

ADDITIONAL DETAILS

Predictive Accuracy

The statistics reported are produced via 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 n th, left out, point. Then, all n predictions are considered to calculate prediction statistics.

Predictive Immune Modeling Results & Analyte Performance

This section shows the Predictive Immune Modeling high level analysis. Shown are the predictive accuracies of estimating cohort assignment with single, isolated analytes ("Individual Biomarker Predictive Accuracy"). Thresholds for single analytes 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. Single analyte accuracies are contrasted against the accuracy of combining these analytes to build the optimal multidimensional biomarker ("Multidimensional Biomarker").

Multidimensional Biomarker Assessment

This section shows the distributions of individual samples from both cohorts as they would be classified by the multidimensional biomarker. The multidimensional values are plotted along the axis, and the frequency of sample values are visualized in the vertical space. The sample distribution visualization is approximate. The cohorts are distinguished by color (green and blue) and shape (circle and square) and estimations are distinguished by outline color (white: correct estimation, yellow: incorrect estimation.) The dashed line at 0 indicates the prediction threshold that separates the cohorts. Samples that are incorrectly estimated are highlighted in yellow, and listed in a separate table on page 3.

ROC Curve Assessment

This section shows the Receiver Operating Characteristic Curve of the multidimensional biomarker. For various thresholds of the multidimensional biomarker, the True Positive Rate (y-axis) is plotted against the False Positive Rate (x-axis) in blue. The area under the curve ('AUC') is included in the lower right corner. The random predictor is shown as a dashed red line.

Performance Matrix

This section shows the confusion matrix of the multidimensional biomarker. This matrix shows how samples are classified based on the assay (rows) versus their known label based on clinical data (columns). In addition, we show the positive predictive value (PPV), negative predictive value (NPV), specificity, and sensitivity of the multidimensional biomarker.

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 visit: <https://cofactorgenomics.com/immunoprism-assay/>.

OUTLIERS

Sample Name	Value
RU-17-594-CC	0.18
RU-17-595-Q	-0.80

SAMPLES INCLUDED IN GROUPINGS

Group 1 includes samples RU-17-594-T, RU-17-594-N, RU-17-594-O, RU-17-594-P, RU-17-594-CC, RU-17-594-WW

Group 2 includes samples RU-17-594-D, RU-17-594-QQ, RU-17-594-J, RU-17-594-Y, RU-17-595-I, RU-17-595-E, RU-17-595-Q