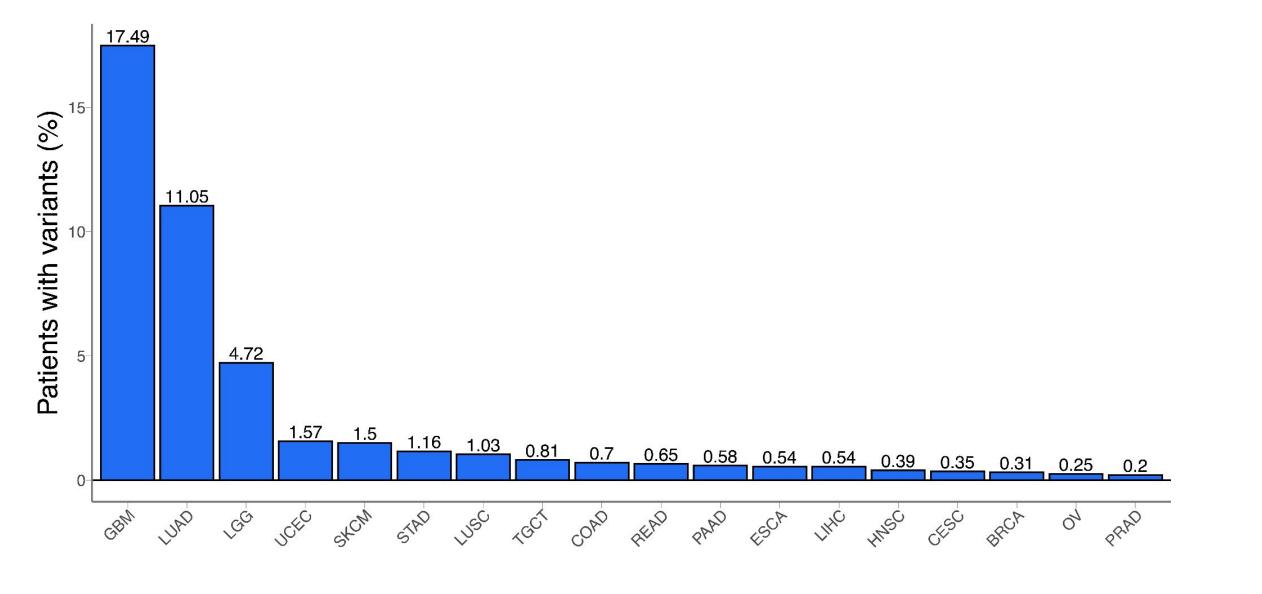


Figure 4. Mutational load showing patient frequency in *EGFR*. Shows percentage of patients with ≥1 variant per indication.

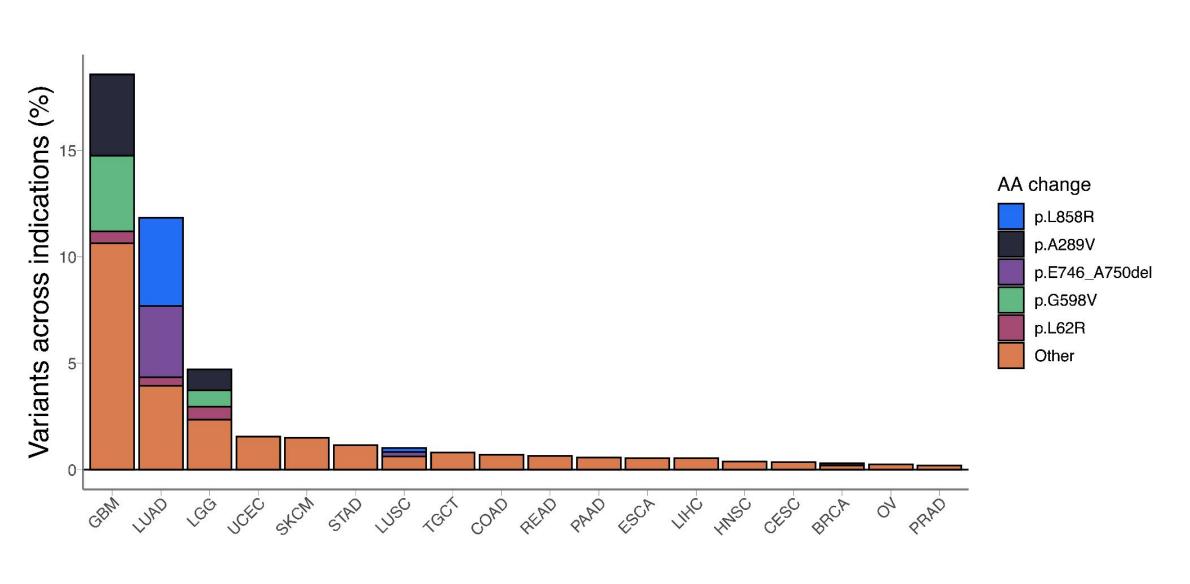


Figure 5. Mutational load by amino acid change in *EGFR*.

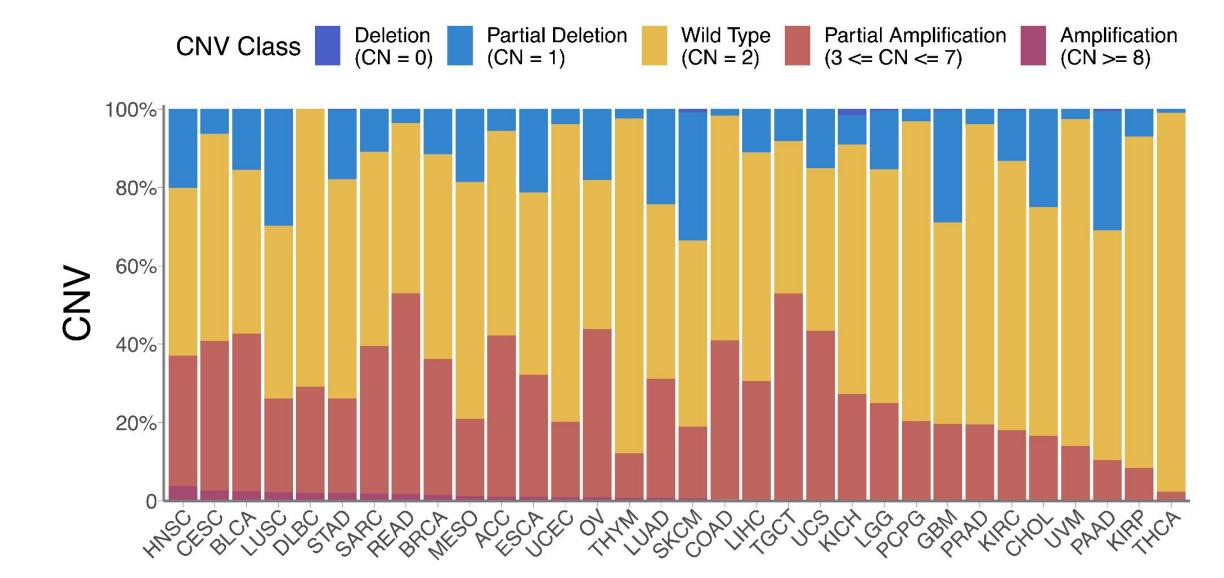


Figure 6. CNV Distributions in CD274.

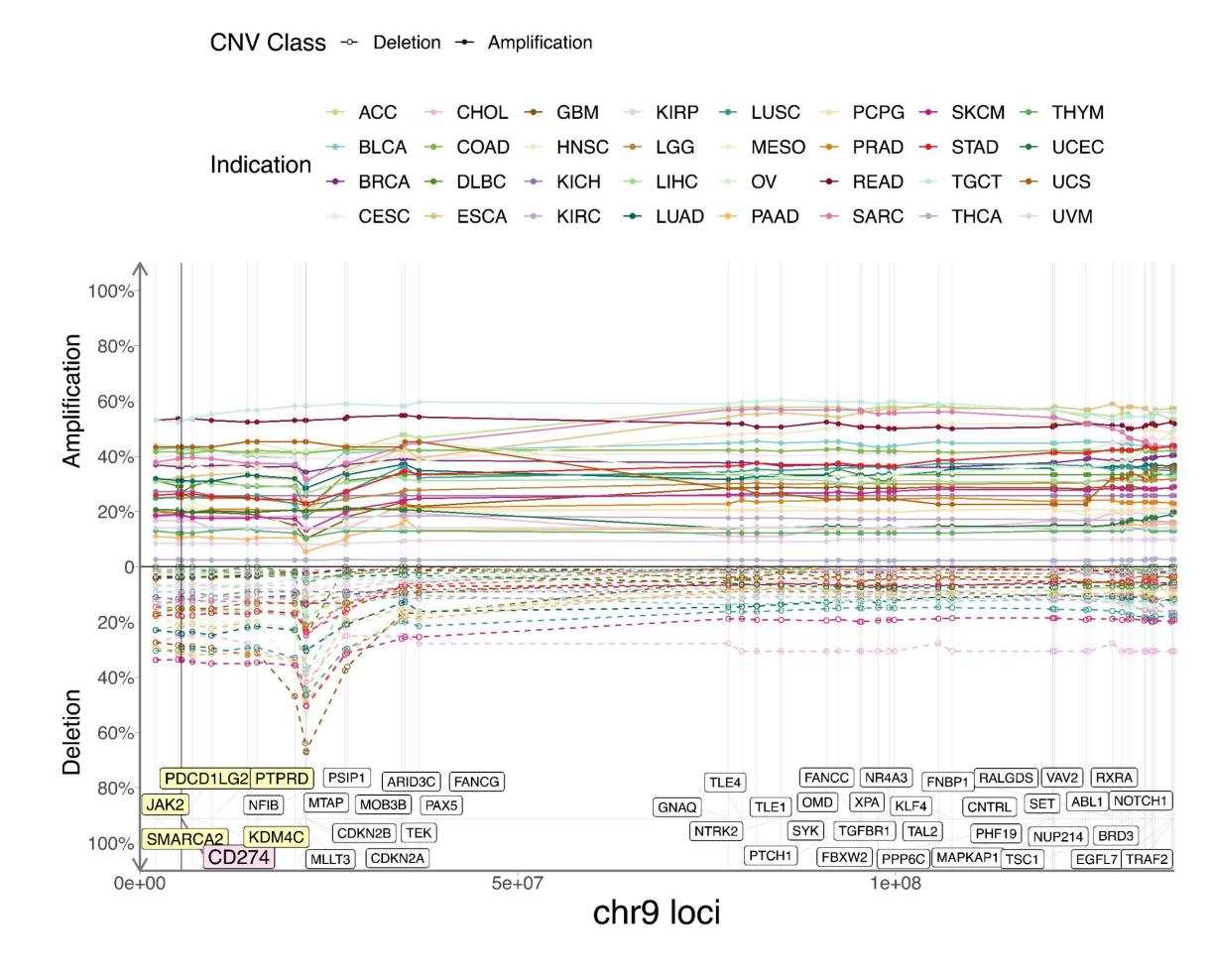


Figure 7. CNV Chromosome Profile in CD274.

X-axis: chromosome loci with cancer-related gene labels; gene of interest in pink, top concordant genes in yellow. Y-axis: percentage of samples with amplification (filled circles, solid lines, top) and deletion (open circles, dashed lines, bottom) in each cancer type (color-coded).

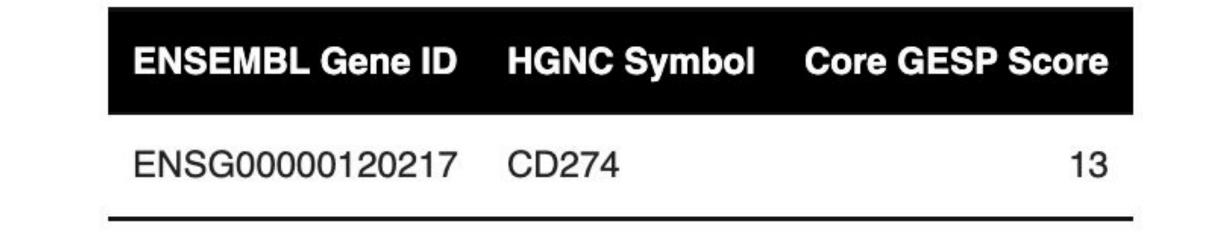
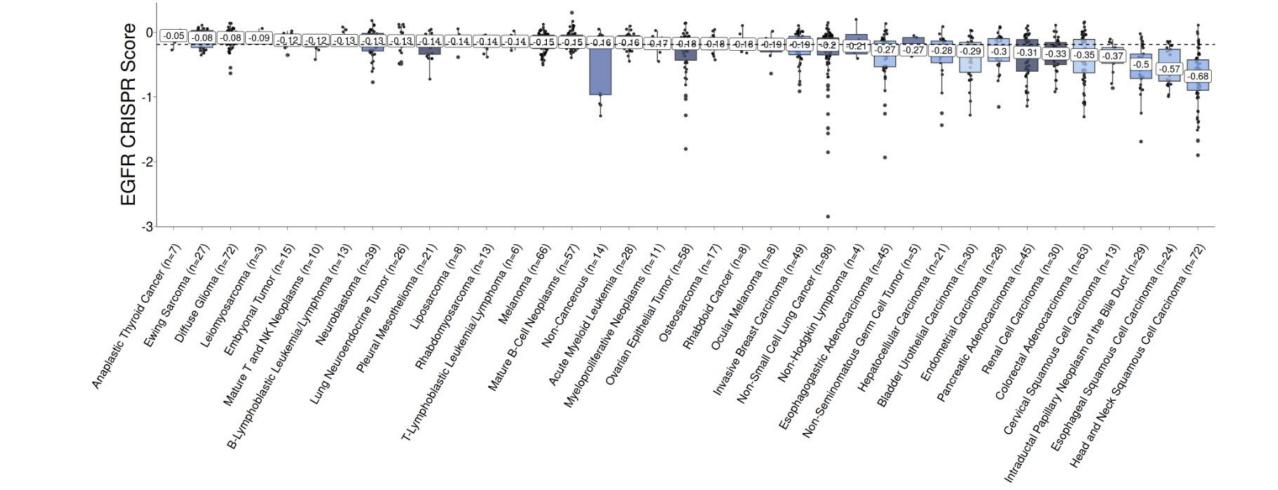


Figure 8. Surface Scores in *CD274*. The core GESP score is calculated for each candidate based on a weighted vote approach to identify potential surface encoded proteins.



**Figure 9. Cell line analysis across primary diseases in** *EGFR***.** Box plot shows CRISPR gene
effect scores by cell line disease; vertical line marks *EGFR* median expression.

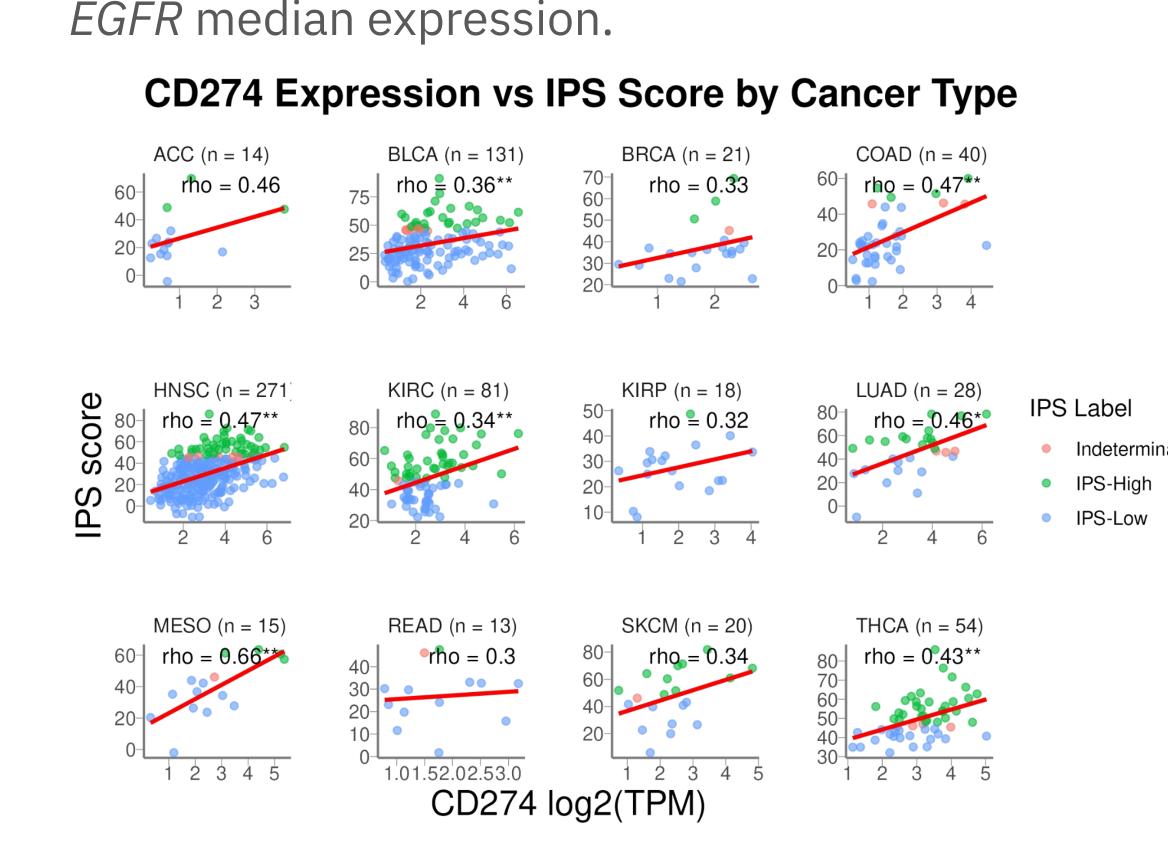


Figure 10. Immune Module Preview in *CD274*. This module is in development to reveal the association between GOI and Tempus Immune Profile Score (IPS)

## Dates to Know and Printing Information

- August 1st: Notifications sent to first author
- August 8th: Withdrawal deadline
- September 22nd October 3rd: Presentation development
- October 2nd: Posters due for SciComm review
- October 9-16th: Presentation review by external authors
- October 16th: Posters submitted for legal/exec leadership review
- October 24th: E-poster deadline [official deadline]
- November 5 9th, 2025: SITC Annual Meeting, National Harbor, MD
- There are no printing guidelines/deadlines, but you must make printing arrangements *prior* to the start of the conference by **November 3rd.**

## Data Visualization Guidelines

## Tempus Color palettes

## Qualitative

## SciComm preferred palette

This is a minor update to the default palette recommended by graphic design (see below) chosen to minimize the grouping of similar colors.



['#5993F7', '#D97C4F', '#62B882', '#CC78A7', '#774D9A', '#515CBE', '#E9C74E', '#B8E382', '#A54A72', '#C8B1F6']

### Graphic design recommendation

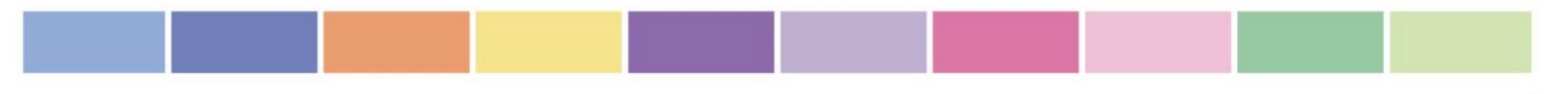
For cases where data are paired or grouped in a logical way, we recommend using this ordering (or any re-ordering) that results in the clearest presentation of the data



['#5993F7', '#515CBE', '#D97C4F', '#E9C74E', '#774D9A', '#C8B1F6', '#A54A72', '#CC78A7', '#62B882', '#B8E382']

#### Graphic design variant

In the event that a slightly lighter look is preferred, this palette (or a logical re-ordering of colors to fit the application) is acceptable



['#86B2FF', '#738AFF', '#F99B6D', '#FCE285', '#AD6CE4', '#CCB2FF', '#E777A8', '#FFC0E3', '#89D3A5', '#D1ECAF']

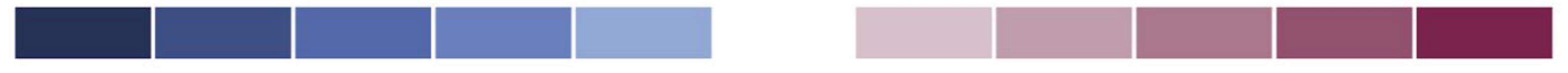
## Continuous

(Note: while these palettes are meant to be used in continuous applications, they are ultimately constructed from discrete color palettes with code examples showing how to properly extrapolate and create a continuous palette for applications such as heatmaps. However, these palettes may also be used in their discrete form [depending on the application], much the same as the qualitative palettes listed above.)

#### Sequential

['#29293C', '#384162', '#485889', '#5770AF', '#6687D6', '#779BEB', '#8BACED', '#9EBDF0', '#B3CCF3', '#C7DDF6']

### Diverging



['#384162', '#475889', '#5770AF', '#6687D6', '#8BACED', '#FFFFFF', '#DDC2CD', '#C99EAD', '#B47A8F', '#9F5773', '#893157']

- 1. SciComms Data Visualization Best Practices
- 2. Figure Sizing and Exporting