COFACTOR genomics

IMMUNOPRISM BIOMARKER REPORT

RESEARCH USE ONLY
VERSION 2.2

PROJECT ID: TRISTAR19
ISSUED: 2019-04-09

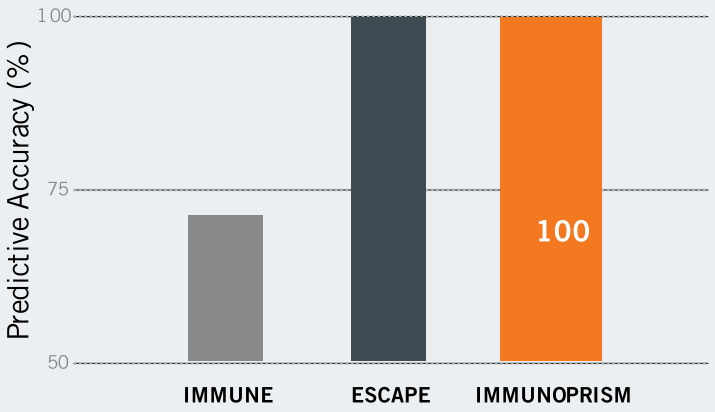
IMMUNOPRISM PREDICTIVE ACCURACY = 100%

HOW TO INTERPRET THESE RESULTS:

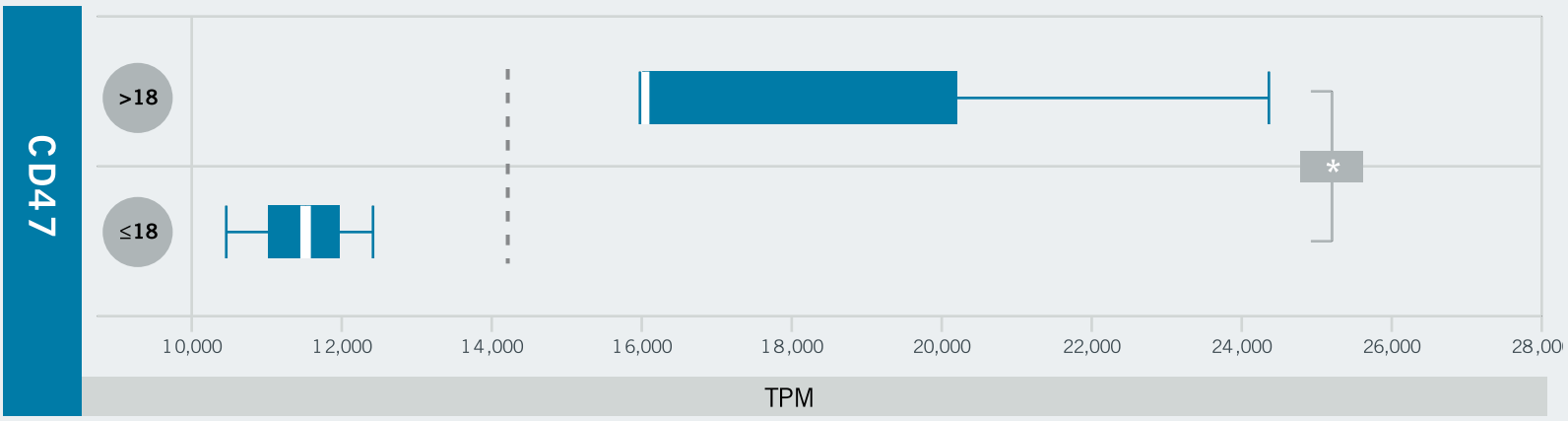
Right: This bar plot shows the most predictive biomarker analytes of the ImmunoPrism assay. "Escape" shows the most predictive escape gene, while "Immune" shows the most predictive immune cell type. "ImmunoPrism" shows the predictive performance of a multi-analyte model created using one or more analytes in the ImmunoPrism assay.

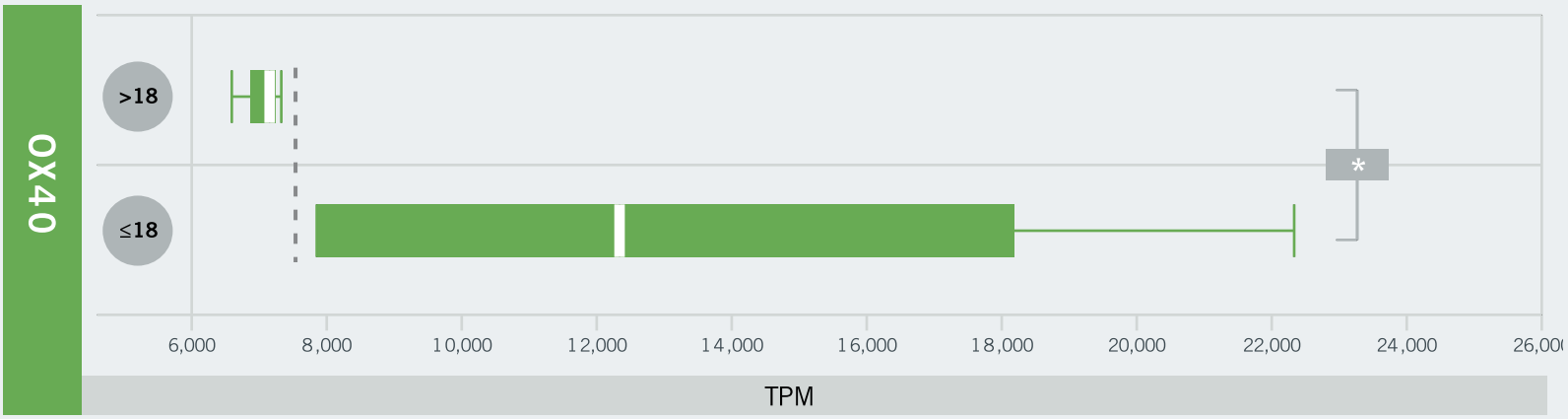
Below: These box-and-whisker plots show the summary statistics of two sample groupings per analyte in the ImmunoPrism Assay. The two analytes shown are those that best discriminate between its groups using a threshold (the grey dotted line.)

More details are found on the 2nd page.



MOST PREDICTIVE BIOMARKERS





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ANALYTE PERFORMANCE

Analyte	>18 Median	≤18 Median	p value	threshold	accuracy (%)	ppv (%)	npv (%)
CD47	16032.42 TPM	11518.23 TPM	0.0339	14213.99 TPM	100	100	100
OX40	7154.26 TPM	12338.12 TPM	0.0339	7537.95 TPM	100	100	100
IDO1	9609.78 TPM	3381.65 TPM	0.0339	5740.94 TPM	85.71	100	80
ARG1	83.05 TPM	250.75 TPM	0.4795	210.87 TPM	71.43	75	66.67
CTLA4	6840.07 TPM	5517.87 TPM	0.7237	5638.75 TPM	71.43	66.67	75
PD-1	4441.55 TPM	2462.25 TPM	0.7237	2613.87 TPM	71.43	66.67	75
TIM-3	8500.03 TPM	6059.33 TPM	1	6169.95 TPM	71.43	66.67	75
PD-L1	2066.41 TPM	1874.61 TPM	0.2888	1913.42 TPM	57.14	50	66.67
ICOS	1956.02 TPM	1733.86 TPM	0.7237	1955.02 TPM	57.14	50	66.67
BTLA	1169.16 TPM	1807.41 TPM	0.7237	1184.99 TPM	57.14	66.67	50
.							
CD56+ NK Cells	5.98 %	1.92 %	0.0339	3.43 %	71.43	66.67	75
CD8+ T Cells	17.2 %	9.41 %	0.0771	15.83 %	71.43	66.67	75
CD14+ Monocytes	8.72 %	6.57 %	0.7237	6.94 %	71.43	66.67	75
CD4+ T Cells	14.5 %	10.09 %	1	11.4 %	71.43	66.67	75
CD19+ B Cells	12.1 %	17.91 %	0.2888	13.6 %	57.14	66.67	50
M1 Macrophages	0.39 %	0.27 %	0.4795	0.32 %	57.14	50	66.67
Treg Cells	6.14 %	11.88 %	0.5959	8.78 %	57.14	66.67	50
M2 Macrophages	1.8 %	1.56 %	0.4795	1.79 %	42.86	33.33	50
.							
ImmunoPrism	N/A	N/A	N/A	N/A	100	100	100

ADDITIONAL DETAILS

Predictive Accuracy Bar Plot: These bars show the predictive accuracy for the most predictive escape gene ("ESCAPE") and immune cell type ("IMMUNE"). Predictive accuracy refers to the leave-one-out cross validation accuracy (See "Leave-one-out Cross Validation", below). Also shown is the predictive accuracy of using one or more analytes in the ImmunoPrism Assay ("IMMUNOPRISM"). This "marker" is created by learning a machine learning model that incorporates information from one or more analytes. **Most Predictive Biomarkers Box Plot:** These box-and-whisker plots visualize the statistics for groups of samples for the 2 most predictive analytes. The left and right sides of the box indicate the 1st and 3rd quartiles of the respective data set. The median is indicated by the white line inside the box. The minimum and maximum inlier datapoints are denoted by the ends of the whiskers, while outliers are shown as empty circles. The optimal threshold for a given analyte is shown as a vertical dotted line. Wilcoxon rank-sum testing is used to test the null hypothesis that the two groups are sampled from the same distribution. Significance of rejecting this hypothesis is denoted for p values of <0.05, <0.01, and <0.001 by 1, 2, and 3 stars, respectively. **Analyte Performance Table:** Leave-one-out cross validation is used to calculate the accuracy, positive predictive value (ppv), and negative predictive value (npv) for each analyte. **Leave-one-out Cross Validation:** For a dataset limited in size, leave-one-out cross validation gives the best approximation to how an estimator will generalize to future, independent samples. The process works by iterating n times (where there are n datapoints), each time learning a threshold considering n-1 points and testing the prediction of the nth, left out, point. Then, all n predictions are considered to calculate prediction statistics. **Thresholds:** Thresholds are determined by optimizing equally for sensitivity and specificity using all samples. For datapoints that are normally distributed, this threshold would be the same threshold optimized for accuracy.

STATEMENT OF PERFORMANCE

The ImmunoPrism assay was developed and characterized by Cofactor Genomics in San Francisco, CA. ImmunoPrism is for Research Use Only and not for use in diagnostics procedures. The results of the included report are subject to change in future releases. For technical support or additional information on assay analytical performance, please contact: support@cofactorgenomics.com